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Paoletti et al.(10) **Pub. No.: US 2008/0188640 A1**(43) **Pub. Date: Aug. 7, 2008**(54) **IMMUNODEFICIENCY RECOMBINANT
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Swiftwater, PA 18370 (US)**(21) Appl. No.: **11/891,027**(22) Filed: **Aug. 8, 2007****Related U.S. Application Data**

(60) Continuation of application No. 10/441,788, filed on May 20, 2003, now abandoned, which is a division of application No. 09/136,159, filed on Aug. 14, 1998, now Pat. No. 6,596,279, which is a division of application No. 08/417,210, filed on Apr. 5, 1995, now Pat. No. 5,863,542, which is a continuation-in-part of application No. 08/223,842, filed on Apr. 6, 1994, now abandoned, which is a continuation-in-part of application No. 07/897,382, filed on Jun. 11, 1992, now abandoned, which is a continuation-in-part of application No. 07/715,921, filed on Jun. 14, 1991, now abandoned, Continuation-in-part of application No. 08/105,483, filed on Aug. 12, 1993, now Pat. No.

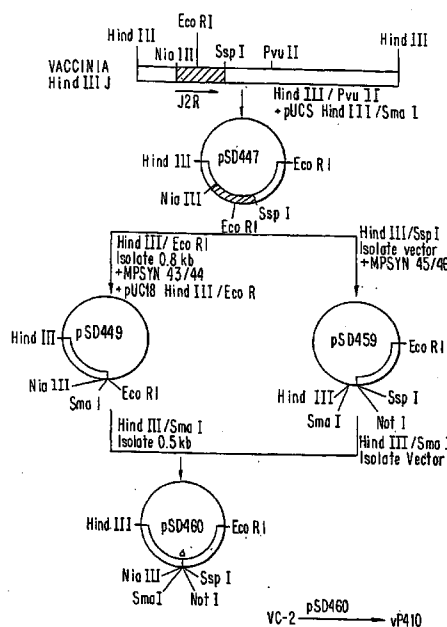
5,494,807, which is a continuation of application No. 07/847,951, filed on Mar. 6, 1992, now abandoned, which is a continuation-in-part of application No. 07/713,967, filed on Jun. 11, 1991, now abandoned, which is a continuation-in-part of application No. 07/666,056, filed on Mar. 7, 1991, now abandoned.

Publication Classification(51) **Int. Cl.****C07K 7/00** (2006.01)**C07K 14/00** (2006.01)**C07H 21/04** (2006.01)(52) **U.S. Cl. 530/329; 530/330; 530/350; 536/23.72**

(57)

ABSTRACT

Attenuated recombinant viruses containing DNA encoding an immunodeficiency virus and/or CTL antigen, as well as methods and compositions employing the viruses, expression products therefrom, and antibodies generated from the viruses or expression products, are disclosed and claimed. The recombinant viruses can be NYVAC or ALVAC recombinant viruses. The DNA can code for at least one of: HIV1gag(+pro) (IIIB), gp120(MN) (+transmembrane), nef (BRU)CTL, pol(IIIB)CTL, ELDKWA or LDKW epitopes, preferably HIV1gag(+pro) (IIIB), gp120(MN) (+transmembrane), two (2) nef(BRU)CTL and three (3) pol(IIIB)CTL epitopes; or two ELDKWA in gp120 V3 or another region or in gp160. The two (2) nef(BRU)CTL and three (3) pol(IIIB)CTL epitopes are preferably CTL1, CTL2, pol1, pol2 and pol3. The recombinant viruses and gene products therefrom and antibodies generated by the viruses and gene products have several preventive, therapeutic and diagnostic uses. DNA from the recombinant viruses are useful as probes or, for generating PCR primers or for immunization. Also disclosed and claimed are HIV immunogens and modified gp160 and gp120.



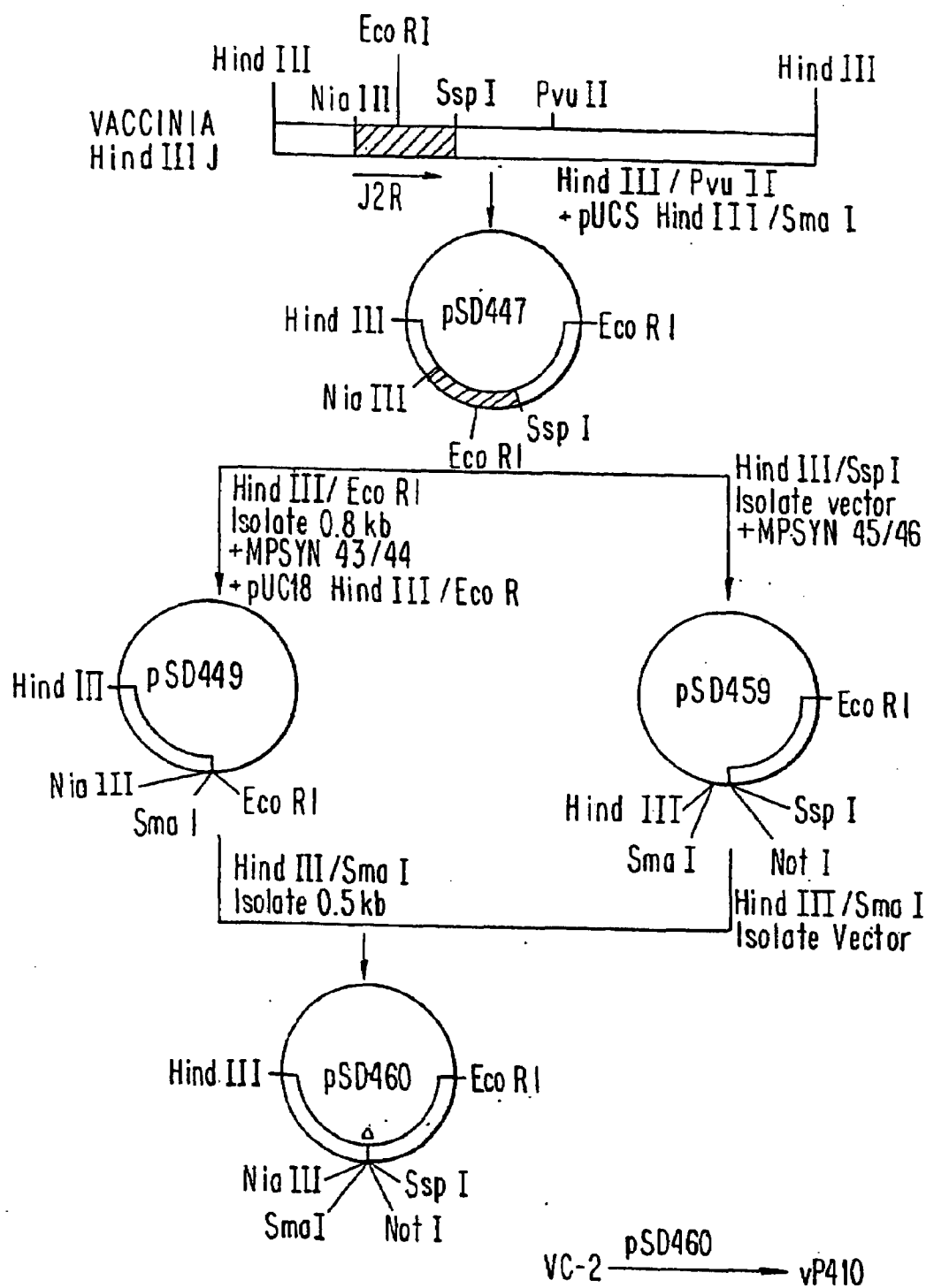


FIG. 1

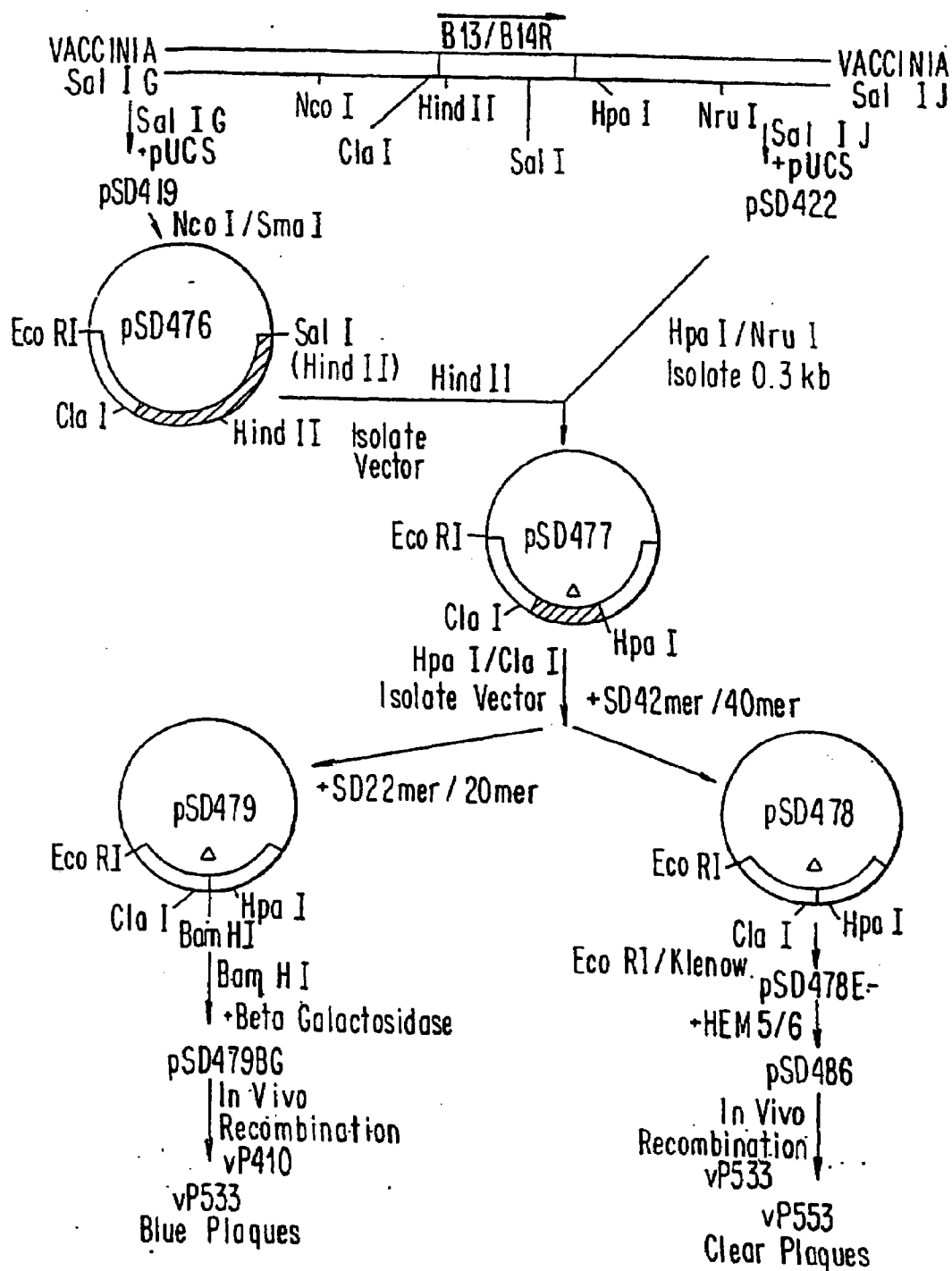


FIG. 2

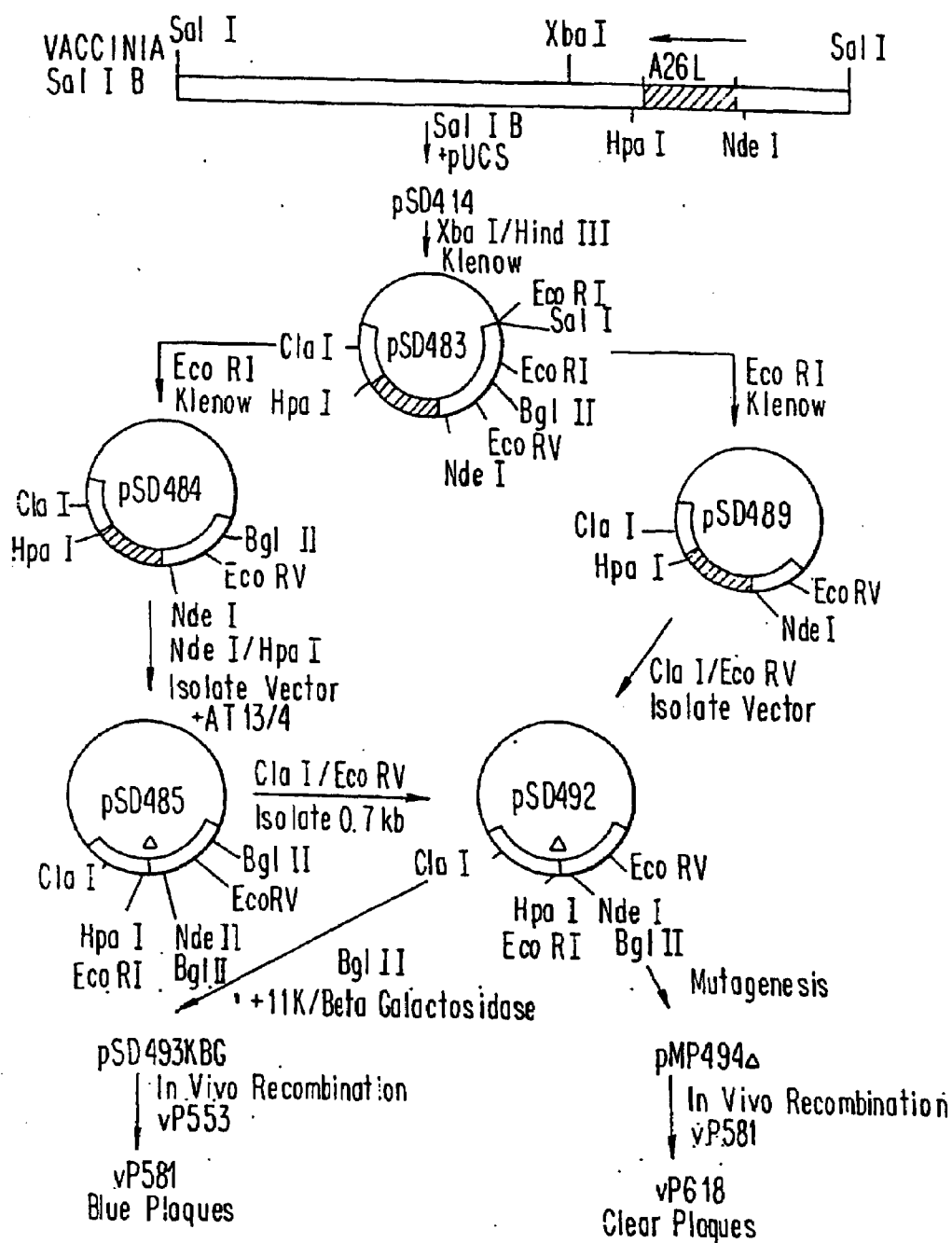


FIG. 3

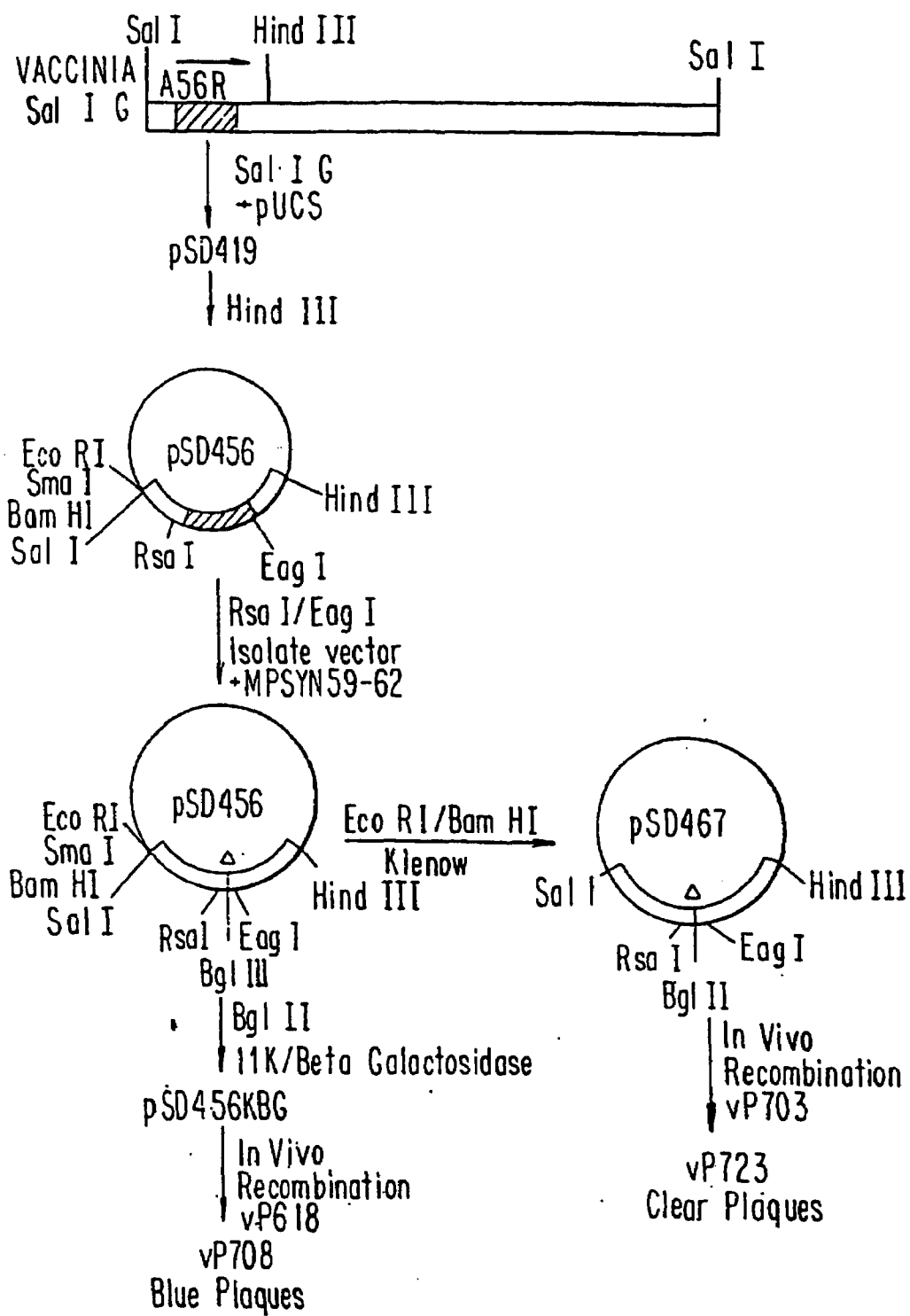


FIG. 4

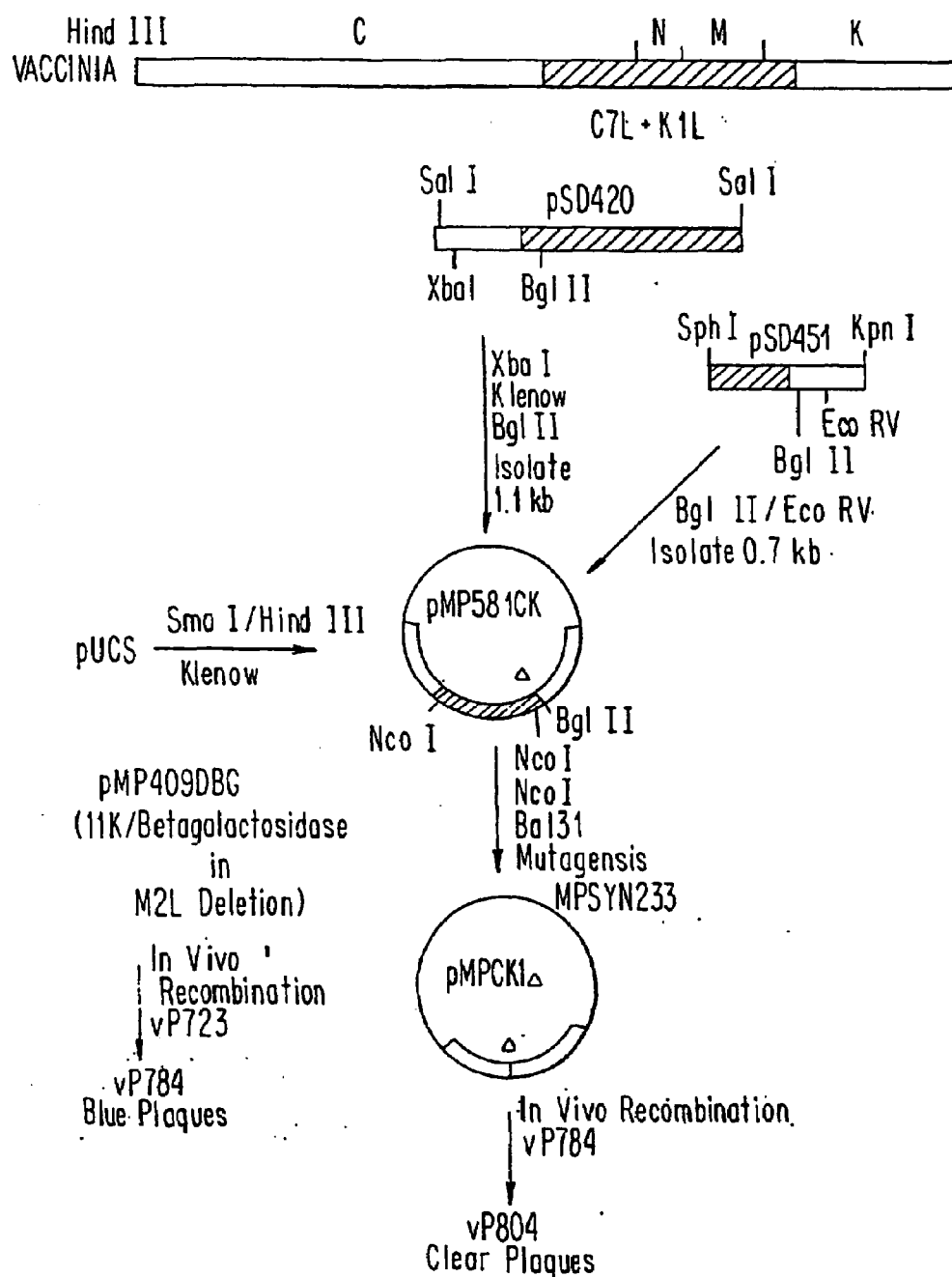


FIG. 5

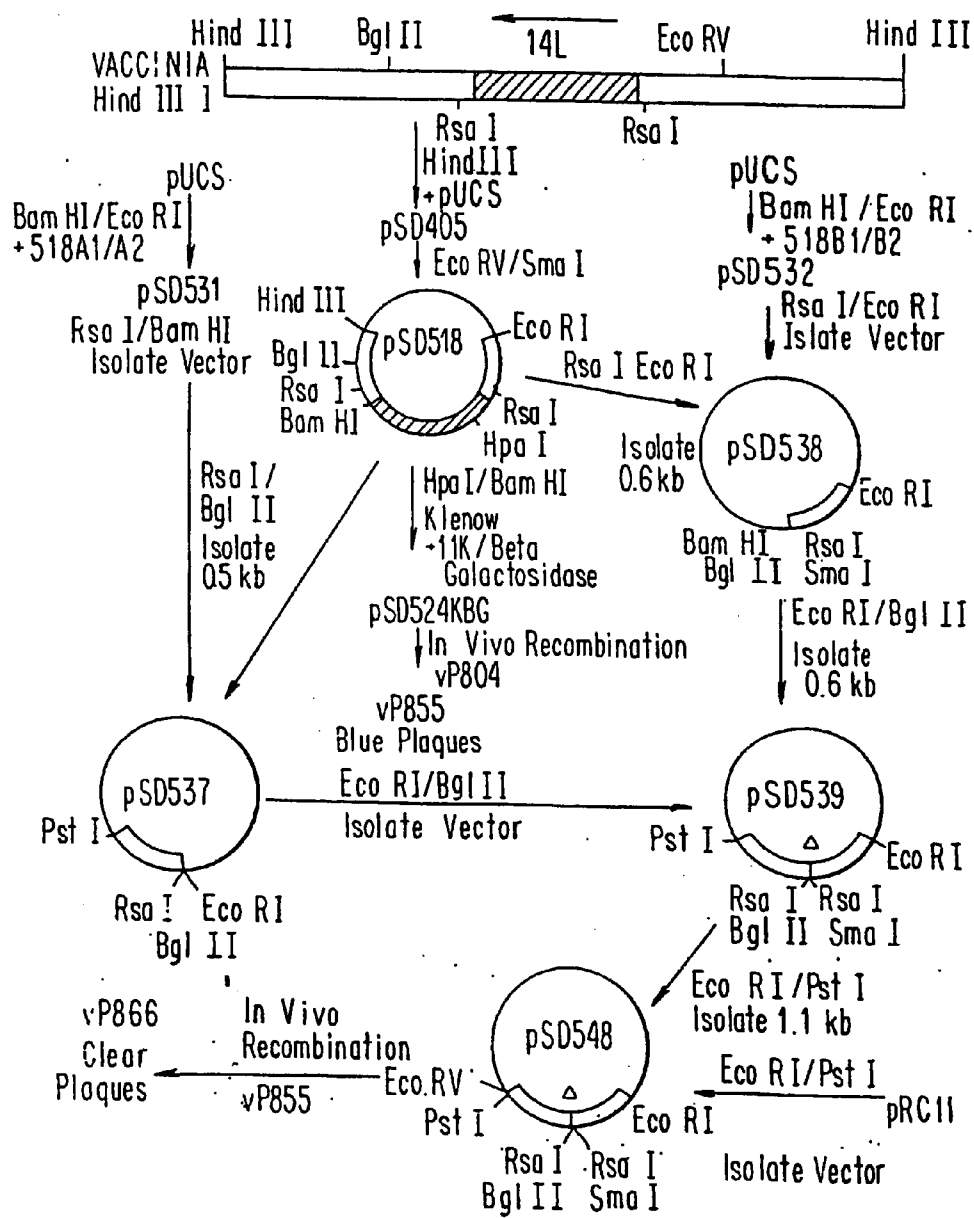


FIG. 6

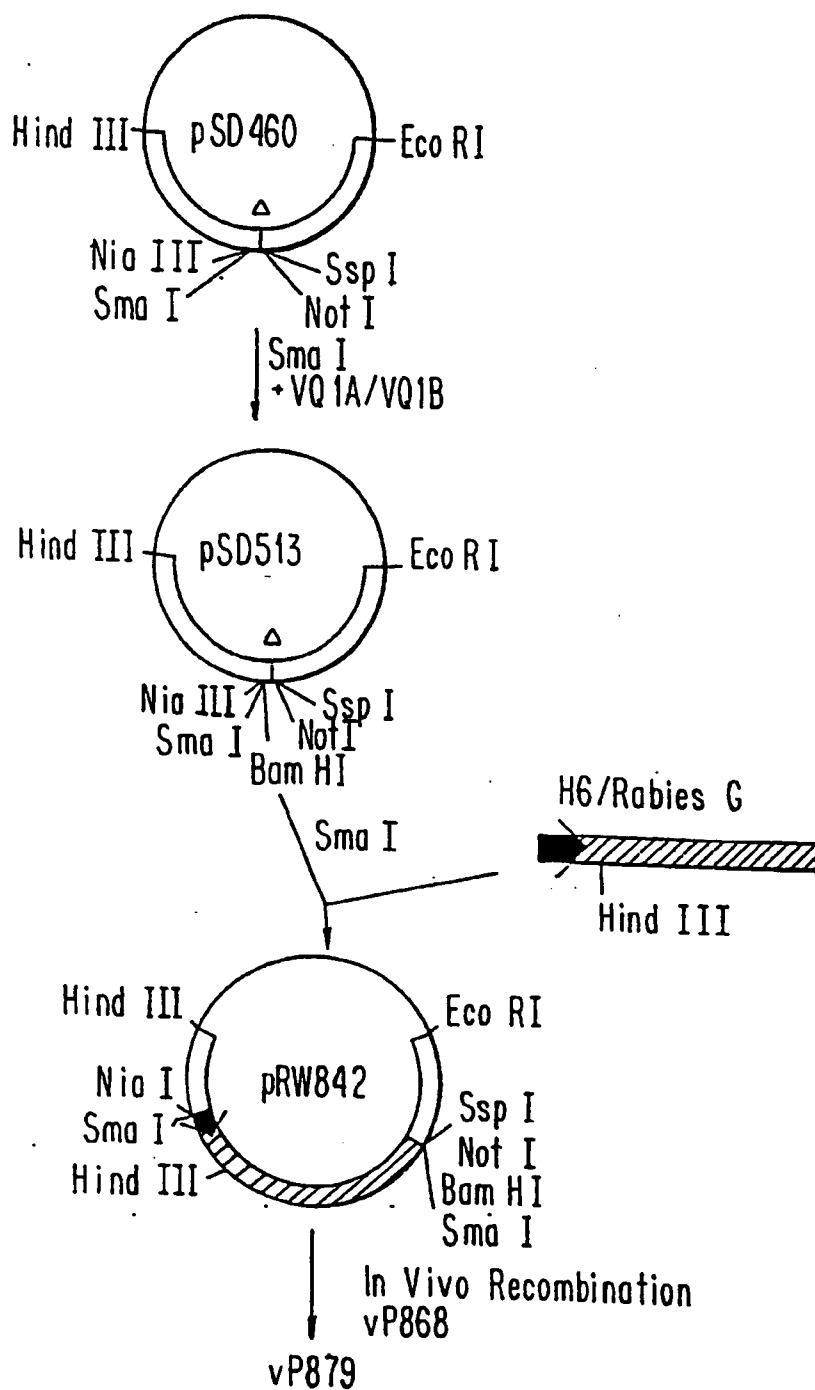
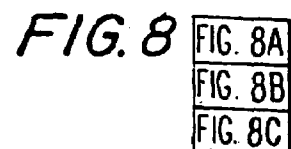


FIG. 7

FIG. 8A



1	TGAATGTAA	ATGTTATACT	TTGGATGAAG
31	CTATAAATAT	GCATTGGAAA	AATAATCCAT
61	TTAAAGAAAG	GATTCAAATA	CTACAAAACC
91	TAAGCGATAA	TATGTAACT	AAGCTTATTC
121	TTAACGACGC	TTTAAATATA	CACAAATAAA
151	CATAATTTTT	GTATAACCTA	ACAAATAACT
181	AAAACATAAA	AATAATAAAA	GGAAATGTAA
211	TATCGTAATT	ATTTTACTCA	GGAATGGGGT
241	TAAATATTTA	TATCACGTGT	ATATCTATAC
271	TGTTATCGTA	TACACTTTAC	AATTACTATT
301	ACGAATATGC	AAGAGATAAT	AAGATTACGT
331	ATTTAAGAGA	ATCTTGTCAT	GATAATTGGG
361	TACGACATAG	TGATAAATGC	TATTTTCGCAT
391	CGTTACATAA	AGTCAGTTGG	AAAGATGGAT
421	TTGACAGATG	TAACCTAATA	GGTGCAAAAA
451	TGTTAAATAA	CAGCATTCTA	TCGGAAGATA
481	GGATACCAGT	TATATTATAC	AAAAATCACT
511	GGTTGGATAA	AACAGATTCT	GCAATATTCG
541	TAAAAGATGA	AGATTACTGC	GAATTTGTAA
571	ACTATGACAA	TAAAAAGCCA	TTTATCTCAA
601	CGACATCGTG	TAATTCTTCC	ATGTTTTATG
631	TATGTGTTTC	AGATATTATG	AGATTACTAT
661	AAACTTTTTG	TATACTTATA	TTCCGTAAAC
691	TATATTAATC	ATGAAGAAAA	TGAAAAAGTA
721	TAGAAGCTGT	TCACGAGCGG	TTGTTGAAAA
751	CAACAAAATT	ATACATTCAA	GATGGCTTAC
781	ATATACGTCT	GTGAGGCTAT	CATGGATAAT
811	GACAATGCAT	CTCTAAATAG	GTTTTTGGAC
841	AATGGATTCTG	ACCCTAACAC	GGAATATGGT
871	ACTCTACAAT	CTCCTCTTGA	AATGGCTGTA
901	ATGTTCAAGA	ATACCGAGGC	TATAAAAATC
931	TTGATGAGGT	ATGGAGCTAA	ACCTGTAGTT
961	ACTGAATGCA	CAACTTCTTG	TCTGCATGAT
991	GCGGTGTTGA	GAGACGACTA	CAAAATAGTG
1021	AAAGATCTGT	TGAAGAATAA	CTATGTAAAC
1051	AATGTTCTTT	ACAGCGGAGG	CTTTACTCCT
1081	TTGTGTTTGG	CAGCTTACCT	TAACAAAGTT
1111	AATTTGGTTA	AACTTCTATT	GGCTCATTCG
1141	GCGGATGTAG	ATATTTCAAA	CACGGATCGG
1171	TAACTCCTC	TACATATAGC	CGTATCAAAT
1201	AAAAATTTAA	CAATGGTTAA	ACTTCTATTG
1231	AACAAAGGTG	CTGATACTGA	CTTGCTGGAT
1261	AACATGGGAC	GTACTCCTTT	AATGATCGCT
1291	GTACAATCTG	GAAATATTGA	AATATGTAGC

FIG. 8B

1321	ACACTACTTA	AAAAAAATAA	AATGTCAGAA
1351	CTGGGAAAAA	TTGATCTTGC	CAGCTGTAAT
1381	TCATGGTAGA	AAAGAAGTGC	TCAGGCTACT
1411	TTTCAACAAA	GGAGCAGATG	TAAACTACAT
1441	CTTTGAAAGA	AATGGAAAAT	CATATACTGT
1471	TTTGGAATTG	ATTAAAGAAA	GTTACTCTGA
1501	GACACAAAAG	AGGTAGCTGA	AGTGGTACTC
1531	TCAAAATGCA	GAACGATGAC	TGCGAAGCAA
1561	GAAGTAGAGA	AATAACACTT	TATGACTTTC
1591	TTAGTTGTAG	AAAAGATAGA	GATATAATGA
1621	TGGTCATAAA	TAACTCTGAT	ATTGCAAGTA
1651	AATGCAATAA	TAAGTTAGAT	TTATTTAAAA
1681	GGATAGTTAA	AAATAGAAAA	AAAGAGTTAA
1711	TTTGTAGGGT	TAAAATAATA	CATAAGATCT
1741	TAAAATTTAT	AAATACGCAT	AATAATAAAA
1771	ATAGATTATA	CTTATTACCT	TCAGAGATAA
1801	AATTTAAGAT	ATTTACTTAT	TTAACTTATA
1831	AAGATCTAAA	ATGCATAATT	TCTAAATAAT
1861	GAAAAAAAAG	TACATCATGA	GCAACGCGTT
1891	AGTATATTTT	ACAATGGAGA	TTAACGCTCT
1921	ATACCGTTCT	ATGTTTATTG	ATTCAGATGA
1951	TGTTTTAGAA	AAGAAAGTTA	TTGAATATGA
1981	AAACTTTAAT	GAAGATGAAG	ATGACGACGA
2211	TGATTATTGT	TGTAAATCTG	TTTLAGATGA
2041	AGAAGATGAC	GCGCTAAAGT	ATACTATGGT
2071	TACAAAGTAT	AAGTCTATAC	TACTAATGGC
2101	GACTTGTGCA	AGAAGGTATA	GTATAGTGAA
2131	AATGTTGTTA	GATTATGATT	ATGAAAAACC
2161	AAATAAATCA	GATCCATATC	TAAAGGTATC
2191	TCCTTTGCAC	ATAATTTTAT	CTATTCCTAG
2221	TTTAGAATAC	TTTTCATTAT	ATTTGTTTAC
2251	AGCTGAAGAC	GAAAAAAATA	TATCGATAAT
2281	AGAAGATTAT	GTTAACTCTG	CTAATAAGAT
2311	GAAATTGAAT	GAGTCTGTGA	TAATAGCTAT
2341	AATCAGAGAA	GTTCTAAAAG	GAAATAAAAA
2371	TCTAACTGAT	CAGGATATAA	AAACATTGGC
2401	TGATGAAATC	AACAAGGAGG	AACTGAATAT
2431	AGCTAAACTA	TTGTTAGATA	GAGGGGCCAA
2461	AGTAAATTAC	AAGGATGTTT	ACGGTTCCTC
2491	AGCTCTCCAT	AGAGCTGCTA	TTGGTAGGAA
2521	ACAGGATATG	ATAAAGCTGT	TAATCGATCA
2551	TGGAGCTGAT	GTAAACTCTT	TAACTATTGC
2581	TAAAGATAAT	CTTATTAAAA	AAAAATAATA
2611	TCACGTTTAG	TAATATTAAA	ATATATTAAT

FIG. 8C

2641	AACCTCTATTA	CTAATAACTC	CAGTGGATAT
2671	GAACATAATA	CGAAGTTTAT	ACATTCTCAT
2701	CAAAATCTTA	TTGACATCAA	GTTAGATTGT
2731	GAAAATGAGA	TTATGAAATT	AAGGAATACA
2761	AAAATAGGAT	GTAAGAACTT	ACTAGAATGT
2791	TTTATCAATA	ATGATATGAA	TACAGTATCT
2821	AGGGCTATAA	ACAATGAAAC	GATTAAAAAT
2851	TATAAAAATC	ATTTCCCTAT	ATATAATACG
2881	CTCATAGAAA	AATTCATTTC	TGAAAGTATA
2911	CTAAGACACG	AATTATTGGA	TGGAGTTATA
2941	AATTCTTTTC	AAGGATTCAA	TAATAAATTG
2971	CCTTACGAGA	TTCAGTACAT	TATACTGGAG
3001	AATCTTAATA	ACCATGAACT	AAAAAAAATT
3031	TTAGATAATA	TACATTAAAA	AGGTAAATAG
3061	ATCATCTGTT	ATTATAAGCA	AAGATGCTTG
3091	TTGCCAATAA	TATACAACAG	GTATTTGTTT
3121	TTATTTTAA	CTACATATTT	GATGTTTCATT
3151	CTCTTTATAT	AGTATACACA	GAAAATTTCAT
3181	AATCCACTTA	GAATTTCTAG	TTATCTAG

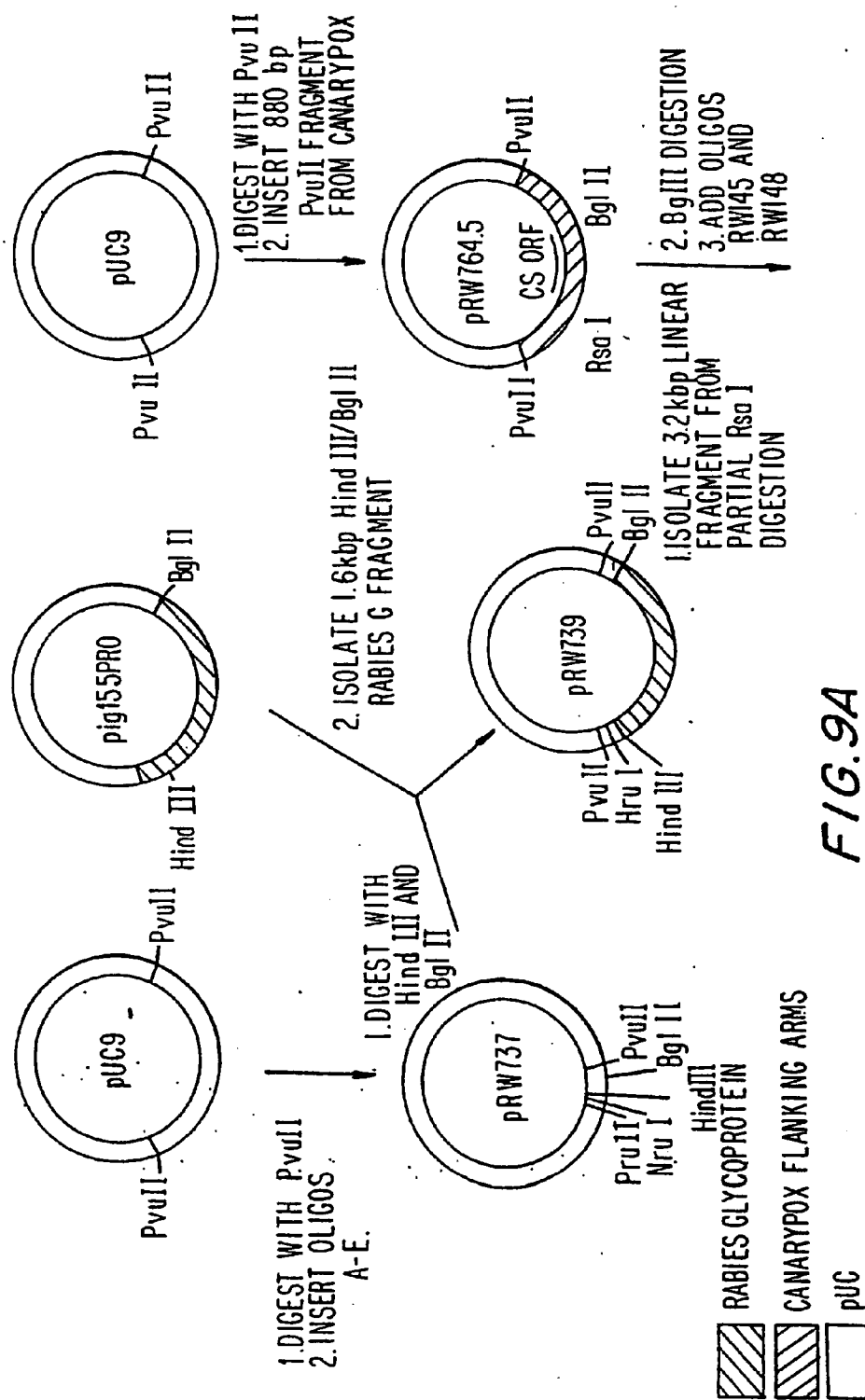
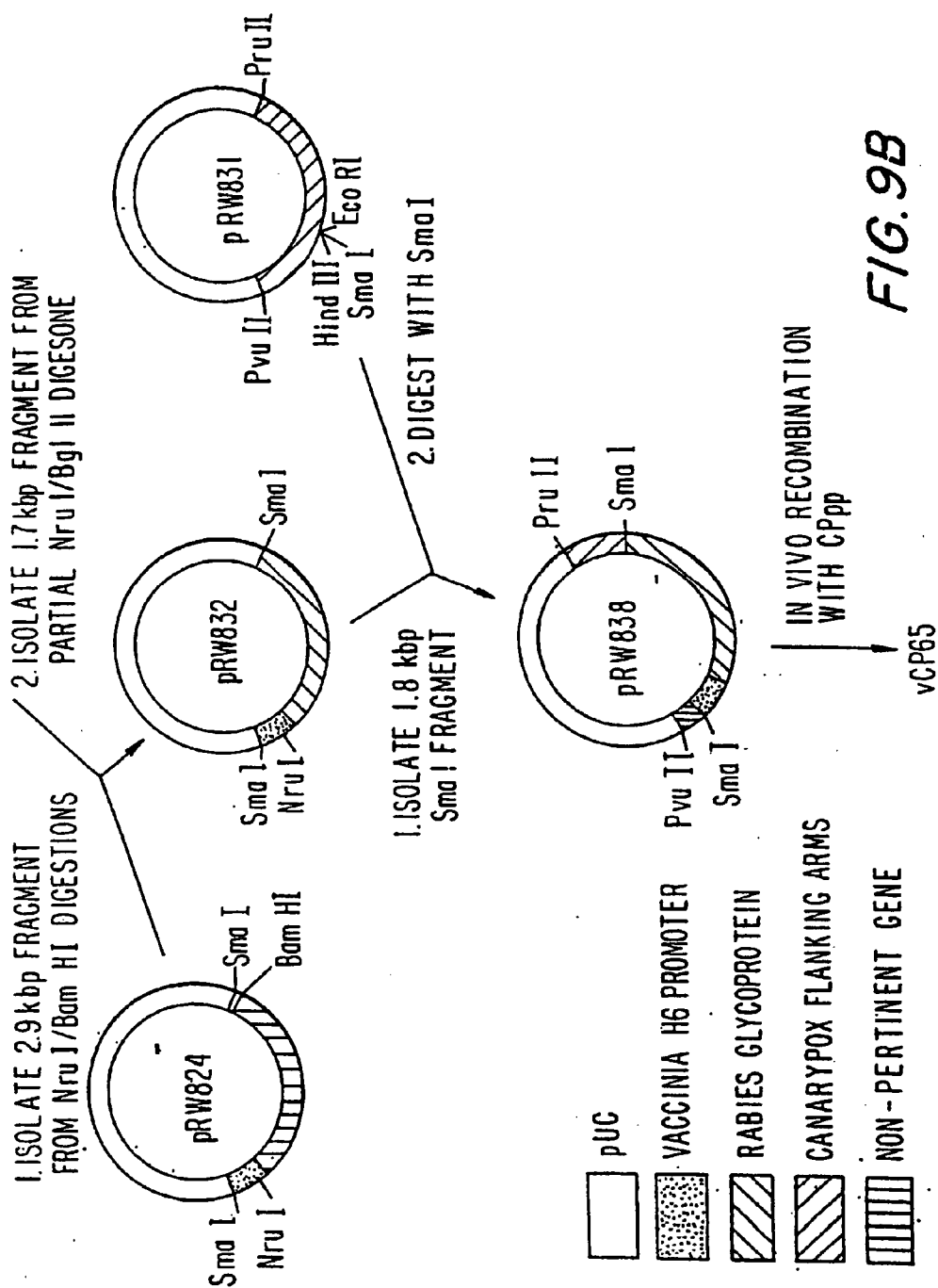


FIG. 9A



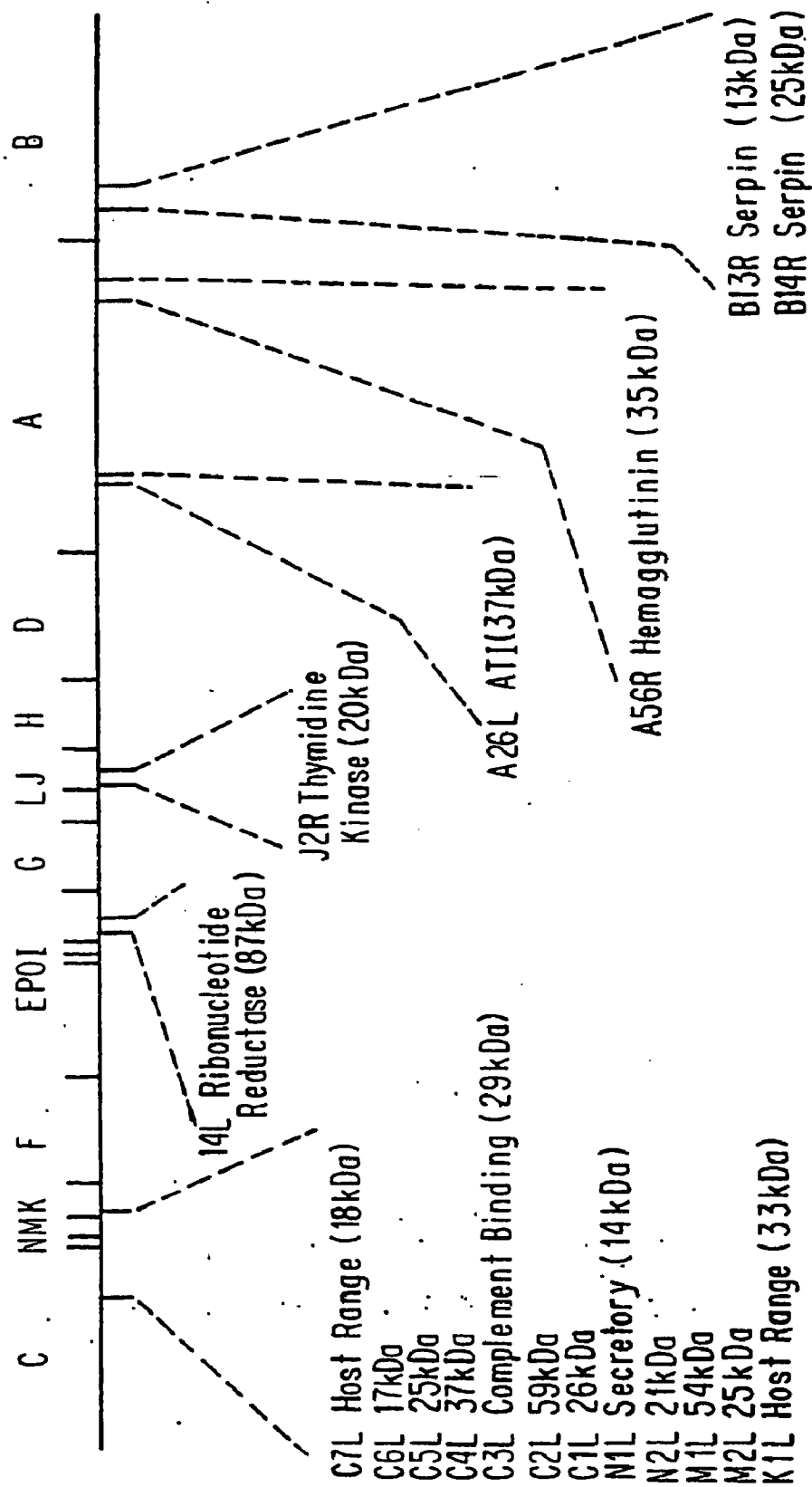


FIG. 10

*FIG. 11A**FIG. 11*

FIG. 11A

FIG. 11B

FIG. 11C

1	GATATCTGTG	GTCTATATAT	ACTACACCCT
31	ACCGATATTA	ACCAACGAGT	TTCTCACAAG
61	AAAACTTGTT	TAGTAGATAG	AGATTCTTTG
91	ATTGTGTTTA	AAAGAAGTAC	CAGTAAAAAG
121	TGTGGCATAT	GCATAGAAGA	AATAAACAAA
151	AAACATATTT	CCGAACAGTA	TTTTGGAATT
181	CTCCCAAGTT	GTAAACATAT	TTTTTGCCTA
211	TCATGTATAA	GACGTTGGGC	AGATACTACC
241	AGAAATACAG	ATACTGAAAA	TACGTGTCCT
271	GAATGTAGAA	TAGTTTTTCC	TTTCATAATA
301	CCCAGTAGGT	ATTGGATAGA	TAATAAATAT
331	GATAAAAAAA	TATTATATAA	TAGATATAAG
361	AAAATGATTT	TTACAAAAAT	ACCTATAAGA
391	ACAATAAAAA	TATAATTACA	TTTACGGAAA
421	ATAGCTGGTT	TTAGTTTACC	AACTTAGAGT
451	AATTATCATA	TTGAATCTAT	ATTGTTTTTT
481	AGTTATATAA	AAACATGATT	AGCCCCCAAT
511	CGGATGAAAA	TATAAAAGAT	GTTGAGAATT
541	TCGAATACAA	CAAAAAGAGG	AATCGTACGT
571	TGTCCATATC	CAAACATATA	AATAAAAATT
601	CAAAAGTAGT	ATTATACTGG	ATGTTTAGAG
631	ATCAACGTGT	ACAAGATAAT	TGGGCTTTAA
661	TTTACGCACA	ACGATTAGCG	TTAAAACTCA
691	AAATACCTCT	AAGAATATGC	TTTTGTGTCG
721	TGCCAAAATT	TCACACTACT	ACTTCTAGAC
751	ACTTTATGTT	TTTAATATCC	GGTCTTAAAG
781	AAGTCGCGGA	AGAATGTAAA	AGACTATGTA
811	TAGGGTTTTTC	ATTGATATAT	GGCGTACCAA
841	AAGTAATAAT	TCCGTGTATA	GTAAAAAAT
871	ACAGAGTCGG	AGTAATCATA	ACGGATTTCT
901	TTCCATTACG	TGTTCCCGAA	AGATTAATGA
931	AACAGACTGT	AATATCTCTT	CCAGATAACA
961	TACCTTTTAT	ACAAGTAGAC	GCTCATAATA
991	TAGTACCTTG	TTGGGAAGCT	TCTGATAAAG
1021	AAGAATACGG	TGCACGAACT	TTAAGAAAAA
1051	AGATATTTGA	TAAATTATAT	GAATATATGA
1081	CAGAATTTCC	TGTTGTTCGT	AAACATCCAT
1111	ACGGTCCATT	TTCTATATCT	ATTGCAAAAC
1141	CCAAAAATAT	ATCATTAGAC	AAGACGGTAT
1171	TACCCGTAAA	ATGGGCAACG	CCTGGAACAA
1201	AAGCTGGAAT	AATTGTTTTA	AAAGAATTTA
1231	TAAAAAACAG	ATTACCGTCA	TACGACGCGG
1261	ATCATAACAA	TCCTACGTGT	GACGCTTTGA
1291	GTAACCTATC	TCCGTGGCTA	CATTTTGGTC

FIG. 11B

1321	ATGTATCCGC	ACAACGTGTT	GCCTTAGAAG
1351	TATTAAAATG	TATACGAGAA	AGCAAAAAAA
1381	ACGTTGAAAC	GTTTATAGAT	GAAATAATTG
1411	TAAGAAGAGA	ACTATCGGAT	AATTTTTGTT
1441	ACTATAACAA	ACATTATGAT	AGTATCCAGT
1471	CTACTCATTC	ATGGGTTAGA	AAAACATTAG
1501	AAGATCACAT	TAATGATCCT	AGAAAGTATA
1531	TATATTCCAT	TAAACAACTC	GAAAAAGCGG
1561	AAACTCATGA	TCCTCTATGG	AACGCGTCAC
1591	AAATGCAGAT	GGTGAGAGAA	GGAAAAATGC
1621	ATAGTTTTTT	ACGAATGTAT	TGGGCTAAGA
1651	AGATACTTGA	ATGGACTAGA	ACACCTGAAG
1681	ACGCTTTGAG	TTATAGTATC	TATTTGAACA
1711	ACAAGTACGA	ACTAGACGGC	ACGGATCCTA
1741	ACGGATACGT	AGGTTGTATG	TGGTCTATTT
1771	GCGGATTACA	CGATAGAGCG	TGGAAAGCAA
1801	GACCGATATT	TGGAAAGATA	AGATATATGA
1831	ATTATGAGAG	TTCTAAGAAG	AAATTTGATG
1861	TTGCTGTATT	TATACAGAAA	TACAATTAAG
1891	ATAAATAATA	TACAGCATTG	TAACCATCGT
1921	CATCCGTTAT	ACGGGGAATA	ATATTACCAT
1951	ACAGTATTAT	TAAATTTTCT	TACGAAGAAT
1981	ATAGATCGGT	ATTTATCGTT	AGTTTATTTT
2011	ACATTTATTA	ATTAAACATG	TCTACTATTA
2041	CCTGTTATGG	AAATGACAAA	TTTAGTTATA
2071	TAATTTATGA	TAAAATTAAG	ATAATAATAA
2101	TGAAATCAAA	TAATTATGTA	AATGCTACTA
2141	GATTATGTGA	ATTACGAGGA	AGAAAGTTTA
2161	CGAACTGGAA	AAAATTAAGT	GAATCTAAAA
2191	TATTAGTCGA	TAATGTAAAA	AAAATAAATG
2221	ATAAACTAA	CCAGTTAAAA	ACGGATATGA
2251	TTATATACGT	TAAGGATATT	GATCATAAAG
2281	GAAGAGATAC	TTGCGGTAC	TATGTACACC
2311	AAGATCTGGT	ATCTTCTATA	TCAAATTGGA
2341	TATCTCCGTT	ATTCGCCGTT	AAGGTAAATA
2371	AAATTATTAA	CTATTATATA	TGTAATGAAT
2401	ATGATATACG	ACTTAGCGAA	ATGGAATCTG
2431	ATATGACAGA	AGTAATAGAT	GTAGTTGATA
2461	AATTAGTAGG	AGGATACAAT	GATGAAATAG
2491	CAGAAATAAT	ATATTTGTTT	AATAAATTTA
2521	TAGAAAAATA	TATTGCTAAC	ATATCGTTAT
2551	CAACTGAATT	ATCTAGTATA	TTAAATAATT
2581	TTATAAATTT	TATAAATTTT	AATAAAAAAT
2611	ACAATAACGA	CATAAAGATA	TTTAATCTTT

FIG. 11C

2641	AATTCCTTGAT	CTGAAAAACA	CATCTATAAA
2671	ACTAGATAAA	AAGTTATTTCG	ATAAAGATAA
2701	TAATGAATCG	AACGATGAAA	AATTGGAAAC
2731	AGAAGTTGAT	AAGCTAATTT	TTTTCATCTA
2761	AATAGTATTA	TTTTATTGAA	GTACGAAGTT
2791	TTACGTTAGA	TAAATAATAA	AGGTCGATTT
2821	TTACTTTGTT	AAATATCAAA	TATGTCATTA
2851	TCTGATAAAG	ATACAAAAAC	ACACGGTGAT
2881	TATCAACCAT	CTAACGAACA	GATATTACAA
2911	AAAATACGTC	GGACTATGGA	AAACGAAGCT
2941	GATAGCCTCA	ATAGAAGAAG	CATTAAAGAA
2971	ATTGTTGTAG	ATGTTATGAA	GAATTGGGAT
3001	CATCCTCAAC	GAAGAAATAG	ATAAAGTTCT
3031	AAACTGGAAA	AATGATACAT	TAAACGATTT
3061	AGATCATCTA	AATACAGATG	ATAATATTAA
3091	GGAAATCATA	CAATGTCTGA	TTAGAGAATT
3121	TGCGTTTAAA	AAGATCAATT	CTATTATGTA
3151	TAGTTATGCT	ATGGTAAAC	TCAATTCAGA
3181	TAACGAACAT	TGAAAGATAA	AATTAAGGAT
3211	TATTTTATAG	AAACTATTCT	TAAAGACAAA
3241	CGTGGTTATA	AACAAAAGCC	ATTACCCGGA
3271	TTGGAAACTA	AAATACTAGA	TAGTATTATA
3301	AGATTTTAAA	AACATAAAAT	TAATAGGTTT
3331	TTATAGATTG	ACTTATTATA	TACAATATGG
3361	ATAAAAGATA	TATATCAACT	AGAAAGTTGA
3391	ATGACGGATT	CTTAATTTTA	TATTATGATT
3421	CAATAGAAAT	TATTGTCATG	TCGTGTAATC
2451	ATTTTATAAA	TATATCAGCG	TTACTAGCTA
3481	AGAAAAACAA	GGACTTTAAT	GAATGGCTAA
3501	AGATAGAATC	ATTTAGAGAA	ATAATAGATA
3541	CTTTAGATAA	AATTAATTAC	GATCTAGGAC
3571	AACGATATTG	TGAAGAACTT	ACGGCGCATC
3601	ACATTCCAGT	GTAATTATTG	AGGTCAAAGC
3631	TAGTAACTTA	ATAGATGACA	GGACAGCTG

FIG. 12A

FIG. 12

FIG. 12A

FIG. 12B

1	TGTCTGGACT	AACTGATTTC	ATGGAACAAT
31	TTTCATCAAA	AATATCAGTT	ATACCTAGTT
61	CTACAAAGAC	AGAACTTTGA	TGTTATGTTT
91	GTGTTTGTAT	AGAAAATTTT	GGGATACTAA
121	CTGATATTTT	TGAATATTTT	TGAATATTTT
151	ATGTTACTTA	CTTACTCCTA	TCTTAGACGA
181	TAATAAAATT	CGAGGCGTAA	TATGTTTTTC
211	CAAATATTTG	AAATTCTTAT	ACGTATCGGC
241	GAAGAAAAGT	AACATACTAT	AAGTGTTATG
271	CAAGTAAGGT	ATGTTAATGA	TATTGGATTT
301	AATTTCAATT	ACAATACATA	TGTCCAAACA
331	TTCCACTCGT	AATTATGTAC	GGAACGACTT
361	TAGTTAAATA	CTTAGTCACA	AAAAACTTAT
391	GACTGTCATT	ATCTGAAAAC	GGTGATTCCC
421	ATAAATCAGA	ATACTTAATA	TTAAATAGAA
461	TGCTCGCTTC	TGGAGGTTTC	CGGATACTAG
481	ATAACATATC	TTCTGTATTA	TAGTTTAATT
511	CACTCATTTT	ATTACATAAT	ACAGTAACAT
541	CTCCCGAAAC	CAATGATGTT	ATATTAGATT
571	TACTTACATA	CTTCTTGTA	CTATCATGAA
601	TACGTTTGTT	ATGATCTATA	AAGAAGATGG
631	ATGTATATTC	TGTTCTAGAT	AGCAAGTTCT
661	TTAAGTTATT	CTTTGTCTGT	ATTACTATCA
691	TCGTCTTCAT	CATCGTCTAA	AGGTAGCATT
721	ATATAATAAA	TCTAATAGTT	GATTTCTCGA
751	TCTATCAGTA	CTCGCTTTCA	ATAACATTTT
781	TACTATAAGC	ATAATAGAAG	GCGGTGATAT
811	CACTATATTT	TTATCGGGTA	TTCTTTTAGT
841	AATTAGTTAG	TTCGTAGAAT	TTCGTAGAGA
871	TAAAAGCCAA	TTTGTTGTTG	ATACTGCTTA
901	CGTTACTCAT	GTTTCTTGTT	TCTGTTAATT
931	AACAGGTATA	CCCTTACAAT	AAGTTTAATT
961	AACTTTTAGG	TTTTTGTGAA	GAACTTT TAG
991	CTTCTAGTTC	CCTTATCCAT	AATTGGGTCT
1021	TAGATCTAGA	TTCTTCCCAT	GTATAAAGGG
1051	GGACATACCC	AAAATCTTTA	AATGCTTTGT
1081	CCGTTTCTAT	AGTAAATGTC	GTACATT CCT
1111	TAATCAAAGT	ATAAGGATTT	AGTAAAGGCG
1141	TGTAAGAACA	AATAGGTGAT	AGTAATACTC
1171	TTAAACCTTT	ATTAATATTA	GCGATAAACC
1201	TTAAACACCA	TAAAGGAAGA	CATGTATTCC
1231	GTAGATCCAT	CCCTAATTGA	TTAAAGAAAT
1261	GCATGT TAAA	ATCATGATAA	TGTT CAGTAG
1291	GAGAGGTATC	GTAACAGTAA	TACACGTTAT

FIG. 12B

1321	TGCAGAGAGG	ACTATGTTGA	CCATTTTCTA
1351	TCATATTTCT	TGCTGCTAAA	ATATGCATCC
1381	AAGCTACGTT	TCCTGCATAG	ACTCTGCTAT
1411	GAAATACTTT	ATCATCCGCA	TATTTATACA
1441	TTTTCCTGCT	TTTATACGAT	CTTCTGTATA
1471	AAGTTTCTAG	TACTGGACAG	TATTCTCCGA
1501	AAACACCTAA	TGGGCGTAGC	GACAAGTGCA
1531	TAATCTAAGT	CCTATATTAG	ACATAGTACC
1561	GTTAGCTTCT	AGTATATATT	TCTCAGATAA
1591	CTTGTTTACT	AAGAGGATAA	GCCTCTTTAT
1621	GGTTAGATTG	ATAATACGTA	TTCTCGTTTC
1651	CTCTTATCAT	CGCATCTCCG	GAGAAAGTTA
1681	GGACCTACCG	CAGAATAACT	ACTCGTATAT
1711	ACTAAGACTC	TTACGCCGTT	ATACAGACAA
1741	GAATCTACTA	CGTTCTTCGT	TCCGTTGATA
1771	TTAACGTCCA	TTATAGAGTC	GTTAGTAAAC
1801	TTACCCGCTA	CATCATTTAT	CGAAGCAATA
1831	TGAATGACCA	CATCTGCTGA	TCTAAGCGCT
1861	TCGTCCAAAG	TACTTTTATT	TCTAACATCT
1891	CCAATCACGG	GAATATCTT	TATTATATTA
1921	CATTTTTCTA	CAAGATCTAG	TAACCATTGG
1951	TCGATTCTAA	TATCGTAAAC	ACGAACTTCT
1981	TTTTAAAGAG	GATTCGAACA	AGATAAGATT
2011	ATTTATAATG	TGTCTACCTA	AAAATCCACA
2041	CCCTCCGGTT	ACCACGTATA	CTAGTGTACG
2071	CATTTTGAGT	ATTAACCTATA	TAAGACCAAA
2101	ATTATATTTT	CATTTTCTGT	TATATTATAC
2131	TATATAATAA	AAACAAATAA	ATATACGAAT
2161	ATTATAAGAA	ATTTAGAACA	CGTTATTAAA
2191	GTATTGCCTT	TTTTATTAAAC	GGCGTGTTCT
2221	TGTAATTGCC	GTTTAGAATA	GTCTTTATTT
2251	ACTTTAGATA	ACTCTTCTAT	CATAACCGTC
2281	TCCTTATTCC	AATCTTCTTC	AGAAGTACAT
2311	GAGTACTTAC	CGAAGTTTAT	CATCATAGAG
2341	ATTATATATG	AAGAAA	

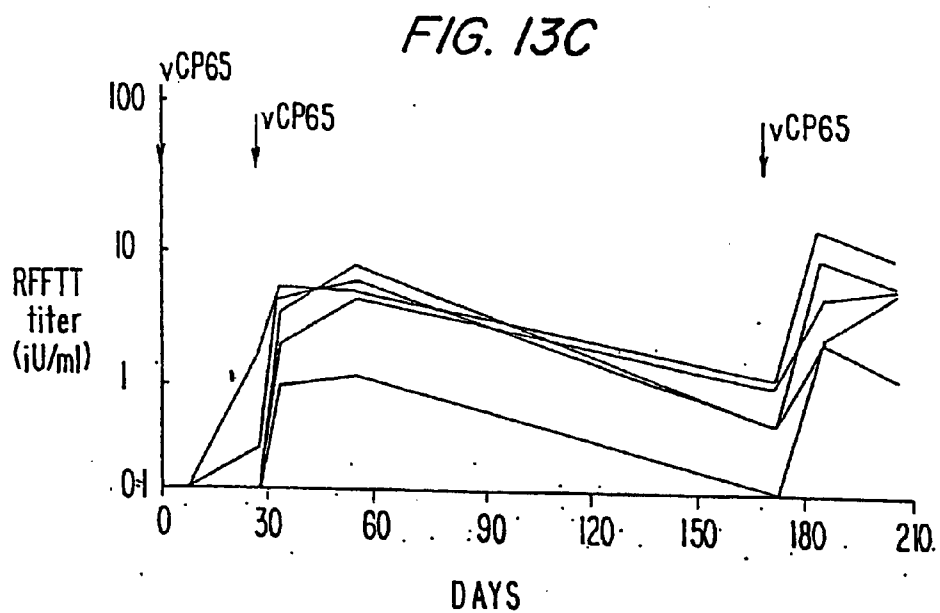
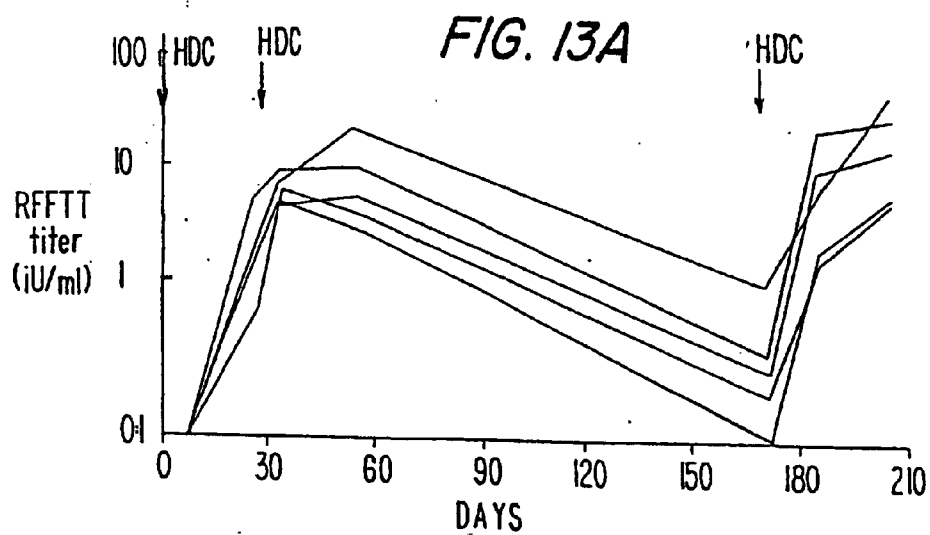


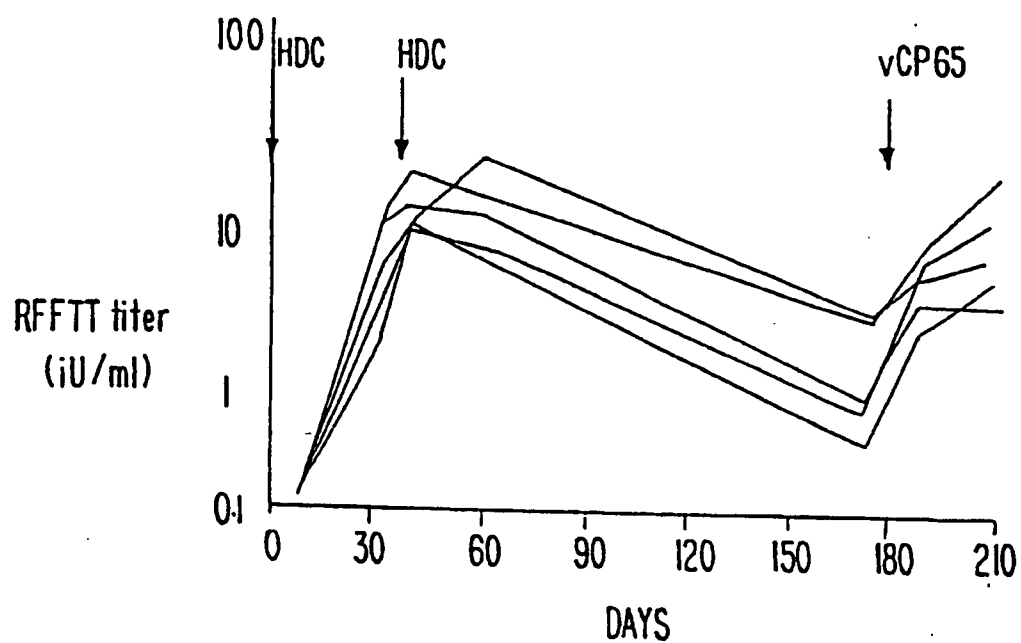
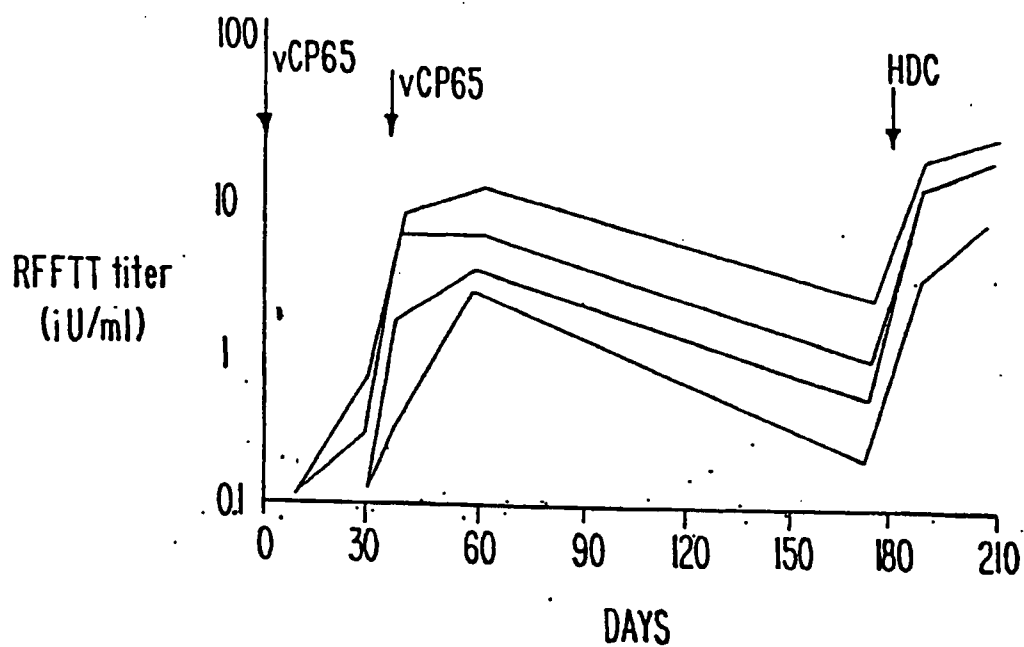
FIG. 13B*FIG. 13D*

FIG. 14A

FIG. 14A-1
FIG. 14A-2
FIG. 14A-3
FIG. 14A-4

FIG. 14A-1

TAATGTAGTA ATTACATCAT _____ C3	TACTAATATT ATGATTATAA FLANKING	AACTCACATT TTGAGTGTAA ARM _____ >	30
TGACTAATTA ACTGATTAAT _____ C3	GCTATAAAAA CGATATTTT FLANKING	CCCGGGATCG GGGCCCTAGC ARM _____ >	60
ATTCTAGAAT TAAGATCTTA	AAAAATTATC TTTTTAATAG _____ <	CCTGCCTAAC GGACGGATTG _____	90
TCTATTCACT AGATAAGTGA _____ < HIV1	ACAGAGAGTA TGTCTCTCAT ENV TRANS	CAGCAAAAAC GTCGTTTTTG MEMBRANE _____	120
TATTCTTAAA ATAAGAATTT _____ < HIV1	CCTACCAAGC GGATGGTTCG ENV TRANS	CTCCTACTAT GAGGATGATA MEMBRANE _____	150
CATTATGAAT GTAATACTTA _____ <	AATCTTTTTT TTAGAAAAAA _____ < HIV1 (MN)	CTCTCTGCAC GAGAGACGTG gp120 _____	180
CACTCTTCTC GTGAGAAGAG _____ < HIV1	TTTGCCTTGG AAACGGAACC (MN) GP120	TGGGTGCTAC ACCCACGATG GENE _____	210
TCCTAATGGT AGGATTACCA _____ < HIV1	TCAATTGTTA AGTTAACAAT (MN) GP120	CTACTTTATA GATGAAATAT GENE _____	240
TTTATATAAT AAATATATTA _____ < HIV1	TCACTTCTCC AGTGAAGAGG (MN) GP120	AATTGTCCTT TTAACAGGGA GENE _____	270
CATATCTCCT GTATAGAGGA _____ < HIV1	CCTCCAGGTC GGAGGTCCAG (MN) GP120	TGAAGATCTC ACTTCTAGAG GENE _____	300
GGTGTCGTTT CCACAGCAAG _____ < HIV1	GTGTCCGTGT CACAGGCACA (MN) GP120	CCTTACCACC GGAATGGTGG GENE _____	330

FIG. 14A-2

TCTTAAAGTG AGAATTTTAC < _____ HIV1	TCATTCCATT AGTAAGGTAA (MN) GP120	TTGCTCTACT AACGAGATGA GENE _____	690
AATGTTACAA TTACAATGTT < _____ HIV1	TGTGCTTGTC ACACGAACAG (MN) GP120	TTATAGTTCC AATATCAAGG GENE _____	720
TATTATATTT ATAATATAAA < _____ HIV1	TTTGTTGTAT AAACAACATA (MN) GP120	AAAATGCTCT TTTTACGAGA GENE _____	750
CCCTGGTCCT GGGACCAGGA < _____ HIV1	ATATGTATCC TATACATAGG (MN) GP120	TTTTTCTTTT AAAAAGAAAA GENE _____	780
ATTGTAGTTG TAACATCAAC < _____ HIV1	GGTCTTGTA CCAGAACATG (MN) GP120	AATTAATTTG TTAATTAAAC GENE _____	810
TACAGATTCA ATGTCTAAGT < _____ HIV1	TTCAGATGTA AAGTCTACAT (MN) GP120	CTATGATGGT GATACTACCA GENE _____	840
TTTAGCATT AAATCGTAAT < _____ HIV1	TCATTGAAAT AGTAACTTTA (MN) GP120	TCTCAGATCT AGAGTCTAGA GENE _____	870
AATTACTACC TTAATGATGG < _____ HIV1	TCTTCTTCTG AGAAGAAGAC (MN) GP120	CTAGACTGCC GATCTGACGG GENE _____	900
ATTTAACAGC TAAATTGTCT < _____ HIV1	AGTTGAGTTG TCAACTCAAC (MN) GP120	ATACTACTGG TATGATGACC GENE _____	930
CCTAATTCCA GGATTAAGGT < _____ HIV1	TGTGTACATT ACACATGTAA (MN) GP120	GTA CTGTGCT CATGACACGA GENE _____	960
GACATTTTTA CTGTAAAAAT < _____ HIV1	CATGATCCTT GTACTAGGAA (MN) GP120	TTCCACTGAA AAGGTGACTT GENE _____	990

FIG. 14A-3

ATCTCTTGTT TAGAGAACAA < _____ HIV1	AATAGTAGCC TTATCATCGG (MN) GP120	CTGTAATATT GACATTATAA GENE _____	360
TGATGAACAT ACTACTTGTA < _____ HIV1	CTAATTTGTC GATTAAACAG (MN) GP120	CTTCAATGGG GAAGTTACCC GENE _____	390
AGGGGCATAT TCCCCGTATA < _____ HIV1	ATTGCTTTTC TAACGAAAAG (MN) GP120	CTACTTCCTG GATGAAGGAC GENE _____	420
CCACATGTTT GGTGTACAAA < _____ HIV1	ATAATTTGTT TATTAAACAA (MN) GP120	TTATTTTGCA AATAAAACGT GENE _____	450
TTGAAGTGTG AACTTCACAC < _____ HIV1	ATATTGTTAT TATAACAATA (MN) GP120	TTGACCCTGT AACTGGGACA GENE _____	480
AGTATTATTC TCATAATAAG < _____ HIV1	CAAGTATTAT GTTCATAATA (MN) GP120	TACCATTCCA ATGGTAAGGT GENE _____	510
AGTACTATTA TCATGATAAT < _____ HIV1	AACAGTGGTG TTGTCACCAC (MN) GP120	ATGAATTACA TACTTAATGT GENE _____	540
GTAGAAGAAT CATCTTCTTA < _____ HIV1	TCCCCTCCAC AGGGGAGGTG (MN) GP120	AATTAAAAC TTAATTTTGA GENE _____	570
GTGCATTACA CACGTAATGT < _____ HIV1	ATTTCTGGGT TAAAGACCCA (MN) GP120	CCCCTCCTGA GGGGAGGACT GENE _____	600
GGATTGATTA CCTAACTAAT < _____ HIV1	AAGACTATTG TTCTGATAAC (MN) GP120	TTTTATTCTT AAAATAAGAA GENE _____	630
AAATTGTTCT TTTAACAAGA < _____ HIV1	TTTAATTTGC AAATTAAACG (MN) GP120	TAACATCTG ATTGATAGAC GENE _____	660

FIG. 14A-4

CTTTTATCG GAAAAATAGC < _____ HIV1	TTACACTTTA AATGTGAAAT (MN) GP120	GAATCGCAAA CTTAGCGTTT GENE _____	1020
ACCAGCCGGG TGGTCGGCCC < _____ HIV1	GCACAATAGT CGTGTTATCA (MN) GP120	GTATGGGAAT CATACCCTTA GENE _____	1050
TGGCTCAAAG ACCGAGTTTC < _____ HIV1	GATATCTTTG CTATAGAAAC (MN) GP120	GACAAGCTTG CTGTTCGAAC GENE _____	1080

*FIG. 14B**FIG. 14B-1*

FIG. 14B-1
FIG. 14B-2
FIG. 14B-3
FIG. 14B-4
FIG. 14B-5

TGTAATGACT ACATTACTGA < _____ HIV1	GAGGTATTAC CTCCATAATG (MN) GP120	AACTTATCAA TTGAATAGTT GENE _____	1110
CCTATAGCTG GGATATCGAC < _____ HIV1	GTACTATCAT CATGATAGTA (MN) GP120	TATTTATTGA ATAAATAACT GENE _____	1140
TACTATATCA ATGATATAGT < _____ HIV1	AGTTTATAAA TCAAATATTT (MN) GP120	GAAGTGCATA CTTCACGTAT GENE _____	1170
TTCTTTCTGC AAGAAAGACG < _____ HIV1	ATCTTATCTC TAGAATAGAG (MN) GP120	TTATGCTTGT AATACGAACA GENE _____	1200
GGTGATATTG CCACTATAAC < _____ HIV1	AAAGAGCAGT TTTCTCGTCA (MN) GP120	TTTTCATTTC AAAAGTAAAG GENE _____	1230
TCCTCCCTTT AGGAGGGAAA < _____ HIV1	ATTGTTCCCT TAACAAGGGA (MN) GP120	CGCTATTACT GCGATAATGA GENE _____	1260
ATTGTTATTA TAACAATAAT < _____ HIV1	GCAGTACTAT CGTCATGATA (MN) GP120	TATTGGTATT ATAACCATAA GENE _____	1290
AGTAGTATTC TCATCATAAG < _____ HIV1	CTCAAATCAG GAGTTTAGTC (MN) GP120	TGCAATTTAA ACGTTAAATT GENE _____	1320
AGTAACACAG TCATTGTGTC < _____ HIV1	AGTGGGGTTA TCACCCCAAT (MN) GP120	ATTTTACACA TAAATGTGT GENE _____	1350
TGGCTTTAGG ACCGAAATCC < _____ HIV1	CTTTGATCCC GAAACTAGGG (MN) GP120	ATAAACTGAT TATTTGACTA GENE _____	1380
TATATCCTCA ATATAGGAGT < _____ HIV1	TGCATCTGTT ACGTAGACAA (MN) GP120	CTACCATGTT GATGGTACAA GENE _____	1410

ATTTTTCAC TAAAAAGGTG < _____ HIV1	ATGTTAAAT TACAATTTTA (MN) GP120	TTTCTGTCAC AAAGACAGTG GENE _____	1440
ATTTACCAAT TAAATGGTTA < _____ HIV1	TCTACTTCTT AGATGAAGAA (MN) GP120	GTGGGTGTTGGG CACCCAACCC GENE _____	1470
GTCTGTGGGT CAGACACCCA < _____ HIV1	ACACAGGCAT TGTGTCCGTA (MN) GP120	GTGTGGCCCA CACACCGGGT GENE _____	1500
AACATTATGT TTGTAATACA < _____ HIV1	ACCTCTGTAT TGGAGACATA (MN) GP120	CATATGCTTT GTATACGAAA GENE _____	1530
AGCATCTGAT TCGTAGACTA < _____ HIV1	GCACAAAATA CGTGTTTTAT (MN) GP120	GAGTGGTGGT CTCACCACCA GENE _____	1560
TGCTTCTTTC ACGAAGAAAG < _____ HIV1	CACACAGGTAC GTGTGTCCATG (MN) GP120	CCCATAATA GGGTATTAT GENE _____	1590
GACTGTGACC CTGACACTGG < _____ HIV1	CACAATTTTT GTGTTAAAAA (MN) GP120	CTGTAGCACT GACATCGTGA GENE _____	1620
ACAGATCATC TGTCTAGTAG < _____ HIV1	AACATCCCAA TTGTAGGGTT (MN) GP120	GGAGCATGGT CCTCGTACCA GENE _____	1650
GCCCCATCTC CGGGGTAGAG < _____ HIV1	CACCCCCATC GTGGGGGTAG (MN) GP120	TCCACAAGTG AGGTGTTTAC GENE _____	1680
CTGATATTTT GACTATAAAG < _____ HIV1	TCCTTCACTC AGGAAGTGAG (MN) GP120	TCATTGCCAC AGTAACGGTG GENE _____	1710
TGTCTTCTGC ACAGAAGACG < HIV1 (MN)	TCTTTCATAT AGAAAGTATA gp120 _____	ACGATACAAA TGCTATGTTT	1740

FIG. 14B-3

CTTAACGCAT GAATTGCGTA < _____ H6	ATCGCGATAA TAGCGCTATT PROMOTER_	TGAAATAATT ACTTTATTAA _____	1770
TATGATTATT ATACTAATAA < _____ H6	TCTCGCTTTC AGAGCGAAAG PROMOTER_	AATTTAACAC TTAAATTGTG _____	1800
AACCCTCAAG TTGGGAGTTC < _____ H6	AACCTTTGTA TTGGAAACAT PROMOTER_	TTTATTTTCA AAATAAAAGT _____	1830
CTTTTTAAGT GAAAAATTCA < _____ H6	ATAGAATAAA TATCTTATTT PROMOTER_	GAAGCTCTAA CTTCGAGATT _____	1860
TTAATTAAGC AATTAATTCTG	TACAAATAGT ATGTTTATCA	TTCGTTTTCA AAGCAAAAGT	1890
CCTTGTCTAA GGAACAGATT	TAACTAATTA ATTGATTAAT	ATTAACCCGG TAATTGGGCC	1920
ATCTTGAGAT TAGAACTCTA _____	AAAGTGAAAA TTTCACTTTT I3L PROMOT	TATATATCAT ATATATAGTA ER _____>	1950
TATATTACAA ATATAATGTT _____	AGTACAATTA TCATGTTAAT I3L PROMOT	TTTAGGTTTA AAATCCAAAT ER _____>	1980
ATCATGGGTG TAGTACCCAC _____ _____ _____ HIV1	CGAGAGCGTC GCTCTCGCAG (IIIB) GAG/	AGTATTAAGC TCATAATTCTG PRO GENE ____>	2010
GGGGGAGAAT CCCCCTCTTA _____ _____ HIV1	TAGATCGATG ATCTAGCTAC (IIIB) GAG/	GGAAAAAATT CCTTTTTTAA PRO GENE ____>	2040
CGGTTAAGGC GCCAATTCCG _____ _____ HIV1	CAGGGGGAAA GTCCCCCTTT (IIIB) GAG/	GAAAAAATAT CTTTTTTATA PRO GENE ____>	2070

FIG. 14B-4

AAATTAAAAC TTTAATTTTG _____HIV1	ATATAGTATG TATATCATAC (IIIB) GAG/	GGCAAGCAGG CCGTTCGTCC PRO GENE__>	2100
GAGCTAGAAC CTCGATCTTG _____HIV1	GATTCGCAGT CTAAGCGTCA (IIIB) GAG/	TAATCCTGGC ATTAGGACCG PRO GENE__>	2130
CTGTTAGAAA GACAATCTTT _____HIV1	CATCAGAAGG GTAGTCTTCC (IIIB) GAG/	CTGTAGACAA GACATCTGTT PRO GENE__>	2160
ATACTGGGAC TATGACCCTG _____HIV1	AGCTACAACC TCGATGTTGG (IIIB) GAG/	ATCCCTTCAG TAGGGAAGTC PRO GENE__>	2190
ACAGGATCAG TGTCCTAGTC _____HIV1	AAGAACTTAG TTCTTGAATC (IIIB) GAG/	ATCATTATAT TAGTAATATA PRO GENE__>	2220
AATACAGTAG TTATGTCATC _____HIV1	CAACCCTCTA GTTGGGAGAT (IIIB) GAG/	TTGTGTGCAT AACACACGTA PRO GENE__>	2250
CAAAGGATAG GTTTCCTATC _____HIV1	AGATAAAAGA TCTATTTTCT (IIIB) GAG/	CACCAAGGAA GTGGTTCCTT PRO GENE__>	2280
GCTTTAGACA CGAAATCTGT _____HIV1	AGATAGAGGA TCTATCTCCT (IIIB) GAG/	AGAGCAAAAC TCTCGTTTTG PRO GENE__>	2310
AAAAGTAAGA TTTTCATTTCT _____HIV1	AAAAAGCACA TTTTTCGTGT (IIIB) GAG/	GCAAGCAGCA CGTTCGTCTG PRO GENE__>	2340
GCTGACACAG CGACTGTGTC _____HIV1	GACACAGCAA CTGTGTCGTT (IIIB) GAG/	TCAGGTCAGC AGTCCAGTCG PRO GENE__>	2370
CAAATTACC GTTTTAATGG _____HIV1	CTATAGTGCA GATATCACGT (IIIB) GAG/	GAACATCCAG CTTGTAAGTC PRO GENE__>	2400

FIG. 14B-5

GGGCAAATGG CCCGTTTACC _____HIV1	TACATCAGGC ATGTAGTCCG (IIIB)GAG/	CATATCACCT GTATAGTGGA PRO GENE__>	2430
AGAACTTTAA TCTTGAAATT _____HIV1	ATGCATGGGT TACGTACCCA (IIIB)GAG/	AAAAGTAGTA TTTTCATCAT PRO GENE__>	2460
GAAGAGAAGG CTTCTCTTCC _____HIV1	CTTTCAGCCC GAAAGTCGGG (IIIB)GAG/	AGAAGTGATA TCTTCACTAT PRO GENE__>	2490
CCCATGTTTT GGGTACAAAA _____HIV1	CAGCATTATC GTCGTAATAG (IIIB)GAG/	AGAAGGAGCC TCTTCCTCGG PRO GENE__>	2520

FIG. 14C

FIG. 14C-1
FIG. 14C-2
FIG. 14C-3
FIG. 14C-4

FIG. 14C-1

ACCCACAAAG TGGGGTGTTC _____ HIV1	ATTTAAACAC TAAATTTGTG (IIIB) GAG/	CATGCTAAAC GTACGATTTG PRO GENE__>	2550
ACAGTGGGGG TGTCAACCCC _____ HIV1	GACATCAAGC CTGTAGTTCG (IIIB) GAG/	AGCCATGCAA TCGGTACGTT PRO GENE__>	2580
ATGTTAAAG TACAATTTTC _____ HIV1	AGACCATCAA TCTGGTAGTT (IIIB) GAG/	TGAGGAAGCT ACTCCTTCGA PRO GENE__>	2610
GCAGAATGGG CGTCTTACCC _____ HIV1	ATAGAGTGCA TATCTCACGT (IIIB) GAG/	TCCAGTGCAT AGGTCACGTA PRO GENE__>	2640
GCAGGGCCTA CGTCCCGGAT _____ HIV1	TTGCACCAGG AACGTGGTCC (IIIB) GAG/	CCAGATGAGA GGTCTACTCT PRO GENE__>	2670
GAACCAAGGG CTTGGTTCCC _____ HIV1	GAAGTGACAT CTTCACTGTA (IIIB) GAG/	AGCAGGAACT TCGTCCTTGA PRO GENE__>	2700
ACTAGTACCC TGATCATGGG _____ HIV1	TTCAGGAACA AAGTCCTTGT (IIIB) GAG/	AATAGGATGG TTATCCTACC PRO GENE__>	2730
ATGACAAATA TACTGTTTAT _____ HIV1	ATCCACCTAT TAGGTGGATA (IIIB) GAG/	CCCAGTAGGA GGGTCATCCT PRO GENE__>	2760
GAAATTTATA CTTTAAATAT _____ HIV1	AAAGATGGAT TTTCTACCTA (IIIB) GAG/	AATCCTGGGA TTAGGACCCT PRO GENE__>	2790
TTAAATAAAA AATTTATTTT _____ HIV1	TAGTAAGAAT ATCATTCTTA (IIIB) GAG/	GTATAGCCCT CATATCGGGA PRO GENE__>	2820
ACCAGCATTC TGGTCGTAAG _____ HIV1	TGGACATAAG ACCTGTATTC (IIIB) GAG/	ACAAGGACCA TGTTCTGGT PRO GENE__>	2850

FIG. 14C-2

AAAGAACCCT TTTCTTGGGA _____HIV1	TTAGAGACTA AATCTCTGAT (IIIB) GAG/	TGTAGACCGG ACATCTGGCC PRO GENE__>	2880
TTCTATAAAA AAGATATTTT _____HIV1	CTCTAAGAGC GAGATTCTCG (IIIB) GAG/	CGAGCAAGCT GCTCGTTCGA PRO GENE__>	2910
TCACAGGAGG AGTGTCCTCC _____HIV1	TAAAAAATTG ATTTTTTAAC (IIIB) GAG/	GATGACAGAA CTACTGTCTT PRO GENE__>	2940
ACCTTGTTGG TGGAACAACC _____HIV1	TCCAAAATGC AGGTTTACG (IIIB) GAG/	GAACCCAGAT CTTGGGTCTA PRO GENE__>	2970
TGTAAGACTA ACATTCTGAT _____HIV1	TTTTAAAAGC AAAATTTTCG (IIIB) GAG/	ATTGGGACCA TAACCCTGGT PRO GENE__>	3000
GCGGCTACAC CGCCGATGTG _____HIV1	TAGAAGAAAT ATCTTCTTTA (IIIB) GAG/	GATGACAGCA CTACTGTCGT PRO GENE__>	3030
TGTCAGGGAG ACAGTCCCTC _____HIV1	TAGGAGGACC ATCCTCCTGG (IIIB) GAG/	CGGCCATAAG GCCGGTATTC PRO GENE__>	3060
GCAAGAGTTT CGTTCTCAA _____HIV1	TGGCTGAAGC ACCGACTTCG (IIIB) GAG/	AATGAGCCAA TTACTCGGTT PRO GENE__>	3090
GTAACAAATT CATTGTTTAA _____HIV1	CAGCTACCAT GTCGATGGTA (IIIB) GAG/	AATGATGCAG TTACTACGTC PRO GENE__>	3120
AGAGGCAATT TCTCCGTAA _____HIV1	TTAGGAACCA AATCCTTGGT (IIIB) GAG/	AAGAAAGATT TTCTTTCTAA PRO GENE__>	3150
GTAAAGTGTT CAATTCACAA _____HIV1	TCAATTGTGG AGTTAACACC (IIIB) GAG/	CAAAGAAGGG GTTTCTTCCC PRO GENE__>	3180

FIG. 14C-3

CACACAGCCA GTGTGTCGGT _____HIV1	GAAATTGCAG CTTTAACGTC (IIIB) GAG/	GGCCCCTAGG CCGGGGATCC PRO GENE__>	3210
AAAAAGGGCT TTTTTCCCGA _____HIV1	GTTGGAAATG CAACCTTTAC (IIIB) GAG/	TGGAAAGGAA ACCTTTCCTT PRO GENE__>	3240
GGACACCAAA CCTGTGGTTT _____HIV1	TGAAAGATTG ACTTTCTAAC (IIIB) GAG/	TACTGAGAGA ATGACTCTCT PRO GENE__>	3270
CAGGCTAATT GTCCGATTAA _____HIV1	TTTtagggAA AAAATCCCTT (IIIB) GAG/	GATCTGGCCT CTAGACCGGA PRO GENE__>	3300
TCCTACAAGG AGGATGTTCC _____HIV1	GAAGGCCAGG CTTCCGGTCC (IIIB) GAG/	GAATTTTCTT CTTAAAAGAA PRO GENE__>	3330
CAGAGCAGAC GTCTCGTCTG _____HIV1	CAGAGCCAAC GTCTCGGTTG (IIIB) GAG/	AGCCCCACCA TCGGGGTGGT PRO GENE__>	3360
GAAGAGAGCT CTTCTCTCGA _____HIV1	TCAGGTCTGG AGTCCAGACC (IIIB) GAG/	GGTAGAGACA CCATCTCTGT PRO GENE__>	3390
ACAACTCCCC TGTTGAGGGG _____HIV1	CTCAGAAGCA GAGTCTTCGT (IIIB) GAG/	GGAGCCGATA CCTCGGCTAT PRO GENE__>	3420
GACAAGGAAC CTGTTCCCTG _____HIV1	TGTATCCTTT ACATAGGAAA (IIIB) GAG/	AACTTCCCTC TTGAAGGGAG PRO GENE__>	3450
AGATCACTCT TCTAGTGAGA _____HIV1	TTGGCAACGA AACCGTTGCT (IIIB) GAG/	CCCCTCGTCA GGGGAGCAGT PRO GENE__>	3480
CAATAAAGAT GTTATTTCTA _____HIV1	AGGGGGGCAA TCCCCCGTT (IIIB) GAG/	CTAAAGGAAG GATTTCCTTC PRO GENE__>	3510

FIG. 14C-4

CTCTATTAGA GAGATAATCT _____HIV1	TACAGGAGCA ATGTCCTCGT (IIIB) GAG/	GATGATACAG CTACTATGTC PRO GENE__>	3540
TATTAGAAGA ATAATCTTCT _____HIV1	AATGAGTTTG TTACTCAAAC (IIIB) GAG/	CCAGGAAGAT GGTCCTTCTA PRO GENE__>	3570
GGAAACCAAA CCTTTGGTTT _____HIV1	AATGATAGGG TTACTATCCC (IIIB) GAG/	GGAATTGGAG CCTTAACCTC PRO GENE__>	3600
GTTTTATCAA CAAAATAGTT _____HIV1	AGTAAGACAG TCATTCTGTC (IIIB) GAG/	TATGATCAGA ATACTAGTCT PRO GENE__>	3630
TACTCATAGA ATGAGTATCT _____HIV1	AATCTGTGGA TTAGACACCT (IIIB) GAG/	CATAAAGCTA GTATTTTCGAT PRO GENE__>	3660
TAGGTACAGT ATCCATGTCA _____HIV1	ATTAGTAGGA TAATCATCCT (IIIB) GAG/	CCTACACCTG GGATGTGGAC PRO GENE__>	3690
TCAACATAAT AGTTGTATTA _____HIV1	TGGAAGAAAT ACCTTCTTTA (IIIB) GAG/	CTGTTGACTC GACAACTGAG PRO GENE__>	3720
AGATTGGTTG TCTAACCAAC _____HIV1 (IIIB)	CACTTTAAAT GTGAAATTTA GAG/PRO	TTTTAACCCG AAAATTGGGC GENE__>	3750
GGGGATCCCG CCCCTAGGGC _____C3	ATTTTTATGA TAAAATACT FLANKING	CTAGTTAATC GATCAATTAG ARM_____>	3780
AAATAAAAAG TTTATTTTTC _____C3	CATACAAGCT GTATGTTTCA FLANKING	ATTGETTC TAACGAAG ARM_____>	3808

FIG. 15A

FIG. 15A-1
FIG. 15A-2

FIG. 15A-1

AGATATTTGT TCTATAAACA _____C3	TAGCTTCTGC ATCGAAGACG FLANKING	CGGAGATAACC GCCTCTATGG ARM _____>	30
GTGAAAATCT CACTTTTAGA _____C3	ATTTTCTGGA TAAAAGACCT FLANKING	AGGAAAGGGA TCCTTTCCT ARM _____>	60
GGTCTTATCT CCAGAATAGA _____C3	ATTCTGTCAG TAAGACAGTC FLANKING	CAGAGTAGGT GTCTCATCCA ARM _____>	90
TCCTCTAATG AGGAGATTAC _____C3	ACGAAGACAA TGCTTCTGTT FLANKING	TAGTGAATAC ATCACTTATG ARM _____>	120
TTGCATGAAG AACGTACTTC _____C3	GTCACTGTGT CAGTGACACA FLANKING	AGAGTTCAAA TCTCAAGTTT ARM _____>	150
ACTGATCATC TGACTIONAG _____C3	AGTGTTTGAT TCACAACTA FLANKING	AACTCTAGCG TTGAGATCGC ARM _____>	180
TGTACGAGTC ACATGCTCAG _____C3	CTTCTAACAC GAAGATTGTG FLANKING	TGTGGTTTAT ACACCAAATA ARM _____>	210
TGGCTGGAAT ACCGACCTTA _____C3	AAAAGGATAA TTTCCTATT FLANKING	AGACACCTAT TCTGTGGATA ARM _____>	240
ACTGATTCAT TGACTIONAG _____C3	TTTCATCTGT AAAGTAGACA FLANKING	CAACGTTTCT GTTGCAAAGA ARM _____>	270
CTAAGAGATT GATTCTCTAA _____C3	CATAGGTATT GTATCCATAA FLANKING	ATTATTACAT TAATAATGTA ARM _____>	300
CGATCTAGAA GCTAGATCTT _____C3	GTCTAATAAC CAGATTATTG FLANKING	TGCTAAGTAT ACGATTCATA ARM _____>	330

FIG. 15A-2

ATTATTGGAT TAATAACCTA _____C3	TTAACGCGCT AATTGCGCGA FLANKING	ATAAACGCAT TATTTGCGTA ARM _____>	360
CCAAAACCTA GGTTTTGGAT _____C3	CAAATATAGG GTTTATATCC FLANKING	AGAAGCTTCT TCTTCGAAGA ARM _____>	390
CTTATGAAAC GAATACTTTG _____C3	TTCTTAAAGC AAGAATTTG FLANKING	TTTACTCTTA AAATGAGAAT ARM _____>	420
CTATTACTAC GATAATGATG _____C3	TCAAAGAGA AGTTTTCTCT FLANKING	TATTACATTA ATAATGTAAT ARM _____>	450
ATTATGTGAT TAATACACTA _____C3	GAGGCATCCA CTCCGTAGGT FLANKING	ACATATAAAG TGTATATTTT ARM _____>	480
AAGACTAAAG TTCTGATTTT _____C3	CTGTAGAAGC GACATCTTCG FLANKING	TGTTATGAAG ACAATACTTC ARM _____>	510
AATATCTTAT TTATAGAATA _____C3	CAGATATATT GTCTATATAA FLANKING	AGATGCATTG TCTACGTAAC ARM _____>	540
TTAGTTCTGT AATCAAGACA _____C3	AGATCAGTAA TCTAGTCATT FLANKING	CGTATAGCAT GCATATCGTA ARM _____>	570
ACGAGTATAA TGCTCATATT _____C3	TTATCGTAGG AATAGCATCC FLANKING	TAGTAGGTAT ATCATCCATA ARM _____>	600
CCTAAAATAA GGATTTTATT _____C3	ATCTGATACA TAGACTATGT FLANKING	GATAATAACT CTATTATTGA ARM _____>	630
TTGTAAATCA AACATTTAGT _____>			640

FIG 15B

FIG. 15B-1

FIG. 15B-2

FIG. 15B-3

FIG. 15B-1

ATTCAGCAAT TAAGTCGTTA _____C3	TTCTCTATTA AAGAGATAAT FLANKING	TCATGATAAT AGTACTATTA ARM _____>	670
GATTAATACA CTAATTATGT _____C3	CAGCGTGTCG GTCGCACAGC FLANKING	TTATTTTTTTG AATAAAAAAC ARM _____>	700
TTACGATAGT AATGCTATCA _____C3	ATTTCTAAAG TAAAGATTTC FLANKING	TAAAGAGCAG ATTTCTCGTC ARM _____>	730
GAATCCCTAG CTTAGGGATC _____C3	TATAATAGAA ATATTATCTT FLANKING	ATAATCCATA TATTAGGTAT ARM _____>	760
TGAAAAATAT ACTTTTTTATA _____C3	AGTAATGTAC TCATTACATG FLANKING	ATATTTCTAA TATAAAGATT ARM _____>	790
TGTTAACATA ACAATTGTAT _____C3	TTTATAGGTA AAATATCCAT FLANKING	AATCCAGGAA TTAGGTCCTT ARM _____>	820
GGGTAATTTT CCCATTAAAA _____C3	TACATATCTA ATGTATAGAT FLANKING	TATACGCTTA ATATGCGAAT ARM _____>	850
TTACAGTTAT AATGTCAATA _____C3	TAAAAATATA ATTTTATAT FLANKING	CTTGCAAACA GAACGTTTGT ARM _____>	880
TGTTAGAAGT ACAATCTTCA _____C3	AAAAAAGAAA TTTTTCTTT FLANKING	GAACATAATT CTTGATTAAA ARM _____>	910
TACAAAGTGC ATGTTTCACG _____C3	TTTACCAAAA AAATGGTTTT FLANKING	TGCCAATGGA ACGGTTACCT ARM _____>	940
AATTACTTAG TTAATGAATC _____C3	TATGTATATA ATACATATAT FLANKING	ATGTATAAAG TACATATTTC ARM _____>	970

FIG. 15B-2

GTATGAATAT CATACTTATA _____C3	CACAAACAGC GTGTTTGTCG FLANKING	AAATCGGCTA TTTAGCCGAT ARM _____>	1000
TTCCCAAGTT AAGGGTTCAA _____C3	GAGAAACGGT CTCTTTGCCA FLANKING	ATAATAGATA TATTATCTAT ARM _____>	1030
TATTTCTAGA ATAAAGATCT _____C3	TACCATTAAT ATGGTAATTA FLANKING	AACCTTATAA TTGGAATATT ARM _____>	1060
GCTTGACGTT CGAACTGCAA _____C3	TCCTATAATG AGGATATTAC FLANKING	CCTACTAAGA GGATGATTCT ARM _____>	1090
AAACTAGAAG TTTGATCTTC _____C3	ATACATACAT TATGTATGTA FLANKING	ACTAACGCCA TGATTGCGGT ARM _____>	1120
TACGAGAGTA ATGCTCTCAT _____C3	ACTACTCATC TGATGAGTAG FLANKING	GTATAACTAC CATATTGATG ARM _____>	1150
TGTTGCTAAC ACAACGATTG _____C3	AGTGACACTG TCACTGTGAC FLANKING	ATGTTATAAC TACAATATTG ARM _____>	1180
TCATCTTTGA AGTAGAAACT _____C3	TGTGGTATAA ACACCATATT FLANKING	ATGTATAATA TACATATTAT ARM _____>	1210
ACTATATTAC TGATATAATG _____C3	ACTGGTATTT TGACCATAAA FLANKING	TATTTCAGTT ATAAAGTCAA ARM _____>	1240
ATATACTATA TATATGATAT _____C3	TAGTATTAAA ATCATAATTT FLANKING	AATTATATTT TTAATATAAA ARM _____>	1270
GTATAATTAT CATATTAATA _____C3	ATTATTATAT TAATAATATA FLANKING	TCAGTGTAGA AGTCACATCT ARM _____>	1300

FIG. 15B-3

AAGTAAAATA TTCATTTTAT _____C3	CTATAAATAT GATATTTATA FLANKING	GTATCTCTTA CATAGAGAAT ARM_____>	1330
TTTATAACTT AAATATTGAA _____C3	ATTAGTAAAG TAATCATTTC FLANKING	TATGTACTAT ATACATGATA ARM_____>	1360
TCAGTTATAT AGTCAATATA _____C3	TGTTTTATAA ACAAAATATT FLANKING	AAGCTAAATG TTCGATTTAC ARM_____>	1390
CTACTAGATT GATGATCTAA _____C3	GATATAAATG CTATATTTAC FLANKING	AATATGTAAT TTATACATTA ARM_____>	1420
AAATTAGTAA TTTAATCATT ___C3 FLANK	TGTAGTATAC ACATCATATG ING ARM___>		1440

FIG. 15C

FIG. 15C-1

FIG. 15C-2

FIG. 15C-3

FIG. 15C-1

TAATATTAAC ATTATAATTG ___C3 FLAN	TCACATTTGA AGTGTAAGCT KING ARM___	CTAATTAGCT GATTAATCGA > ___CLONING	1470
ATAAAAACCC TATTTTTGGG _____	GGGCTGCAGG CCCGACGTCC CLONING	AATTCCTCGA TTAAGGAGCT SITES____>	1500
GTACGATACA CATGCTATGT -> _____H6	AACTTAACGG TTGAATTGCC PROMOTER___	ATATCGCGAT TATAGCGCTA _____ >	1530
AATGAAATAA TTACTTTATT _____H6	TTTATGATTA AAATACTAAT PROMOTER___	TTTCTCGCTT AAAGAGCGAA _____ >	1560
TCAATTTAAC AGTTAAATTG _____H6	ACAACCCTCA TGTTGGGAGT PROMOTER___	AGAACCTTTG TCTTGGAAAC _____ >	1590
TATTTATTTT ATAAATAAAA _____H6	CACTTTTTTAA GTGAAAATT PROMOTER___	GTATAGAATA CATATCTTAT _____ >	1620
AAGAAGCTCT TTCTTCGAGA _____	AATTAATTAA TTAATTAATT	GCTACAAATA CGATGTTTAT	1650
GTTTCGTTTT CAAAGCAAAA	CACCTTGTCT GTGGAACAGA	AATAACTAAT TTATTGATTA	1680
TAATTAACCC ATTAATTGGG	GGATCCCGAT CCTAGGGCTA	TTTTATGACT AAAATACTGA	1710
AGTTAATCAA TCAATTAGTT ___C3	ATAAAAAGCA TATTTTTTCGT FLANKING	TACAAGCTAT ATGTTTCGATA ARM____>	1740

FIG. 15C-2

TGCTTCGCTA ACGAAGCGAT _____C3	TCGTTACAAA AGCAATGTTT FLANKING	ATGGCAGGAA TACCGTCCTT ARM _____>	1770
TTTTGTGTAA AAAACACATT _____C3	ACTAAGCCAC TGATTCGGTG FLANKING	ATACTTGCCA TATGAACGGT ARM _____>	1800
ATGAAAAAAA TACTTTTTTT _____C3	TAGTAGAAAG ATCATCTTTC FLANKING	GATACTATTT CTATGATAAA ARM _____>	1830
TAATGGGATT ATTACCCTAA _____C3	AGATGTTAAG TCTACAATTC FLANKING	G TTCCTTGGG GAAGGAACCC ARM _____>	1860
ATTATAGTAA TAATATCATT _____C3	CTGGGCATCT GACCCGTAGA FLANKING	GT TAACTTTT CAATTGAAAA ARM _____>	1890
ACGACGTTAG TGCTGCAATC _____C3	GTTAGATACT CAATCTATGA FLANKING	GATGTTACAG CTACAATGTC ARM _____>	1920
ATTATAATAA TAATATTATT _____C3	TGTTACAATA ACAATGTTAT FLANKING	AAATACATGA TTTATGTACT ARM _____>	1950
CAGGATGTGA GTCCTACACT _____C3	TATTTTTCCT ATAAAAAGGA FLANKING	CATATAACTC GTATATTGAG ARM _____>	1980
TTGGAATAGC AACCTTATCG _____C3	AAATATGGAT TTTATACCTA FLANKING	CAATGTGATA GTTACACTAT ARM _____>	2010
GATTTGAAAA GTAAACTTTT _____C3	TTTCAAAAAG AAAGTTTTTC FLANKING	CAAATAACTG GTTTATTGAC ARM _____>	2040
ATCAAGATTT TAGTTCTAAA _____C3	ACAGACTATT TGTCTGATAA FLANKING	TCTATAGTCT AGATATCAGA ARM _____>	2070

FIG. 15C-3

GTAAAGAAGA CATTTCTTCT _____C3	GATGTGTTTT CTACACAAAA FLANKING	CCTCAGAGTA GGAGTCTCAT ARM_____>	2100
ACGCCTCTAA TGCGGAGATT _____C3	ACAGTTGGGA TGTC AACCT FLANKING	GCGAAAGGAT CGCTTTCCTA ARM_____>	2130
GCGCTGTAGT CGCGACATCA _____C3	TATGAACTG ATACTTTGAC FLANKING	GAGGTATCTG CTCCATAGAC ARM_____>	2160
ATGAACTTAG TACTTGAATC _____C3	AGCCCTAAGA TCGGGATTCT FLANKING	AATGTTCTGC TTACAAGACG ARM_____>	2190
TGAATGCGGT ACTTACGCCA _____C3	ACCCTGTTCG TGGGACAAGC FLANKING	AAGGACGTGT TTCCTGCACA ARM_____>	2220
TTGGTGATAT AACC ACTATA _____C3 FLANK	CACAGTAGAT GTGTCATCTA ING ARM_____>		2240

FIG. 15D

FIG. 15D-1
FIG. 15D-2
FIG. 15D-3

FIG. 15D-1

AATCCGTGGA TTAGGCACCT _____C3	ATCCTCACAT TAGGAGTGTA FLANKING	AACAGTAGGA TTGTCATCCT ARM _____>	2270
TATGTTAAGG ATACAATTCC _____C3	AGGACGATGT TCCTGCTACA FLANKING	CGAAAACAAG GCTTTTGTTC ARM _____>	2300
AAACGCCTAA TTTGCGGATT _____C3	TGGAGTGCAT ACCTCACGTA FLANKING	GTCCAAGTTT CAGGTTCAAA ARM _____>	2330
AGGGGGCAAG TCCCCCGTTC _____C3	AAATACAAGT TTTATGTTCA FLANKING	TCTAGGATGG AGATCCTACC ARM _____>	2360
TATTAATAAG ATAATTATTC _____C3	TATCTAAGTA ATAGATTCAT FLANKING	TTTGGTATAA AAACCATATT ARM _____>	2390
TTTATTAAAT AAATAATTTA _____C3	AGTATAATTA TCATATTAAT FLANKING	TAACAAATAA ATTGTTTATT ARM _____>	2420
TAAATAACAT ATTTATTGTA _____C3	GATAACGGTT CTATTGCCAA FLANKING	TTTATTAGAA AAATAATCTT ARM _____>	2450
TAAAATAGAG ATTTTATCTC _____C3	ATAATATCAT TATTATAGTA FLANKING	AATGATATAT TTACTATATA ARM _____>	2480
AATACTTCAT TTATGAAGTA _____C3	TACCAGAAAT ATGGTCTTTA FLANKING	GAGTAATGGA CTCATTACCT ARM _____>	2510
AGACTTATAA TCTGAATATT _____C3	ATGAACTGCA TACTTGACGT FLANKING	TAAAGCTATA ATTCGATAT ARM _____>	2540
AGGTATAGAG TCCATATCTC _____C3	ATATAAATTT TATATTTAAA FLANKING	AGTAAGGTAT TCATTCCATA ARM _____>	2570

FIG. 15D-2

ATACTTAAAA TATGAATTTT _____C3	AATGCAAATA TTACGTTTAT FLANKING	CAATAACGTA GTTATTGCAT ARM _____>	2600
AATATACTAT TTATATGATA _____C3	CAACGTCTTT GTTGCAGAAA FLANKING	GTATTTAGCC CATAAATCGG ARM _____>	2630
GTAAGTATTT CATT CATAAA _____C3	CTGATATAGA GACTATATCT FLANKING	AATGGTAAAA TTACCATTTT ARM _____>	2660
TTATTACTAG AATAATGATC _____C3	AACACGGTGC TTGTGCCACG FLANKING	CGATATTTTA GCTATAAAAT ARM _____>	2690
AAATGTAAAA TTTACATTTT _____C3	ATCCTCCTCT TAGGAGGAGA FLANKING	TCATAAAGCT AGTATTTTCGA ARM _____>	2720
GCTAGTTTAG CGATCAAATC _____C3	ATAATACAGA TATTATGTCT FLANKING	AATTGCTAAA TTAACGATTT ARM _____>	2750
CTACTAATAG GATGATTATC _____C3	ATTCTGGCGC TAAGACCGCG FLANKING	TGACATAGAA ACTGTATCTT ARM _____>	2780
CAGATACATT GTCTATGTAA _____C3	CTGGAAATAG GACCTTTATC FLANKING	TCCGTTATAT AGGCAATATA ARM _____>	2710
ATTTCTGTAT TAAAGACATA _____C3	ATAGAAACAA TATCTTTGTT FLANKING	TAAGTCATTA ATTCAGTAAT ARM _____>	2840
ACTAGATATT TGATCTATAA _____C3	TATTAAAAAA ATAATTTTTT FLANKING	AGGTGTTAAT TCCACAATTA ARM _____>	2870
TGTAATAGAT ACATTATCTA _____C3	TCTTTCTAAA AGAAAGATTT FLANKING	TTATTACGAT AATAATGCTA ARM _____>	2890

FIG. 15D-3

GTACTGTATG CATGACATAC _____C3	ATAAGATATC TATTCTATAG FLANKING	TGATGATATG ACTACTATAC ARM_____>	2930
TATAAAATAT ATATTTTATA _____C3	TTATAGATTT AATATCTAAA FLANKING	TAATATTGAT ATTATAACTA ARM_____>	2960
CTTAATATAC GAATTATATG _____C3	AAACTAGAAA TTTGATCTTT FLANKING	TTTGAAACT AAAAC TTTGA ARM_____>	2990
CCGTTACATT GGCAATGTAA _____C3	ACGCTATAAA TGCGATATTT FLANKING	GTATAAGAAT CATATTCTTA ARM_____>	3020
ATAGATTTAA TATCTAAATT ___C3 FLANK	TTAGGATATT AATCCTATAA ING ARM_____>		3040

FIG. 15E

FIG. 15E-1
FIG. 15E-2
FIG. 15E-3

FIG. 15E-1

GTTAGATAAT CAATCTATTA _____C3	AGTATTAAAA TCATAATTTT FLANKING	TAGATAAAAG ATCTATTTTC ARM _____>	3070
TTTATTTTGT AAATAAAAAC _____C3	CATAAACAGT GTATTGTCA FLANKING	ATCTCATAAA TAGAGTATTT ARM _____>	3100
GGCACTTAAA CCGTGAATTT _____C3	AATAATTGTA TTATTAACAT FLANKING	GTTACGATAT CAATGCTATA ARM _____>	3130
AATAGCGTTA TTATCGCAAT _____C3	CTTATAAATC GAATATTTAG FLANKING	ACGGAGTGCC TGCCTCACGG' ARM _____>	3160
TATAAACGAA ATATTTGCTT _____C3	CAAGATGATT GTTCTACTAA FLANKING	TAGGTAAAAC ATCCATTTTG ARM _____>	3190
CCCATTACAT GGGTAATGTA _____C3	CATTCGGTAA GTAAGCCATT FLANKING	TTAATAGAAG AATTATCTTC ARM _____>	3220
AAAAGATGTA TTTTCTACAT _____C3	ACAGCACTTC TGTCGTGAAG FLANKING	TGTTAAATCT ACAATTTAGA ARM _____>	3250
AGGAGCTGAT TCCTCGACTA _____C3	ATAAACGTAA TATTTGCATT FLANKING	TAGATGACTG ATCTACTGAC ARM _____>	3280
TATGGGCAGT ATACCCGTCA _____C3	CCCTTACATT GGGAATGTAA FLANKING	ACGCTGTTTC TGCGACAAAG ARM _____>	3310
ACGTAACGAT TGCATTGCTA _____C3	ATCGAAACAA TAGCTTTGTT FLANKING	CAAAGACACT GTTTCTGTGA ARM _____>	3340
TTTAGAAAGA AAATCTTTCT _____C3	GGATCTAATG CCTAGATTAC FLANKING	TTAATGTGGT AATTACACCA ARM _____>	3370

FIG. 15E-2

TAATAATCAT ATTATTAGTA _____C3	ATAGATACCG TATCTATGGC FLANKING	TTCTAAATAT AAGATTTATA ARM _____>	3400
AGCTGTTGCA TCGACAACGT _____C3	TCTAAAAACA AGATTTTTGT FLANKING	AAACTATAGT TTTGATATCA ARM _____>	3430
AAACTTATTA TTTGAATAAT _____C3	CTGAAGTACG GACTTCATGC FLANKING	GTA CTGATAC CATGACTATG ARM _____>	3460
AAAGTTGGTA TTTCAACCAT _____C3	GGATTAGATA CCTAATCTAT FLANKING	AACATGTTAT TTGTACAATA ARM _____>	3490
TCACATAGCT AGTGTATCGA _____C3	ATAGAAATGA TATCTTTACT FLANKING	AAGATATTAA TTCTATAATT ARM _____>	3520
TATACTGAAT ATATGACTTA _____C3	GCGATCTTAT CGCTAGAATA FLANKING	TATATGGTTG ATATACCAAC ARM _____>	3550
CTATGTAAAC GATACATTTG _____C3	GTCTATAATC CAGATATTAG FLANKING	ATAAAGGTTT TATTTCCAAA ARM _____>	3580
CACTCCTCTA GTGAGGAGAT _____C3	TACATGGCAG ATGTACCGTC FLANKING	TTAGTTCTAT AATCAAGATA ARM _____>	3610
GAAAACAGAA CTTTTGTCTT _____C3	TTTGTTAAAC AAACAATTTG FLANKING	TCTTACTTGA AGAATGAACT ARM _____>	3640
CCACGGTGCT GGTGCCACGA _____C3	TACGTAAATG ATGCATTTAC FLANKING	CTAAAGCTAA GATTTGATT ARM _____>	3670
GTTATCTGGA CAATAGACCT _____C3	AATACTCCTT TTATGAGGAA FLANKING	TACATAAAGC ATGTATTTG ARM _____>	3700

FIG. 15E-3

TATGTTATCT ATACAATAGA _____C3	AATAGTTTTA TTATCAAAAT FLANKING	ATAATATAAA TATTATATTT ARM _____>	3730
ATTACTTTTA TAATGAAAAT _____C3	TCTTATAACG AGAATATTGC FLANKING	CCGACTATAA GGCTGATATT ARM _____>	3760
TTCTCTAAAT AAGAGATTTA _____C3	AATCACGGTA TTAGTGCCAT FLANKING	ATACGCCTCT TATGCCGAGA ARM _____>	3790
AACTTGTGTT TTGAACACAA _____C3	AGCTTTTTTAG TCGAAAAATC FLANKING	ATGACAAGAT TACTGTTCTA ARM _____>	3820
AGCTATTATG TCGATAATAC ___C3 FLANK	ATAATATCTA TATTATAGAT ING ARM _____>		3840

FIG. 15F

FIG. 15F-1
FIG. 15F-2

FIG. 15F-1

AAATGATGTT TTTACTACAA _____C3	AGAAATATCT TCTTTATAGA FLANKING	AAAAATCCTG TTTTTAGGAC ARM _____>	3870
AAATAGCTAA TTTATCGATT _____C3	TTCAGAAGGT AAGTCTTCCA FLANKING	TTTATAGTAA AAATATCATT ARM _____>	3900
ACATGGAACA TGTACCTTGT _____C3	TATAAACAGT ATATTTGTCA FLANKING	AATAAAAGAC TTATTTTCTG ARM _____>	3930
TACTATCTAT ATGATAGATA _____C3	AAAAGAATCA TTTTCTTAGT FLANKING	TGCGAAAAAG ACGCTTTTTTC ARM _____>	3960
AACTAGATGT TTGATCTACA _____C3	TATAACACAT ATATTGTGTA FLANKING	ATAAAGTTAA TATTTCAATT ARM _____>	3990
ATTCTATATA TAAGATATAT _____C3	TTCTTTTAAT AAGAAAATTA FLANKING	ATCTTTCTTG TAGAAAGAAC ARM _____>	4020
ACAATAACAT TGTTATTGTA _____C3	AGATCTTATG TCTAGAATAC FLANKING	GTAAAGTTCG CATTTC AAGC ARM _____>	4050
TAAC TAATCC ATTGATTAGG _____C3	TAGAGTTAAT ATCTCAATTA FLANKING	AAGATACCTG TTCTATGGAC ARM _____>	4080
CATGTATACG GTACATATGC _____C3	TATATATAGG ATATATATCC FLANKING	GAATTAATAC CTTAATTATG ARM _____>	4110
GGAAAAATAA CCTTTTTTATT _____C3	ATCATTAGCT TAGTAATCGA FLANKING	TTTCATAGAC AAAGTATCTG ARM _____>	4140
ATCAGCTAAT TAGTCGATTA _____C3	AGTTAAAGCT TCAATTTCGA FLANKING	GTAAAAGAGA CATTTTCTCT ARM _____>	4170

FIG. 15F-2

GTAAGAATCT CATTCTTAGA _____C3	AGGAATAATA TCCTTATTAT FLANKING	GGTAGGTTAC CCATCCAATG ARM _____>	4200
CTATAGATAT GATATCTATA _____C3	CAAACATATA GTTTGTATAT FLANKING	ATAATGGAAC TATTACCTTG ARM _____>	4230
TATTAAGTAA ATAATTCATT _____C3	TAATGATTTA ATTACTAAAT FLANKING	CATTCTGTTA GTAAGACAAT ARM _____>	4260
TCACCAGCTG AGTGGTCGAC _____C3	TTGTAACCCA AACATTGGGT FLANKING	GTAGTATAAA CATCATATTT ARM _____>	4290
G C _>			4291

FIG. 16

FIG. 16A
FIG. 16B
FIG. 16C

FIG. 16A

AGTACAATAA TCATGTTATT ____C6 LEFT	AAAGTATTAA TTTCATAATT ARM_____	ATAAAAATAC TATTTTTTATG _____>	30
TTACTTACGA AATGAATGCT ____C6 LEFT	AAAAATGACT TTTTTACTGA ARM_____	AATTAGCTAT TTAATCGATA ____>	60
AAAAACCCGG TTTTTGGGCC	GCTGCAGCTC CGACGTCGAG	GAGGATCCTC CTCCTAGGAG	90
TAGATTAACA ATCTAATTGT <C <_____	ATTTTTAAAA TAAAAATTTT N K F _NEF CTL2_	TATTCAGGAT ATAAGTCCTA Y E P H _____	120
GTAATTCTCT CATTAAAGAGA <L E R <_____	AGCTACGTGA TCGATGCACT A V H _NEF CTL2_	TGAAATGCTA ACTTTACGAT H F A L _____	150
ATCTAGAATC TAGATCTTAG <R S D <_____	AAATCTCCAC TTTAGAGGTG F R W _NEF CTL2_	TCCATGATTA AGGTACTAAT E M _____ <_____	180
AACCTAAATA TTGGATTTAT <_____I3L	ATTGTACTTT TAACATGAAA PROMOTER_____	GTAATATAAT CATTATATTA _____	210
GATATATATT CTATATATAA <_____I3L	TTCACTTTAT AAGTGAAATA PROMOTER_____	CTCATTTGAG GAGTAAACTC _____	240
AATAAAAATG TTATTTTTTAC <_____I3L	TTTTTGTTTA AAAAACAAAT PROMOTER_____	ACCACTGCAT TGGTGACGTA _____	270
GATGTCTAAT CTACAGATTA <_____	TAATTAAGCT ATTAATTCGA	ACAAATAGTT TGTTTATCAA	300

FIG. 16B

TCGTTTTTCAC AGCAAAAGTG	CTTGTCTAAT GAACAGATTA	AACTAATTAA TTGATTAATT	330
TTAAGCTTCT AATTCGAAGA _____H6	TTATTCTATA AATAAGATAT PROMOTER_____	CTTAAAAAGT GAATTTTTC _____>	360
GAAAATAAAT CTTTTATTTA _____H6	ACAAAGGTTT TGTTTCCAAG PROMOTER_____	TTGAGGGTTG AACTCCCAAC _____>	390
TGTTAAATTG ACAATTTAAC _____H6	AAAGCGAGAA TTTCGCTCTT PROMOTER_____	ATAATCATAA TATTAGTATT _____>	420
ATTATTTTCAT TAATAAGTA _____H6	TATCGCGATA ATAGCGCTAT PROMOTER_____	TCCGTTAAGT AGGCAATTCA _____>	450
TTGTATCGTA AACATAGCAT _____	ATGGTAGGTT TACCATCCAA M V G > _NEF CTL1_	TTCCAGTAAC AAGGTCATTG F P V T> _____>	480
ACCTCAAGTA TGGAGTTCAT P Q V _____	CCTTTAAGAC GGAAATTCTG P L R _NEF CTL1_	CAATGACTTA GTTACTGAAT P M T Y _____>	510
CAAAGCAGCT GTTTCGTCGA K A A _____	GTAGATCTTT CATCTAGAAA V D L _NEF CTL1_	CTCACTTTTT GAGTGAAAA S H F L _____>	540
AAAAGAAAA TTTTCTTTTT K E K _____	GGAGGTTTAG CCTCCAAATC G G L _NEF CTL1_	AAGGGCTAAT TTCCCGATTA E G L I _____>	570
TCATTCTCAA AGTAAGAGTT H S Q _____	CGAAGACAAG GCTTCTGTTC R R Q _NEF CTL1_	ATATTCTTGA TATAAGAACT D I L D> _____>	600

FIG. 16C

TTTGTGGATT AAACACCTAA L W I _____	TATCATACAC ATAGTATGTG Y H T _NEF CTL1_	AAGGATATTT TTCCTATAAA Q G Y F _____>	630
TCCTGATTGG AGGACTAACC P D W _____	CAGAATTACA GTCTTAATGT Q N Y _NEF CTL1_	CACCAGGACC GTGGTCCTGG T P G P _____>	660
AGGAGTCAGA TCCTCAGTCT G V R _____	TACCCATTAA ATGGGTAATT Y P L _NEF CTL1_	CCTTTGGTTG GGAAACCAAC T F G W _____>	690
GTGCTACAAG CACGATGTTC C Y K _NEF CTL1_	CTAGTACCAT GATCATGGTA L V P> _____>	AATTTTCTC TTAAAAAGAG	720
GAGGAATTCT CTCCTTAAGA	TTTTATTGAT AAAATAACTA	TAACTAGTCA ATTGATCAGT	750
AATGAGTATA T TACTCATAT _____	TATAATTGAA ATATTA ACTT _C6 RIGHT	AAAGTAAAAT TTTCATTTTA ARM_____	780
ATAAATCATA TATTTAGTAT _____C6	TAATAATGAA ATTATTACTT RIGHT ARM	A T _____>	801

FIG. 17A

FIG. 17A-1
FIG. 17A-2

FIG. 17A-1

GAGCTCGCGG CTCGAGCGCC _____C6	CCGCCTATCA GGCGGATAGT FLANKING	AAAGTCTTAA TTTCAGAATT ARM _____>	30
TGAGTTAGGT ACTCAATCCA _____C6	GTAGATAGTA CATCTATCAT FLANKING	TAGATATTAC ATCTATAATG ARM _____>	60
TACAAAGGTA ATGTTTCCAT _____C6	TTCATATTTTC AAGTATAAAG FLANKING	CTATCAATTC GATAGTTAAG ARM _____>	90
TAAAGTAGAT ATTTTCATCTA _____C6	GATATTAATA CTATAATTAT FLANKING	ACTCAAAGAT TGAGTTTCTA ARM _____>	120
GATGATAGTA CTACTATCAT _____C6	GATAATAGAT CTATTATCTA FLANKING	ACGCTCATAT TGCGAGTATA ARM _____>	150
AATGACTGCA TTACTGACGT _____C6	AATTTGGACG TTAAACCTGC FLANKING	GTTACATTT CAAGTGTA ARM _____>	180
TAATCATCAC ATTAGTAGTG _____C6	GCGTTCATAA CGCAAGTATT FLANKING	GTTTCAACTG CAAAGTTGAC ARM _____>	210
CATAGATCAA GTATCTAGTT _____C6	AATCTCACTA TTAGAGTGAT FLANKING	AAAAGATAGC TTTTCTATCG ARM _____>	240
CGATGTATTT GCTACATAAA _____C6	GAGAGAGATT CTCTCTCTAA FLANKING	GGACATCTAA CCTGTAGATT ARM _____>	270
CTACGCTAAA GATGCGATTT _____C6	GAAATTACAG CTTTAATGTC FLANKING	TTATAAATAA AATATTTATT ARM _____>	300
TACATAATGG ATGTATTACC _____C6	ATTTTGTTAT TAAAACAATA FLANKING	CATCAGTTAT GTAGTCAATA ARM _____>	330

FIG. 17A-2

ATTTAACATA TAAATTGTAT _____C6	AGTACAATAA TCATGTTATT flanking	AAAGTATTAA TTTCATAATT arm_____>	360
ATAAAAATAC TATTTTTTATG _____C6	TTACTTACGA AATGAATGCT flanking	AAAAATGACT TTTTTACTGA arm_____> _____>	390
AATTAGCTAT TTAATCGATA _____	AAAAACCCGG TTTTTGGGCC ___Cloning	GCTGCAGCTC CGACGTCGAG sites_____>	420
GAGGAATTCT CTCCTTAAGA _____	TTTTATTGAT AAAATAACTA ___Cloning	TAACTAGTCA ATTGATCAGT sites___> _____>	450
AATGAGTATA TTACTCATAT _____C6	TATAATTGAA ATATTAACTT flanking	AAAGTAAAAT TTTCATTTTA arm_____>	480
ATAAATCATA TATTTAGTAT _____C6	TAATAATGAA ATTATTACTT flanking	ACGAAATATC TGCTTTATAG arm_____>	510
AGTAATAGAC TCATTATCTG _____C6	AGGAACTGGC TCCTTGACCG flanking	AGATTCTTCT TCTAAGAAGA arm_____>	540
TCTAATGAAG AGATTACTTC _____C6	TAAGTACTGC ATTCATGACG flanking	TAAATCTCCA ATTTAGAGGT arm_____>	570
AAATTAGATA TTTAATCTAT _____C6	AAAATGATAC TTTTACTATG flanking	AGCAAATACA TCGTTTATGT arm_____>	600
GCTTCATTCA CGAAGTAAGT _____C6	ACGAATTACC TGCTTAATGG flanking	TTTTAATTTT AAAATTAAAA arm_____>	630

FIG. 17B

FIG. 17B-1

FIG. 17B-1
FIG. 17B-2
FIG. 17B-3

TTCAGACACA AAGTCTGTGT _____C6	CCTTATTACA GGAATAATGT flanking	AACTAACTAA TTGATTGATT arm _____>	660
GTCAGATGAT CAGTCTACTA _____C6	GAGAAAGTAA CTCTTTCATT flanking	ATATAAATTT TATATTTTAA arm _____>	690
AACTTATGGG TTGAATACCC _____C6	TATAATATAA ATATTATATT flanking	TAAAGATTCA ATTTCTAAGT arm _____>	720
TGATATTAAT ACTATAATTA _____C6	AATTTACTTA TTAAATGAAT flanking	ACGATGTTAA TGCTACAATT arm _____>	750
TAGACTTATT ATCTGAATAA _____C6	CCATCAACCC GGTAGTTGGG flanking	CTTCAAACCT GAAGTTTGGG arm _____>	780
TTCTGGATAT AAGACCTATA _____C6	TATAAAATAC ATATTTTATG flanking	CAGTTAATGA GTCAATTACT arm _____>	810
TATTAAAATA ATAATTTTAT _____C6	GATTGTTTAA CTAACAAATT flanking	GAGATGTAAA CTCTACATTT arm _____>	840
TAATTATTTG ATTAATAAAC _____C6	GAGGTAAAGG CTCCATTTC flanking	ATATAAAATT TATATTTTAA arm _____>	870
AGTCTATCTT TCAGATAGAA _____C6	TCACATGGAA AGTGTACCTT flanking	ATGAATTACC TACTTAATGG arm _____>	900
TAATATTAAT ATTATAATTA _____C6	AATTATGATA TTAATACTAT flanking	GGAATTTTTT CCTTAAAAAA arm _____>	930
AGGATTTACA TCCTAAATGT _____C6	GCTGTTATAT CGACAATATA flanking	GTATCAACAA CATAGTTGTT arm _____>	960

FIG. 17B-2

TACAGGCAGA ATGTCCGTCT _____C6	TCTATGGTTA AGATACCAAT flanking	TGGTAAAACA ACCATTTTGT arm_____>	990
CTGTAACGGG GACATTGCCC _____C6	AAGCAGCATT TTCGTGGTAA flanking	CTATGGTAAC GATACCATTG arm_____>	1020
TGGCCTATGT ACCGGATACA _____C6	TTAATAGCCA AATTATCGGT flanking	GATCATTTTA CTAGTAAAAT arm_____>	1050
CTCTATAAAC GAGATATTTG _____C6	ATTTTACCAC TAAAATGGTG flanking	AAATAATAGG TTTATTATCC arm_____>	1080
ATCCTCTAGA TAGGAGATCT _____C6	TATTTAATAT ATAAATTATA flanking	TATATCTAAC ATATAGATTG arm_____>	1110
AACAACAAAA TTGTTGTTTT _____C6	AAATTTAACG TTTAAATTGC flanking	ATGTATGGCC TACATACCGG arm_____>	1140
AGAAGTATTT TCTTCATAAA _____C6	TCTACTAATA AGATGATTAT flanking	AAGATAAAGA TTCTATTTCT arm_____>	1170
TAGTCTATCT ATCAGATAGA _____C6	TATCTACAAG ATAGATGTTC flanking	ATATGAAAGA TATACTTTCT arm_____>	1200
AGATAATGAT TCTATTAGTA _____C6	TTAGTAGTAG AATCATCATC flanking	CTACTAATAT GATGATTATA arm_____>	1230
GGAAAGAAAT CCTTTCTTTA _____C6	GTATACAAAA CATATGTTTT flanking	ACGTGGAAGC TGCACCTTCG arm_____>	1260
TTTTATATTA AAAATATAAT _____C6	AATAGCATAT TTATCGTATA flanking	TACTAGAAGA ATGATCTTCT arm_____>	1290

FIG. 17B-3

AGGAATAAGC TCCTTATTCG _____C6	AATATGCCAA TTATACGGTT flanking	TTATGTCTAA AATACAGATT arm_____>	1440
TATTTTAACT ATAAAATTGA _____C6	TTAGAACTAA AATCTTGATT flanking	AACGTTCTAC TTGCAAGATG arm_____>	1470
CAATACTAAA GTTATGATTT _____C6	AATAGGATAC TTATCCTATG flanking	GTGATAGGCT CACTATCCGA arm_____>	1500
GTTAAAAGCT CAATTTTCGA _____C6	GCAATAAATA CGTTATTTAT flanking	GTAAGGATGT CATTCTACA arm_____>	1530
AGAAGAAATA TCTTCTTTAT _____C6	CTTTGTTCTA GAAACAAGAT flanking	TACCTTCGGA ATGGAAGCCT arm_____>	1560
GGAAAGAACT CCTTTCTTGA _____C6	TTAGAACAAC AATCTTGTTG flanking	TTAAGTTTAA AATTCAAATT arm_____>	1590
TCAAACCTTG AGTTTGAACA _____,C6	ATTTATGAAG TAAATACTTC flanking	GTACC CATGG arm____>	1615

FIG. 17C

TTTAAAATCT AAATTTTAGA _____C6	AGACTTAGTA TCTGAATCAT flanking	TAACAAAACA ATTGTTTTGT arm_____>	1320
GTAAATGCC CAATTTACGG _____C6	AATATCGATT TTATAGCTAA flanking	CTATATTTC GATATAAAGT arm_____>	1350
TCATAACAGT AGTATTGTCA _____C6	AGTACATTAA TCATGTAATT flanking	TCAGTGATAT AGTCACTATA arm_____>	1380
ACTGAAACGA TGACTTTGCT _____C6	TCTACAGACT AGATGTCTGA flanking	CAACTATGCA GTTGATACGT arm_____>	1410

FIG. 18A

FIG. 18A-1
FIG. 18A-2
FIG. 18A-3

FIG. 18A-1

TTAGAAATTA AATCTTTAAT _____C5	TGCATTTTAG ACGTAAAATC LEFT ARM	ATCTTTATAA TAGAAATATT _____	30
GCGGCCGTGA CGCCGGCACT _____	TTAACTAGTC AATTGATCAG _____	ATAAAAACCC TATTTTTGGG >	60
GGGATCGATT CCCTAGCTAA	CTAGACTCGA GATCTGAGCT	GCTATTCAAT CGATAAGTTA	90
TAGGTTGTAA ATCCAACATT <T T L <_____	GTCCCCACCT CAGGGGTGGA G W R POL 2	CAACAGATGT GTTGTCTACA L L H _____	120
TGTCTCAGCT ACAGAGTCGA Q R L E <_____	CCTCTATTTT GGAGATAAAA E I K POL 2	TGTTCTATGC ACAAGATACG T R H _____	150
TGCCCTATTT ACGGGATAAA Q G I E <_____	CTAAGTCAGA GATTCAGTCT L D S POL 2	TCCTACATAC AGGATGTATG G V Y _____	180
AAATCATCCA TTTAGTAGGT L D D M <_____	TGTATTGATA ACATAACTAT Y Q Y POL 2	GATAACTATG CTATTGATAC I V I _____	210
TCTGGATTTT AGACCTAAAA D P N Q <_____	GTTTTCTAAA CAAAAGATTT K R F POL 2	AGGCTCTAAG TCCGAGATTC P E L _____	240
ATTTTTGTCA TAAAAACAGT I K T M <_____	TGCTACTTTG ACGATGAAAC S S Q POL 2	GAATATTGCC CTTATAACGG F I A _____	270

FIG. 18A-2

ATGGCCCAAA TACCGGGTTT D G P K _____ POL1____>	AGTTAAACAA TCAATTTGTT V K Q _____ POL1____>	TGGCCATTGA ACCGGTA ACT W P L _____ ____>	570
CAGAAGAAAA GTCTTCTTTT T E E K _____ POL1____>	AATAAAAGCA TTATTTTCGT I K A _____ POL1____>	TTAGTAGAAA AATCATCTTT L V E _____ ____>	600
TTTGTACAGA AAACATGTCT I C T E _____ POL1____>	GATGGAAAAG CTACCTTTTC M E K _____ POL1____>	GAAGGGAAAA CTTCCCTTTT E G K _____ ____>	630
TTTCAAAAAT AAAGTTTTTA I S K I _____ POL1____>	TGGGCCTTAA ACCCGGAATT G P> _____ POL1____>	TTGATTAGAA AACTAATCTT _____ ____>	660
TTCCTGCAGC AAGGACGTCG _____ 42K	CCAGGTCAAA GGTCCAGTTT _____ 42K	AAAATATAAA TTTTATATTT PROMOTER____>	690
TGATTCACCA ACTAAGTGGT _____ 42K	TCTGATAGAA AGACTATCTT PROMOTER____>	AAAAAATTTA TTTTTTAAAT _____ ____>	720
TTGGGAAGAA AACCCTTCTT _____ 42K	TATGATAATA ATACTATTAT PROMOTER____>	TTTTGGGATT AAAACCCTAA _____ ____>	750
TCAAAATTGA AGTTTTAACT _____ 42K	AAATATATAA TTTATATATT PROMOTER____>	TTACAATATA AATGTTATAT _____ ____>	780
AAATGCCACT TTTACGGTGA M P L _____ ____>	AACAGAAGAA TTGTCTTCTT T E E _____ POL 3____>	GCAGAGCTAG CGTCTCGATC A E L _____ ____>	810
AACTGGCAGA TTGACCGTCT E L A E _____ ____>	AAACAGAGAG TTTGTCTCTC N R E _____ POL 3____>	ATTCTAAAAG TAAGATTTTC I L K> _____ ____>	840

FIG. 18A-3

ATGATTAAAC TACTAATTTG M	CTAAATAATT GATTTATTAA	GTACTTTGTA CATGAAACAT	300
< _____ I3L	PROMOTER _____	_____	
ATATAATGAT TATATTACTA < _____ I3L	ATATATTTTC TATATAAAAG PROMOTER _____	ACTTTATCTC TGAAATAGAG	330
ATTTGAGAAT TAAACTCTTA < _____ I3L	AAAAATGTTT TTTTTACAAA PROMOTER _____	TTGTTTAACC AACAAATTGG	360
ACTGCATGAT TGACGTACTA < _____	GTAAGCTTCT CATTCGAAGA	TTATTCTATA AATAAGATAT	390
	_____	_____ >	
CTTAAAAAGT GAATTTTTC _____ H6	GAAAATAAAT CTTTTATTTA PROMOTER _____	ACAAAGGTTC TGTTTCCAAG	420
		_____ >	
TTGAGGGTTG AACTCCCAAC _____ H6	TGTTAAATTG ACAATTTAAC PROMOTER _____	AAAGCGAGAA TTTCGCTCTT	450
		_____ >	
ATAATCATAA TATTAGTATT _____ H6	ATTATTTTCAT TAATAAAGTA PROMOTER _____	TATCGCGATA ATAGCGCTAT	480
		_____ >	
TCCGTTAAGT AGGCAATTCA _____ H6	TTGTATCGTA AACATAGCAT PROMOTER _____	ATGATTGAGA TACTAACTCT M I E	510
		> _____ >	
CTGTACCAGT GACATGGTCA T V P V	AAAATTAAAG TTTAAATTC K L K POL1 _____	CCAGGAATGG GGTCCTTACC P G M	540
		_____ >	

FIG. 18B

AACCAGTACA TTGGTCATGT E P V H _____	TGGAGTGTAT ACCTCACATA G V Y POL 3	TATGACCCAT ATACTGGGTA Y D P _____>	870
CAAAAGACTT GTTTTCTGAA S K D L _____	AATAGCAGAA TTATCGTCTT I A E POL 3	ATACAGAAGC TATGTCTTCG I Q K _____>	900
AGGGGCAAGG TCCCCGTTCC Q G Q G _____	CCAATGGACA GGTTACCTGT Q W T POL 3	TATCAAATTT ATAGTTTAAA Y Q I _____>	930
ATCAAGAGCC TAGTTCTCGG Y Q E P _____	ATTTAAAAAT TAAATTTTAA F K N POL 3	CTGAAAACAG GACTTTTGTC L K T> _____>	960
GATAATTTTT CTATTAAAAA G> ____>	ATGGATCCTT TACCTAGGAA _____	TTTATAGCTA AAATATCGAT _____>	990
ATTAGTCACG TAATCAGTGC _____C5	TACCTTTGAG ATGGAAACTC RIGHT ARM_	AGTACCACTT TCATGGTGAA _____>	1020
CAGCTACCTC GTCGATGGAG C5 RIGHT	CTTTG GAAAC ARM_>		1035

FIG. 19A-1

FIG. 19A

FIG. 19A-1
FIG. 19A-2
FIG. 19A-3

GAATTGCGGC CTTAACGCCG _____C5	CGCTGAATGT GCGACTTACA FLANKING	TAAATGTTAT ATTTACAATA ARM_____>	30
ACTTTGGATG TGAAACCTAC _____C5	AAGCTATAAA TTCGATATTT FLANKING	TATGCATTGG ATACGTAACC ARM_____>	60
AAAAATAATC TTTTTATTAG _____C5	CATTTAAAGA GTAAATTTCT FLANKING	AAGGATTCAA TTCCTAAGTT ARM_____>	90
ATACTACAAA TATGATGTTT _____C5	ACCTAAGCGA TGGATTCGCT FLANKING	TAATATGTTA ATTATACAAT ARM_____>	120
ACTAAGCTTA TGATTCGAAT _____C5	TTCTTAACGA AAGAATTGCT FLANKING	CGCTTTAAAT GCGAAATTTA ARM_____>	150
ATACACAAAT TATGTGTTTA _____C5	AAACATAATT TTTGTATTAA FLANKING	TTTGTATAAC AAACATATTG ARM_____>	180
CTAACAAATA GATTGTTTAT _____C5	ACTAAAACAT TGATTTTGTA FLANKING	AAAAATAATA TTTTTATTAT ARM_____>	210
AAAGGAAATG TTTCCTTTAC _____C5	TAATATCGTA ATTATAGCAT FLANKING	ATTATTTTAC TAATAAAATG ARM_____>	240
TCAGGAATGG AGTCCTTACC _____C5	GGTTAAATAT CCAATTTATA FLANKING	TTATATCACG AATATAGTGC ARM_____>	270
TGTATATCTA ACATATAGAT _____C5	TACTGTTATC ATGACAATAG FLANKING	GTATACTCTT CATATGAGAA ARM_____>	300
TACAATTACT ATGTTAATGA _____C5	ATTACGAATA TAATGCTTAT FLANKING	TGCAAGAGAT ACGTTCTCTA ARM_____>	330

FIG. 19A-2

AATAAGATTA TTATTCTAAT _____C5	CGTATTTAAG GCATAAATTC FLANKING	AGAATCTTGT TCTTAGAACA ARM_____>	360
CATGATAATT GTACTATTAA _____C5	GGGTACGACA CCCATGCTGT FLANKING	TAGTGATAAA ATCACTATTT ARM_____>	390
TGCTATTTTCG ACGATAAAGC _____C5	CATCGTTACA GTAGCAATGT FLANKING	TAAAGTCAGT ATTCAGTCA ARM_____>	420
TGGAAAGATG ACCTTTCTAC _____C5	GATTTGACAG CTAAACTGTC FLANKING	ATGTAACCTTA TACATTGAAT ARM_____>	450
ATAGGTGCAA TATCCACGTT _____C5	AAATGTTAAA TTTACAATTT FLANKING	TAACAGCATT ATTGTCGTAA ARM_____>	480
CTATCGGAAG GATAGCCTTC _____C5	ATAGGATACC TATCCTATGG FLANKING	AGTTATATTA TCAATATAAT ARM_____>	510
TACAAAAATC ATGTTTTTAG _____C5	ACTGGTTGGA TGACCAACCT FLANKING	TAAAACAGAT ATTTTGTCTA ARM_____>	540
TCTGCAATAT AGACGTTATA _____C5	TCGTAAAAGA AGCATTTTCT FLANKING	TGAAGATTAC ACTTCTAATG ARM_____>	570
TGCGAATTTG ACGCTTAAAC _____C5	TAAACTATGA ATTTGATACT FLANKING	CAATAAAAAG GTTATTTTTC ARM_____>	600
CCATTTATCT GGTAAATAGA _____C5	CAACGACATC GTTGCTGTAG FLANKING	GTGTAATTCT CACATTAAGA ARM_____>	630
TCCATGTTTT AGGTACAAAA _____C5	ATGTATGTGT TACATACACA FLANKING	TTCAGATATT AAGTCTATAA ARM_____>	660

FIG. 19A-3

ATGAGATTAC	TATAAACTTT	TTGTATACTT	690
TACTCTAATG	ATATTTGAAA	AACATATGAA	
_____C5	FLANKING	ARM _____>	
ATATTCCGTA	AACTATATTA	ATCATGAAGA	720
TATAAGGCAT	TTGATATAAT	TAGTACTTCT	
_____C5	FLANKING	ARM _____>	

FIG. 19B

FIG. 19B-1

FIG. 19B-2

FIG. 19B-3

FIG. 19B-1

AAATGAAAAA TTTACTTTTT _____C5	GTATAGAAGC CATATCTTCG FLANKING	TGTTACGAG ACAAGTGCTC ARM_____>	750
CGGTTGTTGA GCCAACAACT _____C5	AAACAACAAA TTTGTTGTTT FLANKING	ATTATACATT TAATATGTAA ARM_____>	780
CAAGATGGCT GTTCTACCGA _____C5	TACATATACG ATGTATATGC FLANKING	TCTGTGAGGC AGACACTCCG ARM_____>	810
TATCATGGAT ATAGTACCTA _____C5	AATGACAATG TTACTGTTAC FLANKING	CATCTCTAAA GTAGAGATTT ARM_____>	840
TAGGTTTTTG ATCCAAAAAC _____C5	GACAATGGAT CTGTTACCTA FLANKING	TCGACCCTAA AGCTGGGATT ARM_____>	870
CACGGAATAT GTGCCTTATA _____C5	GGTACTCTAC CCATGAGATG FLANKING	AATCTCCTCT TTAGAGGAGA ARM_____>	900
TGAAATGGCT ACTTTACCGA _____C5	GTAATGTTCA CATTACAAGT FLANKING	AGAATACCGA TCTTATGGCT ARM_____>	930
GGCTATAAAA CCGATATTTT _____C5	ATCTTGATGA TAGAACTACT FLANKING	GGTATGGAGC CCATACCTCG ARM_____>	960
TAAACCTGTA ATTTGGACAT _____C5	GTTACTGAAT CAATGACTTA FLANKING	GCACAACTTC CGTGTTGAAG ARM_____>	990
TTGTCTGCAT AACAGACGTA _____C5	GATGCGGTGT CTACGCCACA FLANKING	TGAGAGACGA ACTCTCTGCT ARM_____>	1020
CTACAAAATA GATGTTTTAT _____C5	GTGAAAGATC CACTTTCTAG FLANKING	TGTTGAAGAA ACAACCTCTT ARM_____>	1050

FIG. 19B-2

TAAGTATGTA ATTGATACAT _____C5	AACAATGTTC TTGTTACAAG FLANKING	TTTACAGCGG AAATGTCGCC ARM_____>	1080
AGGCTTTACT TCCGAAATGA _____C5	CCTTTGTGTT GGAAACACAA FLANKING	TGGCAGCTTA ACCGTCGAAT ARM_____>	1110
CCTTAACAAA GGAATTGTTT _____C5	GTAAATTTGG CAATTAAACC FLANKING	TTAAACTTCT AATTGAAGA ARM_____>	1140
ATTGGCTCAT TAACCGAGTA _____C5	TCGGCGGATG AGCCGCCTAC FLANKING	TAGATATTTT ATCTATAAAG ARM_____>	1170
AAACACGGAT TTTGTGCCTA _____C5	CGGTAACTC GCCAATTGAG FLANKING	CTCTACATAT GAGATGTATA ARM_____>	1200
AGCCGTATCA TCGGCATAGT _____C5	AATAAAAATT TTATTTTAA FLANKING	TAACAATGGT ATTGTTACCA ARM_____>	1230
TAAACTTCTA ATTTGAAGAT _____C5	TTGAACAAAG AACTTGTTTC FLANKING	GTGCTGATAC CACGACTATG ARM_____>	1260
TGACTTGCTG ACTGAACGAC _____C5	GATAACATGG CTATTGTACC FLANKING	GACGTACTCC CTGCATGAGG ARM_____>	1290
TTTAATGATC AAATTACTAG _____C5	GCTGTACAAT CGACATGTTA FLANKING	CTGGAAATAT GACCTTTATA ARM_____>	1320
TGAAATATGT ACTTTATACA _____C5	AGCACACTAC TCGTGTGATG FLANKING	TTAAAAAAA AATTTTTTTT ARM_____>	1350
TAAAATGTCC ATTTTACAGG _____C5	AGAACTGGGA TCTTGACCCT FLANKING	AAAATTGATC TTTTAACTAG ARM_____>	1380

FIG. 19B-3

TTGCCAGCTG AACGGTCGAC _____C5	TAATTCATGG ATTAAGTACC FLANKING	TAGAAAAGAA ATCTTTTCTT ARM _____>	1410
GTGCTCAGGC CACGAGTCCG _____C5	TACTTTTCAA ATGAAAAGTT FLANKING	CAAAGGAGCA GTTTCCTCGT ARM _____>	1440
GATGTAAACT CTACATTTGA _____C5	ACATCTTTGA TGTAGAACT FLANKING	AAGAAATGGA TTCTTTACCT ARM _____>	1470
AAATCATATA TTTAGTATAT _____C5	CTGTTTTGGA GACAAAACCT FLANKING	ATTGATTAAA TAACTAATT ARM _____>	1500
GAAAGTTACT CTTTCAATGA ___C5 FLANK	CTGAGACACA GACTCTGTGT ING ARM _____>		1520

FIG. 19C

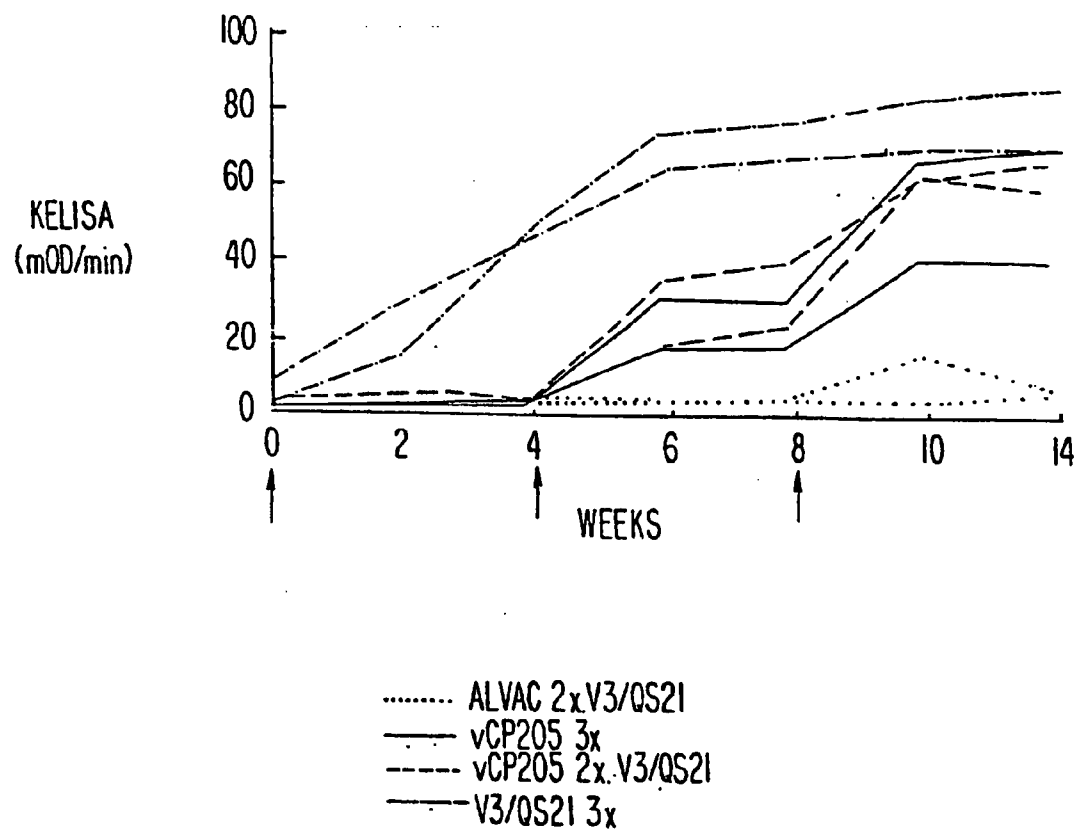
FIG. 19C-1
FIG. 19C-2
FIG. 19C-3

FIG. 19C-1

AAAGAGGTAG TTTCTCCATC _____C5	CTGAAGTGGT GACTTCACCA FLANKING	ACTCTCAAAG TGAGAGTTTC ARM _____>	1550
GTACGTGACT CATGCACTGA _____	AATTAGCTAT TTAATCGATA CLONING	AAAAAGGATC TTTTTCCTAG SITES _____>	1580
CGGTACCCTC GCCATGGGAG _____	GAGTCTAGAA AGCTAGGGCC CLONING	TCGATCCCGG CAAAAATACT SITES _____>	1610
GTTTTTATGA CTCAGATCTT _____	CTAGTTAATC GATCAATTAG CLONING	ACGGCCGCTT TGCCGGCGAA SITES ____>	1640
ATAAAGATCT TATTTCTAGA _____C5	AAAATGCATA TTTTACGTAT FLANKING	ATTTCTAAAT TAAAGATTTA ARM _____>	1670
AATGAAAAAA TTACTTTTTT _____C5	AAGTACATCA TTCATGTAGT FLANKING	TGAGCAACGC ACTCGTTGCG ARM _____>	1700
GTTAGTATAT CAATCATATA _____C5	TTTACAATGG AAATGTTACC FLANKING	AGATTAACGC TCTAATTGCG ARM _____>	1730
TCTATACCGT AGATATGGCA _____C5	TCTATGTTTA AGATACAAAT FLANKING	TTGATTCAGA AACTAAGTCT ARM _____>	1760
TGATGTTTTA ACTACAAAAT _____C5	GAAAAGAAAG CTTTTCTTTC FLANKING	TTATTGAATA AATAACTTAT ARM _____>	1790
TGAAAACCTT ACTTTTGAAA _____C5	AATGAAGATG TTACTTCTAC FLANKING	AAGATGACGA TTCTACTGCT ARM _____>	1820

FIG. 19C-2

CGATGATTAT GCTACTAATA _____C5	TGTTGTAAAT ACAACATTTA FLANKING	CTGTTTTAGA GACAAAATCT ARM _____>	1850
TGAAGAAGAT ACTTCTTCTA _____C5	GACGCGCTAA CTGCGCGATT FLANKING	AGTATACTAT TCATATGATA ARM _____>	1880
GGTTACAAAG CCAATGTTTC _____C5	TATAAGTCTA ATATTCAGAT FLANKING	TACTACTAAT ATGATGATTA ARM _____>	1910
GGCGACTTGT CCGCTGAACA _____C5	GCAAGAAGGT CGTTCTTCCA FLANKING	ATAGTATAGT TATCATATCA ARM _____>	1940
GAAAATGTTG CTTTTACAAC _____C5	TTAGATTATG AATCTAATAC FLANKING	ATTATGAAAA TAATACTTTT ARM _____>	1970
ACCAAATAAA TGGTTTATTT _____C5	TCAGATCCAT AGTCTAGGTA FLANKING	ATCTAAAGGT TAGATTTCCA ARM _____>	2000
ATCTCCTTTG TAGAGGAAAC _____C5	CACATAATTT GTGTATTAAA FLANKING	CATCTATTCC GTAGATAAGG ARM _____>	2030
TAGTTTAGAA ATCAAATCTT _C5 FLANK	TACCTGCAG ATGGACGTC ING ARM ____>		2049

FIG. 20

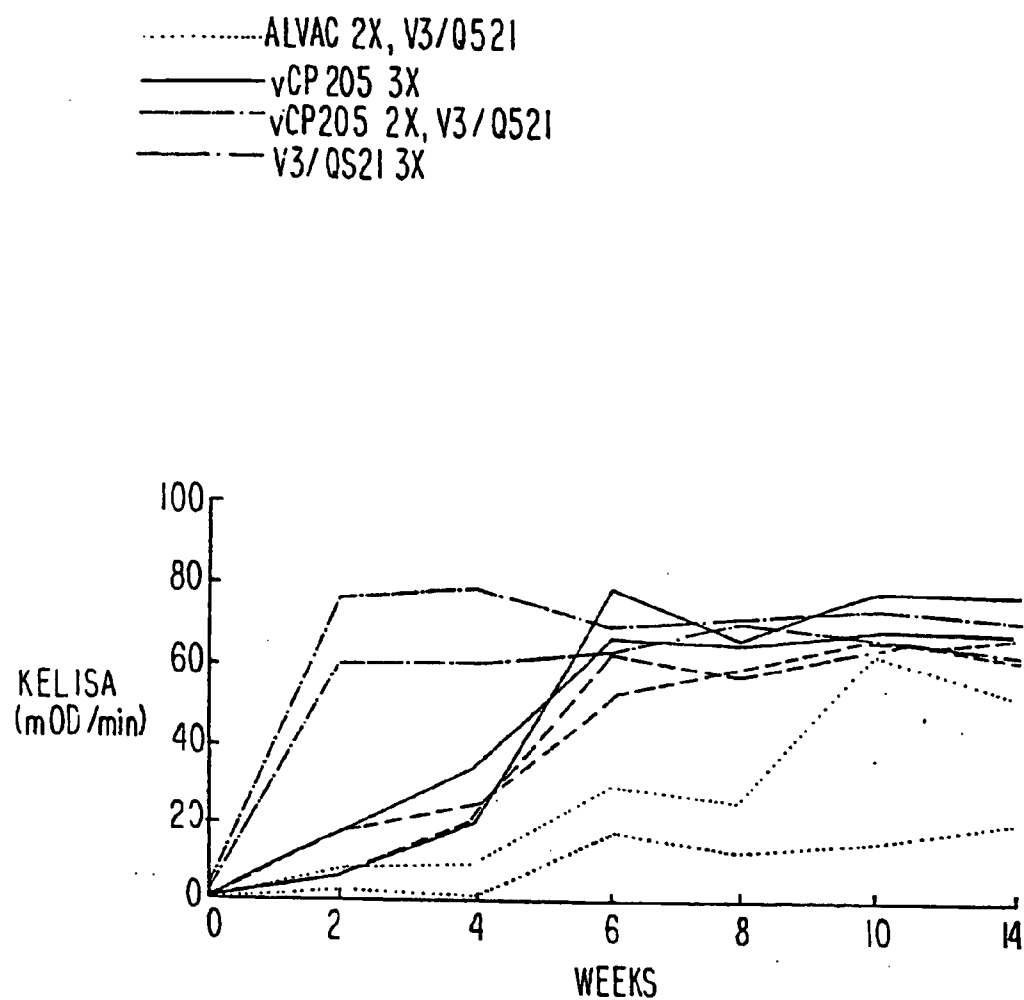
*FIG. 21*

FIG. 22

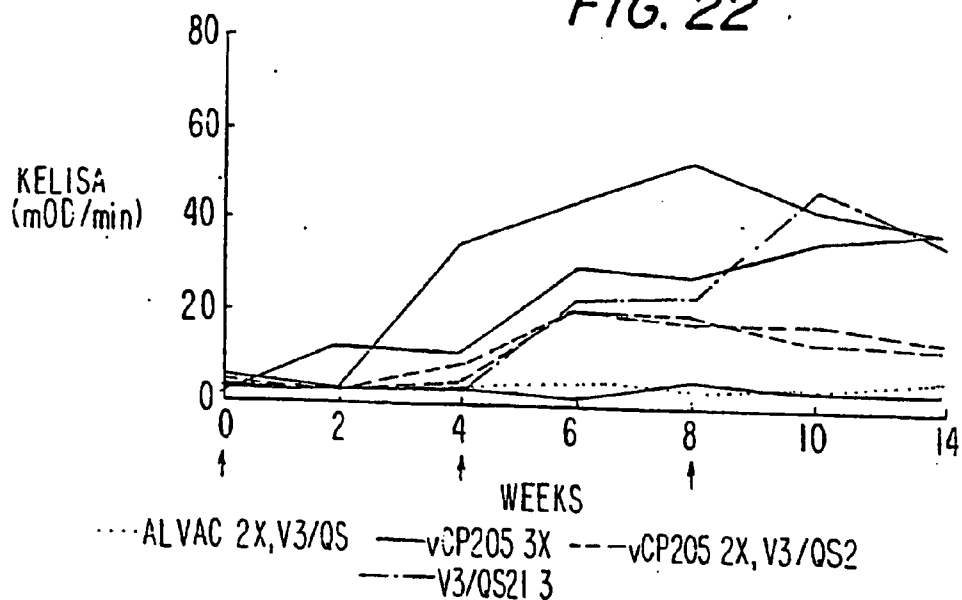
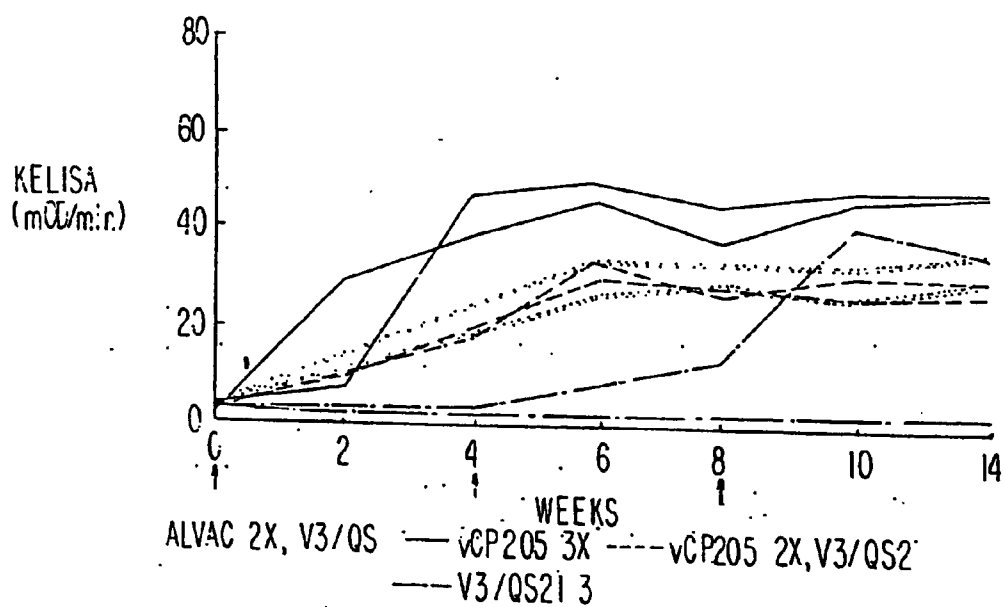


FIG. 23



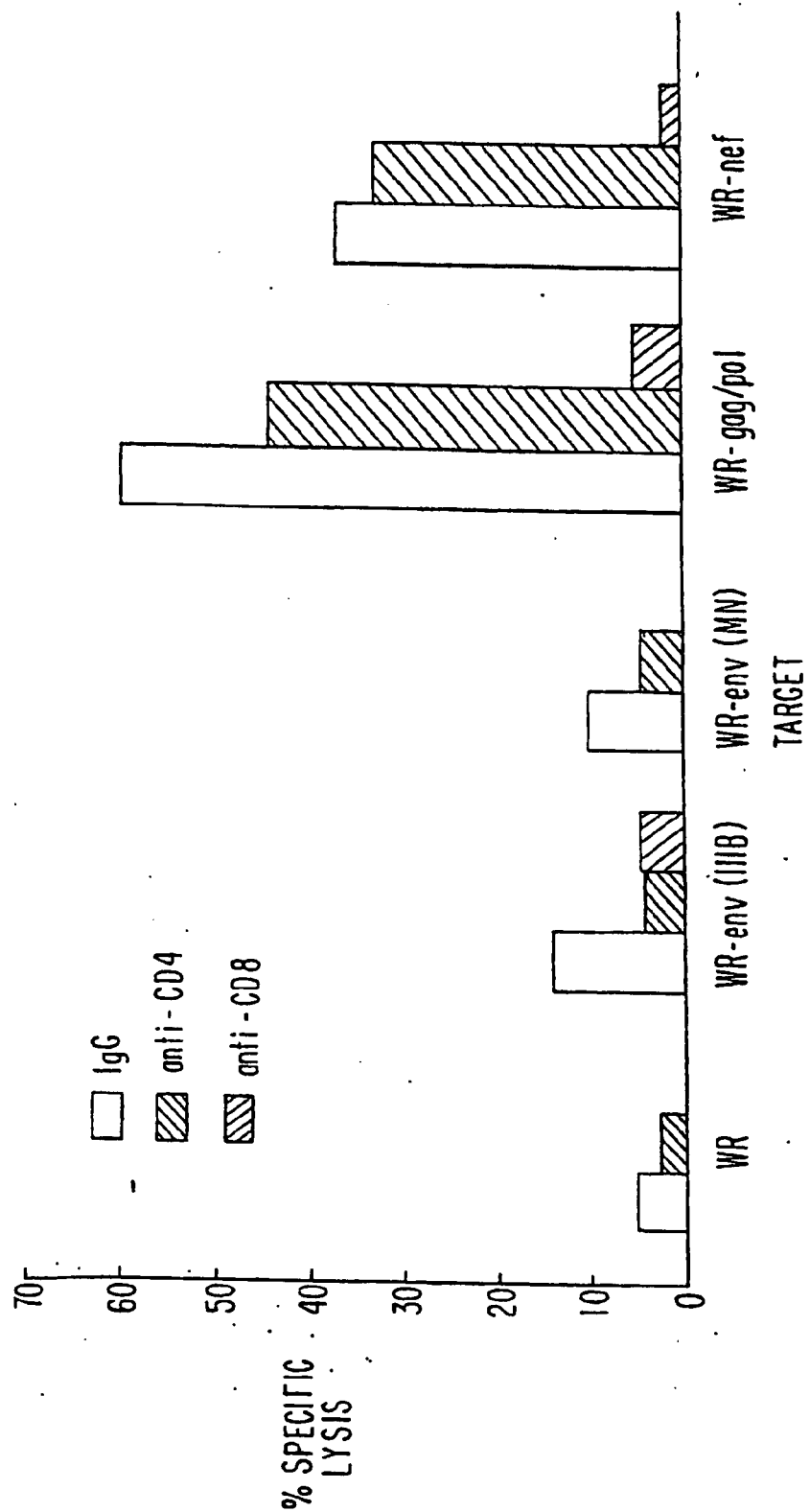


FIG. 24

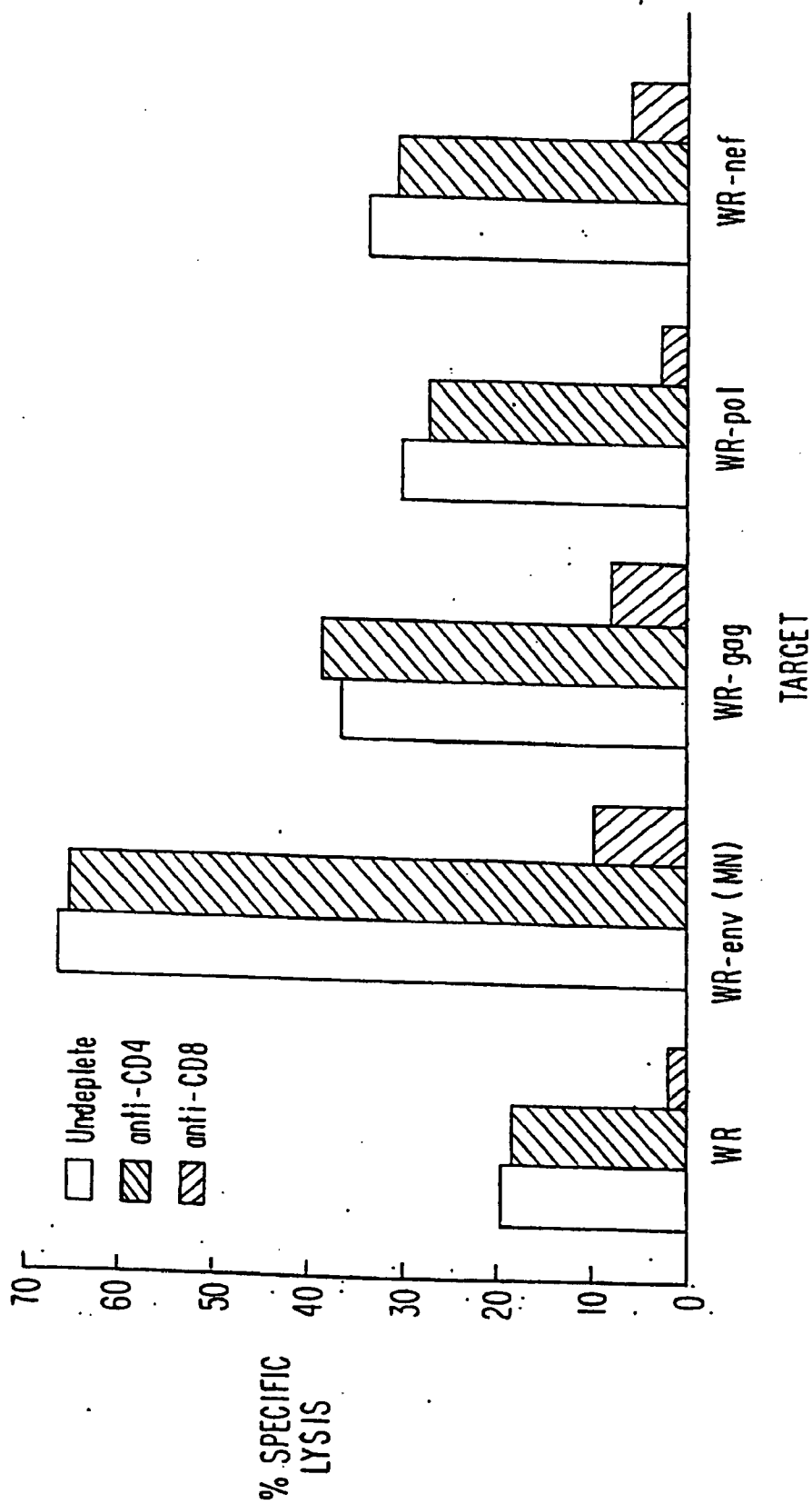


FIG. 25

FIG. 26A

FIG. 26A-1

FIG. 26A-1
FIG. 26A-2
FIG. 26A-3

pHIV59/vCP1307

AGAAAGTTAC TCTTTCAATG _____ C5	TCTGAGACAC AGACTCTGTG FLANKING	AAAAGAGGTA TTTTCTCCAT ARM _____>	30
GCTGAAGTGG CGACTTCACC _____ C5 FLANK	TACTCTCAAA ATGAGAGTTT ING ARM _____>	GGTACGTGAC CCATGCACTG	60
TAATTAGCTA ATTAATCGAT	TAAAAAGGAT ATTTTTCCTA	CCGGGTAAAT GGCCCAATTA	90
TAATTAGTCA ATTAATCAGT	TCAGGCAGGG AGTCCGTCCC	CGAGAACGAG GCTCTTGCTC	120
ACTATCTGCT TGATAGACGA	CGTTAATTAA GCAATTAATT	TTAGAGCTTC AATCTCGAAG _____>	150
TTTATTCTAT AAATAAGATA _____ H6	ACTTAAAAAG TGAATTTTTC PROMOTER _____	TGAAAATAAA ACTTTTATTT _____>	180
TACAAAGGTT ATGTTTCCAA _____ H6	CTTGAGGGTT GAACTCCCAA PROMOTER _____	GTGTAAATT CACAATTTAA _____>	210
GAAAGCGAGA CTTTCGCTCT _____ H6	AATAATCATA TTATTAGTAT PROMOTER _____	AATTATTTCA TTAATAAAGT _____>	240
TTATCGCGAT AATAGCGCTA _____ H6	ATGCGTTAAG TACGCAATTC PROMOTER _____	TTTGTATCGT AAACATAGCA _____>	270
ATATGAAAGA TATACTTTCT M K E	GCAGAAGACA CGTCTTCTGT Q K T	GTGGCAATGA CACC GTTACT V A M>	300
-> _____ HIV1	(MN) GP120	GENE _____>	09

FIG. 26A-2

GAGTGAAGGA CTCACTTCCT R V K E _____HIV1	GAAATATCAG CTTTATAGTC K Y Q (MN) GP120	CACTTGTGGA GTGAACACCT H L W> GENE _____>	330 19
GATGGGGGTG CTACCCCCAC R W G W _____HIV1	GAGATGGGGC CTCTACCCCG R W G (MN) GP120	ACCATGCTCC TGGTACGAGG T M L> GENE _____>	360 29
TTGGGATGTT AACCCTACAA L G M L _____HIV1	GATGATCTGT CTACTAGACA M I C (MN) GP120	AGTGCTACAG TCACGATGTC S A T> GENE _____>	390 39
AAAAATTGTG TTTTTAAACAC E K L W _____HIV1	GGTCACAGTC CCAGTGTGAG V T V (MN) GP120	TATTATGGGG ATAATACCCC Y Y G> GENE _____>	420 49
TACCTGTGTG ATGGACACAC V P V W _____HIV1	GAAAGAAGCA CTTTCTTCGT K E A (MN) GP120	ACCACCACTC TGGTGGTGAG T T T> GENE _____>	450 59
TATTTTGTGC ATAAAACACG L F C A _____HIV1	ATCAGATGCT TAGTCTACGA S D A (MN) GP120	AAAGCATATG TTTCGTATAC K A Y> GENE _____>	480 69
ATACAGAGGT TATGTCTCCA D T E V _____HIV1	ACATAATGTT TGTATTACAA H N V (MN) GP120	TGGGCCACAC ACCCGGTGTG W A T> GENE _____>	510 79
ATGCCTGTGT TACGGACACA H A C V _____HIV1	ACCCACAGAC TGGGTGTCTG P T D (MN) GP120	CCCAACCCAC GGGTGGGGTG P N P> GENE _____>	540 89
AAGAAGTAGA TTCTTCATCT Q E V E _____HIV1	ATTGGTAAAT TAACCATTTA L V N (MN) GP120	GTGACAGAAA CACTGTCTTT V T E> GENE _____>	570 99

FIG. 26A-3

ATTTTAACAT	GTGGA AAAAT	AACATGGTAG	600
TAAAATTGTA	CACCTTTTTA	TTGTACCATC	
N F N M	W K N	N M V>	109
_____HIV1	(MN) GP120	GENE_____>	
AACAGATGC	ATGAGGATATA	ATCAGTTTAT	630
TTGTCTACG	TACTCCTATAT	TAGTCAAATA	
E Q M H	E D I	I S L>	119
_____HIV1	(MN) GP120	GENE_____>	
GGGATCAAAG	CCTAAAGCCA	TGTGTAAAAT	660
CCCTAGTTTC	GGATTTTCGGT	ACACATTTTA	
W D Q S	L K P	C V K>	129
_____HIV1	(MN) GP120	GENE_____>	
TAACCCCACT	CTGTGT TACT	TTAAATTGCA	690
ATTGGGGTGA	GACACAATGA	AATTTAACGT	
L T P L	C V T	L N C>	139
_____HIV1	(MN) GP120	GENE_____>	
CTGATTTGAG	GAATACTACT	AATACCAATA	720
GACTAAACTC	CTTATGATGA	TTATGGTTAT	
T D L R	N T T	N T N>	149
_____HIV1	(MN) GP120	GENE_____>	

FIG. 26B

FIG. 26B-1
FIG. 26B-2
FIG. 26B-3

FIG. 26B-1

pHIV59/vCP1307

ATAGTACTGC	TAATAACAAT	AGTAATAGCG	750
TATCATGACG	ATTATTGTTA	TCATTATCGC	
N S T A	N N N	S N S>	159
_____HIV1	(MN) GP120	GENE_____>	
AGGGAACAAT	AAAGGGAGGA	GAAATGAAAA	780
TCCCTTGTTA	TTTCCCTCCT	CTTTACTTTT	
E G T I	K G G	E M K>	169
_____HIV1	(MN) GP120	GENE_____>	
ACTGCTCTTT	CAATATCACC	ACAAGCATAA	810
TGACGAGAAA	GTTATAGTGG	TGTTCGTATT	
N C S F	N I T	T S I>	179
_____HIV1	(MN) GP120	GENE_____>	
GAGATAAGAT	GCAGAAAGAA	TATGCACTTC	840
CTCTATTCTA	CGTCTTTCTT	ATACGTGAAG	
R D K M	Q K E	Y A L>	189
_____HIV1	(MN) GP120	GENE_____>	
TTTATAAACT	TGATATAGTA	TCAATAAATA	870
AAATATTTGA	ACTATATCAT	AGTTATTTAT	
L Y K L	D I V	S I N>	199
_____HIV1	(MN) GP120	GENE_____>	
ATGATAGTAC	CAGCTATAGG	TTGATAAGTT	900
TACTATCATG	GTCGATATCC	AACTATTCAA	
N D S T	S Y R	L I S>	209
_____HIV1	(MN) GP120	GENE_____>	
GTAATACCTC	AGTCATTACA	CAAGCTTGTC	930
CATTATGGAG	TCAGTAATGT	GTTCGAACAG	
C N T S	V I T	Q A C>	219
_____HIV1	(MN) GP120	GENE_____>	
CAAAGATATC	CTTTGAGCCA	ATTCCCATAC	960
GTTTCTATAG	GAAACTCGGT	TAAGGGTATG	
P K I S	F E P	I P I>	229
_____HIV1	(MN) GP120	GENE_____>	

FIG. 26B-2

ACTATTGTGC	CCCGGCTGGT	TTTGCGATTC	990
TGATAACACG	GGGCCGACCA	AAACGCTAAG	
H Y C A	P A G	F A I>	239
_____HIV1	(MN) GP120	GENE_____>	
TAAAGTGTA	CGATAAAAAG	TTCAGTGGAA	1020
ATTTACACATT	GCTATTTTTC	AAGTCACCTT	
L K C N	D K K	F S G>	249
_____HIV1	(MN) GP120	GENE_____>	
AAGGATCATG	TAAAAATGTC	AGCACAGTAC	1050
TTCCTAGTAC	ATTTTTACAG	TCGTGTCATG	
K G S C	K N V	S T V>	259
_____HIV1	(MN) GP120	GENE_____>	
AATGTACACA	TGGAATTAGG	CCAGTAGTAT	1080
TTACATGTGT	ACCTTAATCC	GGTCATCATA	
Q C T H	G I R	P V V>	269
_____HIV1	(MN) GP120	GENE_____>	
CAACTCAACT	GCTGTTAAAT	GGCAGTCTAG	1110
GTTGAGTTGA	CGACAATTTA	CCGTCAGATC	
S T Q L	L L N	G S L>	279
_____HIV1	(MN) GP120	GENE_____>	
CAGAAGAAGA	GGTAGTAATT	AGATCTGAGA	1140
GTCTTCTTCT	CCATCATTA	TCTAGACTCT	
A E E E	V V I	R S E>	289
_____HIV1	(MN) GP120	GENE_____>	
ATTTCAATGA	TAATGCTAAA	ACCATCATAG	1170
TAAAGTTACT	ATTACGATTT	TGGTAGTATC	
N F N' D	N A K	T I I>	299
_____HIV1	(MN) GP120	GENE_____>	
TACATCTGAA	TGAATCTGTA	CAAATTAATT	1200
ATGTAGACTT	ACTTAGACAT	GTTTAATTAA	
V H L N	E S V	Q I N>	309
_____HIV1	(MN) GP120	GENE_____>	
GTACAAGACC	CAACTACGAG	CTCGACAAAT	1230
CATGTTCTGG	GTTGATGCTC	GAGCTGTTTA	
C T R P	N Y E	L D K	319
_____GP120	GENE____<KAT	EPITOPE_____>	

FIG. 26B-3

GGGCCCATAT	AGGACCAGGG	AGAGAATTGG	1260
CCCGGGTATA	TCCTGGTCCC	TCTCTTAACC	
W A H I	G P G	R E L	329
____><____GP120 GENE____		____><____	
ATAAGTGGGC	GAATATAATA	GGAACTATAA	1290
TATTCACCCG	CTTATATTAT	CCTTGATATT	
D K W A	N I I	G T I>	339
KAT EPITOP	><____GP	120 GENE____>	
GACAAGCACA	TTGTAACATT	AGTAGAGCAA	1320
CTGTTTCGTGT	AACATTGTAA	TCATCTCGTT	
R Q A H	C N I	S R A>	349
____HIV1	(MN) GP120	GENE____>	
AATGGAATGA	CACTTTAAGA	CAGATAGTTA	1350
TTACCTTACT	GTGAAATTCT	GTCTATCAAT	
K W N D	T L R	Q I V>	359
____HIV1	(MN) GP120	GENE____>	
GCAAATTAAA	AGAACAATTT	AAGAATAAAA	1380
CGTTTAATTT	TCTTGTTAAA	TTCTTATTTT	
S K L K	E Q F	K N K>	369
____HIV1	(MN) GP120	GENE____>	
CAATAGTCTT	TAATCAATCC	TCAGGAGGGG	1410
GTTATCAGAA	ATTAGTTAGG	AGTCCTCCCC	
T I V F	N Q S	S G G>	379
____HIV1	(MN) GP120	GENE____>	
ACCCAGAAAT	TGTAATGCAC	AGTTTTAATT	1440
TGGGTCTTTA	ACATTACGTG	TCAAATTTAA	
D P E' I	V M H	S F N>	389
____HIV1	(MN) GP120	GENE____>	

FIG. 26C-1

FIG. 26C

FIG. 26C-1

FIG. 26C-2

FIG. 26C-3

pHIV59/vCP1307

GTGGAGGGGA CACCTCCCCT C G G E _____HIV1	ATTCTTCTAC TAAGAAGATG F F Y (MN) GP120	TGTAATTCAT ACATTAAGTA C N S> GENE _____>	1470 399
CACCACTGTT GTGGTGACAA S P L F _____HIV1	TAATAGTACT ATTATCATGA N S T (MN) GP120	TGGAATGGTA ACCTTACCAT W N G> GENE _____>	1500 409
ATAATACTTG TATTATGAAC N N T W _____HIV1	GAATAATACT CTTATTATGA N N T (MN) GP120	ACAGGGTCAA TGTCCCAGTT T G S> GENE _____>	1530 419
ATAACAATAT TATTGTTATA N N N I _____HIV1	CACACTTCAA GTGTGAAGTT T L Q (MN) GP120	TGCAAAATAA ACGTTTTATT C K I> GENE _____>	1560 429
AACAAATTAT TTGTTTAATA K Q I I _____HIV1	AAACATGTGG TTTGTACACC N M W (MN) GP120	CAGGAAGTAG GTCCTTCATC Q E V> GENE _____>	1590 439
GAAAAGCAAT CTTTTCGTTA G K A I _____HIV1	ATATGCCCCCT TATACGGGGA Y A P (MN) GP120	CCCATTGAAG GGGTAACCTC P I E> GENE _____>	1620 449
GACAAATTAG CTGTTTAATC G Q I R _____HIV1	ATGTTTCATCA TACAAGTAGT C S S (MN) GP120	AATATTACAG TTATAATGTC N I T> GENE _____>	1650 459
GGCTACTATT CCGATGATAA G L L L _____HIV1	AACAAGAGAT TTGTTCTCTA T R D (MN) GP120	GGTGGTAAGG CCACCATTCC G G K> GENE _____>	1680 469
ACACGGACAC TGTGCTGTG D T D T _____HIV1	GAACGACACC CTTGCTGTGG N D T (MN) GP120	GAGATCTTCA CTCTAGAAGT E I F> GENE _____>	1710 479

FIG. 26C-2

GACCTGGAGG	AGGAGATATG	AGGGACAATT	1740
CTGGACCTCC	TCCTCTATAC	TCCCTGTTAA	
R P G G	G D M	R D N>	489
_____HIV1	(MN) GP120	GENE_____>	
GGAGAAGTGA	ATTATATAAA	TATAAAGTAG	1770
CCTCTTCACT	TAATATATTT	ATATTTTCATC	
W R S E	L Y K	Y K V>	499
_____HIV1	(MN) GP120	GENE_____>	
TAACAATTGA	ACCATTAGGA	GTAGCACCCA	1800
ATTGTTAACT	TGGTAATCCT	CATCGTGGGT	
V T I E	P L G	V A P>	509
_____HIV1	(MN) GP120	GENE_____>	
CCAAGGCAAA	GAGAAGAGTG	GTGCAGAGAG	1830
GGTTCCGTTT	CTCTTCTCAC	CACGTCTCTC	
T K A K	R R V	V Q R>	519
_____HIV1	(MN) GP120	GENE_____>	
AAAAAAGATT	ATTCATAATG	ATAGTAGGAG	1860
TTTTTTCTAA	TAAGTATTAC	TATCATCCTC	
E K R L	F I M	I V G>	529
_____	TRANSMEMBR	ANE REGION>	
GCTTGGTAGG	TTTAAGAATA	GTTTTTGCTG	1890
CGAACCATCC	AAATTCTTAT	CAAAAACGAC	
G L V G	L R I	V F A>	539
_____HIV1 TRAN	SMEMBRANE	REGION_____>	
TACTCTCTGT	AGTGAATAGA	GTTAGGCAGG	1920
ATGAGAGACA	TCACTTATCT	CAATCCGTCC	
V L S V	V N R	V R Q>	549
_____HIV1 TRAN	SMEMBRANE	REGION_____>	
GATAATTTTT	ATTCTAGAAT	CGATCCCGGG	1950
CTATTAAAAA	TAAGATCTTA	GCTAGGGCCC	
G *>			550
_____>			
TTTTTATGAC	TAGTTAATCA	CGGCCGCTTA	1980
AAAAATACTG	ATCAATTAGT	GCCGGCGAAT	

FIG. 26C-3

TAAAGATCTA	AAATGCATAA	TTTCTAAATA	2010
ATTTCTAGAT	TTTACGTATT	AAAGATTTAT	
_____C5	FLANKING	ARM_____>	
ATGAAAAAAAA			2020
TACTTTTTTT			
_____>			

FIG.27

FIG.27a
FIG.27b

#12/98/95028007 FLI-H FLI-Height

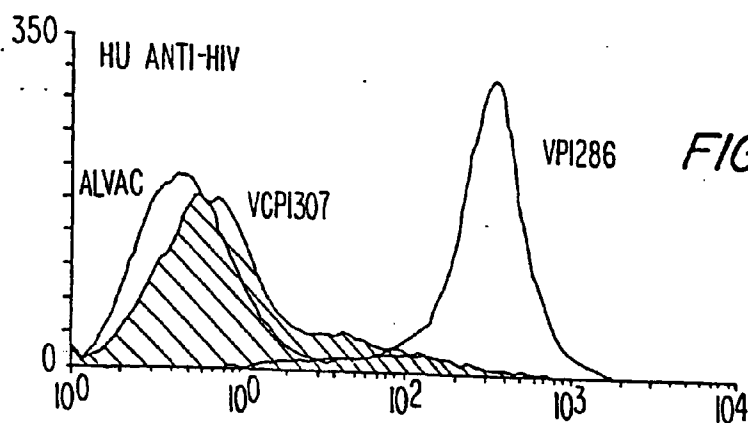


FIG.27a

#12/98/95028014 FLI-H FLI-Height
HU MAB- ELDKWA

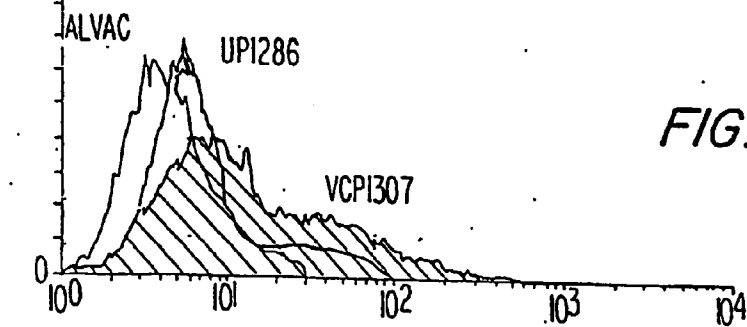


FIG.27b

FIG. 28A

FIG. 28A-1

FIG. 28A-2

FIG. 28A-3

FIG. 28A-1

pHIV60/vP1313

TACTTTGTAA ATGAAACATT _____14L	TATAATGATA ATATTACTAT FLANKING	TATATTTTCA ATATAAAAGT ARM _____>	30
CTTTATCTCA GAAATAGAGT _____14L	TTTGAGAATA AAACTCTTAT FLANKING	AAAAGATCAC TTTTCTAGTG ARM _____>	60
AAAAATTAAC TTTTTAATTG	TAATCAGGAT ATTAGTCCTA	CCGGGTAAAT GGCCAATTA	90
TAATTAGTCA ATTAATCAGT	TCAGGCAGGG AGTCCGTCCC	CGAGAACGAG GCTCTTGCTC	120
ACTATCTGCT TGATAGACGA	CGTTAATTAA GCAATTAATT	TTAGAGCTTC AATCTCGAAG _____>	150
TTTATTCTAT AAATAAGATA _____H6	ACTTAAAAAG TGAATTTTTC PROMOTER _____	TGAAAATAAA ACTTTTATTT _____>	180
TACAAAGGTT ATGTTTCCAA _____H6	CTTGAGGGTT GAACTCCCAA PROMOTER _____	GTGTAAATT CACAATTAA _____>	210
GAAAGCGAGA CTTTCGGTCT _____H6	AATAATCATA TTATTAGTAT PROMOTER _____	AATTATTTCA TTAATAAAGT _____>	240
TTATCGCGAT AATAGCGCTA _____H6	ATGCGTTAAG TACGCAATTC PROMOTER _____	TTTGTATCGT AAACATAGCA _____>	270
ATATGAAAGA TATACTTTCT M K E -> _____HIV1	GCAGAAGACA CGTCTTCTGT Q K T (MN) GP120	GTGGCAATGA CACCGTTACT V A M> GENE _____>	300

FIG. 28A-2

GAGTGAAGGA CTCACTTCCT R V K E _____ HIV1	GAAATATCAG CTTTATAGTC K Y Q (MN) GP120	CACTTGTGGA GTGAACACCT H L W> GENE _____>	330
GATGGGGGTG CTACCCCCAC R W G W _____ HIV1	GAGATGGGGC CTCTACCCCG R W G (MN) GP120	ACCATGCTCC TGGTACGAGG T M L> GENE _____>	360
TTGGGATGTT AACCCTACAA L G M L _____ HIV1	GATGATCTGT CTACTAGACA M I C (MN) GP120	AGTGCTACAG TCACGATGTC S A T> GENE _____>	390
AAAAATTGTG TTTTTAACAC E K L W _____ HIV1	GGTCACAGTC CCAGTGTGAG V T V (MN) GP120	TATTATGGGG ATAATACCCC Y Y G> GENE _____>	420
TACCTGTGTG ATGGACACAC V P V W _____ HIV1	GAAAGAAGCA CTTTCTTCGT K E A (MN) GP120	ACCACCACTC TGGTGGTGAG T T T> GENE _____>	450
TATTTTGTGC ATAAAACACG L F C A _____ HIV1	ATCAGATGCT TAGTCTACGA S D A (MN) GP120	AAAGCATATG TTTCGTATAC K A Y> GENE _____>	480
ATACAGAGGT TATGTCTCCA D T E V _____ HIV1	ACATAATGTT TGTATTACAA H N V (MN) GP120	TGGGCCACAC ACCCGGTGTG W A T> GENE _____>	510
ATGCCTGTGT TACGGACACA H A C V _____ HIV1	ACCCACAGAC TGGGTGTCTG P T D (MN) GP120	CCCAACCCAC GGGTTGGGTG P N P> GENE _____>	540
AAGAAGTAGA TTCTTCATCT Q E V E _____ HIV1	ATTGGTAAAT TAACCATTTA L V N (MN) GP120	GTGACAGAAA CACTGTCTTT V T E> GENE _____>	570

FIG. 28A-3

ATTTTAACAT TAAAATTGTA N F N M _____HIV1	GTGGAAAAAT CACCTTTTTA W K N (MN) GP120	AACATGGTAG TTGTACCATC N M V> GENE_____>	600
AACAGATGCA TTGTCTACGT E Q M H _____HIV1	TGAGGATATA ACTCCTATAT E D I (MN) GP120	ATCAGTTTAT TAGTCAAATA I S L> GENE_____>	630
GGGATCAAAG CCCTAGTTTC W D Q S _____HIV1	CCTAAAGCCA GGATTTCGGT L K P (MN) GP120	TGTGTAAAAT ACACATTTTA C V K> GENE_____>	660
TAACCCCACT ATTGGGGTGA L T P L _____HIV1	CTGTGTTACT GACACAATGA C V T (MN) GP120	TTAAATTGCA AATTTAACGT L N C> GENE_____>	690
CTGATTTGAG GACTAAACTC T D L R _____HIV1	GAATACTACT CTTATGATGA N T T (MN) GP120	AATACCAATA TTATGGTTAT N T N> GENE_____>	720

FIG. 28B

FIG. 28B-1

FIG.28B-1
FIG.28B-2
FIG.28B-3

ATAGTACTGC TATCATGACG N S T A _____ HIV1	TAATAACAAT ATTATTGTTA N N N (MN) GP120	AGTAATAGCG TCATTATCGC S N S> GENE _____>	750
AGGGAACAAT TCCCTTGTTA E G T I _____ HIV1	AAAGGGAGGA TTTCCCTCCT K G G (MN) GP120	GAAATGAAAA CTTTACTTTT E M K> GENE _____>	780
ACTGCTCTTT TGACGAGAAA N C S F _____ HIV1	CAATATCACC GTTATAGTGG N I T (MN) GP120	ACAAGCATAA TGTTTCGTATT T S I> GENE _____>	810
GAGATAAGAT CTCTATTCTA R D K M _____ HIV1	GCAGAAAGAA CGTCTTTCTT Q K E (MN) GP120	TATGCACTTC ATACGTGAAG Y A L> GENE _____>	840
TTTATAAACT AAATATTTGA L Y K L _____ HIV1	TGATATAGTA ACTATATCAT D I V (MN) GP120	TCAATAAATA AGTTATTTAT S I N> GENE _____>	870
ATGATAGTAC TACTATCATG N D S T _____ HIV1	CAGCTATAGG GTCGATATCC S Y R (MN) GP120	TTGATAAGTT AACTATTCAA L I S> GENE _____>	900
GTAATACCTC CATTATGGAG C N T S _____ HIV1	AGTCATTACA TCAGTAATGT V I T (MN) GP120	CAAGCTTGTC GTTCGAACAG Q A C> GENE _____>	930
CAAAGATATC GTTTCATAG P K I S _____ HIV1	CTTTGAGCCA GAAACTCGGT F E P (MN) GP120	ATTCCCATAC TAAGGGTATG I P I> GENE _____>	960
ACTATTGTGC TGATAACACG H Y C A _____ HIV1	CCCGGCTGGT GGGCCGACCA P A G (MN) GP120	TTTGCGATTC AAACGCTAAG F A I> GENE _____>	990

FIG. 28B-2

TAAAGTGTAA ATTTACATT L K C N _____ HIV1	CGATAAAAAG GCTATTTTTC D K K (MN) GP120	TTCAGTGGAA AAGTCACCTT F S G> GENE _____>	1020
AAGGATCATG TTCCTAGTAC K G S C _____ HIV1	TAAAAATGTC ATTTTACAG K N V (MN) GP120	AGCACAGTAC TCGTGTCATG S T V> GENE _____>	1050
AATGTACACA TTACATGTGT Q C T H _____ HIV1	TGGAATTAGG ACCTTAATCC G I R (MN) GP120	CCAGTAGTAT GGTCATCATA P V V> GENE _____>	1080
CAACTCAACT GTTGAGTTGA S T Q L _____ HIV1	GCTGTAAAT CGACAATTTA L L N (MN) GP120	GGCAGTCTAG CCGTCAGATC G S L> GENE _____>	1110
CAGAAGAAGA GTCTTCTTCT A E E E _____ HIV1	GGTAGTAATT CCATCATTAA V V I (MN) GP120	AGATCTGAGA TCTAGACTCT R S E> GENE _____>	1140
ATTTCAATGA TAAAGTTACT N F N D _____ HIV1	TAATGCTAAA ATTACGATTT N A K (MN) GP120	ACCATCATAG TGGTAGTATC T I I> GENE _____>	1170
TACATCTGAA ATGTAGACTT V H L N _____ HIV1	TGAATCTGTA ACTTAGACAT E S V (MN) GP120	CAAATTAATT GTTTAATTAA Q I N> GENE _____>	1200
GTACAAGACC CATGTTCTGG C T R P _____ GP120	CAACTACGAG GTTGATGCTC N Y E GENE _____><KAT	CTCGACAAAT GAGCTGTTTA L D K> EPITOPE _____>	1230
GGGCCCATAT CCCGGGTATA W A H I _____>< GP	AGGACCAGGG TCCTGGTCCC G P G 120 GENE _____	AGAGAATTGG TCTCTTAACC R E L> _____><_____	1260

FIG. 28B-3

ATAAGTGGGC TATTCACCCG D K W A KAT EPITOP	GAATATAATA CTTATATTAT N I I ><_____GP	GGAAGTATAA CCTTGATATT G T I> 120 GENE____>	1290
GACAAGCACA CTGTTCGTGT R Q A H _____HIV1	TTGTAACATT AACATTGTAA C N I (MN) GP120	AGTAGAGCAA TCATCTCGTT S R A> GENE____>	1320
AATGGAATGA TTACCTTACT K W N D _____HIV1	CACTTTAAGA GTGAAATTCT T L R (MN) GP120	CAGATAGTTA GTCTATCAAT Q I V> GENE____>	1350
GCAAATTAAA CGTTTAATTT S K L K _____HIV1	AGAACAATTT TCTTGTTAAA E Q F (MN) GP120	AAGAATAAAA TTCTTATTTT K N K> GENE____>	1380
CAATAGTCTT GTTATCAGAA T I V F _____HIV1	TAATCAATCC ATTAGTTAGG N Q S (MN) GP120	TCAGGAGGGG AGTCCTCCCC S G G> GENE____>	1410
ACCCAGAAAT TGGGTCTTTA D P E I _____HIV1	TGTAATGCAC ACATTACGTG V M H (MN) GP120	AGTTTTAATT TCAAAATTAA S F N> GENE____>	1440

FIG. 28C

FIG. 28C-1

FIG. 28C-2

FIG. 28C-3

FIG. 28C-1

GTGGAGGGGA CACCTCCCCT C G G E _____ HIV1	ATTCTTCTAC TAAGAAGATG F F Y (MN) GP120	TGTAATTCAT ACATTAAGTA C N S> GENE _____>	1470
CACCACTGTT GTGGTGACAA S P L F _____ HIV1	TAATAGTACT ATTATCATGA N S T (MN) GP120	TGGAATGGTA ACCTTACCAT W N G> GENE _____>	1500
ATAATACTTG TATTATGAAC N N T W _____ HIV1	GAATAATACT CTTATTATGA N N T (MN) GP120	ACAGGGTCAA TGTCCCAGTT T G S> GENE _____>	1530
ATAACAATAT TATTGTTATA N N N I _____ HIV1	CACACTTCAA GTGTGAAGTT T L Q (MN) GP120	TGCAAAATAA ACGTTTTATT C K I> GENE _____>	1560
AACAAATTAT TTGTTTAATA K Q I I _____ HIV1	AAACATGTGG TTTGTAACCC N M W (MN) GP120	CAGGAAGTAG GTCCTTCATC Q E V> GENE _____>	1590
GAAAAGCAAT CTTTTCGTTA G K A I _____ HIV1	ATATGCCCCCT TATACGGGGA Y A P (MN) GP120	CCCATTGAAG GGGTAAC TTC P I E> GENE _____>	1620
GACAAATTAG CTGTTTAATC G Q I R _____ HIV1	ATGTTTCATCA TACAAGTAGT C S S (MN) GP120	AATATTACAG TTATAATGTC N I T> GENE _____>	1650
GGCTACTATT CCGATGATAA G L L L _____ HIV1	AACAAGAGAT TTGTTCTCTA T R D (MN) GP120	GGTGGTAAGG CCACCATTCC G G K> GENE _____>	1680
ACACGGACAC TGTGCCTGTG D T D T _____ HIV1	GAACGACACC CTTGCTGTGG N D T (MN) GP120	GAGATCTTCA CTCTAGAAGT E I F> GENE _____>	1710

FIG. 28C-2

GACCTGGAGG CTGGACCTCC R P G G _____ HIV1	AGGAGATATG TCCTCTATAC G D M (MN) GP120	AGGGACAATT TCCCTGTTAA R D N> GENE _____>	1740
GGAGAAGTGA CCTCTTCACT W R S E _____ HIV1	ATTATATAAA TAATATATTT L Y K (MN) GP120	TATAAAGTAG ATATTTTCATC Y K V> GENE _____>	1770
TAACAATTGA ATTGTTAACT V T I E _____ HIV1	ACCATTAGGA TGGTAATCCT P L G (MN) GP120	GTAGCACCCA CATCGTGGGT V A P> GENE _____>	1800
CCAAGGCAAA GGTTCCGTTT T K A K _____ HIV1	GAGAAGAGTG CTCTTCTCAC R R V (MN) GP120	GTGCAGAGAG CACGTCTCTC V Q R> GENE _____>	1830
AAAAAAGATT TTTTTTCTAA E K R L _____	ATTCATAATG TAAGTATTAC F I M _____ TRANS	ATAGTAGGAG TATCATCCTC I V G> MEMBRANE _____>	1860
GCTTGGTAGG CGAACCATCC G L V G _____ HIV1	TTTAAGAATA AAATTCTTAT L R I TRANSMEMBR	GTTTTTGCTG CAAAAACGAC V F A> ANE _____>	1890
TACTCTCTGT ATGAGAGACA V L S V _____ HIV1	AGTGAATAGA TCACTTATCT V N R TRANSMEMBR	GTTAGGCAGG CAATCCGTCC V R Q> ANE _____>	1920
GATAATTTTT CTATTAAAAA G *> _____>	ATTCTAGAAT TAAGATCTTA	CGATCCCGGG GCTAGGGCCC	1950
AGATCTTAGC TCTAGAATCG	TAAGTGAATTT ATTGACTAAA	TTCTGGGAAA AAGACCCTTT _____>	1980

FIG. 28C-3

AAAATTATTT TTTTAATAAA _____14L	AACTTTTCAT TTGAAAAGTA FLANKING	TAATAGGGAT ATTATCCCTA ARM_____>	2010
TTGACGTATG AACTGCATAC _14L FLANK	TAGCGTAC ATCGCATG ING ARM_>		2028

FIG.29

#121:98/95028005\FLI-H\FLI-Height

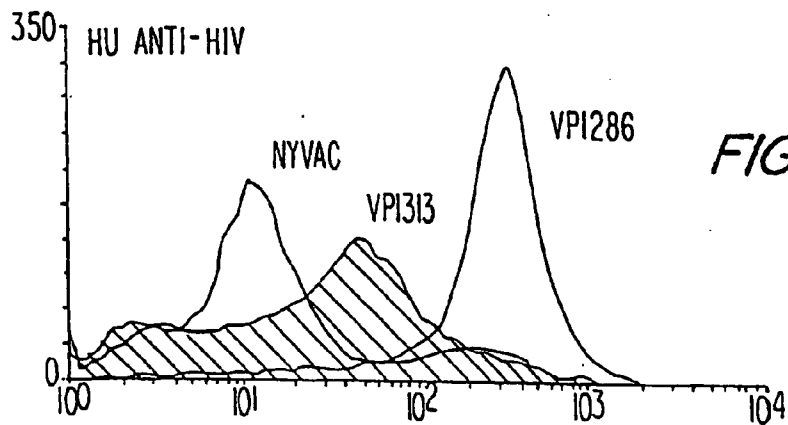


FIG.29a

#121:98/95028012\FLI-H\FLI-Height

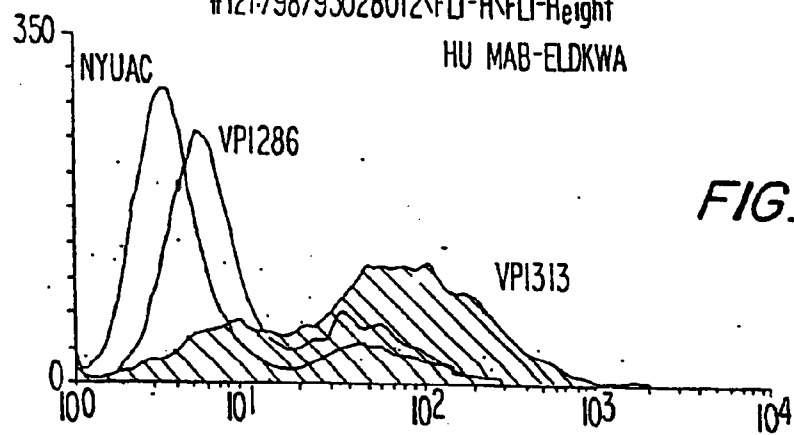


FIG.29b

FIG. 30A

FIG. 30A-1
FIG. 30A-2
FIG. 30A-3

FIG. 30A-1

pHIV61/vCP1319

ATAAACCATT TATTTGGTAA _____A24R	AGATAAAGTT TCTATTTCAA FLANKING	GATCTCAAGC CTAGAGTTCG ARM_____>	30
GCTCTTTTCT CGAGAAAAGA _____	GGTGTAATAA CCACATTATT _____>	AAATTAATTA TTTAATTAAT	60
ATTACTCGAG TAATGAGCTC	GGTACCGGAT CCATGGCCTA	CCGGGTTAAT GGCCCAATTA	90
TAATTAGTCA ATTAATCAGT	TCAGGCAGGG AGTCCGTCCC	CGAGAACGAG GCTCTTGCTC	120
ACTATCTGCT TGATAGACGA	CGTTAATTAA GCAATTAATT	TTAGAGCTTC AATCTCGAAG _____>	150
TTTATTCTAT AAATAAGATA _____H6	ACTTAAAAAG TGAATTTTTC PROMOTER_____	TGAAAATAAA ACTTTTATTT _____>	180
TACAAAGGTT ATGTTTCCAA _____H6	CTTGAGGGTT GAACTCCCAA PROMOTER_____	GTGTTAAATT CACAATTTAA _____>	210
GAAAGCGAGA CTTTCGCTCT _____H6	AATAATCATA TTATTAGTAT PROMOTER_____	AATTATTTCA TTAATAAAGT _____>	240
TTATCGCGAT AATAGCGCTA _____H6	ATGCGTTAAG TACGCAATTC PROMOTER_____	TTTGTATCGT AAACATAGCA _____>	270
ATATGAAAGA TATACTTTCT M K E _____ _____ _____HIV1	GCAGAAGACA CGTCTTCTGT Q K T (MN) GP120	GTGGCAATGA CACCGTTACT V A M> GENE_____	300 09

FIG. 30A-2

GAGTGAAGGA CTCACTTCCT R V K E _____HIV1	GAAATATCAG CTTTATAGTC K Y Q (MN) GP120	CACTTGTGGA GTGAACACCT H L W> GENE _____>	330 19
GATGGGGGTG CTACCCCCAC R W G W _____HIV1	GAGATGGGGC CTCTACCCCG R W G (MN) GP120	ACCATGCTCC TGGTACGAGG T M L> GENE _____>	360 29
TTGGGATGTT AACCCTACAA L G M L _____HIV1	GATGATCTGT CTACTAGACA M I C (MN) GP120	AGTGCTACAG TCACGATGTC S A T> GENE _____>	390 39
AAAAATTGTG TTTTTAACAC E K L W _____HIV1	GGTCACAGTC CCAGTGTGAG V T V (MN) GP120	TATTATGGGG ATAATACCCC Y Y G> GENE _____>	420 49
TACCTGTGTG ATGGACACAC V P V W _____HIV1	GAAAGAAGCA CTTTCTTCGT K E A (MN) GP120	ACCACCACTC TGGTGGTGAG T T T> GENE _____>	450 59
TATTTTGTGC ATAAAACACG L F C A _____HIV1	ATCAGATGCT TAGTCTACGA S D A (MN) GP120	AAAGCATATG TTTCGTATAC K A Y> GENE _____>	480 69
ATACAGAGGT TATGTCTCCA D T E V _____HIV1	ACATAATGTT TGTATTACAA H N V (MN) GP120	TGGGCCACAC ACCCGGTGTG W A T> GENE _____>	510 79
ATGCCTGTGT TACGGACACA H A C V _____HIV1	ACCCACAGAC TGGGTGTCTG P T D (MN) GP120	CCCAACCCAC GGGTTGGGTG P N P> GENE _____>	540 89
AAGAAGTAGA TTCTTCATCT Q E V E _____HIV1	ATTGGTAAAT TAACCATTTA L V N (MN) GP120	GTGACAGAAA CACTGTCTTT V T E> GENE _____>	570 99

FIG. 30A-3

ATTTTAACAT	GTGGAAAAAT	AACATGGTAG	600
TAAAATTGTA	CACCTTTTTA	TTGTACCATC	
N F N M	W K N	N M V>	109
_____HIV1	(MN) GP120	GENE_____>	
AACAGATGC	ATGAGGATATA	ATCAGTTTAT	630
TTGTCTACG	TACTCCTATAT	TAGTCAAATA	
E Q M H	E D I	I S L>	119
_____HIV1	(MN) GP120	GENE_____>	
GGGATCAAAG	CCTAAAGCCA	TGTGTAAAAT	660
CCCTAGTTTC	GGATTTCGGT	ACACATTTTA	
W D Q S	L K P	C V K>	129
_____HIV1	(MN) GP120	GENE_____>	
TAACCCCACT	CTGTGTTACT	TTAAATTGCA	690
ATTGGGGTGA	GACACAATGA	AATTTAACGT	
L T P L	C V T	L N C>	139
_____HIV1	(MN) GP120	GENE_____>	
CTGATTTGAG	GAATACTACT	AATACCAATA	720
GACTAAACTC	CTTATGATGA	TTATGGTTAT	
T D L R	N T T	N T N>	149
_____HIV1	(MN) GP120	GENE_____>	

FIG. 30B

FIG. 30B-1

FIG. 30B-1
FIG. 30B-2
FIG. 30B-3

ATAGTACTGC	TAATAACAAT	AGTAATAGCG	750
TATCATGACG	ATTATTGTTA	TCATTATCGC	
N S T A	N N N	S N S>	159
_____HIV1	(MN) GP120	GENE_____>	
AGGGAACAAT	AAAGGGAGGA	GAAATGAAAA	780
TCCCTTGTTA	TTTCCCTCCT	CTTTACTTTT	
E G T I	K G G	E M K>	169
_____HIV1	(MN) GP120	GENE_____>	
ACTGCTCTTT	CAATATCACC	ACAAGCATAA	810
TGACGAGAAA	GTTATAGTGG	TGTTTCGTATT	
N C S F	N I T	T S I>	179
_____HIV1	(MN) GP120	GENE_____>	
GAGATAAGAT	GCAGAAAGAA	TATGCACTTC	840
CTCTATTCTA	CGTCTTTCTT	ATACGTGAAG	
R D K M	Q K E	Y A L>	189
_____HIV1	(MN) GP120	GENE_____>	
TTTATAAACT	TGATATAGTA	TCAATAAATA	870
AAATATTTGA	ACTATATCAT	AGTTATTTAT	
L Y K L	D I V	S I N>	199
_____HIV1	(MN) GP120	GENE_____>	
ATGATAGTAC	CAGCTATAGG	TTGATAAGTT	900
TACTATCATG	GTCGATATCC	AACTATTCAA	
N D S T	S Y R	L I S>	209
_____HIV1	(MN) GP120	GENE_____>	
GTAATACTC	AGTCATTACA	CAAGCTTGTC	930
CATTATGGAG	TCAGTAATGT	GTTCGAACAG	
C N T S	V I T	Q A C>	219
_____HIV1	(MN) GP120	GENE_____>	
CAAAGATATC	CTTTGAGCCA	ATTCCCATAC	960
GTTTCTATAG	GAAACTCGGT	TAAGGGTATG	
P K I S	F E P	I P I>	229
_____HIV1	(MN) GP120	GENE_____>	
ACTATTGTGC	CCCGGCTGGT	TTTGCGATTC	990
TGATAACACG	GGGCCGACCA	AAACGCTAAG	
H Y C A	P A G	F A I>	239
_____HIV1	(MN) GP120	GENE_____>	

FIG. 30B-2

TAAAGTGTAA ATTTCACATT L K C N _____HIV1	CGATAAAAAG GCTATTTTTC D K K (MN) GP120	TTCAGTGGAA AAGTCACCTT F S G> GENE _____>	1020 249
AAGGATCATG TTCCTAGTAC K G S C _____HIV1	TAAAAATGTC ATTTTACAG K N V (MN) GP120	AGCACAGTAC TCGTGTCATG S T V> GENE _____>	1050 259
AATGTACACA TTACATGTGT Q C T H _____HIV1	TGGAATTAGG ACCTTAATCC G I R (MN) GP120	CCAGTAGTAT GGTCATCATA P V V> GENE _____>	1080 269
CAACTCAACT GTTGAGTTGA S T Q L _____HIV1	GCTGTAAAT CGACAATTA L L N (MN) GP120	GGCAGTCTAG CCGTCAGATC G S L> GENE _____>	1110 279
CAGAAGAAGA GTCTTCTTCT A E E E _____HIV1	GGTAGTAATT CCATCATTA V V I (MN) GP120	AGATCTGAGA TCTAGACTCT R S E> GENE _____>	1140 289
ATTTCAATGA TAAAGTTACT N F N D _____HIV1	TAATGCTAAA ATTACGATTT N A K (MN) GP120	ACCATCATAG TGGTAGTATC T I I> GENE _____>	1170 299
TACATCTGAA ATGTAGACTT V H L'N _____HIV1	TGAATCTGTA ACTTAGACAT E S V (MN) GP120	CAAATTAATT GTTTAATTAA Q I N> GENE _____>	1200 309
GTACAAGACC CATGTTCTGG C T R P _____GP120	CAACTACGAG GTTGATGCTC N Y E GENE _____><KAT	CTCGACAAAT GAGCTGTTTA L D K EPITOPE _____>	1230 319
GGGCCCATAT CCCGGGTATA W A H I _____>< GP120	AGGACCAGGG TCCTGGTCCC G P G GENE _____><	AGAGAATTGG TCTCTTAACC R E L _____><	1260 329

FIG. 30B-3

ATAAGTGGGC	GAATATAATA	GGAACTATAA	1290
TATTCACCCG	CTTATATTAT	CCTTGATATT	
D K W A	N I I	G T I>	339
KAT EPITOP	>< _____ GP	120 GENE _____>	
GACAAGCACA	TTGTAACATT	AGTAGAGCAA	1320
CTGTTCGTGT	AACATTGTAA	TCATCTCGTT	
R Q A H	C N I	S R A>	349
_____ HIV1	(MN) GP120	GENE _____>	
AATGGAATGA	CACTTTAAGA	CAGATAGTTA	1350
TTACCTTACT	GTGAAATTCT	GTCTATCAAT	
K W N D	T L R	Q I V>	359
_____ HIV1	(MN) GP120	GENE _____>	
GCAAATTAAA	AGAACAATTT	AAGAATAAAA	1380
CGTTTAATTT	TCTTGTTAAA	TTCTTATTTT	
S K L K	E Q F	K N K>	369
_____ HIV1	(MN) GP120	GENE _____>	
CAATAGTCTT	TAATCAATCC	TCAGGAGGGG	1410
GTTATCAGAA	ATTAGTTAGG	AGTCCTCCCC	
T I V F	N Q S	S G G>	379
_____ HIV1	(MN) GP120	GENE _____>	
ACCCAGAAAT	TGTAATGCAC	AGTTTTAATT	1440
TGGGTCTTTA	ACATTACGTG	TCAAATTTAA	
D P E I	V M H	S F N>	389
_____ HIV1	(MN) GP120	GENE _____>	

FIG. 30C

FIG. 30C-1
FIG. 30C-2
FIG. 30C-3

FIG. 30C-1

GTGGAGGGGA CACCTCCCCT C G G E _____HIV1	ATTCTTCTAC TAAGAAGATG F F Y (MN) GP120	TGTAATTCAT ACATTAAGTA C N S> GENE _____>	1470 399
CACCACTGTT GTGGTGACAA S P L F _____HIV1	TAATAGTACT ATTATCATGA N S T (MN) GP120	TGGAATGGTA ACCTTACCAT W N G> GENE _____>	1500 409
ATAATACTTG TATTATGAAC N N T W _____HIV1	GAATAATACT CTTATTATGA N N T (MN) GP120	ACAGGGTCAA TGTCCCAGTT T G S> GENE _____>	1530 419
ATAACAATAT TATTGTTATA N N N I _____HIV1	CACACTTCAA GTGTGAAGTT T L Q (MN) GP120	TGCAAAATAA ACGTTTTATT C K I> GENE _____>	1560 429
AACAAATTAT TTGTTTAATA K Q I I _____HIV1	AAACATGTGG TTTGTACACC N M W (MN) GP120	CAGGAAGTAG GTCCTTCATC Q E V> GENE _____>	1590 439
GAAAAGCAAT CTTTTCGTTA G K A I _____HIV1	ATATGCCCCCT TATACGGGGA Y A P (MN) GP120	CCCATTGAAG GGGTAACCTC P I E> GENE _____>	1620 449
GACAAATTAG CTGTTTAATC G Q I R _____HIV1	ATGTTTCATCA TACAAGTAGT C S S (MN) GP120	AATATTACAG TTATAATGTC N I T> GENE _____>	1650 459
GGCTACTATT CCGATGATAA G L L L _____HIV1	AACAAGAGAT TTGTTCTCTA T R D (MN) GP120	GGTGGTAAGG CCACCATTCC G G K> GENE _____>	1680 469
ACACGGACAC TGTGCCTGTG D T D T _____HIV1	GAACGACACC CTTGCTGTGG N D T (MN) GP120	GAGATCTTCA CTCTAGAAGT E I F> GENE _____>	1710 479

FIG. 30C-2

GACCTGGAGG CTGGACCTCC R P G G _____HIV1	AGGAGATATG TCCTCTATAC G D M (MN) GP120	AGGGACAATT TCCCTGTAA R D N> GENE _____>	1740 489
GGAGAAGTGA CCTCTTCACT W R S E _____HIV1	ATTATATAAA TAATATATTT L Y K (MN) GP120	TATAAAGTAG ATATTTTCATC Y K V> GENE _____>	1770 499
TAACAATTGA ATTGTAACT V T I E _____HIV1	ACCATTAGGA TGGTAATCCT P L G (MN) GP120	GTAACACCCA CATCGTGGGT V A P> GENE _____>	1800 509
CCAAGGCAAA GGTTCCGTTT T K A K _____HIV1	GAGAAGAGTG CTCTTCTCAC R R V (MN) GP120	GTGCAGAGAG CACGTCTCTC V Q R> GENE _____>	1830 519
AAAAAAGATT TTTTTTCTAA E K R L _____	ATTCATAATG TAAGTATTAC F I M TRANSMEMBR	ATAGTAGGAG TATCATCCTC I V G> ANE REGION>	1860 529
GCTTGGTAGG CGAACCATCC G L V G _HIV1 TRAN	TTTAAGAATA AAATTCTTAT L R I SMEBRANE	GTTTTTGCTG CAAAAACGAC V F A> REGION _____>	1890 539
TACTCTCTGT ATGAGAGACA V L S V _HIV1 TRAN	AGTGAATAGA TCACTTATCT V N R SMEBRANE	GTTAGGCAGG CAATCCGTCC V R Q> REGION _____>	1920 549
GATAATTTTT CTATTAAAA G * ____>	ATTCGAGAAT TAAGATCTTA	CGATCCCGGG GCTAGGGCCC	1950 550
AATCGATTGG TTAGCTAAGC	CGATAGCTGA GCTATCGACT	TTAGTTTTTG AATCAAAAAC	1980

FIG. 30C-3

TTAACAAAA AATTGTTTT	TGTGGGAGAA ACACCCTCTT	TCTAATTAGT AGATTAATCA <_____	2010
TTTTCTTTAC AAAAGAAATG <_____K1L	ACAATTGACG TGTTAACTGC FLANKING	TACATGAGTC ATGTACTCAG ARM_____	2040
TGAGTTCCTT ACTCAAGGAA <_K1L FLAN	GTTTTTGCTA CAAAAACGAT KING ARM__		2060

FIG. 3I

FIG. 3Ia
FIG. 3Ib
FIG. 3Ic

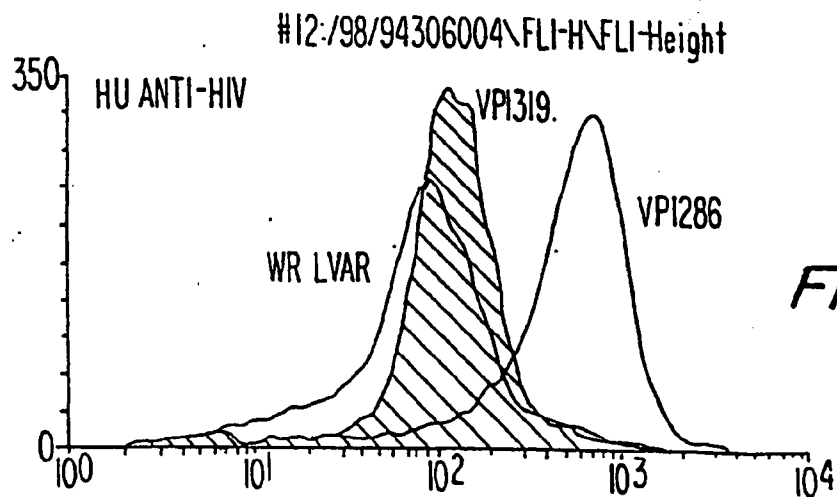


FIG. 3Ia

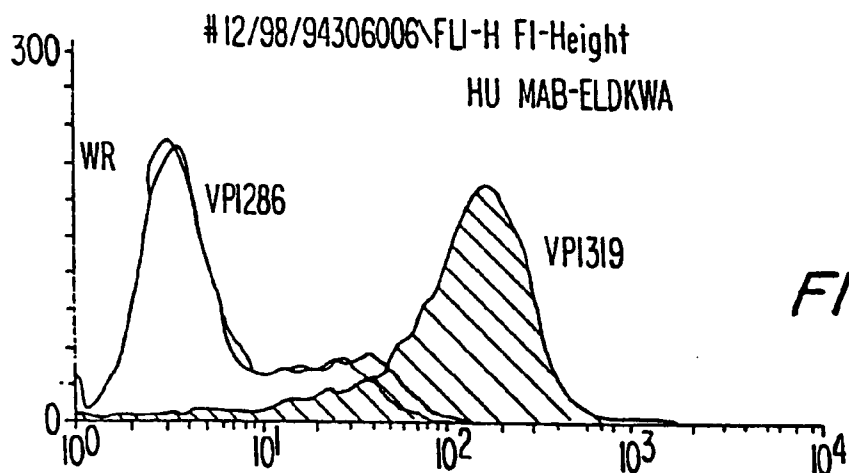


FIG. 3Ib

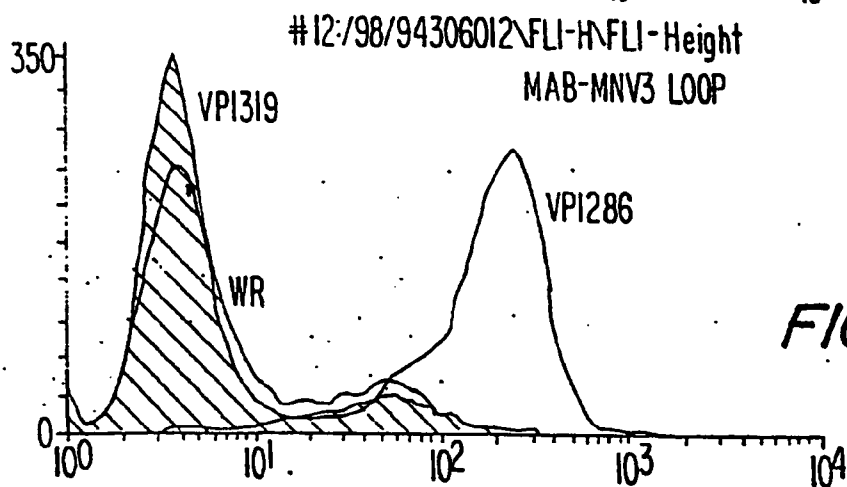
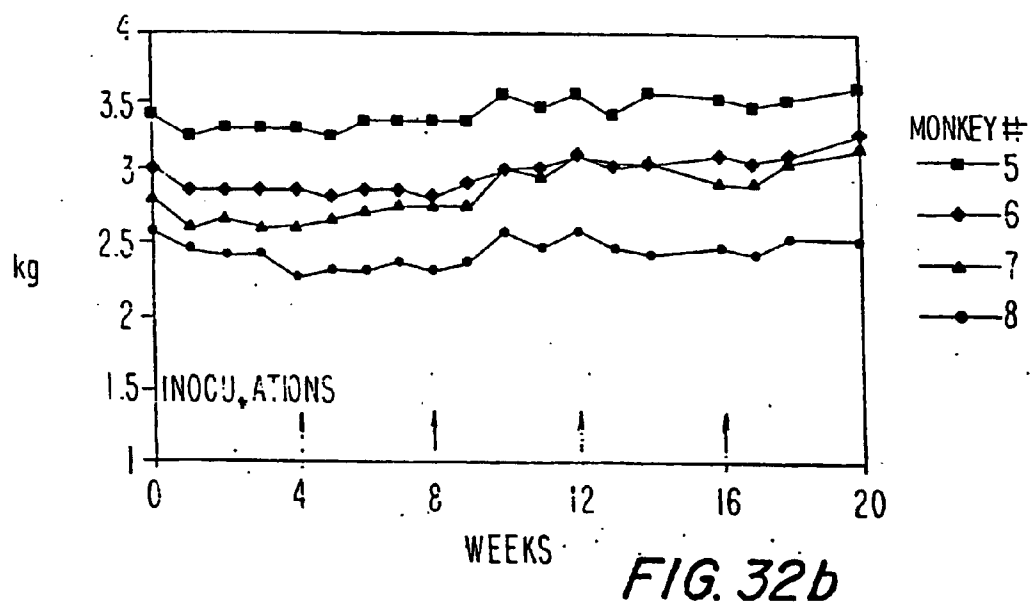
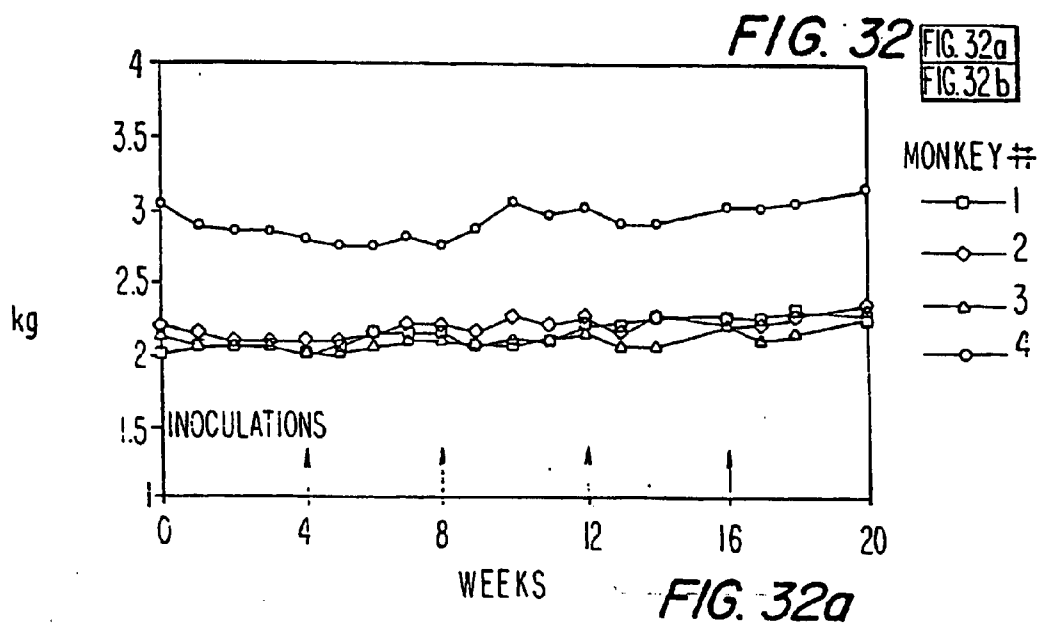


FIG. 3Ic



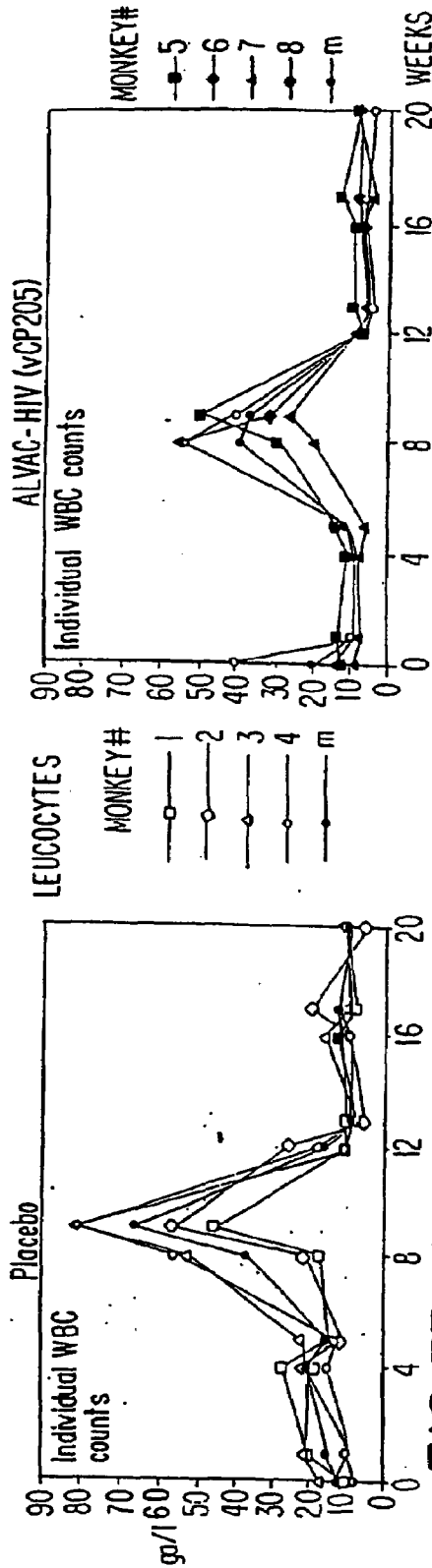


FIG. 33a-1

FIG. 33a-2

FIG. 33a-3
FIG. 33a-4

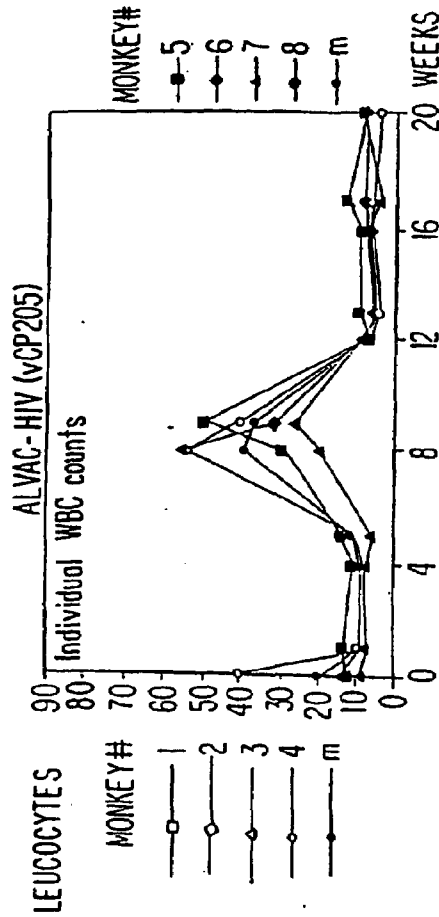


FIG. 33a-2

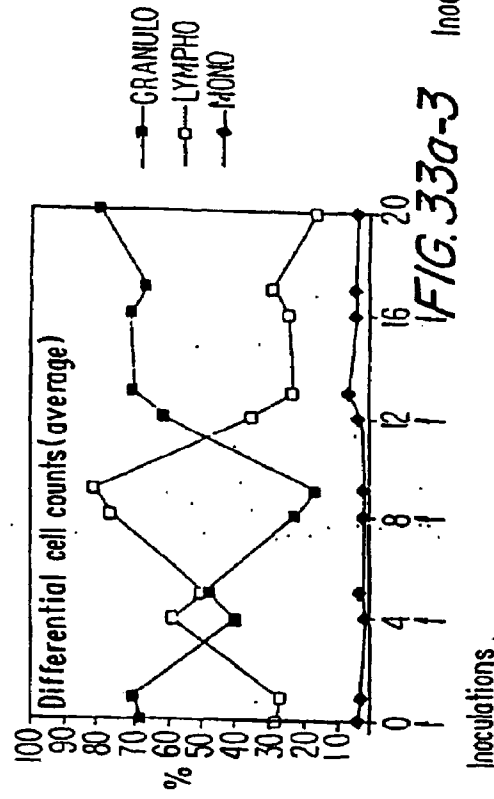


FIG. 33a-3

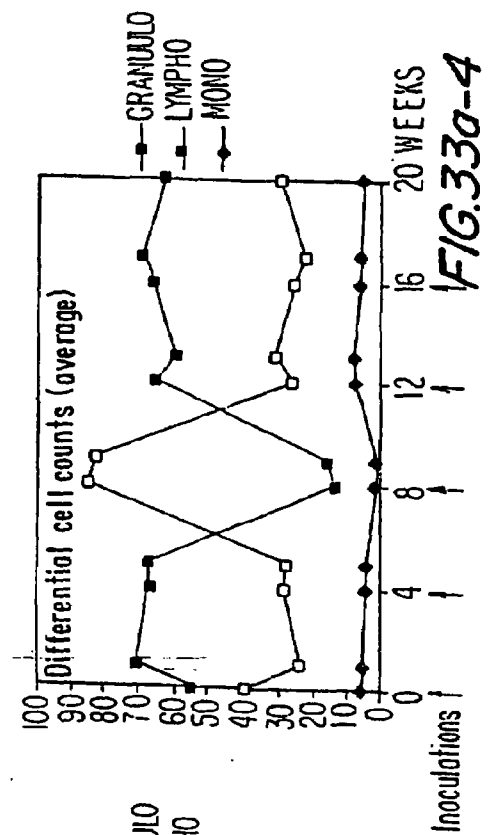
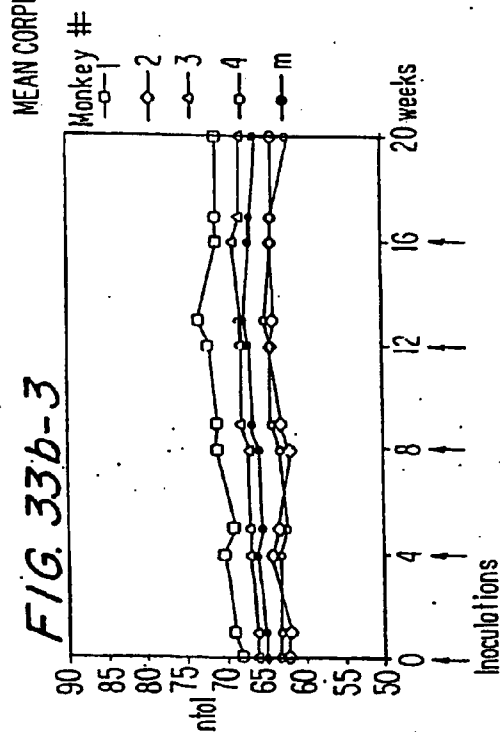
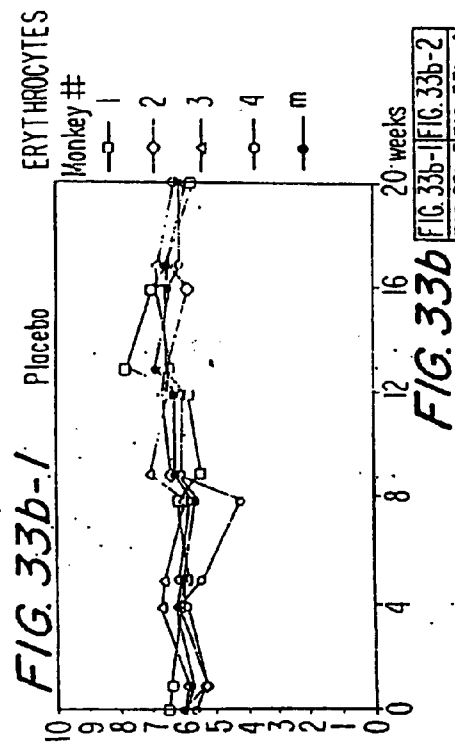
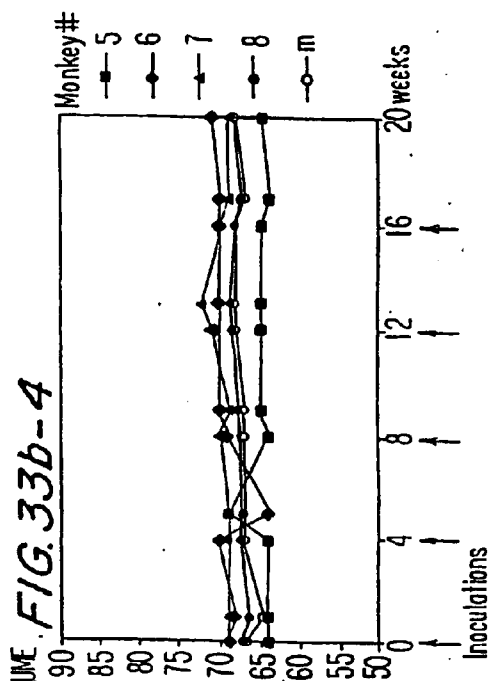
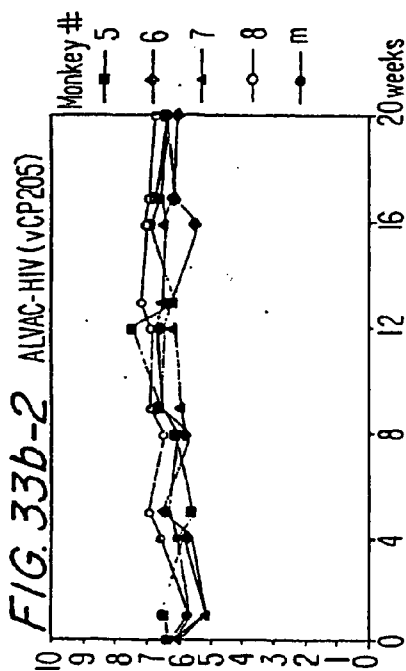
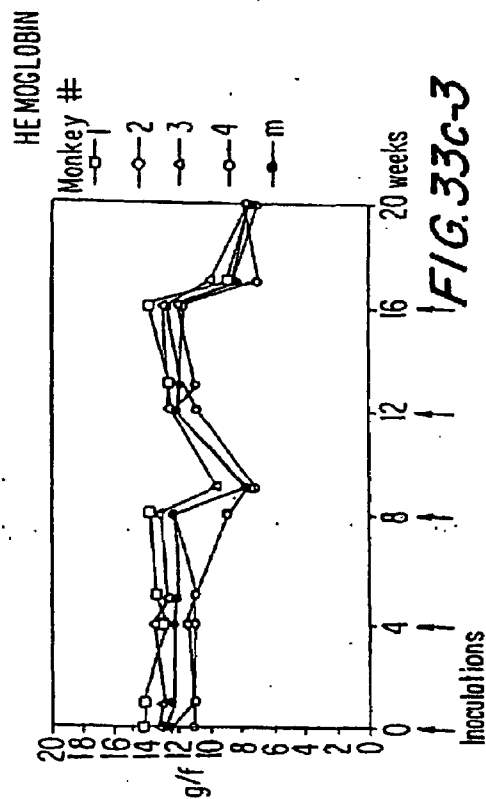
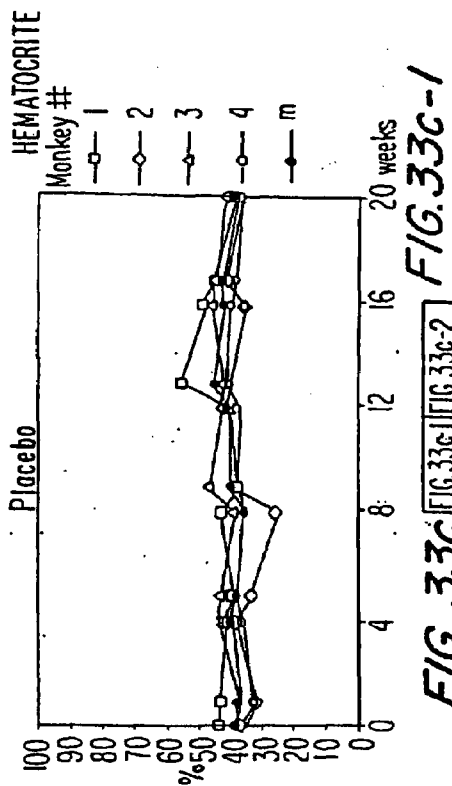
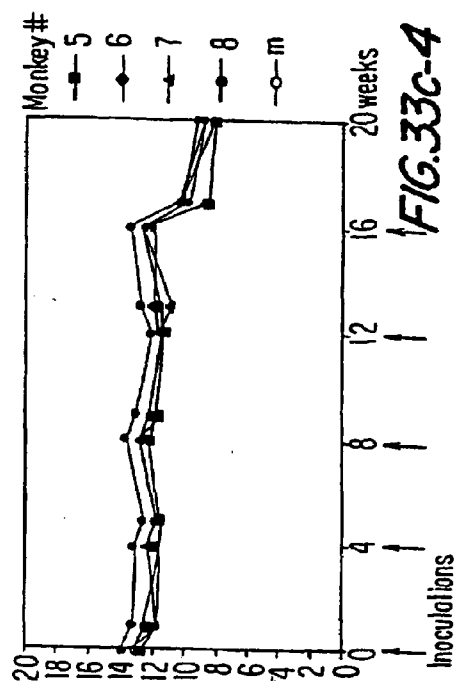
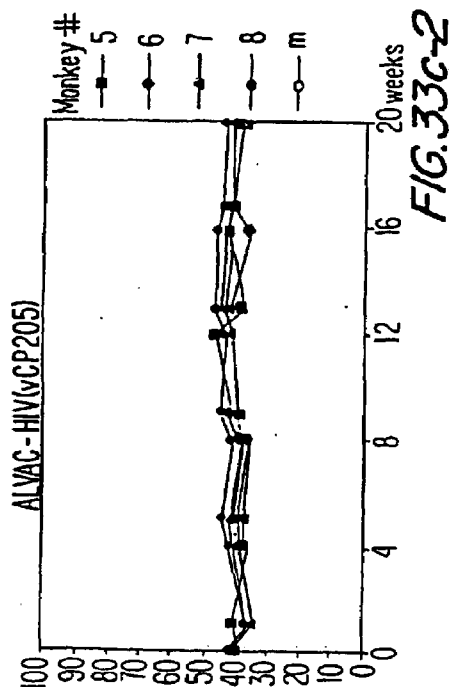
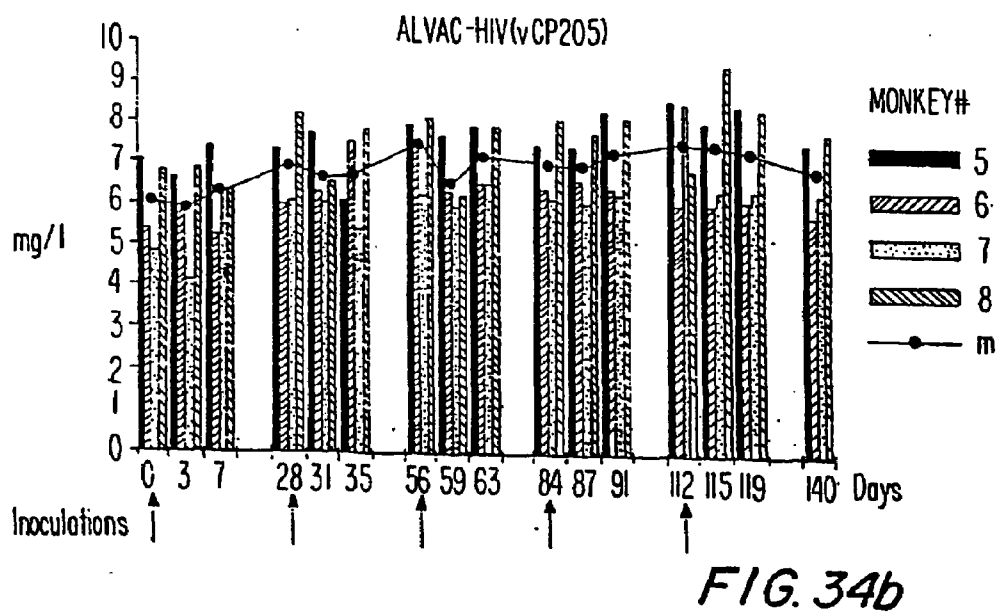
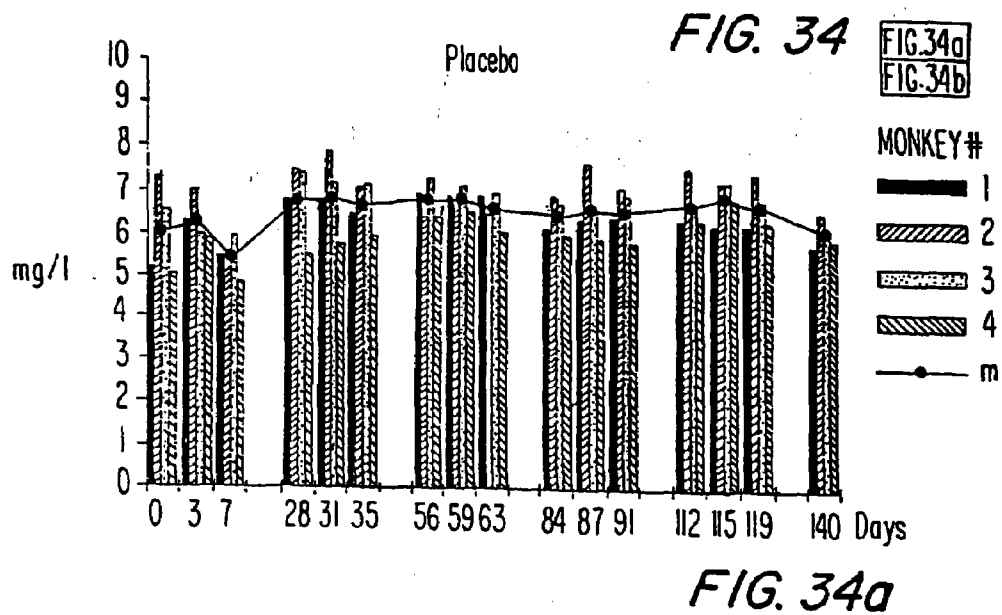
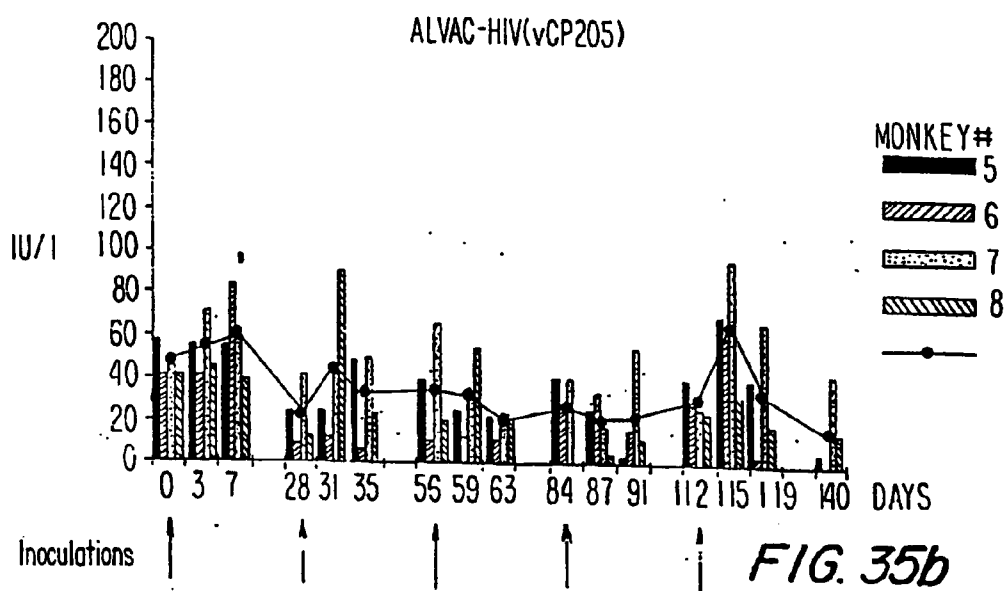
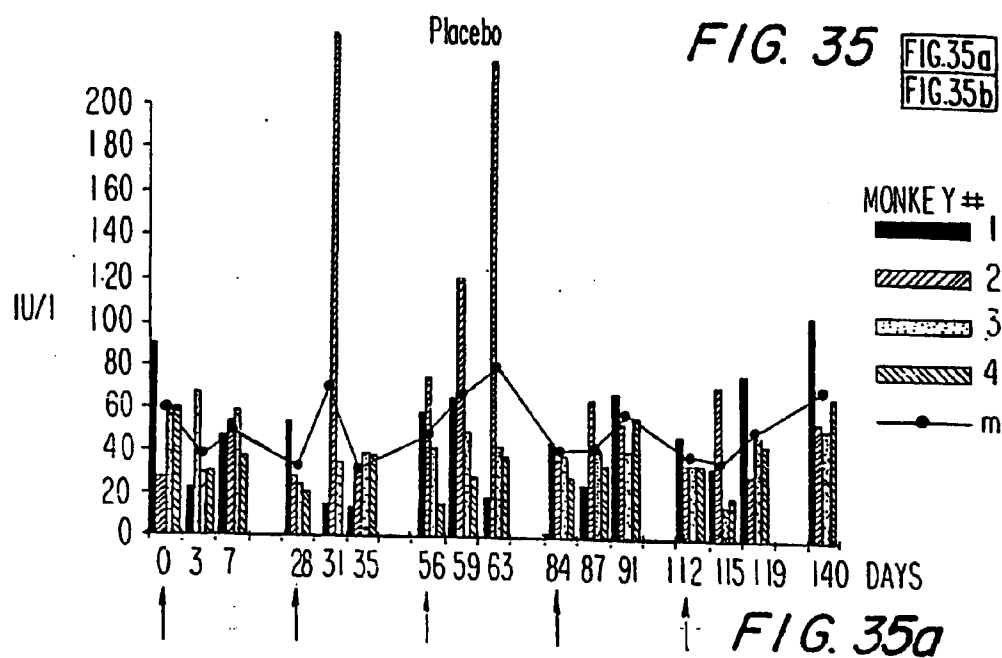


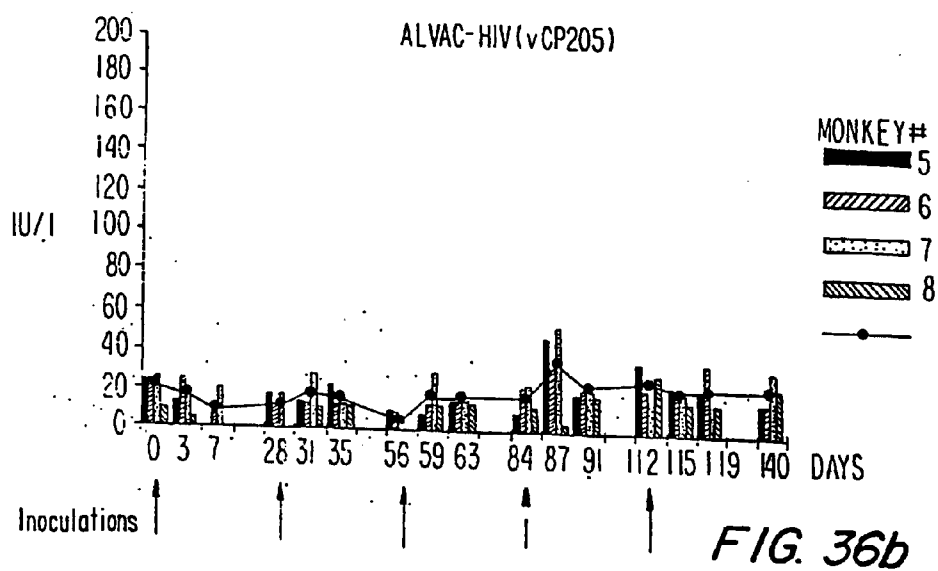
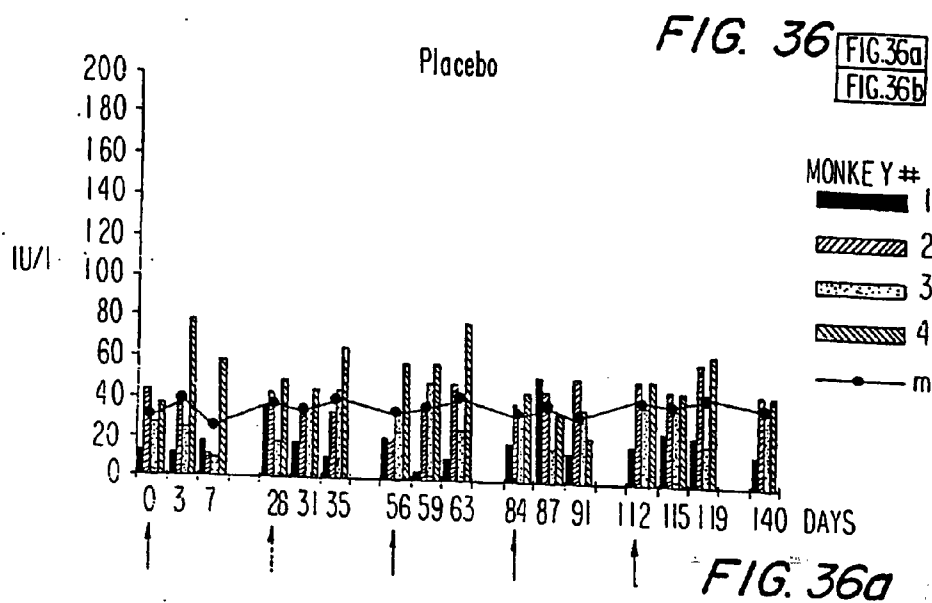
FIG. 33a-4

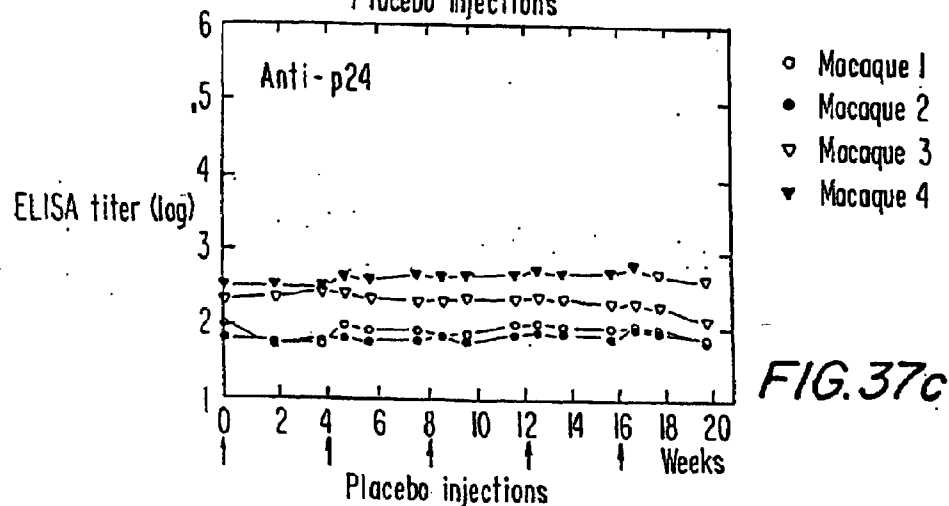
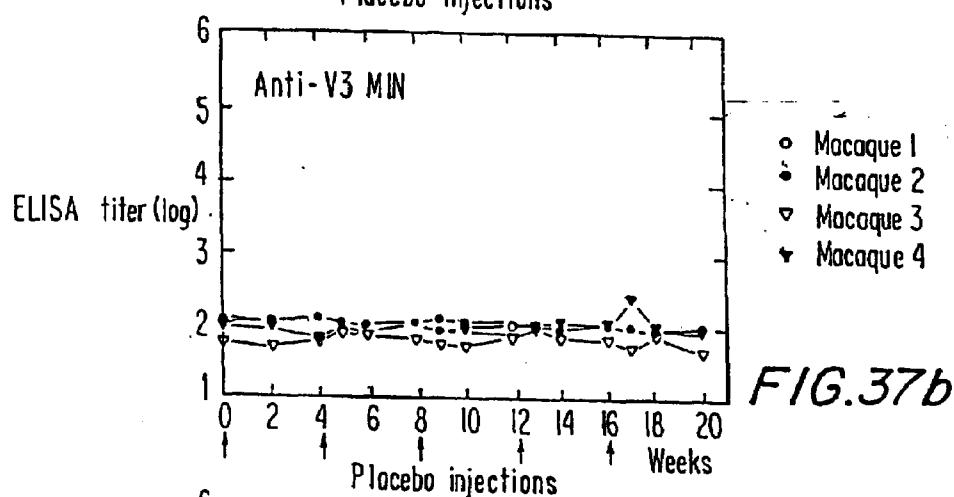
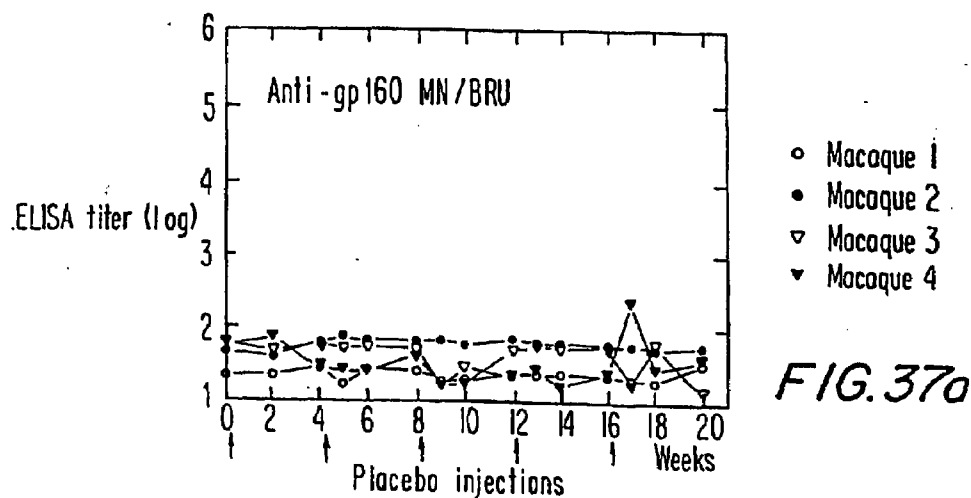












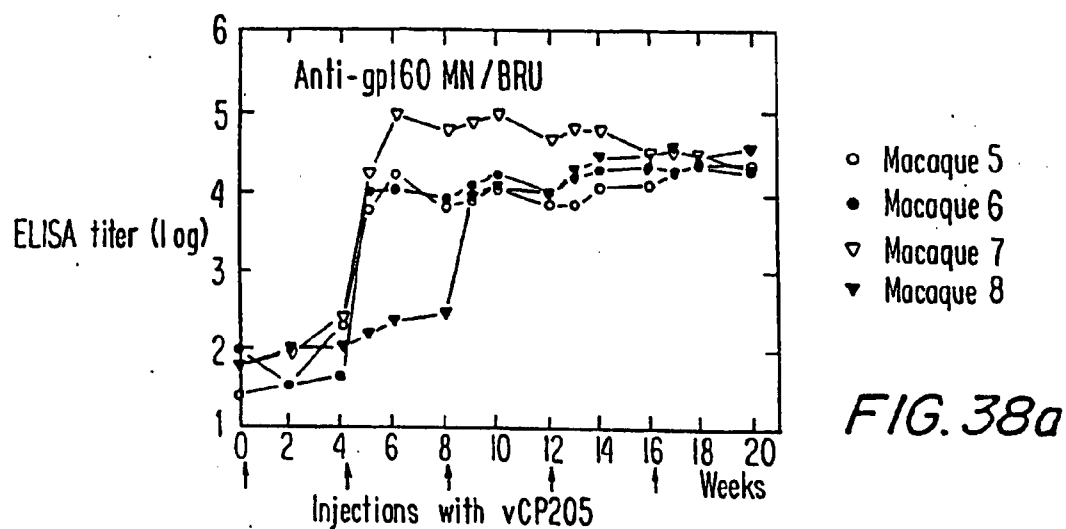


FIG. 38a

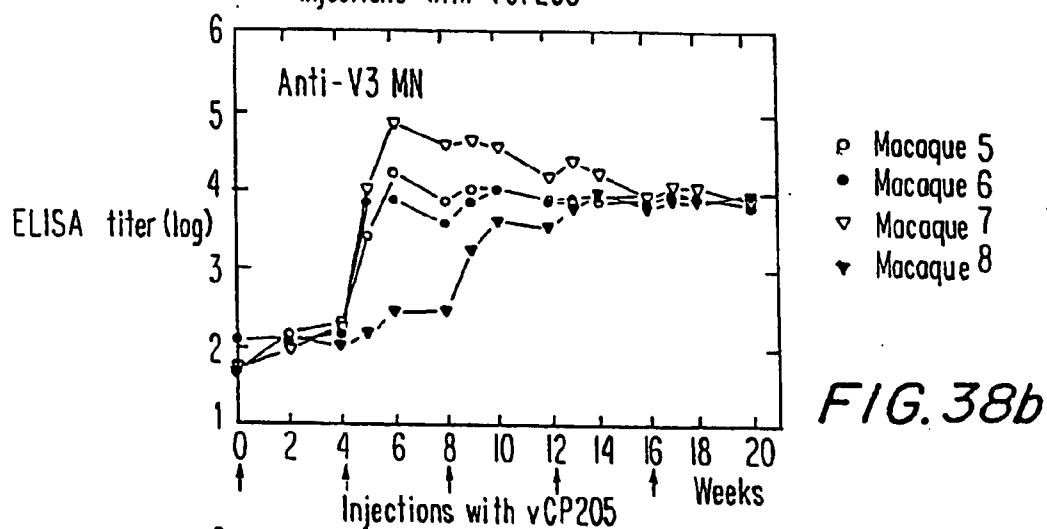


FIG. 38b

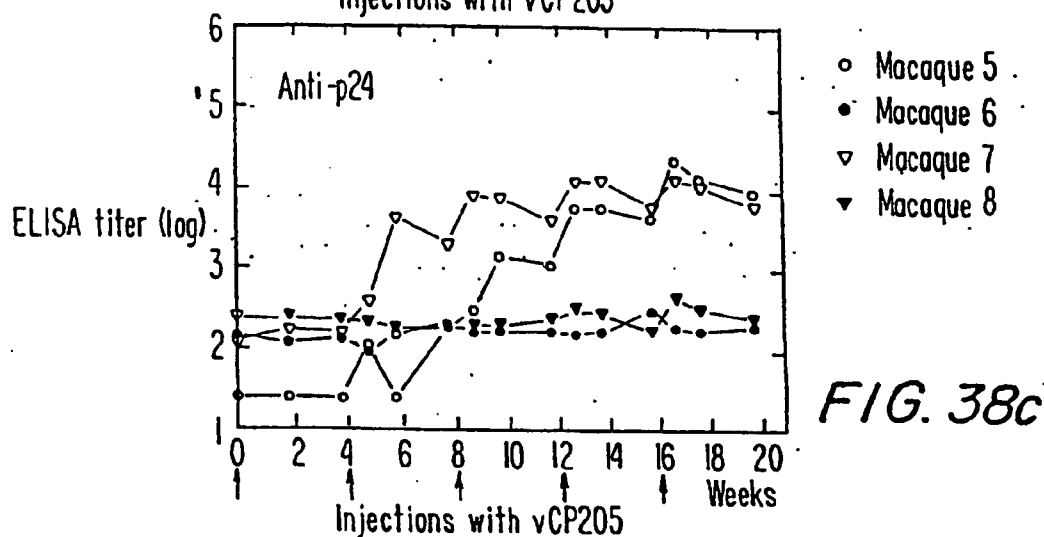


FIG. 38c

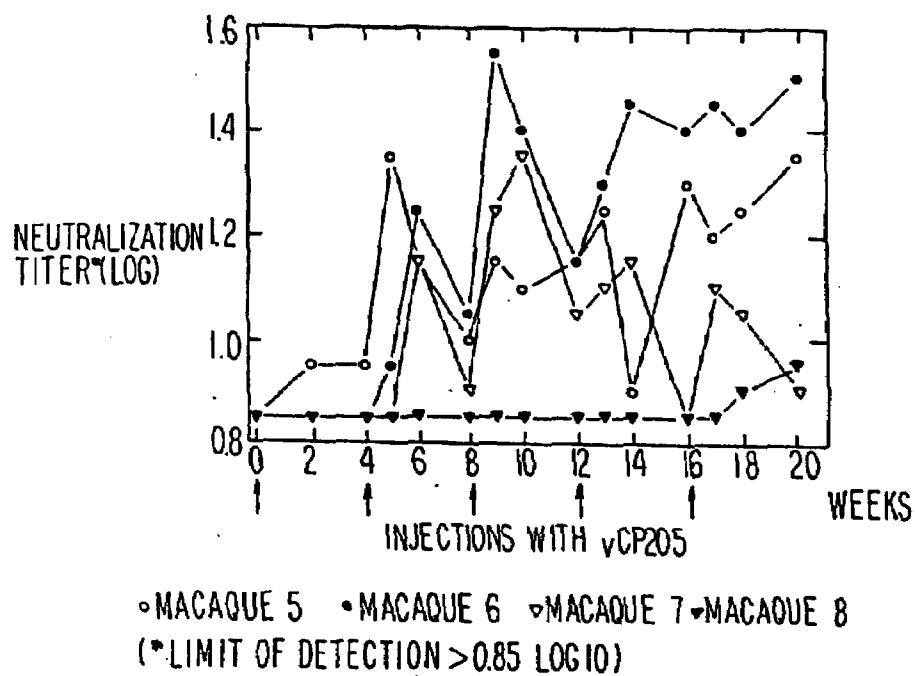


FIG. 39

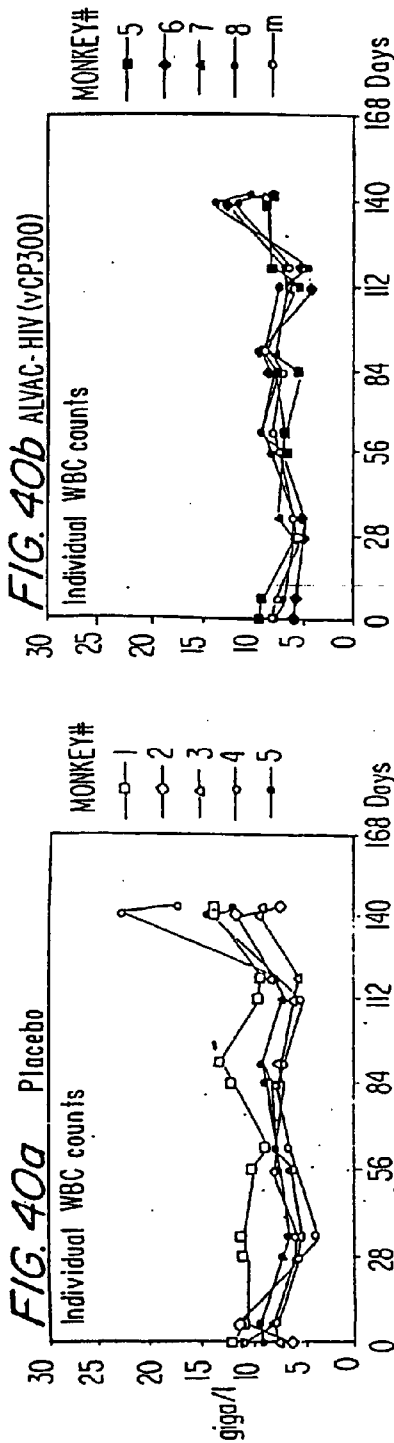
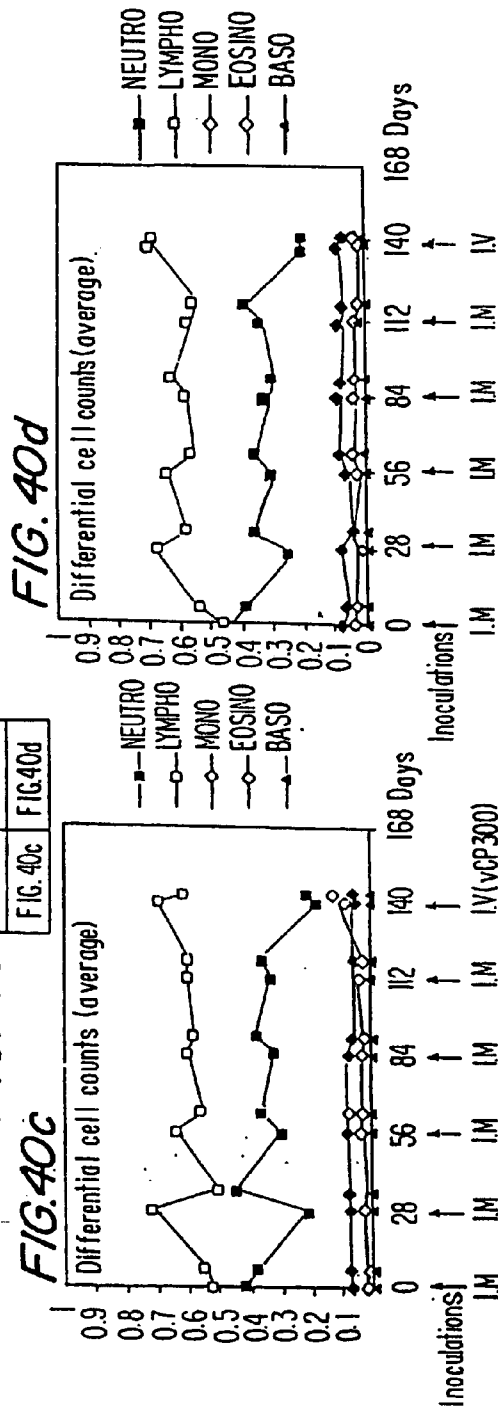


FIG. 40

FIG. 40a	FIG. 40b
FIG. 40c	FIG. 40d



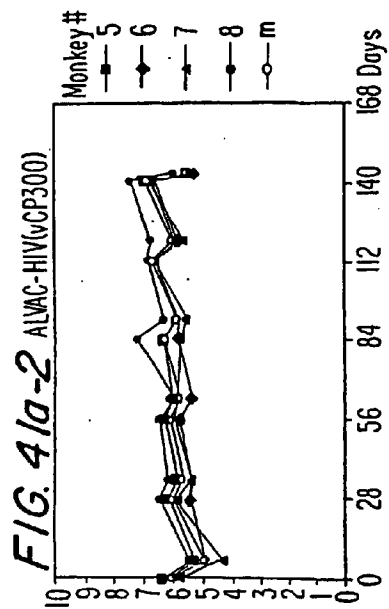
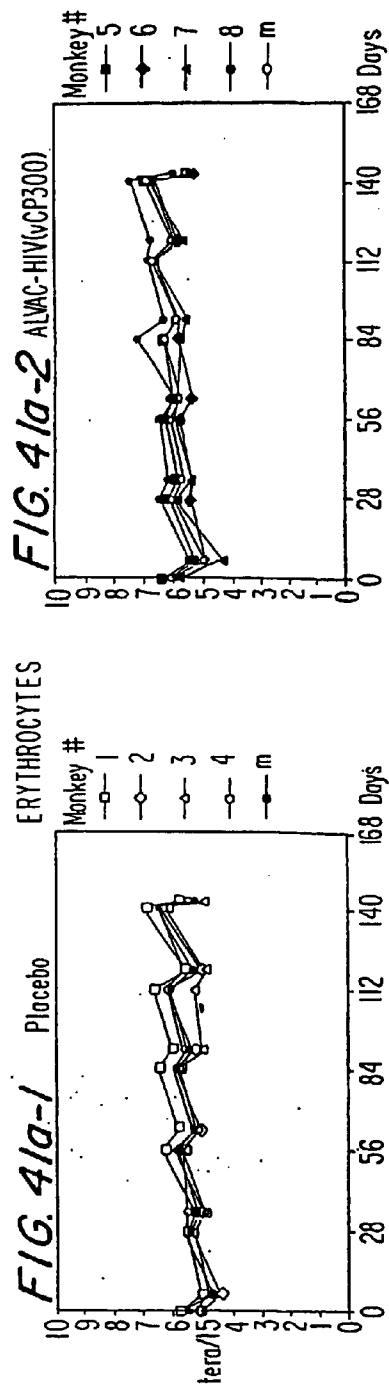
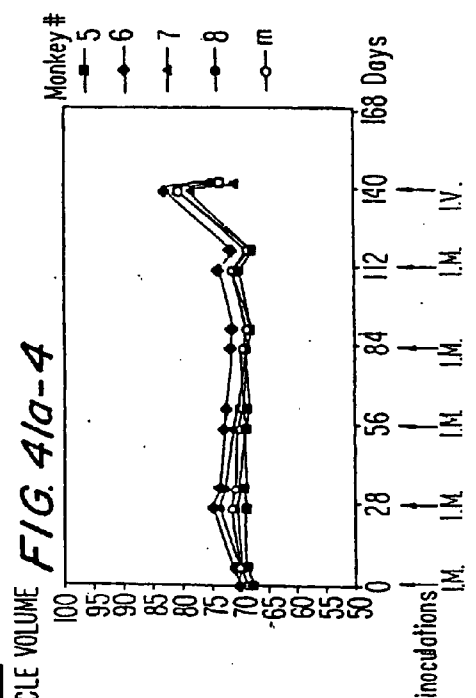
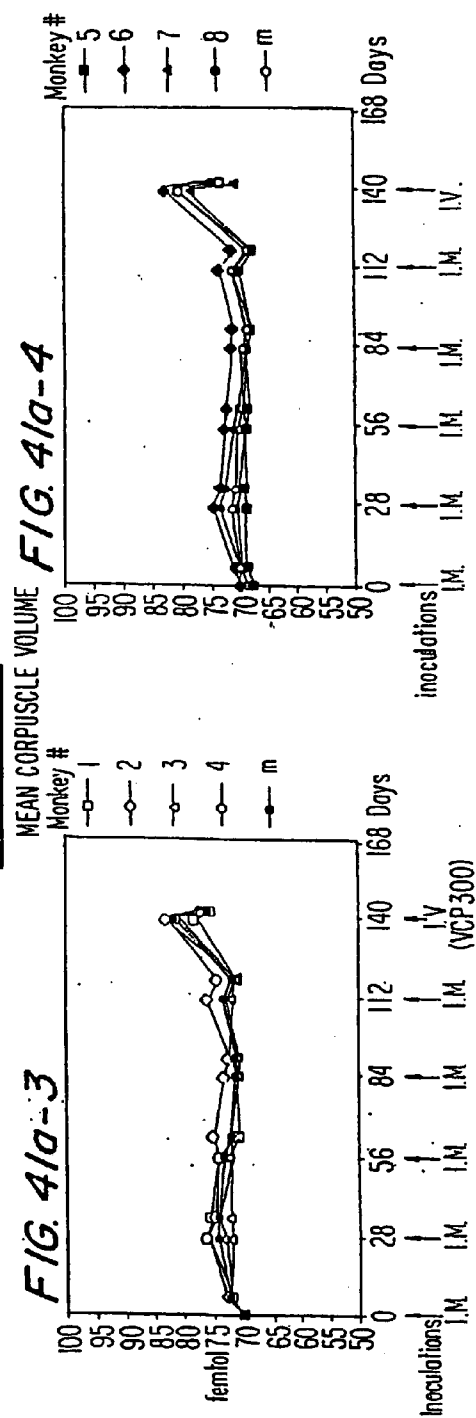


FIG. 41a

FIG. 41a-1
FIG. 41a-2
FIG. 41a-3
FIG. 41a-4



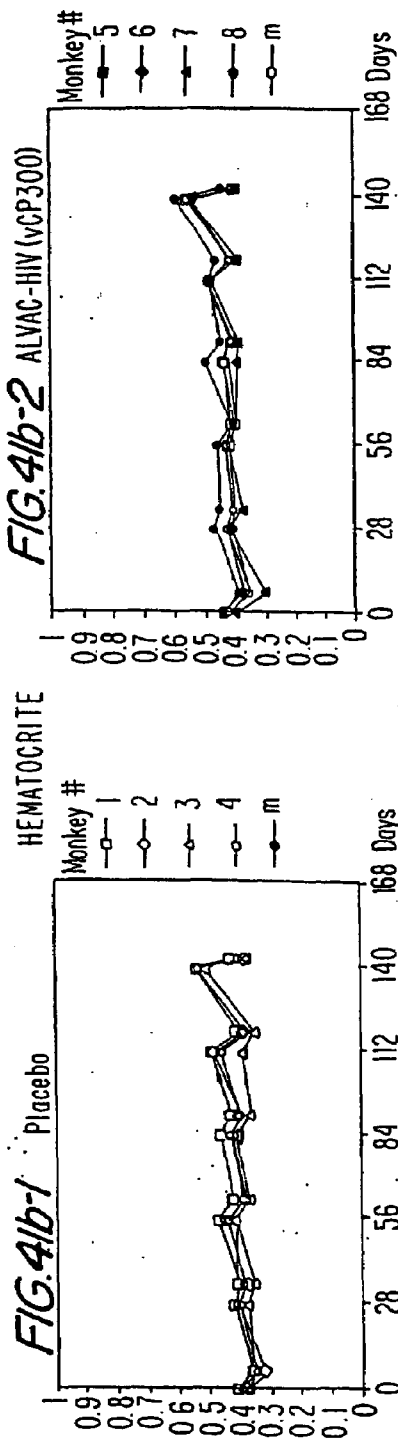


FIG. 41b

FIG. 41b-1 FIG. 41b-2
FIG. 41b-3 FIG. 41b-4

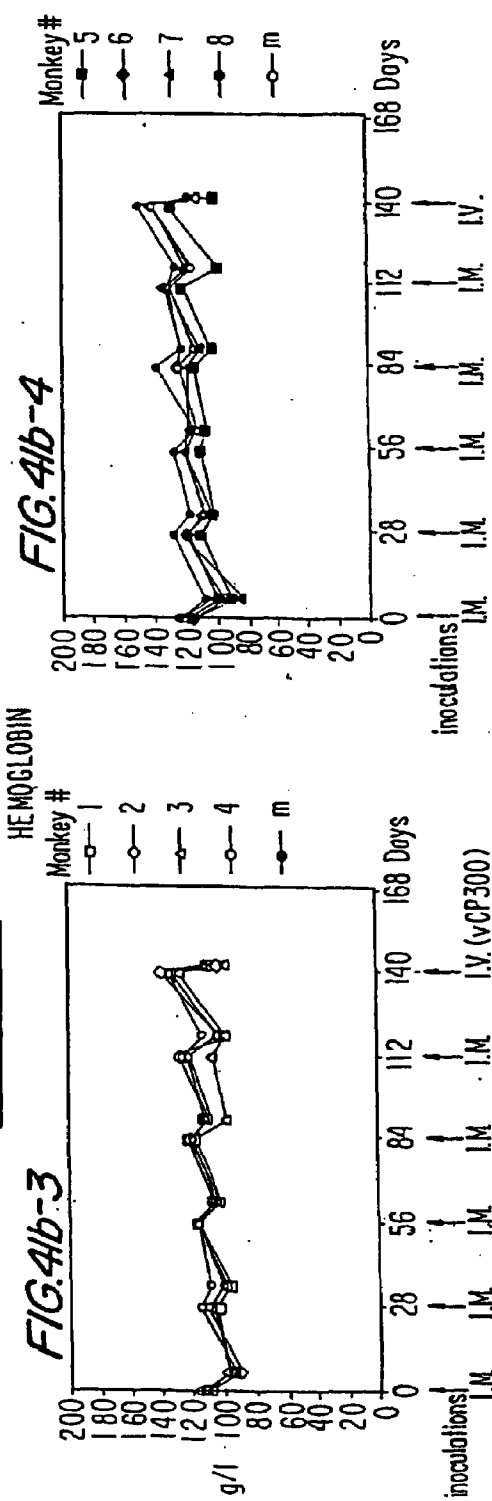
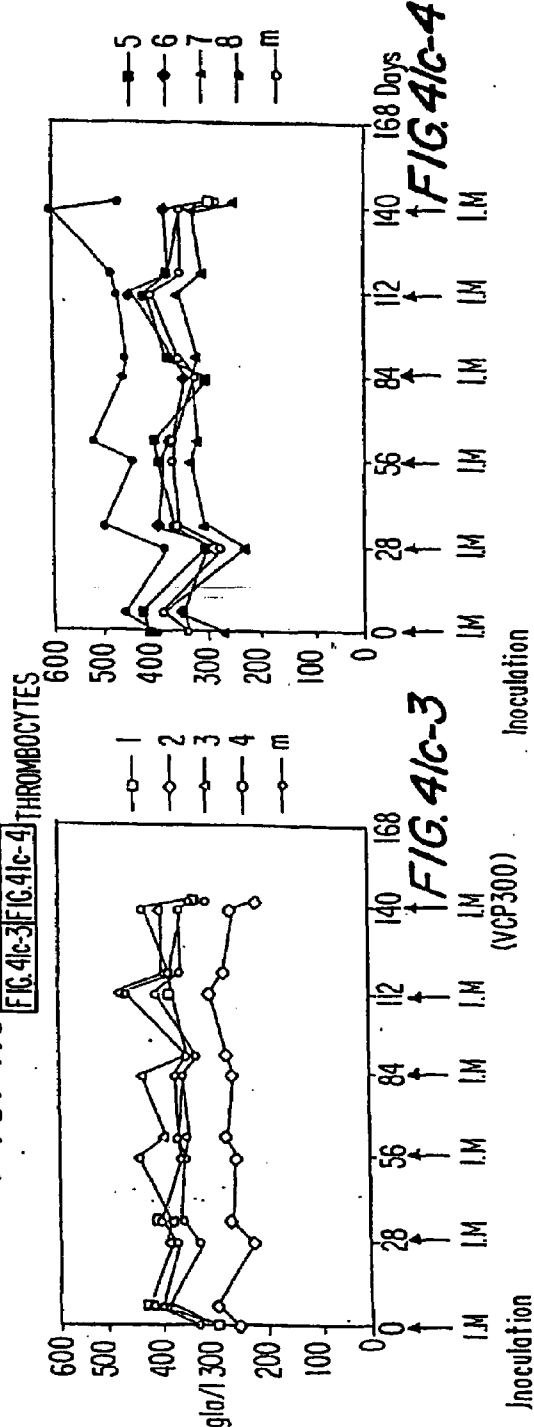
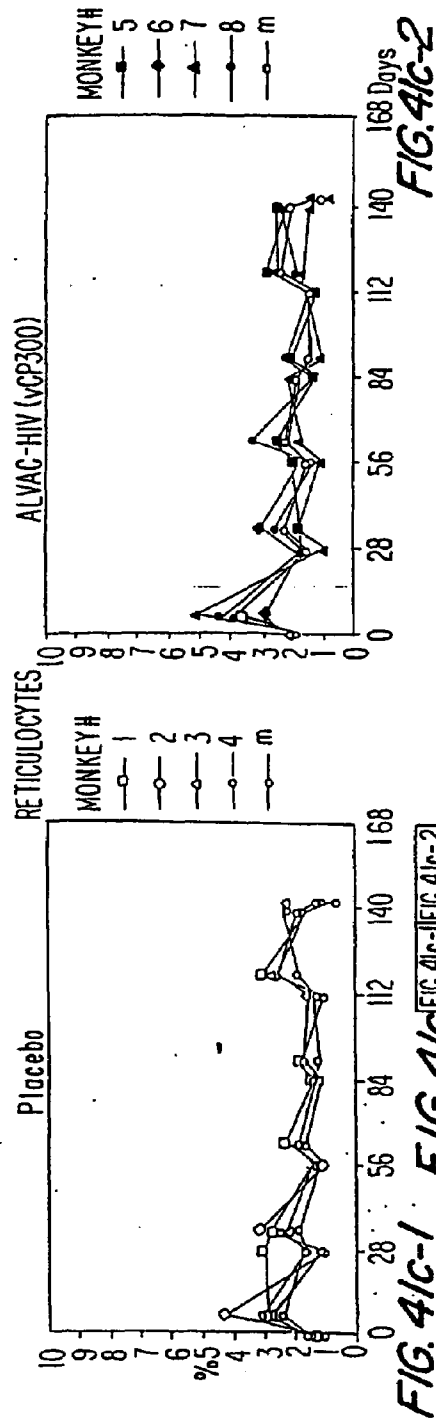
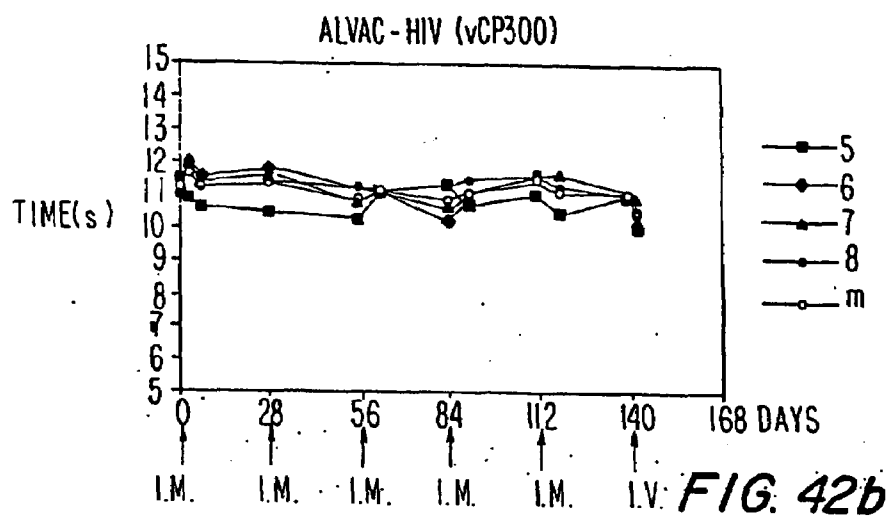
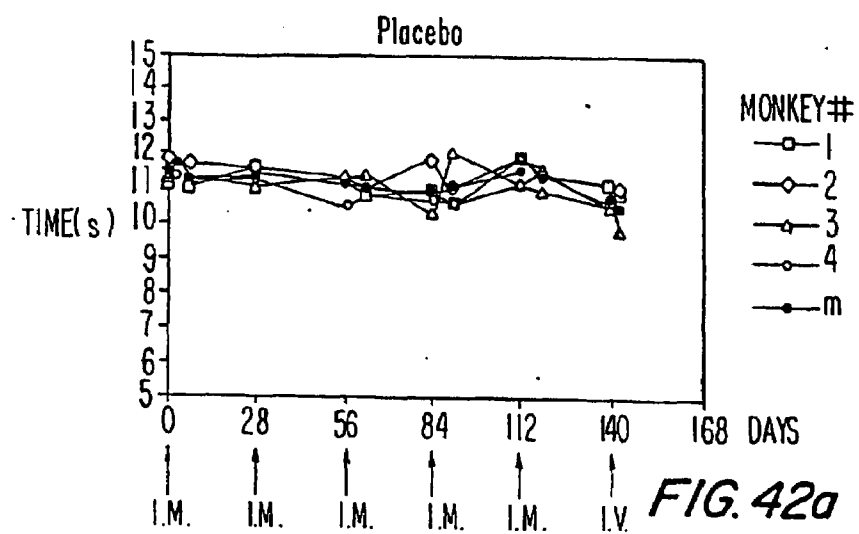
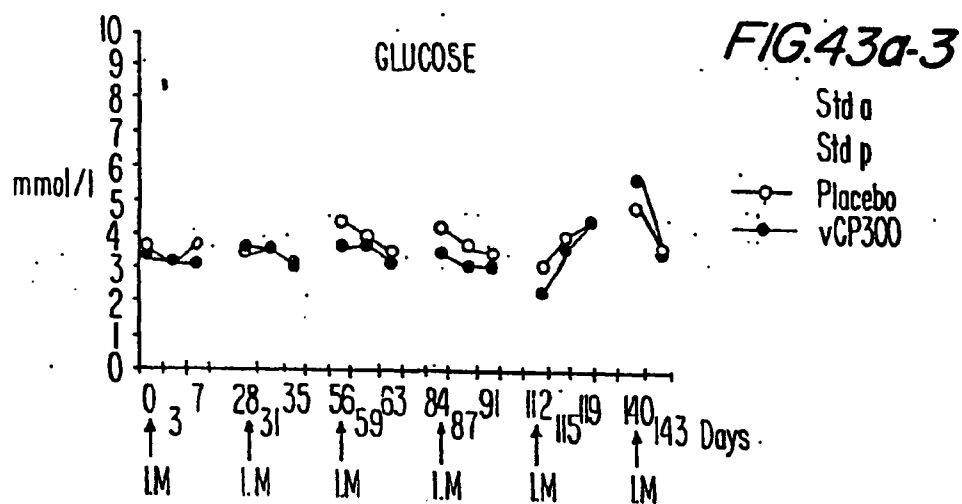
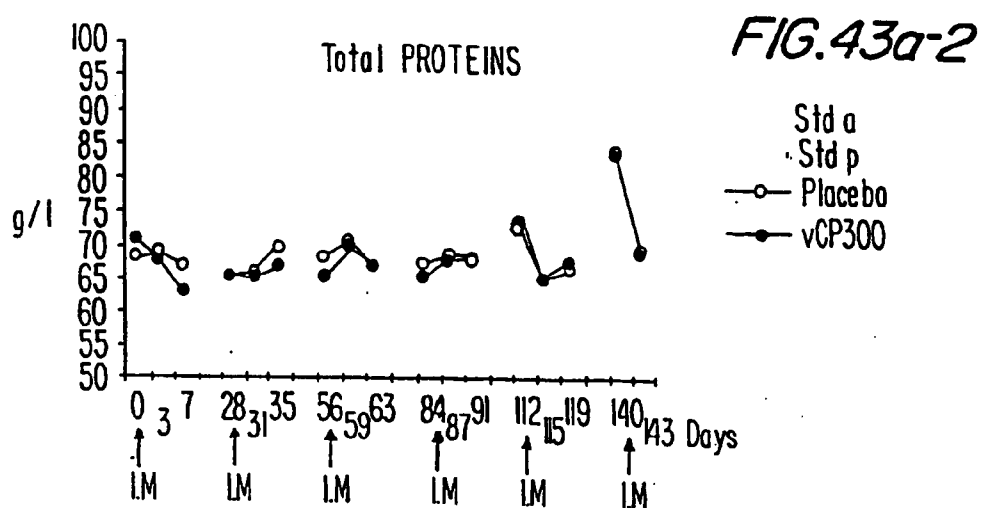
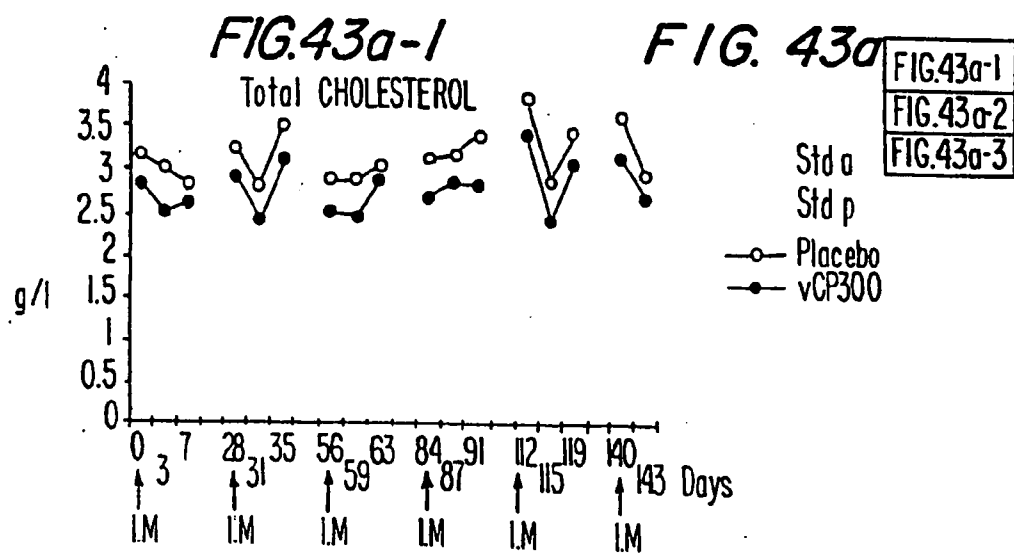


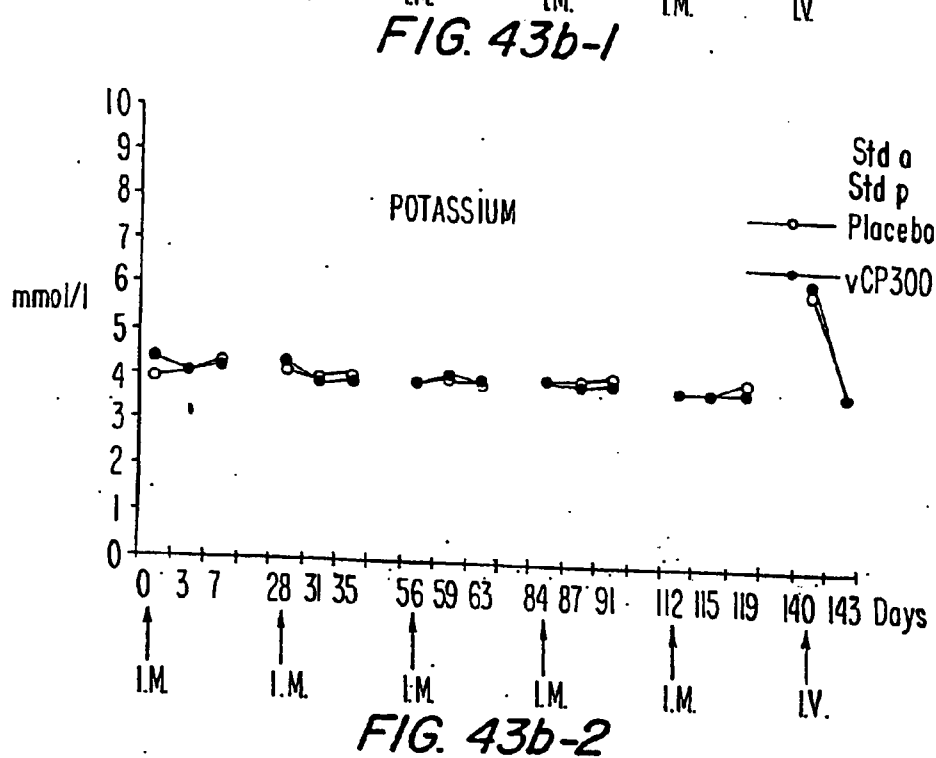
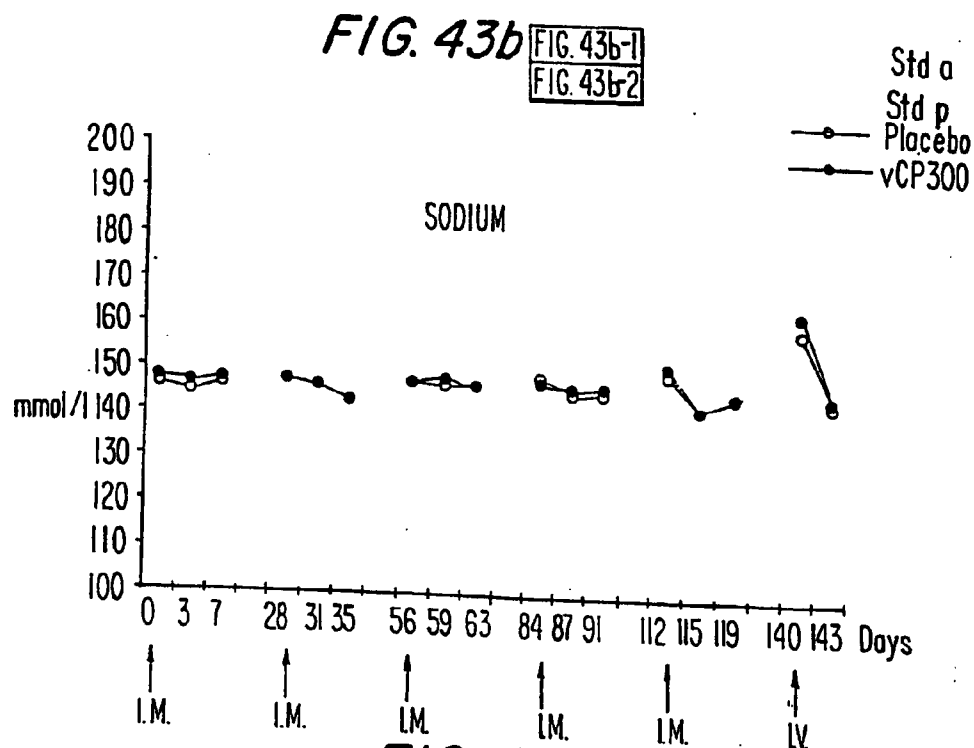
FIG. 41b-2 ALVAC-HIV (vCP300)

FIG. 41b-4









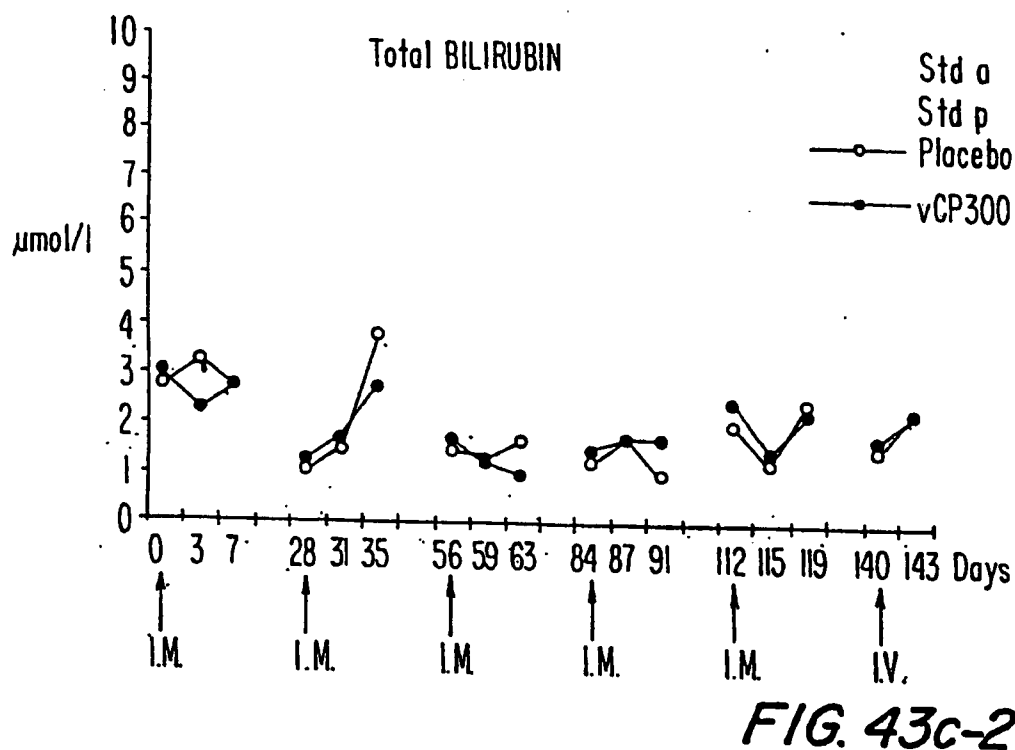
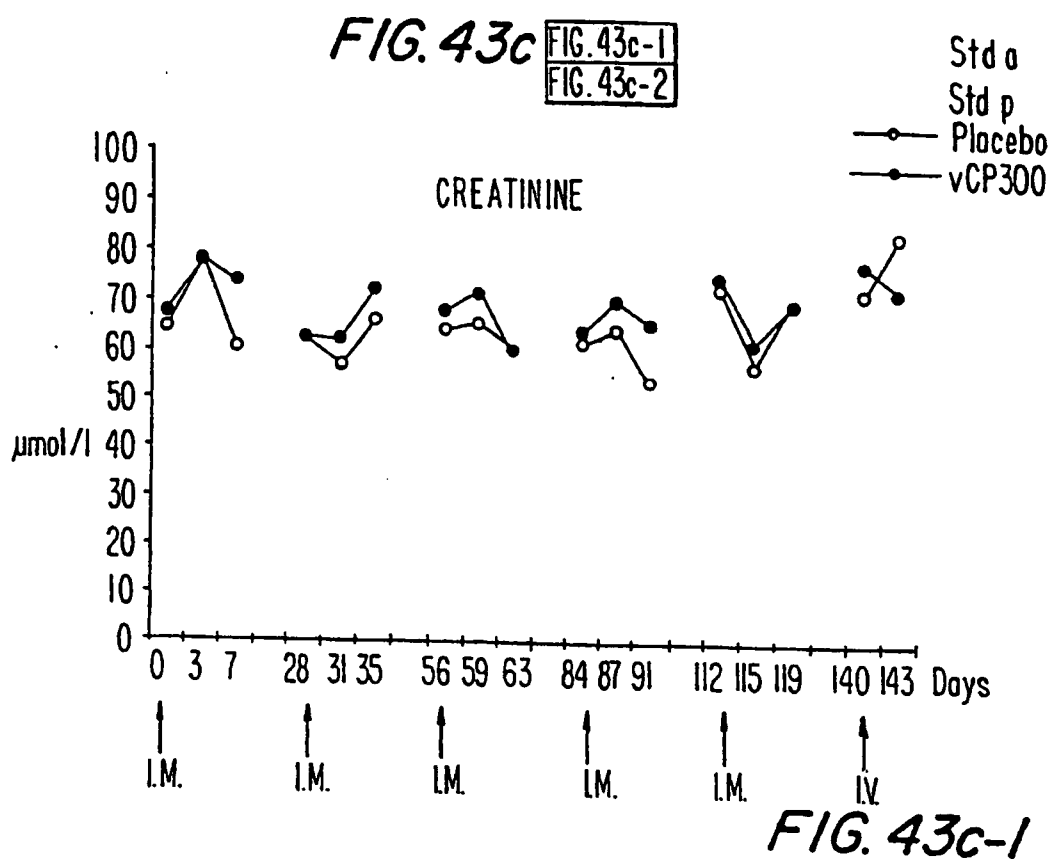
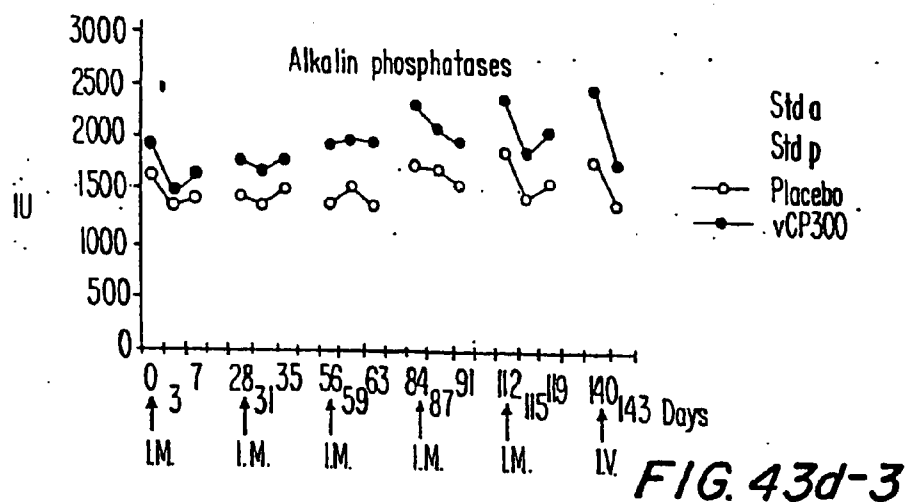
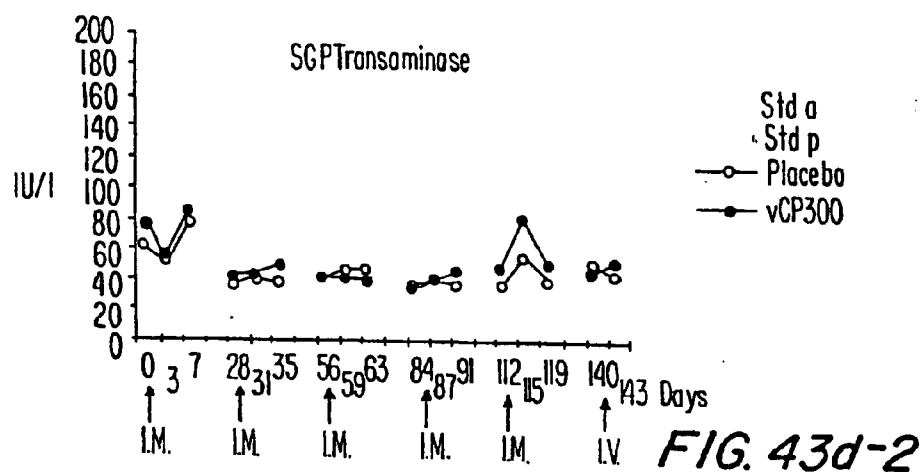
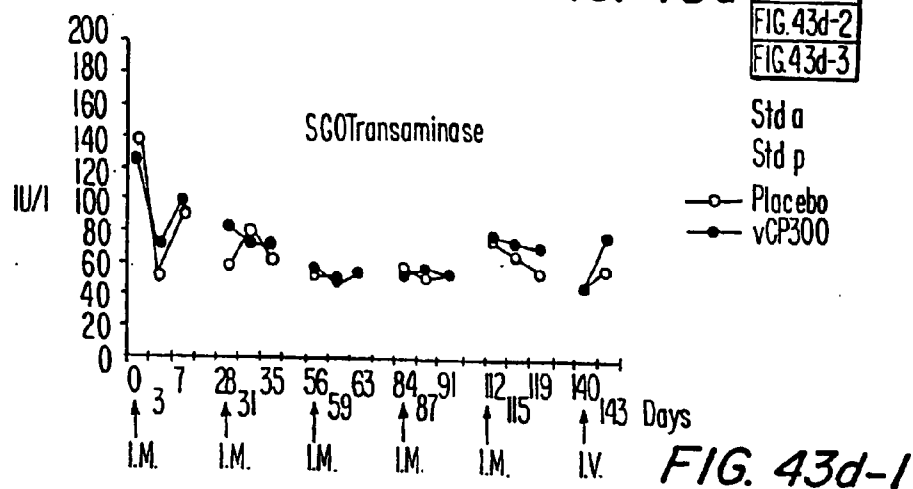
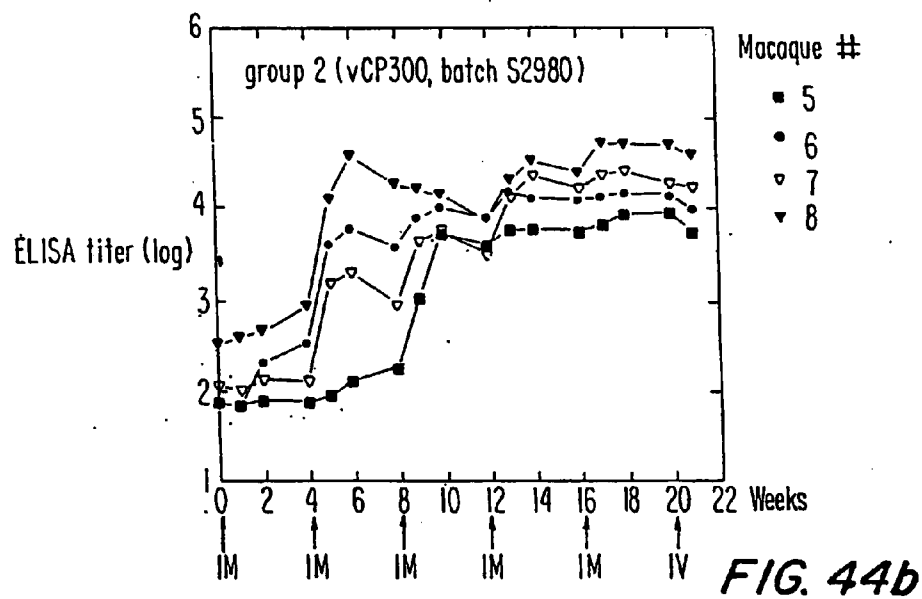
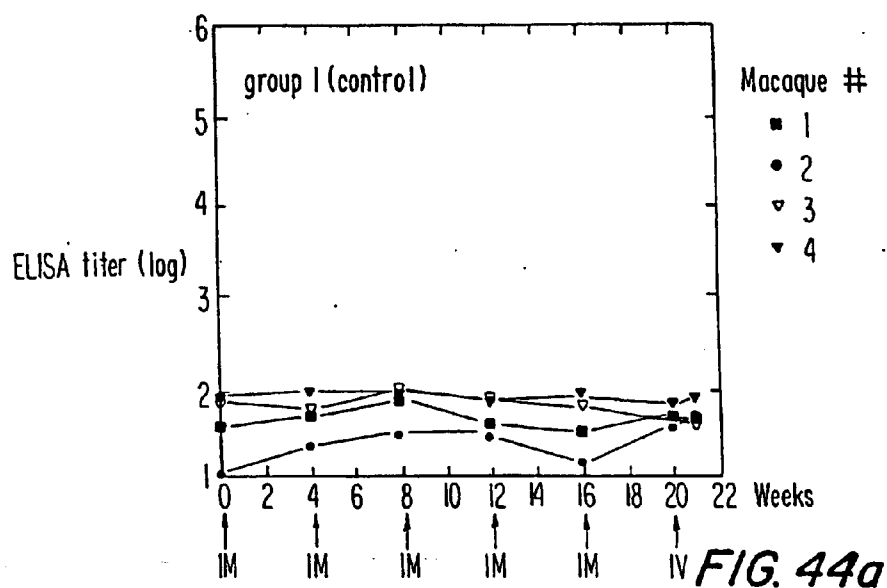


FIG. 43d

FIG. 43d-1
FIG. 43d-2
FIG. 43d-3





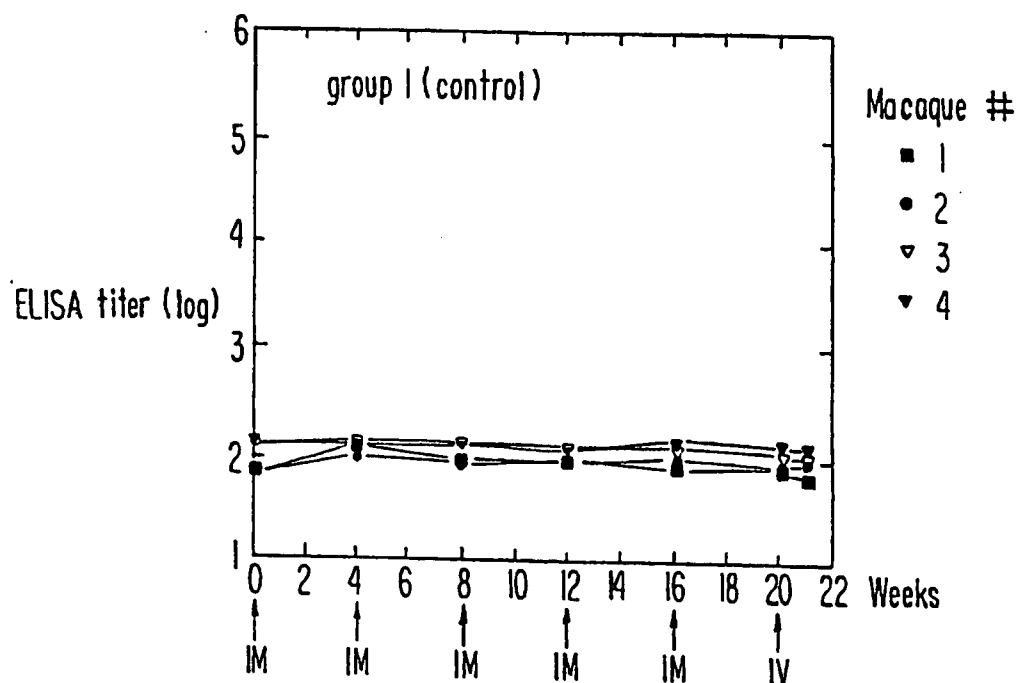


FIG.45a

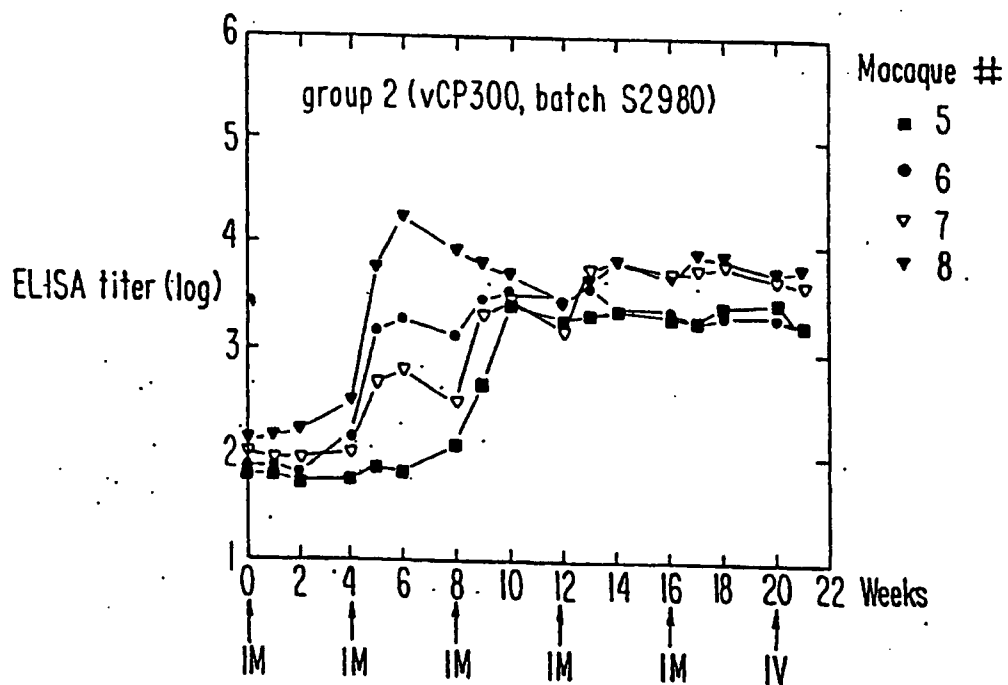
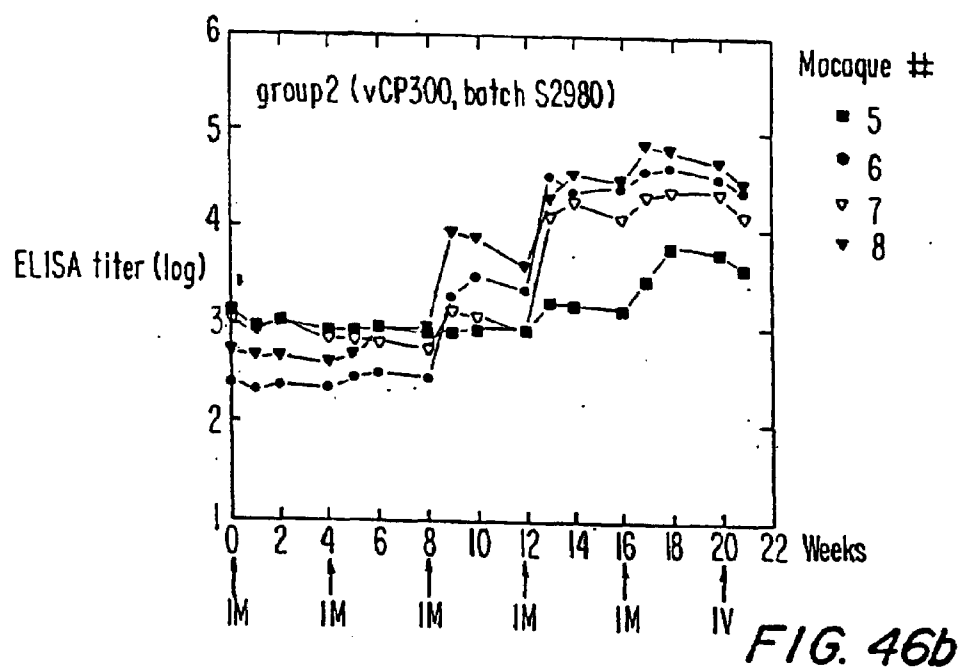
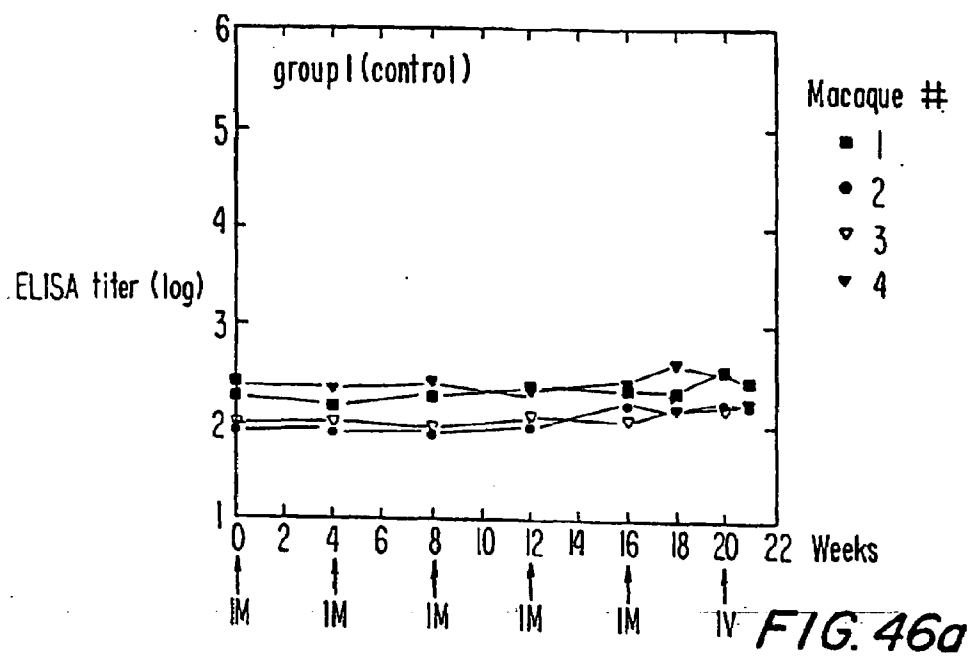
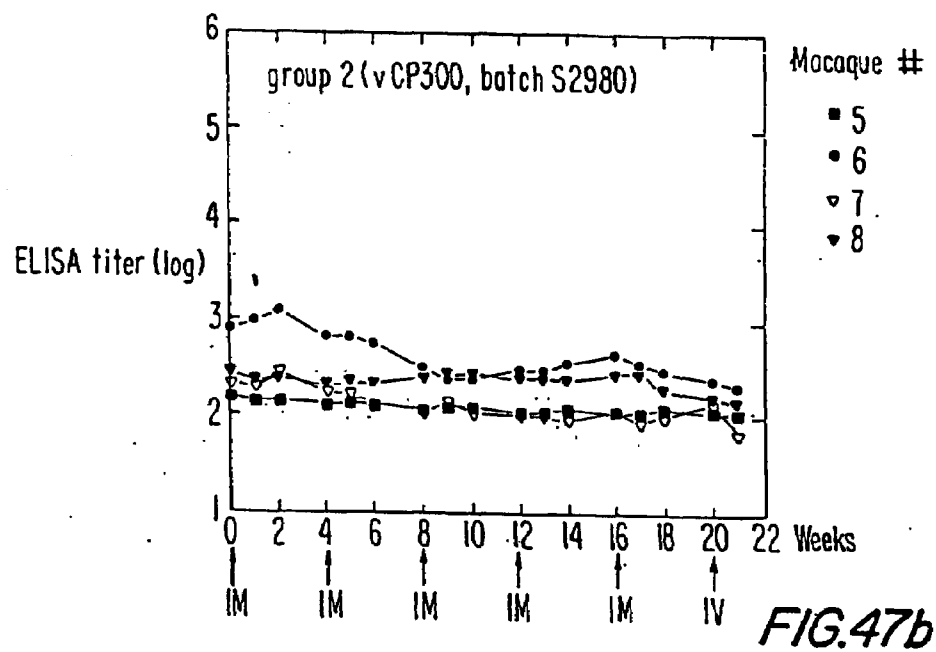
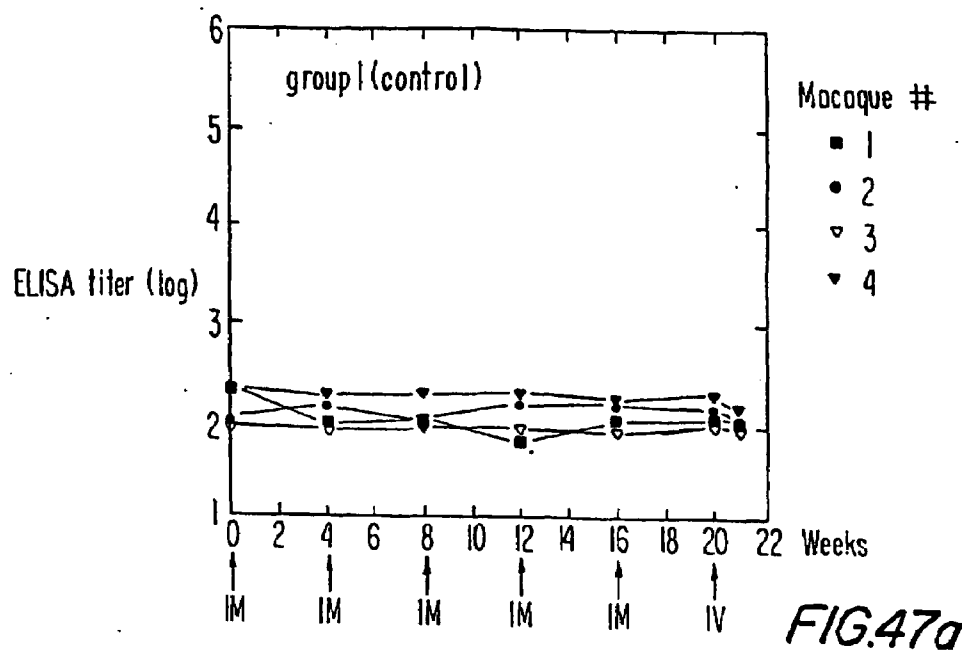


FIG.45b





IMMUNODEFICIENCY RECOMBINANT POXVIRUS

RELATED APPLICATIONS

[0001] This application is a continuation of application Ser. No. 10/441,788, filed May 20, 2003, which in turn is a divisional of application Ser. No. 09/136,159, filed Aug. 14, 1998, now U.S. Pat. No. 6,596,279, which in turn is a divisional of application Ser. No. 08/417,210, filed Apr. 5, 1995, now U.S. Pat. No. 5,863,542, which in turn is a continuation-in-part of application Ser. No. 08/223,842, filed Apr. 6, 1994, abandoned, which in turn is a continuation-in-part of application Ser. No. 07/897,382, filed Jun. 11, 1992, abandoned, which in turn is a continuation-in-part of application Ser. No. 07/715,921, filed Jun. 14, 1991, abandoned. This application is also a continuation-in-part of application Ser. No. 08/105,483, filed Aug. 12, 1993, now U.S. Pat. No. 5,494,807 which in turn is a continuation of application Ser. No. 07/847,951, filed Mar. 6, 1992, abandoned, which in turn is a continuation-in-part of application Ser. No. 07/713,967, filed Jun. 11, 1991, abandoned, which in turn is a continuation in part of application Ser. No. 07/666,056, filed Mar. 7, 1991, abandoned. Mention is also made of co-pending application Ser. No. 08/184,009, filed Jan. 19, 1994, now U.S. Pat. No. 5,833,975, as a continuation-in-part of application Ser. No. 08/007,115, filed Jan. 21, 1993, abandoned. Each of the aforementioned and above-referenced applications is hereby incorporated herein by reference.

FIELD OF THE INVENTION

[0002] The present invention relates to a modified poxvirus and to methods of making and using the same. More in particular, the invention relates to improved vectors for the insertion and expression of foreign genes for use as safe immunization vehicles to elicit an immune response against immunodeficiency virus. Thus, the invention relates to a recombinant poxvirus, which virus expresses gene products of immunodeficiency virus and to immunogenic compositions which induce an immunological response against immunodeficiency virus infections when administered to a host, or in vitro (e.g. ex vivo modalities) as well as to the products of expression of the poxvirus which by themselves are useful for eliciting an immune response e.g., raising antibodies, which antibodies are useful against immunodeficiency virus infection, in either seropositive or seronegative individuals, or are useful if isolated from an animal or human for preparing a diagnostic kit, test or assay for the detection of the virus or infected cells.

[0003] Several publications are referenced in this application. Full citation to these references is found at the end of the specification immediately preceding the claims or where the publication is mentioned; and each of these publications is hereby incorporated herein by reference.

BACKGROUND OF THE INVENTION

[0004] Vaccinia virus and more recently other poxviruses have been used for the insertion and expression of foreign genes. The basic technique of inserting foreign genes into live infectious poxvirus involves recombination between pox DNA sequences flanking a foreign genetic element in a donor plasmid and homologous sequences present in the rescuing poxvirus (Piccini et al., 1987).

[0005] Specifically, the recombinant poxviruses are constructed in two steps known in the art and analogous to the methods for creating synthetic recombinants of poxviruses such as the vaccinia virus and avipox virus described in U.S. Pat. Nos. 4,769,330, 4,772,848, 4,603,112, 5,100,587, and 5,179,993, the disclosures of which are incorporated herein by reference.

[0006] First, the DNA gene sequence to be inserted into the virus, particularly an open reading frame from a non-pox source, is placed into an *E. coli* plasmid construct into which DNA homologous to a section of DNA of the poxvirus has been inserted. Separately, the DNA gene sequence to be inserted is ligated to a promoter. The promoter-gene linkage is positioned in the plasmid construct so that the promoter-gene linkage is flanked on both ends by DNA homologous to a DNA sequence flanking a region of pox DNA containing a nonessential locus. The resulting plasmid construct is then amplified by growth within *E. coli* bacteria (Clewell, 1972) and isolated (Clewell et al., 1969; Maniatis et al., 1982).

[0007] Second, the isolated plasmid containing the DNA gene sequence to be inserted is transfected into a cell culture, e.g. chick embryo fibroblasts, along with the poxvirus. Recombination between homologous pox DNA in the plasmid and the viral genome respectively gives a poxvirus modified by the presence, in a nonessential region of its genome, of foreign DNA sequences. The term "foreign" DNA designates exogenous DNA, particularly DNA from a non-pox source, that codes for gene products not ordinarily produced by the genome into which the exogenous DNA is placed.

[0008] Genetic recombination is in general the exchange of homologous sections of DNA between two strands of DNA. In certain viruses RNA may replace DNA. Homologous sections of nucleic acid are sections of nucleic acid (DNA or RNA) which have the same sequence of nucleotide bases.

[0009] Genetic recombination may take place naturally during the replication or manufacture of new viral genomes within the infected host cell. Thus, genetic recombination between viral genes may occur during the viral replication cycle that takes place in a host cell which is co-infected with two or more different viruses or other genetic constructs. A section of DNA from a first genome is used interchangeably in constructing the section of the genome of a second co-infecting virus in which the DNA is homologous with that of the first viral genome.

[0010] However, recombination can also take place between sections of DNA in different genomes that are not perfectly homologous. If one such section is from a first genome homologous with a section of another genome except for the presence within the first section of, for example, a genetic marker or a gene coding for an antigenic determinant inserted into a portion of the homologous DNA, recombination can still take place and the products of that recombination are then detectable by the presence of that genetic marker or gene in the recombinant viral genome. Additional strategies have recently been reported for generating recombinant vaccinia virus.

[0011] Successful expression of the inserted DNA genetic sequence by the modified infectious virus requires two conditions. First, the insertion must be into a nonessential region of the virus in order that the modified virus remain viable. The second condition for expression of inserted DNA is the presence of a promoter in the proper relationship to the inserted DNA. The promoter must be placed so that it is located upstream from the DNA sequence to be expressed.

[0012] Vaccinia virus has been used successfully to immunize against smallpox, culminating in the worldwide eradication of smallpox in 1980. In the course of its history, many strains of vaccinia have arisen. These different strains demonstrate varying immunogenicity and are implicated to varying degrees with potential complications, the most serious of which are post-vaccinial encephalitis and generalized vaccinia (Behbehani, 1983).

[0013] With the eradication of smallpox, a new role for vaccinia became important, that of a genetically engineered vector for the expression of foreign genes. Genes encoding a vast number of heterologous antigens have been expressed in vaccinia, often resulting in protective immunity against challenge by the corresponding pathogen (reviewed in Tartaglia et al., 1990a).

[0014] The genetic background of the vaccinia vector has been shown to affect the protective efficacy of the expressed foreign immunogen. For example, expression of Epstein Barr Virus (EBV) gp340 in the Wyeth vaccine strain of vaccinia virus did not protect cottontop tamarins against EBV virus induced lymphoma, while expression of the same gene in the WR laboratory strain of vaccinia virus was protective (Morgan et al., 1988).

[0015] A fine balance between the efficacy and the safety of a vaccinia virus-based recombinant vaccine candidate is extremely important. The recombinant virus must present the immunogen(s) in a manner that elicits a protective immune response in the vaccinated animal but lacks any significant pathogenic properties. Therefore attenuation of the vector strain would be a highly desirable advance over the current state of technology.

[0016] A number of vaccinia genes have been identified which are non-essential for growth of the virus in tissue culture and whose deletion or inactivation reduces virulence in a variety of animal systems.

[0017] The gene encoding the vaccinia virus thymidine kinase (TK) has been mapped (Hruby et al., 1982) and sequenced (Hruby et al., 1983; Weir et al., 1983). Inactivation or complete deletion of the thymidine kinase gene does not prevent growth of vaccinia virus in a wide variety of cells in tissue culture. TK⁻ vaccinia virus is also capable of replication in vivo at the site of inoculation in a variety of hosts by a variety of routes.

[0018] It has been shown for herpes simplex virus type 2 that intravaginal inoculation of guinea pigs with TK⁻ virus resulted in significantly lower virus titers in the spinal cord than did inoculation with TK⁺ virus (Stanberry et al., 1985). It has been demonstrated that herpesvirus encoded TK activity in vitro was not important for virus growth in actively metabolizing cells, but was required for virus growth in quiescent cells (Jamieson et al., 1974).

[0019] Attenuation of TK⁻ vaccinia has been shown in mice inoculated by the intracerebral and intraperitoneal routes (Buller et al., 1985). Attenuation was observed both for the WR neurovirulent laboratory strain and for the Wyeth vaccine strain. In mice inoculated by the intradermal route, TK⁻ recombinant vaccinia generated equivalent anti-vaccinia neutralizing antibodies as compared with the parental TK⁺ vaccinia virus, indicating that in this test system the loss of TK function does not significantly decrease immunogenicity of the vaccinia virus vector. Following intranasal inoculation of mice with TK⁻ and TK⁺ recombinant vaccinia virus (WR

strain), significantly less dissemination of virus to other locations, including the brain, has been found (Taylor et al., 1991a).

[0020] Another enzyme involved with nucleotide metabolism is ribonucleotide reductase. Loss of virally encoded ribonucleotide reductase activity in herpes simplex virus (HSV) by deletion of the gene encoding the large subunit was shown to have no effect on viral growth and DNA synthesis in dividing cells in vitro, but severely compromised the ability of the virus to grow on serum starved cells (Goldstein et al., 1988). Using a mouse model for acute HSV infection of the eye and reactivatable latent infection in the trigeminal ganglia, reduced virulence was demonstrated for HSV deleted of the large subunit of ribonucleotide reductase, compared to the virulence exhibited by wild type HSV (Jacobson et al., 1989).

[0021] Both the small (Slabaugh et al., 1988) and large (Schmidt et al., 1988) subunits of ribonucleotide reductase have been identified in vaccinia virus. Insertional inactivation of the large subunit of ribonucleotide reductase in the WR strain of vaccinia virus leads to attenuation of the virus as measured by intracranial inoculation of mice (Child et al., 1990).

[0022] The vaccinia virus hemagglutinin gene (HA) has been mapped and sequenced (Shida, 1986). The HA gene of vaccinia virus is nonessential for growth in tissue culture (Ichihashi et al., 1971). Inactivation of the HA gene of vaccinia virus results in reduced neurovirulence in rabbits inoculated by the intracranial route and smaller lesions in rabbits at the site of intradermal inoculation (Shida et al., 1988). The HA locus was used for the insertion of foreign genes in the WR strain (Shida et al., 1987), derivatives of the Lister strain (Shida et al., 1988) and the Copenhagen strain (Guo et al., 1989) of vaccinia virus. Recombinant HA vaccinia virus expressing foreign genes have been shown to be immunogenic (Guo et al., 1989; Itamura et al., 1990; Shida et al., 1988; Shida et al., 1987) and protective against challenge by the relevant pathogen (Guo et al., 1989; Shida et al., 1987).

[0023] Cowpox virus (Brighton red strain) produces red (hemorrhagic) pocks on the chorioallantoic membrane of chicken eggs. Spontaneous deletions within the cowpox genome generate mutants which produce white pocks (Pickup et al., 1984). The hemorrhagic function (u) maps to a 38 kDa protein encoded by an early gene (Pickup et al., 1986). This gene, which has homology to serine protease inhibitors, has been shown to inhibit the host inflammatory response to cowpox virus (Palumbo et al., 1989) and is an inhibitor of blood coagulation.

[0024] The u gene is present in WR strain of vaccinia virus (Kotwal et al., 1989b). Mice inoculated with a WR vaccinia virus recombinant in which the u region has been inactivated by insertion of a foreign gene produce higher antibody levels to the foreign gene product compared to mice inoculated with a similar recombinant vaccinia virus in which the u gene is intact (Zhou et al., 1990). The u region is present in a defective nonfunctional form in Copenhagen strain of vaccinia virus (open reading frames B13 and B14 by the terminology reported in Goebel et al., 1990a,b).

[0025] Cowpox virus is localized in infected cells in cytoplasmic A type inclusion bodies (ATI) (Kato et al., 1959). The function of ATI is thought to be the protection of cowpox virus virions during dissemination from animal to animal (Bergoin et al., 1971). The ATI region of the cowpox genome encodes a 160 kDa protein which forms the matrix of the ATI bodies (Funahashi et al., 1988; Patel et al., 1987). Vaccinia

virus, though containing a homologous region in its genome, generally does not produce ATI. In WR strain of vaccinia, the ATI region of the genome is translated as a 94 kDa protein (Patel et al., 1988). In Copenhagen strain of vaccinia virus, most of the DNA sequences corresponding to the ATI region are deleted, with the remaining 3' end of the region fused with sequences upstream from the ATI region to form open reading frame (ORF) A26L (Goebel et al., 1990a,b).

[0026] A variety of spontaneous (Altenburger et al., 1989; Drillien et al., 1981; Lai et al., 1989; Moss et al., 1981; Paez et al., 1985; Panicali et al., 1981) and engineered (Perkus et al., 1991; Perkus et al., 1989; Perkus et al., 1986) deletions have been reported near the left end of the vaccinia virus genome. A WR strain of vaccinia virus with a 10 kb spontaneous deletion (Moss et al., 1981; Panicali et al., 1981) was shown to be attenuated by intracranial inoculation in mice (Buller et al., 1985). This deletion was later shown to include 17 potential ORFs (Kotwal et al., 1988b). Specific genes within the deleted region include the virokinin N1L and a 35 kDa protein (C3L, by the terminology reported in Goebel et al., 1990a,b). Insertional inactivation of N1L reduces virulence by intracranial inoculation for both normal and nude mice (Kotwal et al., 1989a). The 35 kDa protein is secreted like N1L into the medium of vaccinia virus infected cells. The protein contains homology to the family of complement control proteins, particularly the complement 4B binding protein (C4 bp) (Kotwal et al., 1988a). Like the cellular C4 bp, the vaccinia 35 kDa protein binds the fourth component of complement and inhibits the classical complement cascade (Kotwal et al., 1990). Thus the vaccinia 35 kDa protein appears to be involved in aiding the virus in evading host defense mechanisms.

[0027] The left end of the vaccinia genome includes two genes which have been identified as host range genes, K1L (Gillard et al., 1986) and C7L (Perkus et al., 1990). Deletion of both of these genes reduces the ability of vaccinia virus to grow on a variety of human cell lines (Perkus et al., 1990).

[0028] Two additional vaccine vector systems involve the use of naturally host-restricted poxviruses, avipoxviruses. Both fowlpoxvirus (FPV) and canarypoxvirus (CPV) have been engineered to express foreign gene products. Fowlpox virus (FPV) is the prototypic virus of the Avipox genus of the Poxvirus family. The virus causes an economically important disease of poultry which has been well controlled since the 1920's by the use of live attenuated vaccines. Replication of the avipox viruses is limited to avian species (Matthews, 1982) and there are no reports in the literature of avipoxvirus causing a productive infection in any non-avian species including man. This host restriction provides an inherent safety barrier to transmission of the virus to other species and makes use of avipoxvirus based vaccine vectors in veterinary and human applications an attractive proposition.

[0029] FPV has been used advantageously as a vector expressing antigens from poultry pathogens. The hemagglutinin protein of a virulent avian influenza virus was expressed in an FPV recombinant (Taylor et al., 1988a). After inoculation of the recombinant into chickens and turkeys, an immune response was induced which was protective against either a homologous or a heterologous virulent influenza virus challenge (Taylor et al., 1988a). FPV recombinants expressing the surface glycoproteins of Newcastle Disease Virus have also been developed (Taylor et al., 1990; Edbauer et al., 1990).

[0030] Despite the host-restriction for replication of FPV and CPV to avian systems, recombinants derived from these

viruses were found to express extrinsic proteins in cells of nonavian origin. Further, such recombinant viruses were shown to elicit immunological responses directed towards the foreign gene product and where appropriate were shown to afford protection from challenge against the corresponding pathogen (Tartaglia et al., 1993a,b; Taylor et al., 1992; 1991b; 1988b).

[0031] In 1983, human immunodeficiency virus type 1 (HIV1) was identified as the causative agent of AIDS. Twelve years later, despite a massive, worldwide effort, an effective HIV1 vaccine is still not available. Recently, however, several reports have suggested that an efficacious HIV1 vaccine may be attainable. For example, macaques have been protected against a simian immunodeficiency virus (SIV) challenge by a vaccination protocol involving a primary immunization with a vaccinia virus recombinant expressing the SIV gp160 glycoprotein and a booster immunization with purified SIV gp160 glycoprotein (Hu et al., 1992). In addition, chimpanzees have been protected against an HIV1 challenge with an HIV1 gp120 subunit vaccine (Berman et al., 1990). Chimps have also been protected against an HIV1 challenge by a vaccination protocol involving multiple injections of either inactivated HIV1, gp160 and/or V3 peptide or gp160, p17 (a Gag protein) and/or V3 peptide (Girard et al., 1991). A similar protocol involving multiple injections of gp160, p17, p24 (a Gag protein), Vif, Nef and/or V3 peptide has also protected chimps against a challenge of HIV1-infected cells (Fultz et al., 1992). Furthermore, chimps have been passively protected by the infusion of HIV1 V3-specific antibodies (Emini et al., 1992).

[0032] Most of these vaccination protocols have focused on eliciting an immune response against the HIV1 or SIV envelope glycoprotein, or more specifically, against the V3 epitope of the envelope glycoprotein. Unfortunately, different strains of HIV1 exhibit extensive genetic and antigenic variability, especially in the envelope glycoprotein. Therefore, an effective HIV1 vaccine may need to elicit an immune response against more than one HIV1 antigen, or one epitope of one HIV1 antigen.

[0033] Contrary to the extensive sequence variability observed in B-cell epitopes, T-cell epitopes are relatively conserved. For example, cytotoxic T-lymphocytes (CTL) clones, isolated from an HIV1-seronegative individual vaccinated with a vaccinia virus recombinant expressing HIV1 gp160 (LAI strain) and boosted with purified HIV1 gp160 (LAI), lyse target cells expressing the HIV1 MN or RF envelope glycoprotein as efficiently as cells expressing the HIV1 LAI envelope glycoprotein (Hammond et al., 1992). Therefore, a vaccine that elicits an immune response against relatively conserved T-cell epitopes may not only be more efficacious against a homologous challenge, but also more efficacious against a heterologous challenge.

[0034] HIV1-seronegative individuals have been vaccinated with an ALVAC recombinant (vCP125) expressing HIV1 gp160, in a prime-boost protocol similar to the regimen used to vaccinate macaques against SIV. These ALVAC-based protocols demonstrated the ability of vCP125 to elicit HIV1 envelope-specific CD8⁺ CTLs and to enhance envelope-specific humoral responses observed following a subunit booster (Pialoux et al., 1995). These results justify the rationale for a recombinant ALVAC-based HIV1 vaccine.

[0035] Individuals infected with human immunodeficiency virus type 1 (HIV1) initially generate a relatively dynamic and extensive antiviral immune response, including HIV1-

specific neutralizing antibodies and HIV1-specific CTLs. Despite these responses, however, the vast majority of HIV1-infected people eventually succumb to HIV1-associated diseases. Since the immune response generated by most HIV1-infected people is not protective, generation of an effective immune response may necessitate that the immune response be modulated or redirected against HIV1 epitopes that are not normally or efficiently seen by HIV1-infected individuals.

[0036] Approximately 40% of the HIV1-specific antibody in HIV1-seropositive individuals capable of binding HIV1-infected cells is specific to the third variable region (V3) of the HIV1 envelope glycoprotein (Spear et al, 1994). These results indicate that the V3 loop is 1) highly immunogenic and 2) exposed on the surface of infected cells. The amino acid sequence of the V3 loop varies considerably between different HIV1 isolates. Therefore, a moderate level of sequence variation does not appear to alter the structure or immunogenicity of this region of the envelope glycoprotein. Since the V3 loop is highly immunogenic and its structure and immunogenicity is not severely affected by sequence variation, this region of the envelope glycoprotein may be useful as an immunogenic platform for presenting normally non-immunogenic linear HIV1 epitopes or heterologous epitopes to the immune system.

[0037] Sera from HIV1-seropositive individuals can neutralize lab-adapted strains of HIV1. These sera can also neutralize primary HIV1 isolates (although 100× higher titers are required). Conversely, sera from individuals vaccinated with HIV1 gp120 can neutralize lab-adapted strains of HIV1 (although 10× higher titers relative to sera from seropositive individuals are required), but can not neutralize (at assayable levels) primary isolates (Hanson, 1994). A significant portion of the neutralizing activity found in sera from seropositive and gp120-vaccinated individuals appears to be specific to the V3 loop (Spear et al., 1994; Berman et al., 1994). Since the V3 loop is hypervariable and since antibodies against this region may not neutralize primary isolates or heterologous strains of HIV1, it may be necessary to develop vaccines that elicit an immune response against epitopes other than the V3 loop, epitopes that can neutralize a broad spectrum of HIV1 strains, including primary isolates.

[0038] A monoclonal antibody capable of neutralizing primary HIV1 isolates, as well as a broad spectrum of lab-adapted HIV1 strains, has been isolated (Conley et al., 1994; Katinger et al., 1992). The epitope recognized by this monoclonal antibody has been mapped between amino acids 662 and 667 of HIV1 gp41 and has the amino acid sequence, ELDKWA (Buchacher et al, 1994). Approximately 80% of the HIV1 strains from which sequence information has been derived, including strains from the various HIV1 clades, express the core binding sequence of this epitope, LDKW (Conley et al., 1994). Therefore, unlike the V3 loop, this epitope appears to be relatively well conserved. Unfortunately, this epitope does not appear to be very immunogenic in its normal configuration. Only approximately 50% of HIV1-seropositive individuals have a detectable antibody response to the region of gp41 containing this epitope (Broliden et al., 1992).

[0039] It can thus be appreciated that provision of an immunodeficiency virus recombinant poxvirus, and of an immunogenic composition which induces an immunological response against immunodeficiency virus infections when administered to host, particularly a composition having enhanced safety such as NYVAC or ALVAC based recombi-

nants containing coding for any or all of HIV1gag(+pro) (IIIB), gp120(MN) (+transmembrane), nef(BRU)CTL epitopes, pol(IIIB)CTL epitopes; for instance, HIV1gag(+pro) (IIIB), gp120(MN) (+transmembrane), nefCTL1, nefCTL2, pol1(PolCTL1), pol2(PolCTL2), pol3(PolCTL3), ELDKWA or LDKW epitopes (SEQ ID NOS: 147 and 148), especially in an immunogenic configuration, or any combination thereof, for example all of them in combination, would be a highly desirable advance over the current state of technology.

OBJECTS AND SUMMARY OF THE INVENTION

[0040] It is therefore an object of this invention to provide modified recombinant viruses, which viruses have enhanced safety, and to provide a method of making such recombinant viruses.

[0041] It is an additional object of this invention to provide a recombinant poxvirus antigenic, vaccine or immunological composition having an increased level of safety compared to known recombinant poxvirus vaccines.

[0042] It is a further object of this invention to provide a modified vector for expressing a gene product in a host, wherein the vector is modified so that it has attenuated virulence in the host.

[0043] It is another object of this invention to provide a method for expressing a gene product in a cell cultured in vitro using a modified recombinant virus or modified vector having an increased level of safety.

[0044] These and other objects and advantages of the present invention will become more readily apparent after consideration of the following.

[0045] In one aspect, the present invention relates to a modified recombinant virus having inactivated virus-encoded genetic functions so that the recombinant virus has attenuated virulence and enhanced safety. The functions can be non-essential, or associated with virulence. The virus is advantageously a poxvirus, particularly a vaccinia virus or an avipox virus, such as fowlpox virus and canarypox virus. The modified recombinant virus can include, within a non-essential region of the virus genome, a heterologous DNA sequence which encodes an antigen or epitope derived from immunodeficiency virus and/or CTL epitope such as, e.g., HIV1gag(+pro) (IIIB), gp120(MN) (+transmembrane), nef (BRU)CTL, pol(IIIB)CTL, ELDKWA, LDKW epitopes or any combination thereof, preferably all of them in combination.

[0046] In another aspect, the present invention relates to an antigenic, immunological or vaccine composition or a therapeutic composition for inducing an antigenic or immunological response in a host animal inoculated with the composition, said vaccine including a carrier and a modified recombinant virus having inactivated nonessential virus-encoded genetic functions so that the recombinant virus has attenuated virulence and enhanced safety. The virus used in the composition according to the present invention is advantageously a poxvirus, particularly a vaccinia virus or an avipox virus, such as fowlpox virus and canarypox virus. The modified recombinant virus can include, within a non-essential region of the virus genome, a heterologous DNA sequence which encodes an antigenic protein, e.g., derived from immunodeficiency virus and/or CTL such as, HIV1gag(+pro) (IIIB), gp120 (MN) (+transmembrane), nef(BRU)CTL, pol(IIIB)CTL,

ELDKWA, LDKW epitopes or any combination thereof, preferably all of them in combination.

[0047] In yet another aspect, the present invention relates to an immunogenic composition containing a modified recombinant virus having inactivated nonessential virus-encoded genetic functions so that the recombinant virus has attenuated virulence and enhanced safety. The modified recombinant virus includes, within a non-essential region of the virus genome, a heterologous DNA sequence which encodes an antigenic protein (e.g., derived from an immunodeficiency virus and/or CTL such as, HIV1gag(+pro) (IIIB), gp120 (MN) (+transmembrane), nef(BRU)CTL, pol(IIIB)CTL, ELDKWA, LDKW epitopes or any combination thereof, preferably all of them in combination) wherein the composition, when administered to a host, is capable of inducing an immunological response specific to the antigen.

[0048] In a further aspect, the present invention relates to a method for expressing a gene product in a cell (e.g. peripheral blood mononuclear cells (PBMCs) or lymph node mononuclear cells (LNMN) in vitro by introducing into the cell a modified recombinant virus having attenuated virulence and coenhanced safety. The modified recombinant virus can include, within a nonessential region of the virus genome, a heterologous DNA sequence which encodes an antigenic protein, e.g. derived from an immunodeficiency virus such as HIV/gag (+pro) (IIIB), gp120(MN) (+transmembrane), nef (BRU)CTL, pol (IIIB)CTL, ELDKWA, LDKW epitopes or any combination thereof, preferably all of them in combination. The cells can then be reinfused directly into the individual or used to amplify specific CD8⁺ CTL reactivities for reinfusion (Ex vivo therapy).

[0049] In a further aspect, the present invention relates to a method for expressing a gene product in a cell cultured in vitro by introducing into the cell a modified recombinant virus having attenuated virulence and enhanced safety. The modified recombinant virus can include, within a non-essential region of the virus genome, a heterologous DNA sequence which encodes an antigenic protein, e.g., derived from an immunodeficiency virus such as HIV1gag (+pro) (IIIB), gp120(MN) (+transmembrane), nef(BRU)CTL, pol (IIIB)CTL, ELDKWA, LDKW epitopes or any combination thereof, preferably all of them in combination. The product can then be administered to individuals or animals to stimulate an immune response. The antibodies raised can be useful in individuals for the prevention or treatment of immunodeficiency virus and, the antibodies from animals can be used in diagnostic kits, assays or tests to determine the presence or absence in a sample such as sera of immunodeficiency virus or CTL antigens (and therefore the absence or presence of the virus of an immune response to the virus or antibodies).

[0050] In a still further aspect, the present invention relates to a modified recombinant virus having nonessential virus-encoded genetic functions inactivated therein so that the virus has attenuated virulence, and wherein the modified recombinant virus further contains DNA from a heterologous source in a nonessential region of the virus genome. The DNA can code for an immunodeficiency virus and/or CTL antigen such as HIV1gag(+pro) (IIIB), gp120(MN) (+transmembrane), nef(BRU)CTL, pol(IIIB)CTL, ELDKWA, LDKW epitopes or any combination thereof, preferably all of them in combination. In particular, the genetic functions are inactivated by deleting an open reading frame encoding a virulence factor or by utilizing naturally host restricted viruses. The virus used according to the present invention is advantageously a pox-

virus, particularly a vaccinia virus or an avipox virus, such as fowlpox virus and canarypox virus. Advantageously, the open reading frame is selected from the group consisting of J2R, B13R+B14R, A26L, A56R, C7L-K1L, and 14L (by the terminology reported in Goebel et al., 1990a,b); and, the combination thereof. In this respect, the open reading frame comprises a thymidine kinase gene, a hemagglutinin gene, an A type inclusion body region, a hemagglutinin gene, a host range gene region or a large subunit, ribonucleotide reductase; or, the combination thereof. The modified Copenhagen strain of vaccinia virus is identified as NYVAC (Tartaglia et al., 1992). However, the COPAK strain can also be used in the practice of the invention.

[0051] Most preferably, in recombinant viruses of the invention, the exogenous DNA codes for HIV1gag(+pro) (IIIB), gp120(MN) (+transmembrane), two (2) nef(BRU) CTL and three (3) pol(IIIB)CTL epitopes; or, the exogenous DNA codes for the ELDKWA or LDKW epitopes, and, is inserted so as to be expressed in a region of gp120 or gp160 (i.e., the exogenous DNA codes for a ELDKWA or LDKW modified gp120 or gp160, for instance ELDKWA or LDKW or repeats of either or both in the V3 loop) such that the epitope is expressed in an immunogenic configuration. In this most preferred embodiment it is even more preferred that the two (2) nef(BRU)CTL and three (3) pol(IIIB)CTL epitopes are CTL1, CTL2, pol1, pol2, and pol3. In another most preferred embodiment the exogenous DNA codes for HIV1 gp120+TM in which the V3 loop has been modified to contain at least one, and preferably two ELDKWA epitopes.

[0052] In further embodiments, the invention comprehends HIV immunogens and modified gp160 or gp120. Thus, the invention includes an HIV immunogen preferably selected from the group consisting of: HIV1gag(+pro) (IIIB), gp120 (MN) (+transmembrane), nef (BRU)CTL, pol(IIIB)CTL, and ELDKWA or LDKW epitopes. The HIV immunogen of the invention can be part of gp160 or gp120. Thus the HIV immunogens ELDKWA or LDKWA, for example, can be a part of a region of gp120 or a region of gp160; for instance, part of gp120V3. Accordingly, the invention comprehends a gp120 or gp160 modified so as to contain an epitope not naturally occurring in gp160. The epitope can be a B-cell epitope. The epitope, more specifically, can be at least one of HIV1gag(+pro) (IIIB), gp120(MN) (+transmembrane), nef (BRU)CTL, pol(IIIB)CTL, and ELDKWA or LDKW epitopes. The gp120 can be modified in the V3 loop. The immunogen and modified gp120 or gp160 can be synthesized by any suitable vector, including a poxvirus, such as a recombinant of the invention; or, by any suitable chemical synthesis method such as the Merrifield Synthesis Method.

[0053] The invention in yet a further aspect relates to the product of expression of the inventive recombinant poxvirus and uses therefor, as well as to uses for the inventive immunogens and modified gp120 and gp160, such as to form antigenic, immunological or vaccine compositions for treatment, prevention, diagnosis or testing. The invention in still a further embodiment relates to the uses of DNA from the recombinants as probes for detecting the presence or absence of HIV DNA in a sample or for DNA immunization using an appropriate expression plasmid.

[0054] These and other embodiments are disclosed or are obvious from and encompassed by the following detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0055] The following detailed description, given by way of example, but not intended to limit the invention solely to the specific embodiments described, may best be understood in conjunction with the accompanying drawings, in which:

[0056] FIG. 1 schematically shows a method for the construction of plasmid pSD460 for deletion of thymidine kinase gene and generation of recombinant vaccinia virus vP410;

[0057] FIG. 2 schematically shows a method for the construction of plasmid pSD486 for deletion of hemorrhagic region and generation of recombinant vaccinia virus vP553;

[0058] FIG. 3 schematically shows a method for the construction of plasmid pMP494Δ for deletion of ATI region and generation of recombinant vaccinia virus vP618;

[0059] FIG. 4 schematically shows a method for the construction of plasmid pSD467 for deletion of hemagglutinin gene and generation of recombinant vaccinia virus vP723;

[0060] FIG. 5 schematically shows a method for the construction of plasmid pMPCK1Δ for deletion of gene cluster [C7L-K1L] and generation of recombinant vaccinia virus vP804;

[0061] FIG. 6 schematically shows a method for the construction of plasmid pSD548 for deletion of large subunit, ribonucleotide reductase and generation of recombinant vaccinia virus vP866 (NYVAC);

[0062] FIG. 7 schematically shows a method for the construction of plasmid pRW842 for insertion of rabies glycoprotein G gene into the TK deletion locus and generation of recombinant vaccinia virus vP879;

[0063] FIG. 8 shows the DNA sequence (SEQ ID NO:66) of a canarypox PvuII fragment containing the C5 ORF.

[0064] FIGS. 9A and 9B schematically show a method for the construction of recombinant canarypox virus vCP65 (ALVAC-RG);

[0065] FIG. 10 shows schematically the ORFs deleted to generate NYVAC;

[0066] FIG. 11 shows the nucleotide sequence (SEQ ID NO:67) of a fragment of TROVAC DNA containing an F8 ORF;

[0067] FIG. 12 shows the DNA sequence (SEQ ID NO:68) of a 2356 base pair fragment of TROVAC DNA containing the F7 ORF;

[0068] FIGS. 13A to 13D show graphs of rabies neutralizing antibody titers (RFFIT, IU/ml), booster effect of HDC and vCP65 ($10^{5.5}$ TCID₅₀) in volunteers previously immunized with either the same or the alternate vaccine (vaccines given at days 0, 28 and 180, antibody titers measured at days 0, 7, 28, 35, 56, 173, 187 and 208);

[0069] FIG. 14A to 14C shows the nucleotide sequence of the H6-promoted HIV1 gp120 (+transmembrane) gene and the I3L-promoted HIV1gag(+pro) gene contained in pHIV32 (SEQ ID NOS: 78 and 79);

[0070] FIG. 15A to 15F shows the nucleotide sequence of the C3 locus in pVQH6CP3L (SEQ ID NOS: 80 and 81);

[0071] FIG. 16 shows the nucleotide sequence of the I3L-promoted nef CTL2 epitope and H6-promoted nef CTL1 epitope contained in p2-60-HIV.3 (SEQ ID NOS: 93-96);

[0072] FIG. 17A to 17C shows the nucleotide sequence of the C6 locus in pC6L (SEQ ID NOS: 97 and 98);

[0073] FIG. 18A to 18B shows the nucleotide sequence of the I3L-promoted pol2 epitope, H6-promoted pol1 epitope and 42K-promoted pol3 epitope contained in pC5POLT5A (SEQ ID NOS: 111-115);

[0074] FIG. 19A to 19C shows the nucleotide sequence of the C5 locus in pNC5L-SP5 (SEQ ID NOS: 116 and 117);

[0075] FIG. 20 shows the rabbit antibody responses to the HIV envelope glycoprotein following immunization with ALVAC, vCP205, or with peptide CLTB-36;

[0076] FIG. 21 shows the rabbit antibody responses to the HIV MN V3 loop following immunization with ALVAC, vCP205, or with peptide CLTB-36;

[0077] FIG. 22 shows the guinea pig antibody responses to the HIV envelope glycoprotein following immunization with ALVAC, vCP205, or with peptide CLTB-36;

[0078] FIG. 23 shows the guinea pig antibody responses to the HIV MN V3 loop following immunization with ALVAC, vCP205, or with peptide CLTB-36;

[0079] FIG. 24 shows in vitro stimulation of HIV-1-specific CTLs from PBMCs of an HIV-seropositive individual—Patient 1;

[0080] FIG. 25 is as in FIG. 24 but with Patient 2;

[0081] FIG. 26a-c, shows the nucleotide sequence of the H6-promoted HIV1 gp120+TM (with ELDKWA epitopes) gene (SEQ ID NOS: 135 and 136) contained in pHIV59 and vCP1307 and the protein expressed (SEQ ID NO: 137);

[0082] FIG. 27 shows FACS analysis of vCP1307-infected cells (FACS analysis was performed on HeLa cells infected with ALVAC, vP1286 or vCP1307 with sera from HIV1-seropositive humans (upper panel) or a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (lower panel));

[0083] FIG. 28a-c shows the nucleotide sequence of the H6-promoted HIV1 gp120+TM (with ELDKWA epitopes) gene (SEQ ID NOS: 138 and 139) contained in pHIV60 and vP1313 and the protein expressed (SEQ ID NO: 140);

[0084] FIG. 29 shows FACS analysis of vP1313-infected cells (FACS analysis was performed on HeLa cells infected with NYVAC, vP1286 or vP1313 with sera from HIV1-seropositive humans (upper panel) or a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (lower panel));

[0085] FIG. 30a-c shows the nucleotide sequence of the H6-promoted HIV1 gp120+TM (with ELDKWA epitopes) gene (SEQ ID NOS: 141 to 142) contained in pHIV61 and vP1319 and the protein expressed (SEQ ID NO: 143);

[0086] FIG. 31 shows the FACS analysis of vP1319-infected cells (FACS analysis was performed on HeLa cells infected with WR, vP1286 or vP1319 with sera from HIV1-seropositive humans (upper panel), a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (middle panel) or a mouse monoclonal antibody specific for the V3 loop, 50.1 (lower panel));

[0087] FIGS. 32, 33a, 33b, 33c, 34, 35, 36, 37a, 37b, 37c, 38a, 38b, 38c show comparative body weights (FIG. 32), blood counts (FIG. 33a-c), creatinine (FIG. 34), SGOT (35), SGPT (FIG. 36), ELISA (Anti-gp160 MN/BR, -v3MN, -p24, FIGS. 37a-c, 38a-c) of monkeys inoculated with vCP205 and placebo (FIG. 32). upper panel=monkeys 1-4, placebo; lower panel=monkeys 5-8 vCP205; monkeys: 1=open square, 2=open diamond, 3=open triangle, 4=open circle, 5=darkened square, 6=darkened diamond, 7=darkened triangle, 8=darkened circle; plots of Kg (wt) vs. weeks (inoculations indicated with arrow). FIG. 33a: leucocytes: left top and bot-

tom panels=monkeys 1-4, placebo; right top and bottom panels=monkeys 5-8, vCP205; top panels individual WBC counts, key same as FIG. 32 except small darkened circle is mean (m); lower panels differential cell counts, darkened square=granulo, open square=lympho, darkened diamond=mono. FIG. 33b: same layout and keying as FIG. 33a, with upper panels indicating erythrocytes and lower panels indicating mean corpuscle volume and mean indicated by smaller darkened circle. FIG. 33c: same layout as FIG. 33b with upper panels indicating hematocrite and lower panels indicating hemoglobin. FIG. 34: upper bar graphs=monkeys 1-4, placebo; lower bar graph=monkeys 5-8, vCP205; mg/l vs. days, arrow indicates inoculation; monkeys 1 and 5=dark bars, monkeys 2 and 6=double stippling bars (slanted lines in opposite directions), monkeys 3 and 7=dotted bars, monkeys 4 and 8=single stippling bar (slant lines in one direction), mean is darkened circles. FIG. 35: same keying as FIG. 34, except IU/l vs. days. FIG. 36: same keying as FIG. 35. FIGS. 37a-c and 38a-c: ELISA in placebo administered monkeys (FIGS. 37a-c) and in vCP205 administered monkeys (FIGS. 38a-c), titer (log) vs. weeks, arrow indicates injection; FIGS. 37a and 38a=anti-gp160 MN/BRU, FIGS. 37b and 38b=anti-V3MN, FIGS. 37c and 38c=anti-p24; monkeys 1 and 5=open circle; monkeys 2 and 6=darkened circle; monkeys 3 and 7=open inverted triangle; monkeys 4 and 8=darkened inverted triangle);

[0088] FIG. 39 shows anti-HIV1 (MN) neutralizing antibodies in monkeys inoculated with vCP205 (keying same as FIG. 38a-c); and,

[0089] FIGS. 40, 41a, 41b, 41c, 42, 43a, 43b, 43c, 43d, 44a, 44b, 45a, 45b, 46a, 46b, 47a, and 47b show leucocyte counts (FIG. 40), blood counts (erythrocytes FIG. 41a, hematocrite FIG. 41b, reticulocytes FIG. 41c), prothrombin (FIG. 42), biochemical results (total cholesterol, total proteins, glucose FIG. 43a; sodium, potassium FIG. 43b; creatinine, bilirubin FIG. 43c; SGOTransaminase, SGPTransaminase, alkaline phosphatase FIG. 43d), gp160 MN/BRU ELISA (control FIG. 44a, test animals FIG. 44b), V3 MN ELISA (control FIG. 46a, test animals FIG. 46b), and nef ELISA (control FIG. 47a, test animals FIG. 47b) in monkeys inoculated with vCP300 and a placebo (FIG. 40: layout same as FIG. 33a; keying same as FIG. 33a, except in upper panels, mean is dotted circle (left) and open circle (right) and in lower panels decimal instead of percentage and darkened square=neutro, open diamond=eosino, and darkened triangle=baso. FIG. 41a: layout same as FIG. 33b, keying same as FIG. 33a, except mean is dotted circle (left) and open circle (right). FIG. 41b: layout same as FIG. 33c, keying same as FIG. 41a. FIG. 41c: layout and keying same as FIG. 41b, upper panels=reticulocytes, lower panels=thrombocytes. FIG. 42: upper panel=placebo, lower panel=vCP300, keying same as FIG. 41c. FIG. 43a: top=cholesterol, middle=proteins, lower=glucose; open circle=placebo, darkened circle=vCP300. FIG. 43b: top=sodium, lower=potassium; keying same as FIG. 43a. FIG. 43c: top=creatinine, lower=bilirubin; keying same as FIG. 43a. FIG. 43d: top=SGOT, middle=SGPT, lower=alkaline phosphatases; keying same as FIG. 43a. FIGS. 44a, 44b: gp160 MN/BRU ELISA, control and vCP300, respectively; keying same as FIGS. 37a and 38a, respectively. FIGS. 45a, 45b: V3 MN ELISA, control and vCP300, respectively; keying same as FIGS. 37b and 38b, respectively. FIGS. 46a, 46b: p34 ELISA, control and vCP300, respectively; keying same as FIGS. 37c

and 38c, respectively. FIG. 47a, 47b, nef ELISA, control and vCP300, respectively; keying as in FIGS. 44a-46b).

DETAILED DESCRIPTION OF THE INVENTION

[0090] To develop a new vaccinia vaccine strain, NYVAC (vP866), the Copenhagen vaccine strain of vaccinia virus was modified by the deletion of six nonessential regions of the genome encoding known or potential virulence factors. The sequential deletions are detailed below. All designations of vaccinia restriction fragments, open reading frames and nucleotide positions are based on the terminology reported in Goebel et al., 1990a,b.

[0091] The deletion loci were also engineered as recipient loci for the insertion of foreign genes.

[0092] The regions deleted in NYVAC are listed below. Also listed are the abbreviations and open reading frame designations for the deleted regions (Goebel et al., 1990a,b) and the designation of the vaccinia recombinant (vP) containing all deletions through the deletion specified:

[0093] (1) thymidine kinase gene (TK; J2R) vP410;

[0094] (2) hemorrhagic region (u; B13R+B14R) vP553;

[0095] (3) A type inclusion body region (ATI; A26L) vP618;

[0096] (4) hemagglutinin gene (HA; A56R) vP723;

[0097] (5) host range gene region (C7L-K1L) vP804; and

[0098] (6) large subunit, ribonucleotide reductase (14L) vP866 (NYVAC).

[0099] NYVAC is a genetically engineered vaccinia virus strain that was generated by the specific deletion of eighteen open reading frames encoding gene products associated with virulence and host range. NYVAC is highly attenuated by a number of criteria including i) decreased virulence after intracerebral inoculation in newborn mice, ii) innocuity in genetically (nu⁺/nu⁺) or chemically (cyclophosphamide) immunocompromised mice, iii) failure to cause disseminated infection in immunocompromised mice, iv) lack of significant induration and ulceration on rabbit skin, v) rapid clearance from the site of inoculation, and vi) greatly reduced replication competency on a number of tissue culture cell lines including those of human origin. Nevertheless, NYVAC based vectors induce excellent responses to extrinsic immunogens and provided protective immunity.

[0100] TROVAC refers to an attenuated fowlpox that was a plaque-cloned isolate derived from the FP-1 vaccine strain of fowlpoxvirus which is licensed for vaccination of 1 day old chicks. ALVAC is an attenuated canarypox virus-based vector that was a plaque-cloned derivative of the licensed canarypox vaccine, Kanapox (Tartaglia et al., 1992). ALVAC has some general properties which are the same as some general properties of Kanapox. ALVAC-based recombinant viruses expressing extrinsic immunogens have also been demonstrated efficacious as vaccine vectors (Tartaglia et al., 1993 a,b). This avipox vector is restricted to avian species for productive replication. On human cell cultures, canarypox virus replication is aborted early in the viral replication cycle prior to viral DNA synthesis. Nevertheless, when engineered to express extrinsic immunogens, authentic expression and processing is observed in vitro in mammalian cells and inoculation into numerous mammalian species induces antibody and cellular immune responses to the extrinsic immunogen and provides protection against challenge with the cognate pathogen (Taylor et al., 1992; Taylor et al., 1991). Recent Phase I clinical trials in both Europe and the United States of

a canarypox/rabies glycoprotein recombinant (ALVAC-RG) demonstrated that the experimental vaccine was well tolerated and induced protective levels of rabiesvirus neutralizing antibody titers (Cadoz et al., 1992; Fries et al., 1992). Additionally, peripheral blood mononuclear cells (PBMCs) derived from the ALVAC-RG vaccinees demonstrated significant levels of lymphocyte proliferation when stimulated with purified rabies virus (Fries et al., 1992).

[0101] NYVAC, ALVAC and TROVAC have also been recognized as unique among all poxviruses in that the National Institutes of Health ("NIH") (U.S. Public Health Service), Recombinant DNA Advisory Committee, which issues guidelines for the physical containment of genetic material such as viruses and vectors, i.e., guidelines for safety procedures for the use of such viruses and vectors which are based upon the pathogenicity of the particular virus or vector, granted a reduction in physical containment level: from BSL2 to BSL1. No other poxvirus has a BSL1 physical containment level. Even the Copenhagen strain of vaccinia virus—the common smallpox vaccine—has a higher physical containment level; namely, BSL2. Accordingly, the art has recognized that NYVAC, ALVAC and TROVAC have a lower pathogenicity than any other poxvirus.

[0102] Both NYVAC- and ALVAC-based recombinant viruses have been shown to stimulate *in vitro* specific CD8⁺ CTLs from human PBMCs (Tartaglia et al., 1993a). Mice immunized with NYVAC or ALVAC recombinants expressing various forms of the HIV-1 envelope glycoprotein generated both primary and memory HIV specific CTL responses which could be recalled by a second inoculation (Tartaglia et al., 1993a; Cox et al., 1993). ALVAC-env and NYVAC-env recombinants (expressing the HIV-1 envelope glycoprotein) stimulated strong HIV-specific CTL responses from peripheral blood mononuclear cells (PBMC) of HIV-1 infected individuals (Tartaglia et al., 1993a; Cox et al., 1993). Acutely infected autologous PBMC were used as stimulator cells for the remaining PBMC. After 10 days incubation in the absence of exogenous IL-2, the cells were evaluated for CTL activities. NYVAC-env and ALVAC-env stimulated high levels of anti-HIV activities in mice.

[0103] Applicants have generated an ALVAC recombinant, vCP300 (ALVAC-MN120TMGNP), that expresses numerous HIV1 antigens and HIV1 T-cell epitopes. vCP300 expresses the HIV1 (IIIB) gag (and protease) proteins. (Expression of the protease protein allows the gag polyprotein to be correctly processed.) vCP300 also expresses a form of the HIV1 (MN) envelope glycoprotein in which gp120 is fused to the transmembrane anchor sequence derived from gp41. vCP300 also expresses two (2) HIV1 (BRU) nef CTL epitopes and three (3) HIV1 (IIIB) pol CTL epitopes. vCP300 does not, however, express a functional reverse transcriptase activity. vCP300 also does not express a functional nef gene product; a protein associated with pathogenicity in the SIV-macaque model system and HIV1 virulence (Miller et al, 1994; Spina et al, 1994). Therefore, vCP300 expresses immunologically important antigens and/or epitopes from gag, env, pol and nef, but does not express the potentially detrimental enzymatic and/or pathogenic activities associated with pol and nef.

[0104] As previously mentioned, vCP300 expresses a form of HIV1 envelope glycoprotein in which the vast majority of the gp41 sequence is deleted. Since most of the immunologically important epitopes associated with the HIV1 envelope glycoprotein are found on gp120, rather than gp41, it is

assumed that the immunogenicity of the envelope glycoprotein expressed by this recombinant is not adversely affected. In fact, in a side-by-side analysis, an HIV1 gp120 subunit vaccine was able to protect chimpanzees against an HIV1 challenge, whereas an HIV1 gp160 subunit vaccine was not (Berman et al., 1990). It is not known why the efficacy of these two vaccines is different. However, it is known that antibodies against an epitope gp41 can enhance HIV1 infection *in vitro* (Robinson et al., 1990). Furthermore, it is known that antibodies to a putative immunosuppressive region of gp41 are associated with the absence of AIDS in HIV1-seropositive individuals, suggesting a potential role in pathogenicity for this region (Klasse et al., 1988). In addition, it is known that antibodies to the C-terminal region of gp41 can cross-react with HLA class II antigens (Golding et al., 1988) and inhibit antigen-specific lymphoproliferative responses (Golding et al., 1989). Since the envelope glycoprotein expressed by vCP300 does not contain any gp41 sequence, except for the 28 amino acids associated with the transmembrane region, the potentially detrimental effects associated with gp41 are avoided. Furthermore, the envelope glycoprotein expressed by vCP300 does not contain the immunodominant epitope on gp41 that is recognized by antisera from every HIV1-seropositive individual from every stage of an HIV1 infection (Shafferman et al., 1989). Therefore, diagnostic tests based upon reactivity against this epitope can be used to distinguish between vaccinated and infected individuals. The ability to differentiate vCP300-vaccinated individuals from HIV1-infected individuals with a gp41 antibody assay is important because the most commonly used diagnostic kit (which assays for the presence of HIV1 p24 antibodies) would be useless, since vCP300-vaccinated individuals would be expected to have a high level of p24 antibodies. Alternatively, HIV-1 infected individuals would be expected to make anti-gp41 antibodies but those vaccinated with vCP205 or vCP300 would not since gp41 is absent from vCP205 or vCP300.

[0105] Rabbits and guinea pigs have been inoculated with an ALVAC recombinant (vCP205; ALVAC-MN120TMG) expressing the same cell surface-associated form of HIV1 gp120 (120TM) and Gag/pro as expressed by vCP300. Rabbits and guinea pigs have also been inoculated with vCP205 and boosted with an HIV1 T-B peptide. Both ALVAC-based protocols were able to elicit HIV1 gp160- and V3 loop-specific antibodies, thereby indicating that an ALVAC recombinant expressing the cell surface form of HIV1 gp120 induces an HIV1-specific immune response.

[0106] vCP300 expresses the HIV1 Gag proteins, a cell surface-associated form of the HIV1 gp120 envelope glycoprotein, two (2) regions from HIV1 nef containing CTL epitopes and three (3) regions from HIV1 pol containing CTL epitopes. The expression of an HIV1 envelope glycoprotein that does not contain gp41 allows vaccinated individuals to be differentiated from HIV1-infected individuals via an assay for gp41 antibodies and eliminates potentially detrimental responses associated with various gp41 epitopes. Since a previous ALVAC recombinant expressing HIV1 gp160 has been shown to elicit HIV1-specific humoral and cellular immune responses in humans (Pialoux et al., 1995), the addition of Gag and the Pol and Nef epitopes (and the deletion of

the potentially detrimental gp41 epitopes) heightens and broadens the immune response elicited by vCP300, relative to vCP125, and, may provide an efficacious HIV1 vaccine, or immunological or antigenic composition.

[0107] In *Macaca fascicularis* (monkeys; macaques) immunized with vCP205 or vCP300, an antibody response (anti-HIV) was observed, thereby further demonstrating the utility and efficacy of these recombinants.

[0108] Since the ELDKWA or LDKW epitope does not appear to be very immunogenic in its normal configuration, to increase its immunogenicity, recombinants of the invention present it to the immune system in a more immunogenic setting, such as within the V3 loop of gp120 or within other regions of gp120 and/or as part of an intact gp160 envelope.

[0109] ALVAC recombinant (vCP1307), NYVAC recombinant (vP1313) and COPAK recombinant (vP1319) express a form of the HIV1 gp120+TM gene product in which the V3 loop has been modified to contain two copies of the ELDKWA epitope. The ELDKWA epitopes of this gp120+TM (with ELDKWA epitopes) gene product are expressed on the surface of vCP1307-, vP1313- and vP1319-infected cells.

[0110] The V3 loop of HIV1 gp120+TM (or gp160) can be used as an immunological platform for any linear epitope, not just linear HIV1 epitopes. The gp120+TM (with epitopes of interest) protein generated by these recombinants can also be isolated from poxvirus-infected cells and used to inoculate individuals in a subunit vaccine configuration (composition, or an antigenic or immunological composition). The proteins generated by the recombinants and antibodies elicited therefrom can also be used in assays to detect the presence or absence of HIV. Accordingly, the invention comprehends HIV immunogens and modified gp120 and gp160. Further, such envelope-based immunogens (HIV immunogens or unmodified gp120 or gp160 (can be derived from any eukaryotic or prokaryotic expression vector and used as subunit preparations or can be administered through DNA immunization using an appropriate expression plasmid. Techniques for DNA immunization are known in the art. With respect to techniques for DNA immunization, mention is particularly made of Nabel and Felgner, "Direct gene transfer for immunotherapy and immunization", Tibtech, May 1993, 11: 211-215, and Webster et al., "protection of ferrets against influenza challenge with a DNA vaccine to the haemagglutinin", vaccine, 1994, 12(16): 1495-1498, incorporated herein by reference. Also, the DNA from the recombinants vP1313, vP1319 and vCP1307 can be used to probe for the presence of HIV DNA in a sample of interest using known hybridization techniques, or, to generate PCR primers using known techniques.

[0111] Clearly based on the attenuation profiles of the NYVAC, ALVAC, and TROVAC vectors and their demonstrated ability to elicit both humoral and cellular immunological responses to extrinsic immunogens (Tartaglia et al., 1993a,b; Taylor et al., 1992; Konishi et al., 1992) such recombinant viruses offer a distinct advantage over previously described vaccinia-based recombinant viruses.

[0112] The administration procedure for recombinant virus, immunogen, modified gp120 or gp160, DNA or expression product compositions of the invention such as immunological, antigenic or vaccine compositions or therapeutic compositions can be via a parenteral route (intradermal, intramuscular or subcutaneous). Such an administration enables a systemic immune response.

[0113] More generally, the inventive antigenic, immunological or vaccine compositions or therapeutic compositions

(compositions containing the poxvirus recombinants, expression products, immunogens, DNA, modified gp120 or gp160 of the invention) can be prepared in accordance with standard techniques well known to those skilled in the pharmaceutical art. Such compositions can be administered in dosages and by techniques well known to those skilled in the medical arts taking into consideration such factors as the age, sex, weight, and condition of the particular patient, and the route of administration. The compositions can be administered alone, or can be co-administered or sequentially administered with compositions of the invention or with other immunological, antigenic or vaccine or therapeutic compositions in seropositive individuals. The compositions can be administered alone, or can be co-administered or sequentially administered with compositions of the invention or with other antigenic, immunological, vaccine or therapeutic compositions in seronegative individuals. Such other compositions can include purified antigens from immunodeficiency virus or from the expression of such antigens by a recombinant poxvirus or other vector system or, such other compositions can include a recombinant poxvirus which expresses other immunodeficiency antigens or biological response modifiers (e.g. cytokines; co-stimulating molecules). Again, co-administration is performed by taking into consideration such known factors as the age, sex, weight, and condition of the particular patient, and, the route of administration.

[0114] Examples of compositions of the invention include liquid preparations for orifice, e.g., oral, nasal, anal, vaginal, etc., administration such as suspensions, syrups or elixirs; and, preparations for parenteral, subcutaneous, intradermal, intramuscular or intravenous administration (e.g., injectable administration) such as sterile suspensions or emulsions. In such compositions the recombinant poxvirus, expression product, immunogen, DNA, or modified gp120 or gp160 may be in admixture with a suitable carrier, diluent, or excipient such as sterile water, physiological saline, glucose or the like.

[0115] Further, the products of expression of the inventive recombinant poxviruses can be used directly to stimulate an immune response in either seronegative or seropositive individuals or in animals. Thus, the expression products can be used in compositions of the invention instead or in addition to the inventive recombinant poxvirus in the aforementioned compositions. The immunogens of the invention can be similarly used.

[0116] Additionally, the inventive recombinant poxvirus and the expression products therefrom and immunogens and modified gp120 or gp160 of the invention stimulate an immune or antibody response in humans and animals. From those antibodies or by techniques well-known in the art, monoclonal antibodies can be prepared and, those monoclonal antibodies, can be employed in well known antibody binding assays, diagnostic kits or tests to determine the presence or absence of particular immunodeficiency virus antigen (s) and therefore the presence or absence of the virus, or to determine whether an immune response to the virus or antigen(s) has simply been stimulated. Those monoclonal antibodies can also be employed in immunoadsorption chromatography to recover immunodeficiency virus or expression products of the inventive recombinant poxvirus.

[0117] Monoclonal antibodies are immunoglobulins produced by hybridoma cells. A monoclonal antibody reacts with a single antigenic determinant and provides greater specificity than a conventional, serum-derived antibody. Furthermore, screening a large number of monoclonal antibodies

makes it possible to select an individual antibody with desired specificity, avidity and isotype. Hybridoma cell lines provide a constant, inexpensive source of chemically identical antibodies and preparations of such antibodies can be easily standardized. Methods for producing monoclonal antibodies are well known to those of ordinary skill in the art, e.g., Koprowski, H. et al., U.S. Pat. No. 4,196,265, issued Apr. 1, 1989, incorporated herein by reference.

[0118] Uses of monoclonal antibodies are known. One such use is in diagnostic methods, e.g., David, G. and Greene, H. U.S. Pat. No. 4,376,110, issued Mar. 8, 1983; incorporated herein by reference. Monoclonal antibodies have also been used to recover materials by immunoadsorption chromatography, e.g., Milstein, C. 1980, *Scientific American* 243:66, 70, incorporated herein by reference.

[0119] Furthermore, the inventive recombinant poxvirus or expression products therefrom or the inventive immunogens or modified gp120 or gp160 can be used to stimulate a response in cells such as lymphocytes or CTLs in vitro or ex vivo for subsequent reinfusion into a patient. If the patient is seronegative, the reinfusion is to stimulate an immune response, e.g., an immunological or antigenic response such as active immunization. In a seropositive individual, the reinfusion is to stimulate or boost the immune system against immunodeficiency virus.

[0120] Additionally, the DNA from inventive recombinants can be used as probes to detect the presence of HIV DNA in a sample or, to generate PCR primers, or for DNA immunization using an appropriate expression plasmid, by methods known in the art. (See Nabel and Felger and Webster et al, *Supra*)

[0121] Accordingly, the inventive recombinant poxvirus has several utilities: In antigenic, immunological or vaccine compositions such as for administration to seronegative individuals. In therapeutic compositions in seropositive individuals in need of therapy to stimulate or boost the immune system against immunodeficiency virus. In vitro to produce antigens or the inventive immunogens or the inventive modified gp120 or gp160 which can be further used in antigenic, immunological or vaccine compositions or in therapeutic compositions. To generate antibodies (either by direct administration or by administration of an expression product of the inventive recombinant poxvirus) which can be further used: in diagnosis, tests or kits to ascertain the presence or absence of antigens in a sample such as sera, for instance, to ascertain the presence or absence of immunodeficiency virus or CTLs in a sample such as sera or, to determine whether an immune response has elicited to the virus or, to particular antigen(s); or, in immunoadsorption chromatography (the inventive immunogens and modified gp120 or gp160 can also be used to generate antibodies which can be also so further used). To generate DNA for use as hybridization probes or to prepare PCR primers or for DNA immunization. And, the inventive recombinant poxvirus, expression products therefrom, immunogens and modified gp120 or gp160 can be used to generate stimulated cells which can be further used (reinfused) to stimulate an immune response (antigenic, or immunological response; or active immunization) or, to boost or stimulate the immune system (for instance, of an immunocompromised or seropositive individual). Other utilities also exist for embodiments of the invention.

[0122] A better understanding of the present invention and of its many advantages will be had from the following examples, given by way of illustration.

EXAMPLES

[0123] DNA Cloning and Synthesis. Plasmids were constructed, screened and grown by standard procedures (Maniatis et al., 1982; Perkus et al., 1985; Piccini et al., 1987). Restriction endonucleases were obtained from Bethesda Research Laboratories, Gaithersburg, Md., New England Biolabs, Beverly, Mass.; and Boehringer Mannheim Biochemicals, Indianapolis, Ind. Klenow fragment of *E. coli* polymerase was obtained from Boehringer Mannheim Biochemicals. BAL-31 exonuclease and phage T4 DNA ligase were obtained from New England Biolabs. The reagents were used as specified by the various suppliers.

[0124] Synthetic oligodeoxyribonucleotides were prepared on a Biosearch 8750 or Applied Biosystems 380B DNA synthesizer as previously described (Perkus et al., 1989). DNA sequencing was performed by the dideoxy-chain termination method (Sanger et al., 1977) using Sequenase (Tabor et al., 1987) as previously described (Guo et al., 1989). DNA amplification by polymerase chain reaction (PCR) for sequence verification (Engelke et al., 1988) was performed using custom synthesized oligonucleotide primers and GeneAmp DNA amplification Reagent Kit (Perkin Elmer Cetus, Norwalk, Conn.) in an automated Perkin Elmer Cetus DNA Thermal Cycler. Excess DNA sequences were deleted from plasmids by restriction endonuclease digestion followed by limited digestion by BAL-31 exonuclease and mutagenesis (Mandecki, 1986) using synthetic oligonucleotides.

[0125] Cells, Virus, and Transfection. The origins and conditions of cultivation of the Copenhagen strain of vaccinia virus has been previously described (Guo et al., 1989). Generation of recombinant virus by recombination, in situ hybridization of nitrocellulose filters and screening for B-galactosidase activity are as previously described (Piccini et al., 1987).

[0126] The origins and conditions of cultivation of the Copenhagen strain of vaccinia virus and NYVAC has been previously described (Guo et al., 1989; Tartaglia et al., 1992). Generation of recombinant virus by recombination, in situ hybridization of nitrocellulose filters and screening for B-galactosidase activity are as previously described (Panicali et al., 1982; Perkus et al., 1989).

[0127] The parental canarypox virus (Rentschler strain) is a vaccinal strain for canaries. The vaccine strain was obtained from a wild type isolate and attenuated through more than 200 serial passages on chick embryo fibroblasts. A master viral seed was subjected to four successive plaque purifications under agar and one plaque clone was amplified through five additional passages after which the stock virus was used as the parental virus in in vitro recombination tests. The plaque purified canarypox isolate is designated ALVAC.

[0128] The strain of fowlpox virus (FPV) designated FP-1 has been described previously (Taylor et al., 1988a). It is an attenuated vaccine strain useful in vaccination of day old chickens. The parental virus strain Duvette was obtained in France as a fowlpox scab from a chicken. The virus was attenuated by approximately 50 serial passages in chicken embryonated eggs followed by 25 passages on chicken embryo fibroblast cells. The virus was subjected to four suc-

cessive plaque purifications. One plaque isolate was further amplified in primary CEF cells and a stock virus, designated as TROVAC, established.

[0129] NYVAC, ALVAC and TROVAC viral vectors and their derivatives were propagated as described previously (Piccini et al., 1987; Taylor et al., 1988a,b). Vero cells and chick embryo fibroblasts (CEF) were propagated as described previously (Taylor et al., 1988a,b).

Example 1

Construction of Plasmid pSD460 for Deletion of Thymidine Kinase Gene (J2R)

[0130] Referring now to FIG. 1, plasmid pSD406 contains vaccinia HindIII J (pos. 83359-88377) cloned into pUC8. pSD406 was cut with HindIII and PvuII, and the 1.7 kb fragment from the left side of HindIII J cloned into pUC8 cut with HindIII/SmaI, forming pSD447. pSD447 contains the entire gene for J2R (pos. 83855-84385). The initiation codon is contained within an NlaIII site and the termination codon is contained within an SspI site. Direction of transcription is indicated by an arrow in FIG. 1.

[0131] To obtain a left flanking arm, a 0.8 kb HindIII/EcoRI fragment was isolated from pSD447, then digested with NlaIII and a 0.5 kb HindIII/NlaIII fragment isolated. Annealed synthetic oligonucleotides MPSYN43/MPSYN44 (SEQ ID NO:1/SEQ ID NO:2)

```

MPSYN43  5'      TAATTAAGTACGCTACCCGGG      3'
              SmaI
MPSYN44  3'  GTACATTAATTGATCGATGGGCCCTTAA  5'
              NlaIII      EcoRI

```

were ligated with the 0.5 kb HindIII/NlaIII fragment into pUC18 vector plasmid cut with HindIII/EcoRI, generating plasmid pSD449.

[0132] To obtain a restriction fragment containing a vaccinia right flanking arm and pUC vector sequences, pSD447 was cut with SspI (partial) within vaccinia sequences and HindIII at the pUC/vaccinia junction, and a 2.9 kb vector fragment isolated. This vector fragment was ligated with annealed synthetic oligonucleotides MPSYN45/MPSYN46 (SEQ ID NO:3/SEQ ID NO:4)

```

MPSYN45  5'      AGCTTCCCGGTAAGTAATACGTCAGGAGAAAACGAA
MPSYN46  3'      AGGGCCCATTCATTATGCAGTTCCTCTTTGCTT
              HindIII SmaI

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              NotI      SspI
ACGATCTGTAGTTAGCGGCGCCTAATTAATAAT  3'
TGCTAGACATCAATCGCCGGCGGATTAATTGATTA  5'

```

generating pSD459.

[0133] To combine the left and right flanking arms into one plasmid, a 0.5 kb HindIII/SmaI fragment was isolated from pSD449 and ligated with pSD459 vector plasmid cut with HindIII/SmaI, generating plasmid pSD460. pSD460 was used as donor plasmid for recombination with wild type parental vaccinia virus Copenhagen strain VC-2. ³²P labelled probe was synthesized by primer extension using MPSYN45 (SEQ ID NO:3) as template and the complementary 20mer oligonucleotide MPSYN47 (SEQ ID NO:5) (5' TTAGT-TAATTAGGCGGCCGC 3') as primer. Recombinant virus vP410 was identified by plaque hybridization.

Example 2

Construction of Plasmid pSD486 for Deletion of Hemorrhagic Region (B13R+B14R)

[0134] Referring now to FIG. 2, plasmid pSD419 contains vaccinia SalI G (pos. 160, 744-173,351) cloned into pUC8. pSD422 contains the contiguous vaccinia SalI fragment to the right, SalI J (pos. 173, 351-182,746) cloned into pUC8. To construct a plasmid deleted for the hemorrhagic region, u, B13R-B14R (pos. 172, 549-173,552), pSD419 was used as the source for the left flanking arm and pSD422 was used as the source of the right flanking arm. The direction of transcription for the u region is indicated by an arrow in FIG. 2.

[0135] To remove unwanted sequences from pSD419, sequences to the left of the NcoI site (pos. 172,253) were removed by digestion of pSD419 with NcoI/SmaI followed by blunt ending with Klenow fragment of *E. coli* polymerase and ligation generating plasmid pSD476. A vaccinia right flanking arm was obtained by digestion of pSD422 with HpaI at the termination codon of B14R and by digestion with NruI 0.3 kb to the right. This 0.3 kb fragment was isolated and ligated with a 3.4 kb HincII vector fragment isolated from pSD476, generating plasmid pSD477. The location of the partial deletion of the vaccinia u region in pSD477 is indicated by a triangle. The remaining B13R coding sequences in pSD477 were removed by digestion with ClaI/HpaI, and the resulting vector fragment was ligated with annealed synthetic oligonucleotides SD22mer/SD20mer (SEQ ID NO:6/SEQ ID NO:7)

```

SD22mer  5'      CGATTACTATGAAGGATCCGTT      3'
              ClaI      BamHI HpaI
SD20mer  3'      TAATGATACTTCCTAGGCAA      5'

```

generating pSD479. pSD479 contains an initiation codon (underlined) followed by a BamHI site. To place *E. coli* Beta-galactosidase in the B13-B14 (u) deletion locus under the control of the u promoter, a 3.2 kb BamHI fragment containing the Beta-galactosidase gene (Shapira et al., 1983) was inserted into the BamHI site of pSD479, generating

pSD479BG. pSD479BG was used as donor plasmid for recombination with vaccinia virus vP410. Recombinant vaccinia virus vP533 was isolated as a blue plaque in the presence of chromogenic substrate X-gal. In vP533 the B13R-B14R region is deleted and is replaced by Beta-galactosidase.

[0136] To remove Beta-galactosidase sequences from vP533, plasmid pSD486, a derivative of pSD477 containing a polylinker region but no initiation codon at the u deletion junction, was utilized. First the ClaI/HpaI vector fragment from pSD477 referred to above was ligated with annealed synthetic oligonucleotides SD42mer/SD40mer (SEQ ID NO:8/SEQ ID NO:9)

SD42mer 5' ClaI SacI XhoI HpaI 3'
 CGATTACTAGATCTGAGCTCCCCGGGCTCGAGGGATCCGTT
 SD40mer 3' TAATGATCTAGACTCGAGGGCCCGAGCTCCCTAGGCAA 5'
BglII SmaI BamHI

generating plasmid pSD478. Next the EcoRI site at the pUC/vaccinia junction was destroyed by digestion of pSD478 with EcoRI followed by blunt ending with Klenow fragment of *E. coli* polymerase and ligation, generating plasmid pSD478E⁻. pSD478E⁻ was digested with BamHI and HpaI and ligated with annealed synthetic oligonucleotides HEM5/HEM6 (SEQ ID NO:10/SEQ ID NO:11)

HEM5 5' BamHI EcoRI HpaI 3'
 GATCCGAATTCTAGCT
 HEM6 3' GCTTAAGATCGA 5'

generating plasmid pSD486. pSD486 was used as donor plasmid for recombination with recombinant vaccinia virus vP533, generating vP553, which was isolated as a clear plaque in the presence of X-gal.

Example 3

Construction of Plasmid pMP494Δ for Deletion of ATI Region (A26L)

[0137] Referring now to FIG. 3, pSD414 contains SalI B cloned into pUC8. To remove unwanted DNA sequences to the left of the A26L region, pSD414 was cut with XbaI within vaccinia sequences (pos. 137,079) and with HindIII at the pUC/vaccinia junction, then blunt ended with Klenow fragment of *E. coli* polymerase and ligated, resulting in plasmid pSD483. To remove unwanted vaccinia DNA sequences to the right of the A26L region, pSD483 was cut with EcoRI (pos. 140,665 and at the pUC/vaccinia junction) and ligated, forming plasmid pSD484. To remove the A26L coding region, pSD484 was cut with NdeI (partial) slightly upstream from the A26L ORF (pos. 139,004) and with HpaI (pos. 137,889) slightly downstream from the A26L ORF. The 5.2 kb vector fragment was isolated and ligated with annealed synthetic oligonucleotides ATI3/ATI4 (SEQ ID NO:12/SEQ ID NO:13)

NdeI
 ATI3 5' TATGAGTAACTTAACTCTTTTGTTAATTAAGTATATTCAA
 ATI4 3' ACTCATTTGAATTGAGAAACAATTAATTTTCATATAAGTT
BglII EcoRI HpaI
 AAAATAAGTTATATAAATAGATCTGAATTCGTT 3' ATI3
 TTTTATTCAATATATTATCTAGACTTAAGCAA 5' ATI4

reconstructing the region upstream from A26L and replacing the A26L ORF with a short polylinker region containing the restriction sites BglII, EcoRI and HpaI, as indicated above. The resulting plasmid was designated pSD485. Since the BglII and EcoRI sites in the polylinker region of pSD485 are not unique, unwanted BglII and EcoRI sites were removed from plasmid pSD483 (described above) by digestion with BglII (pos. 140,136) and with EcoRI at the pUC/vaccinia

junction, followed by blunt ending with Klenow fragment of *E. coli* polymerase and ligation. The resulting plasmid was designated pSD489. The 1.8 kb ClaI (pos. 137,198)/EcoRV (pos. 139,048) fragment from pSD489 containing the A26L ORF was replaced with the corresponding 0.7 kb polylinker-containing ClaI/EcoRV fragment from pSD485, generating pSD492. The BglII and EcoRI sites in the polylinker region of pSD492 are unique.

[0138] A 3.3 kb BglII cassette containing the *E. coli* Beta-galactosidase gene (Shapira et al., 1983) under the control of the vaccinia 11 kDa promoter (Bertholet et al., 1985; Perkus et al., 1990) was inserted into the BglII site of pSD492, forming pSD493KBG. Plasmid pSD493KBG was used in recombination with rescuing virus vP553. Recombinant vaccinia virus, vP581, containing Beta-galactosidase in the A26L deletion region, was isolated as a blue plaque in the presence of X-gal.

[0139] To generate a plasmid for the removal of Beta-galactosidase sequences from vaccinia recombinant virus vP581, the polylinker region of plasmid pSD492 was deleted by mutagenesis (Mandecki, 1986) using synthetic oligonucleotide MPSYN177 (SEQ ID NO:14) (5' AAAATGGGCGTGGATTGTAACTT-TATATAACTTATTTTTTGAATATAC 3'). In the resulting plasmid, pMP494Δ, vaccinia DNA encompassing positions [137,889-138,937], including the entire A26L ORF is deleted. Recombination between the pMP494L and the Beta-galactosidase containing vaccinia recombinant, vP581, resulted in vaccinia deletion mutant vP618, which was isolated as a clear plaque in the presence of X-gal.

Example 4

Construction of Plasmid pSD467 for Deletion of Hemagglutinin Gene (A56R)

[0140] Referring now to FIG. 4, vaccinia SalI G restriction fragment (pos. 160, 744-173,351) crosses the HindIII A/B junction (pos. 162,539). pSD419 contains vaccinia SalI G cloned into pUC8. The direction of transcription for the hemagglutinin (HA) gene is indicated by an arrow in FIG. 4. Vaccinia sequences derived from HindIII B were removed by digestion of pSD419 with HindIII within vaccinia sequences and at the pUC/vaccinia junction followed by ligation. The resulting plasmid, pSD456, contains the HA gene, A56R, flanked by 0.4 kb of vaccinia sequences to the left and 0.4 kb of vaccinia sequences to the right. A56R coding sequences were removed by cutting pSD456 with RsaI (partial; pos. 161,090) upstream from A56R coding sequences, and with EagI (pos. 162,054) near the end of the gene. The 3.6 kb RsaI/EagI vector fragment from pSD456 was isolated and ligated with annealed synthetic oligonucleotides MPSYN59 (SEQ ID NO:15), MPSYN62 (SEQ ID NO:16), MPSYN60 (SEQ ID NO:17), and MPSYN61 (SEQ ID NO:18)

RsaI
 MPSYN59 5' ACACGAATGATTTTCTAAAGTATTGGAAAGTTTATAGGT-
 MPSYN62 3' TGTGCTTACTAAAGATTTTATAAACCTTTCAAATATCCA-

- continued

MPSYN59 AGTTGATAGAACAAATACATAATTT 3'

MPSYN62 TCAACTATCT 5'

MPSYN60 5' TGTAATAAATAATCACTTTTTATA-

MPSYN61 3' TGTTTTATGTATTAAACATTTTTATTAGTGAATAATAT-

BglII SmaI PstI EaqI

MPSYN60 CTAAGATCTCCCGGGCTGCAGC 3'

MPSYN61 GATTCTAGAGGGGCCGACGTCGCCGG 5'

reconstructing the DNA sequences upstream from the A56R ORF and replacing the A56R ORF with a polylinker region as indicated above. The resulting plasmid is pSD466. The vaccinia deletion in pSD466 encompasses positions [161,185-162,053]. The site of the deletion in pSD466 is indicated by a triangle in FIG. 4.

[0141] A 3.2 kb BglIII/BamHI (partial) cassette containing the *E. coli* Beta-galactosidase gene (Shapira et al., 1983) under the control of the vaccinia 11 kDa promoter (Bertholet et al., 1985; Guo et al., 1989) was inserted into the BglIII site of pSD466, forming pSD466 KBG. Plasmid pSD466 KBG was used in recombination with rescuing virus vP618. Recombinant vaccinia virus, vP708, containing Beta-galactosidase in the A56R deletion, was isolated as a blue plaque in the presence of X-gal.

[0142] Beta-galactosidase sequences were deleted from vP708 using donor plasmid pSD467. pSD467 is identical to pSD466, except that EcoRI, SmaI and BamHI sites were removed from the pUC/vaccinia junction by digestion of pSD466 with EcoRI/BamHI followed by blunt ending with Klenow fragment of *E. coli* polymerase and ligation. Recombination between vP708 and pSD467 resulted in recombinant vaccinia deletion mutant, vP723, which was isolated as a clear plaque in the presence of X-gal.

Example 5

Construction of Plasmid pMPCSK1Δ for Deletion of Open Reading Frames [C7L-K1L]

[0143] Referring now to FIG. 5, the following vaccinia clones were utilized in the construction of pMPCSK1Δ. pSD420 is Sall H cloned into pUC8. pSD435 is KpnI F cloned into pUC18. pSD435 was cut with SphI and religated, forming pSD451. In pSD451, DNA sequences to the left of the SphI site (pos. 27,416) in HindIII M are removed (Perkus et al., 1990). pSD409 is HindIII M cloned into pUC8.

[0144] To provide a substrate for the deletion of the [C7L-K1L] gene cluster from vaccinia, *E. coli* Beta-galactosidase was first inserted into the vaccinia M2L deletion locus (Guo et al., 1990) as follows. To eliminate the BglII site in pSD409, the plasmid was cut with BglIII in vaccinia sequences (pos. 28,212) and with BamHI at the pUC/vaccinia junction, then ligated to form plasmid pMP409B. pMP409B was cut at the unique SphI site (pos. 27,416). M2L coding sequences were removed by mutagenesis (Guo et al., 1990; Mandecki, 1986) using synthetic oligonucleotide

MPSYN82 (SEQ ID NO: 19)

5' TTTCTGTATATTTGCACCAATTAGATCTT-BglIIACTCAAAATATGTAAC

ATAA 3'

The resulting plasmid, pMP409D, contains a unique BglII site inserted into the M2L deletion locus as indicated above. A 3.2 kb BamHI (partial)/BglII cassette containing the *E. coli* Beta-galactosidase gene (Shapira et al., 1983) under the control of the 11 kDa promoter (Bertholet et al., 1985) was inserted into pMP409D cut with BglII. The resulting plasmid, pMP409DBG (Guo et al., 1990), was used as donor plasmid for recombination with rescuing vaccinia virus vP723. Recombinant vaccinia virus, vP784, containing Beta-galactosidase inserted into the M2L deletion locus, was isolated as a blue plaque in the presence of X-gal.

[10415] A plasmid deleted for vaccinia genes [C7L-K1L] was assembled in pUC8 cut with SmaI, HindIII and blunt ended with Klenow fragment of *E. coli* polymerase. The left flanking arm consisting of vaccinia HindIII C sequences was obtained by digestion of pSD420 with XbaI (pos. 18,628) followed by blunt ending with Klenow fragment of *E. coli* polymerase and digestion with BglII (pos. 19,706). The right flanking arm consisting of vaccinia HindIII K sequences was obtained by digestion of pSD451 with BglII (pos. 29,062) and EcoRV (pos. 29,778). The resulting plasmid, pMP581CK is deleted for vaccinia sequences between the BglII site (pos. 19,706) in HindIII C and the BglII site (pos. 29,062) in HindIII K. The site of the deletion of vaccinia sequences in plasmid pMP581CK is indicated by a triangle in FIG. 5.

[0146] To remove excess DNA at the vaccinia deletion junction, plasmid pMP581CK, was cut at the NcoI sites within vaccinia sequences (pos. 18,811; 19,655), treated with Bal-31 exonuclease and subjected to mutagenesis (Mandel, 1986) using synthetic oligonucleotide MPSYN233 (SEQ ID NO:20) 5'-TGTCATTTAACTACTACTCATATTAATAAAAAATAATATTTATT-3'. The resulting plasmid, pMPCSK18, is deleted for vaccinia sequences positions 18,805-29,108, encompassing 12 vaccinia open reading frames [C7L-K1L]. Recombination between pMPCSK18 and the Beta-galactosidase containing vaccinia recombinant, vP784, resulted in vaccinia deletion mutant, vP804, which was isolated as a clear plaque in the presence of X-gal.

Example 6

Construction of Plasmid pSD548 for Deletion of Large Subunit, Ribonucleotide Reductase (I4L)

[0147] Referring now to FIG. 6, plasmid pSD405 contains vaccinia HindIII I (pos. 63, 875-70,367) cloned in pUC8. pSD405 was digested with EcoRV within vaccinia sequences (pos. 67,933) and with SmaI at the pUC/vaccinia junction, and ligated, forming plasmid pSD518. pSD518 was used as the source of all the vaccinia restriction fragments used in the construction of pSD548.

[0148] The vaccinia I4L gene extends from position 67,371–65,059. Direction of transcription for I4L is indicated by an arrow in FIG. 6. To obtain a vector plasmid fragment deleted for a portion of the I4L coding sequences, pSD518

was digested with BamHI (pos. 65,381) and HpaI (pos. 67,001) and blunt ended using Klenow fragment of *E. coli* polymerase. This 4.8 kb vector fragment was ligated with a 3.2 kb SmaI cassette containing the *E. coli* Beta-galactosidase gene (Shapira et al., 1983) under the control of the vaccinia 11 kDa promoter (Bertholet et al., 1985; Perkus et al., 1990), resulting in plasmid pSD524 KBG. pSD524 KBG was used as donor plasmid for recombination with vaccinia virus vP804. Recombinant vaccinia virus, vP855, containing Beta-galactosidase in a partial deletion of the I4L gene, was isolated as a blue plaque in the presence of X-gal.

[0149] To delete Beta-galactosidase and the remainder of the I4L ORF from vP855, deletion plasmid pSD548 was constructed. The left and right vaccinia flanking arms were assembled separately in pUC8 as detailed below and presented schematically in FIG. 6.

[0150] To construct a vector plasmid to accept the left vaccinia flanking arm, pUC8 was cut with BamHI/EcoRI and ligated with annealed synthetic oligonucleotides 518A1/518A2

```
(SEQ ID NO: 21/SEQ ID NO: 22)
      BamHI   RsaI
518A1  5'  GATCCTGAGTACTTTGTAATATAATGATATATATTTTCACT
518A2  3'  GACTCATGAACATTATATTACTATATATAAAAGTGA

      BglII   EcoRI
      TTTATCTCATTTGAGAATAAAAAGATCTTAGG 3'
      AATAGAGTAAACTCTTATTTTCTAGAATCCTTAA 5'

518A1
518A2
```

forming plasmid pSD531. pSD531 was cut with RsaI (partial) and BamHI and a 2.7 kb vector fragment isolated. pSD518 was cut with BglII (pos. 64,459)/RsaI (pos. 64,994) and a 0.5 kb fragment isolated. The two fragments were ligated together, forming pSD537, which contains the complete vaccinia flanking arm left of the I4L coding sequences.

[0151] To construct a vector plasmid to accept the right vaccinia flanking arm, pUC8 was cut with BamHI/EcoRI and ligated with annealed synthetic oligonucleotides 518B1/518B2

```
(SEQ ID NO: 23/SEQ ID NO: 24)
      BamHI BglII SmaI
518B1  5'  GATCCAGATCTCCCGGAAAAAATTATTTAACTTTTCAT
518B2  3'  GTCTAGAGGCCCTTTTAAATAAATTGAAAAGTA

      RsaI   EcoRI
      TAATAG-GGATTGACGTATGTAGCGTACTAGG 3'
      ATTATC-CCTAAACTGCATACTACGCATGATCCTTAA 5'

518B1
518B2
```

forming plasmid pSD532. pSD532 was cut with RsaI (partial)/EcoRI and a 2.7 kb vector fragment isolated. pSD518 was cut with RsaI within vaccinia sequences (pos. 67,436) and EcoRI at the vaccinia/pUC junction, and a 0.6 kb frag-

ment isolated. The two fragments were ligated together, forming pSD538, which contains the complete vaccinia flanking arm to the right of I4L coding sequences.

[0152] The right vaccinia flanking arm was isolated as a 0.6 kb EcoRI/BglII fragment from pSD538 and ligated into pSD537 vector plasmid cut with EcoRI/BglII. In the resulting plasmid, pSD539, the I4L ORF (pos. 65, 047-67,386) is replaced by a polylinker region, which is flanked by 0.6 kb vaccinia DNA to the left and 0.6 kb vaccinia DNA to the right, all in a pUC background. The site of deletion within vaccinia sequences is indicated by a triangle in FIG. 6. To avoid possible recombination of Beta-galactosidase sequences in the pUC-derived portion of pSD539 with Beta-galactosidase sequences in recombinant vaccinia virus vP855, the vaccinia I4L deletion cassette was moved from pSD539 into pRC11, a pUC derivative from which all Beta-galactosidase sequences have been removed and replaced with a polylinker region (Colinas et al., 1990). pSD539 was cut with EcoRI/PstI and the 1.2 kb fragment isolated. This fragment was ligated into pRC11 cut with EcoRI/PstI (2.35 kb), forming pSD548. Recombination between pSD548 and the Beta-galactosidase containing vaccinia recombinant, vP855, resulted in vaccinia deletion mutant vP866, which was isolated as a clear plaque in the presence of X-gal.

[0153] DNA from recombinant vaccinia virus vP866 was analyzed by restriction digests followed by electrophoresis on an agarose gel. The restriction patterns were as expected. Polymerase chain reactions (PCR) (Engelke et al., 1988) using vP866 as template and primers flanking the six deletion loci detailed above produced DNA fragments of the expected sizes. Sequence analysis of the PCR generated fragments around the areas of the deletion junctions confirmed that the junctions were as expected. Recombinant vaccinia virus vP866, containing the six engineered deletions as described above, was designated vaccinia vaccine strain "NYVAC."

[0154] NYVAC was deposited under the terms of the Budapest Treaty on Mar. 6, 1997 with the American Type Culture Collection (ATCC), P.O. Box 1549, Manassas, Va. 20108 USA under ATCC accession number VR-2559.

Example 7

Insertion of a Rabies Glycoprotein G Gene into NYVAC

[0155] The gene encoding rabies glycoprotein G under the control of the vaccinia H6 promoter (Taylor et al., 1988a,b) was inserted into TK deletion plasmid pSD513. pSD513 is identical to plasmid pSD460 (FIG. 1) except for the presence of a polylinker region.

[0156] Referring now to FIG. 7, the polylinker region was inserted by cutting pSD460 with SmaI and ligating the plasmid vector with annealed synthetic oligonucleotides VQ1A/VQ1B (SEQ ID NO:25/SEQ ID NO:26)

```
      SmaI BglII XhoI PstI NarI BamHI
VQ1A  5'  GGGAGATCTCTCGAGCTGCAGGGCGCCGATCCTTTTCT 3'
VQ1B  3'  CCCTCTAGAGAGCTCGACGTCCCGCGCCTAGGAAAAAGA 5'
```

to form vector plasmid pSD513. pSD513 was cut with SmaI and ligated with a SmaI ended 1.8 kb cassette containing the gene encoding the rabies glycoprotein G gene under the control of the vaccinia H6 promoter (Taylor et al., 1988a,b). The

resulting plasmid was designated pRW842. pRW842 was used as donor plasmid for recombination with NYVAC rescuing virus (vP866). Recombinant vaccinia virus vP879 was identified by plaque hybridization using ³²P-labelled DNA probe to rabies glycoprotein G coding sequences.

[0157] The modified recombinant viruses of the present invention provide advantages as recombinant vaccine vectors. The attenuated virulence of the vector advantageously reduces the opportunity for the possibility of a runaway infection due to vaccination in the vaccinated individual and also diminishes transmission from vaccinated to unvaccinated individuals or contamination of the environment.

[0158] The modified recombinant viruses are also advantageously used in a method for expressing a gene product in a cell cultured in vitro by introducing into the cell the modified recombinant virus having foreign DNA which codes for and expresses gene products in the cell.

Example 8

Construction of TROVAC-NDV Expressing the Fusion and Hemagglutinin-Neuraminidase Glycoproteins of Newcastle Disease Virus

[0159] This example describes the development of TROVAC, a fowlpox virus vector and, of a fowlpox Newcastle Disease Virus recombinant designated TROVAC-NDV and its safety and efficacy. A fowlpox virus (FPV) vector expressing both F and HN genes of the virulent NDV strain Texas was constructed. The recombinant produced was designated TROVAC-NDV. TROVAC-NDV expresses authentically processed NDV glycoproteins in avian cells infected with the recombinant virus and inoculation of day old chicks protects against subsequent virulent NDV challenge.

[0160] Cells and Viruses. The Texas strain of NDV is a velogenic strain. Preparation of cDNA clones of the F and HN genes has been previously described (Taylor et al., 1990; Edbauer et al., 1990). The strain of FPV designated FP-1 has been described previously (Taylor et al., 1988a). It is a vaccine strain useful in vaccination of day old chickens. The parental virus strain Duvette was obtained in France as a fowlpox scab from a chicken. The virus was attenuated by approximately 50 serial passages in chicken embryonated eggs followed by 25 passages on chicken embryo fibroblast cells. The virus was subjected to four successive plaque purifications. One plaque isolate was further amplified in primary CEF cells and a stock virus, designated as TROVAC, established. The stock virus used in the in vitro recombination test to produce TROVAC-NDV had been subjected to twelve passages in primary CEF cells from the plaque isolate.

[0161] TROVAC was deposited under the terms of the Budapest Treaty on Feb. 6, 1997 with the American Type Culture Collection (ATCC), P.O. Box 1549, Manassas, Va. 20108 USA under ATCC accession number VR-2553.

[0162] Construction of a Cassette for NDV-F. A 1.8 kbp BamHI fragment containing all but 22 nucleotides from the 5' end of the F protein coding sequence was excised from pNDV81 (Taylor et al., 1990) and inserted at the BamHI site of pUC18 to form pCE13. The vaccinia virus H6 promoter previously described (Taylor et al., 1988a,b; Guo et al., 1989; Perkus et al., 1989) was inserted into pCE13 by digesting pCE13 with SalI, filling in the sticky ends with Klenow fragment of *E. coli* DNA polymerase and digesting with HindIII. A HindIII-EcoRV fragment containing the H6 promoter sequence was then inserted into pCE13 to form pCE38. A

perfect 5' end was generated by digesting pCE38 with KpnI and NruI and inserting the annealed and kinased oligonucleotides CE75 (SEQ ID NO:27) and CE76 (SEQ ID NO:28) to generate pCE47.

CE75 :
CGATATCCGTTAAGTTTGTATCGTAATGGGCTCCAGATCTTCTACCAGGA
TCCCCGTAC

CE76 :
CGGGATCCTGGTAGAAGATCTGGAGCCCATTACGATACAACTTAACGGA
TATCG.

In order to remove non-coding sequence from the 3' end of the NDV-F a SmaI to PstI fragment from pCE13 was inserted into the SmaI and PstI sites of pUC18 to form pCE23. The non-coding sequences were removed by sequential digestion of pCE23 with SacI, BamHI, Exonuclease III, SI nuclease and EcoRI. The annealed and kinased oligonucleotides CE42 (SEQ ID NO:29) and CE43 (SEQ ID NO:30) were then inserted to form pCE29.

CE42 : AATTCGAGCTCCCCGGG
CE43 : CCCGGGAGCTCG

The 3' end of the NDV-F sequence was then inserted into plasmid pCE20 already containing the 5' end of NDV-F by cloning a PstI-SacI fragment from pCE29 into the PstI and SacI sites of pCE20 to form pCE32. Generation of pCE20 has previously been described in Taylor et al., 1990.

[0163] In order to align the H6 promoter and NDV-F 5' sequences contained in pCE47 with the 3' NDV-F sequences contained in pCE32, a HindIII-PstI fragment of pCE47 was inserted into the HindIII and PstI sites of pCE32 to form pCE49. The H6 promoted NDV-F sequences were then transferred to the de-ORF8 locus (described below) by cloning a HindIII-NruI fragment from pCE49 into the HindIII and SmaI sites of pJCA002 (described below) to form pCE54. Transcription stop signals were inserted into pCE54 by digesting pCE54 with SacI, partially digesting with BamHI and inserting the annealed and kinased oligonucleotides CE166 (SEQ ID NO:31) and CE167 (SEQ ID NO:32) to generate pCE58.

CE166 : CTTTTTATAAAAAGTTAACTACGTAG
CE167 : GATCCTACGTAGTTAACTTTTTTATAAAAAGAGCT

A perfect 3' end for NDV-F was obtained by using the polymerase chain reaction (PCR) with pCE54 as template and oligonucleotides CE182 (SEQ ID NO:33) and CE183 (SEQ ID NO:34) as primers.

CE182 : CTTAACTCAGCTGACTATCC
CE183 : TACGTAGTTAACTTTTTTATAAAAATCATATTTTGTAGTGCTC

[0164] The PCR fragment was digested with PvuII and HpaI and cloned into pCE58 that had been digested with HpaI and partially digested with PvuII. The resulting plasmid was designated pCE64. Translation stop signals were inserted by cloning a HindIII-HpaI fragment which contains the com-

plete H6 promoter and F coding sequence from pCE64 into the HindIII and HpaI sites of pRW846 to generate pCE71, the final cassette for NDV-F. Plasmid pRW846 is essentially equivalent to plasmid pJCA002 (described below) but containing the H6 promoter and transcription and translation stop signals. Digestion of pRW846 with HindIII and HpaI eliminates the H6 promoter but leaves the stop signals intact.

[0165] Construction of Cassette for NDV-HN. Construction of plasmid pRW802 was previously described in Edbauer et al., 1990. This plasmid contains the NDV-HN sequences linked to the 3' end of the vaccinia virus H6 promoter in a pUC9 vector. A HindIII-EcoRV fragment encompassing the 5' end of the vaccinia virus H6 promoter was inserted into the HindIII and EcoRV sites of pRW802 to form pRW830. A perfect 3' end for NDV-HN was obtained by inserting the annealed and kinased oligonucleotides CE162 (SEQ ID NO:35) and CE163 (SEQ ID NO:36) into the EcoRI site of pRW830 to form pCE59, the final cassette for NDV-HN.

CE162:
AATTGAGGATCGTTCCTTACTAGTTGAGATTCTCAAGGATGATGGGATT
TAATTTTATAAGCTTG

CE163:
AATTCAAGCTTATAAAATTAATCCCATCATCCTTGAGAATCTCAACTA
GTAAAGGAACGATCCTTG

[0166] Construction of FPV Insertion Vector. Plasmid pRW731-15 contains a 10 kb PvuII-PvuII fragment cloned from genomic DNA. The nucleotide sequence was determined on both strands for a 3660 bp PvuII-EcoRV fragment and is shown in FIG. 11 (SEQ ID NO:67). The limits of an open reading frame designated here as F8 were determined. Plasmid pRW761 is a sub-clone of pRW731-15 containing a 2430 bp EcoRV-EcoRV fragment. The F8 ORF was entirely contained between an XbaI site and an SspI site in pRW761. In order to create an insertion plasmid which on recombination with TROVAC genomic DNA would eliminate the F8 ORF, the following steps were followed. Plasmid pRW761 was completely digested with XbaI and partially digested with SspI. A 3700 bp XbaI-SspI band was isolated from the gel and ligated with the annealed double-stranded oligonucleotides JCA017 (SEQ ID NO:37) and JCA018 (SEQ ID NO:38).

JCA017:
5' CTAGACACTTTATGTTTTTAAATATCCGGTCTTAAAGCTTCCCGG
GATCCTTATACGGGGAATAAT

JCA018:
5' ATTATTTCCCGGTATAAGGATCCCCGGGAAGCTTTTAAGACCGGATA
TTAAAAACATAAAGTGT

The plasmid resulting from this ligation was designated pJCA002.

[0167] Construction of Double Insertion Vector for NDV F and HN. The H6 promoted NDV-HN sequence was inserted into the H6 promoted NDV-F cassette by cloning a HindIII fragment from pCE59 that had been filled in with Klenow fragment of *E. coli* DNA polymerase into the HpaI site of pCE71 to form pCE80. Plasmid pCE80 was completely digested with NdeI and partially digested with BglII to generate an NdeI-BglII 4760 bp fragment containing the NDV F

and HN genes both driven by the H6 promoter and linked to F8 flanking arms. Plasmid pJCA021 was obtained by inserting a 4900 bp PvuII-HindIII fragment from pRW731-15 into the SmaI and HindIII sites of pBSSK+. Plasmid pJCA021 was then digested with NdeI and BglII and ligated to the 4760 bp NdeI-BglII fragment of pCE80 to form pJCA024. Plasmid pJCA024 therefore contains the NDV-F and HN genes inserted in opposite orientation with 3' ends adjacent between FPV flanking arms. Both genes are linked to the vaccinia virus H6 promoter. The right flanking arm adjacent to the NDV-F sequence consists of 2350 bp of FPV sequence. The left flanking arm adjacent to the NDV-HN sequence consists of 1700 bp of FPV sequence.

[0168] Development of TROVAC-NDV. Plasmid pJCA024 was transfected into TROVAC infected primary CEF cells by using the calcium phosphate precipitation method previously described (Panicali et al., 1982; Piccini et al., 1987). Positive plaques were selected on the basis of hybridization to specific NDV-F and HN radiolabelled probes and subjected to five sequential rounds of plaque purification until a pure population was achieved. One representative plaque was then amplified and the resulting TROVAC recombinant was designated TROVAC-NDV (vFP96).

[0169] Immunofluorescence. Indirect immunofluorescence was performed as described (Taylor et al., 1990) using a polyclonal anti-NDV serum and, as mono-specific reagents, sera produced in rabbits against vaccinia virus recombinants expressing NDV-F or NDV-HN.

[0170] Immunoprecipitation. Immunoprecipitation reactions were performed as described (Taylor et al., 1990) using a polyclonal anti-NDV serum obtained from SPAFAS Inc., Storrs, Conn.

[0171] The stock virus was screened by in situ plaque hybridization to confirm that the F8 ORF was deleted. The correct insertion of the NDV genes into the TROVAC genome and the deletion of the F8 ORF was also confirmed by Southern blot hybridization.

[0172] In NDV-infected cells, the F glycoprotein is anchored in the membrane via a hydrophobic transmembrane region near the carboxyl terminus and requires post-translational cleavage of a precursor, F₀, into two disulfide linked polypeptides F₁ and F₂. Cleavage of F₀ is important in determining the pathogenicity of a given NDV strain (Homma and Ohuchi, 1973; Nagai et al., 1976; Nagai et al., 1980), and the sequence of amino acids at the cleavage site is therefore critical in determining viral virulence. It has been determined that amino acids at the cleavage site in the NDV-F sequence inserted into FPV to form recombinant vFP29 had the sequence Arg-Arg-Gln-Arg-Arg (SEQ ID NO: 149) (Taylor et al., 1990) which conforms to the sequence found to be a requirement for virulent NDV strains (Chambers et al., 1986; Espion et al., 1987; Le et al., 1988; McGinnes and Morrison, 1986; Toyoda et al., 1987). The HN glycoprotein synthesized in cells infected with virulent strains of NDV is an uncleaved glycoprotein of 74 kDa. Extremely avirulent strains such as Ulster and Queensland encode an HN precursor (HNo) which requires cleavage for activation (Garten et al., 1980).

[0173] The expression of F and HN genes in TROVAC-NDV was analyzed to confirm that the gene products were authentically processed and presented. Indirect-immunofluorescence using a polyclonal anti-NDV chicken serum confirmed that immunoreactive proteins were presented on the infected cell surface. To determine that both proteins were presented on the plasma membrane, mono-specific rabbit

sera were produced against vaccinia recombinants expressing either the F or HN glycoproteins. Indirect immunofluorescence using these sera confirmed the surface presentation of both proteins.

[0174] Immunoprecipitation experiments were performed by using (35 S) methionine labeled lysates of CEF cells infected with parental and recombinant viruses. The expected values of apparent molecular weights of the glycosylated forms of F₁ and F₂ are 54.7 and 10.3 kDa respectively (Chambers et al., 1986). In the immunoprecipitation experiments using a polyclonal anti-NDV serum, fusion specific products of the appropriate size were detected from the NDV-F single recombinant vFP29 (Taylor et al., 1990) and the TROVAC-NDV double recombinant vFP96. The HN glycoprotein of appropriate size was also detected from the NDV-HN single recombinant VFP-47 (Edbauer et al., 1990) and TROVAC-NDV. No NDV specific products were detected from uninfected and parental TROVAC infected CEF cells.

[0175] In CEF cells, the F and HN glycoproteins are appropriately presented on the infected cell surface where they are recognized by NDV immune serum. Immunoprecipitation analysis indicated that the F₀ protein is authentically cleaved to the F₁ and F₂ components required in virulent strains. Similarly, the HN glycoprotein was authentically processed in CEF cells infected with recombinant TROVAC-NDV.

[0176] Previous reports (Taylor et al., 1990; Edbauer et al., 1990; Bourns et al., 1990a,b,c; Ogawa et al., 1990) would indicate that expression of either HN or F alone is sufficient to elicit protective immunity against NDV challenge. Work on other paramyxoviruses has indicated, however, that antibody to both proteins may be required for full protective immunity. It has been demonstrated that SV5 virus could spread in tissue culture in the presence of antibody to the HN glycoprotein but not to the F glycoprotein (Merz et al., 1980). In addition, it has been suggested that vaccine failures with killed measles virus vaccines were due to inactivation of the fusion component (Norrbj et al., 1975). Since both NDV glycoproteins have been shown to be responsible for eliciting virus neutralizing antibody (Avery et al., 1979) and both glycoproteins, when expressed individually in a fowlpox vector are able to induce a protective immune response, it can be appreciated that the most efficacious NDV vaccine should express both glycoproteins.

Example 9

Construction of ALVAC Recombinants Expressing Rabies Virus Glycoprotein G

[0177] This example describes the development of ALVAC, a canarypox virus vector and, of a canarypox-rabies recombinant designated as ALVAC-RG (vCP65) and its safety and efficacy.

[0178] Cells and Viruses. The parental canarypox virus (Rentschler strain) is a vaccinal strain for canaries. The vaccine strain was obtained from a wild type isolate and attenuated through more than 200 serial passages on chick embryo fibroblasts. A master viral seed was subjected to four successive plaque purifications under agar and one plaque clone was amplified through five additional passages after which the stock virus was used as the parental virus in in vitro recombination tests. The plaque purified canarypox isolate is designated ALVAC.

[0179] ALVAC was deposited under the terms of the Budapest Treaty with the American Type Culture Collection

(ATCC), 12301 Parklawn Drive, Rockville, Md., 20852, USA: ALVAC under ATCC accession number VR-2547 on Nov. 14, 1996.

[0180] Construction of a Canarypox Insertion Vector. An 880 bp canarypox PvuII fragment was cloned between the PvuII sites of pUC9 to form pRW764.5. The sequence of this fragment is shown in FIG. 8 (SEQ ID NO:66) between positions 1372 and 2251. The limits of an open reading frame designated as C5 were defined. It was determined that the open reading frame was initiated at position 166 within the fragment and terminated at position 487. The C5 deletion was made without interruption of open reading frames. Bases from position 167 through position 455 were replaced with the sequence (SEQ ID NO:39) GCTTCCCGGGAAT-TCTAGCTAGCTAGTTT. This replacement sequence contains HindIII, SmaI and EcoRI insertion sites followed by translation stops and a transcription termination signal recognized by vaccinia virus RNA polymerase (Yuen et al., 1987). Deletion of the C5 ORF was performed as described below. Plasmid pRW764.5 was partially cut with RsaI and the linear product was isolated. The RsaI linear fragment was recut with BglII and the pRW764.5 fragment now with a RsaI to BglII deletion from position 156 to position 462 was isolated and used as a vector for the following synthetic oligonucleotides:

RW145 (SEQ ID NO: 40):
ACTCTCAAAGCTTCCCGGAATTCTAGCTAGCTAGTTTATATAAA

RW146 (SEQ ID NO: 41):
GATCTTTATAAACTAGCTAGCTAGCTAGCTAGCTTTGAGAGT

Oligonucleotides RW145 and RW146 were annealed and inserted into the pRW 764.5 RsaI and BglII vector described above. The resulting plasmid is designated pRW831.

[0181] Construction of Insertion Vector Containing the Rabies G Gene. Construction of pRW838 is illustrated below. Oligonucleotides A through E, which overlap the translation initiation codon of the H6 promoter with the ATG of rabies G, were cloned into pUC9 as pRW737. Oligonucleotides A through E contain the H6 promoter, starting at NruI, through the HindIII site of rabies G followed by BglII. Sequences of oligonucleotides A through E ((SEQ ID NO:42)-(SEQ ID NO:46)) are:

A (SEQ ID NO: 42):
CTGAAATTATTTTCATTATCGCGATATCCGTTAAGTTTGTATCGTAATGGT

TCCTCAGGCTCTCCTGTTTGT

B (SEQ ID NO: 43):
CATTACGATACAACTTAACGGATATCGCGATAATGAAATAATTTTCTAG

C (SEQ ID NO: 44):
ACCCCTTCTGGTTTTTCGGTTGTGTTTGGGAAATTCCTATTTACACGA

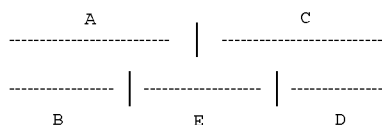
TCCCAGACAAGCTTAGATCTCTAG

D (SEQ ID NO: 45):
CTGAGATCTAAGCTTGTCTGGGATCGTGTAATAGGGAATTTCCCAAAAC

A

E (SEQ ID NO: 46):
CAACGGAAAAACAGAGGGGTACAAACAGGAGAGCCTGAGGAAC

The diagram of annealed oligonucleotides A through E is as follows:



[0182] Oligonucleotides A through E were kinased, annealed (95° C. for 5 minutes, then cooled to room temperature), and inserted between the PvuII sites of pUC9. The resulting plasmid, pRW737, was cut with HindIII and BglII and used as a vector for the 1.6 kbp HindIII-BglII fragment of pgt155PRO (Kieny et al., 1984) generating pRW739. The pgt155PRO HindIII site is 86 bp downstream of the rabies G translation initiation codon. BglII is downstream of the rabies G translation stop codon in pgt155PRO. pRW739 was partially cut with NruI, completely cut with BglII, and a 1.7 kbp NruI-BglII fragment, containing the 3' end of the H6 promoter previously described (Taylor et al., 1988a,b; Guo et al., 1989; Perkus et al., 1989) through the entire rabies G gene, was inserted between the NruI and BamHI sites of pRW824. The resulting plasmid is designated pRW832. Insertion into pRW824 added the H6 promoter 5' of NruI. The pRW824 sequence of BamHI followed by SmaI is (SEQ ID NO:47): GGATCCCCGGG. pRW824 is a plasmid that contains a nonpertinent gene linked precisely to the vaccinia virus H6 promoter. Digestion with NruI and BamHI completely excised this nonpertinent gene. The 1.8 kbp pRW832 SmaI fragment, containing H6 promoted rabies G, was inserted into the SmaI of pRW831, to form plasmid pRW838.

[0183] Development of ALVAC-RG. Plasmid pRW838 was transfected into ALVAC infected cells by using the calcium phosphate precipitation method previously described (Panicali et al., 1982; Piccini et al., 1987). Positive plaques were selected on the basis of hybridization to a specific rabies G probe and subjected to 6 sequential rounds of plaque purification until a pure population was achieved. One representative plaque was then amplified and the resulting ALVAC recombinant was designated ALVAC-RG (vCP65) (see also FIGS. 9A and 9B). The correct insertion of the rabies G gene into the ALVAC genome without subsequent mutation was confirmed by sequence analysis.

[0184] Immunofluorescence. During the final stages of assembly of mature rabies virus particles, the glycoprotein component is transported from the golgi apparatus to the plasma membrane where it accumulates with the carboxy terminus extending into the cytoplasm and the bulk of the protein on the external surface of the cell membrane. In order to confirm that the rabies glycoprotein expressed in ALVAC-RG was correctly presented, immunofluorescence was performed on primary CEF cells infected with ALVAC or ALVAC-RG. Immunofluorescence was performed as previously described (Taylor et al., 1990) using a rabies G monoclonal antibody. Strong surface fluorescence was detected on CEF cells infected with ALVAC-RG but not with the parental ALVAC.

[0185] Immunoprecipitation. Preformed monolayers of primary CEF, Vero (a line of African Green monkey kidney cells ATCC # CCL81) and MRC-5 cells (a fibroblast-like cell line derived from normal human fetal lung tissue ATCC # CCL171) were inoculated at 10 pfu per cell with parental

virus ALVAC and recombinant virus ALVAC-RG in the presence of radiolabelled ³⁵S-methionine and treated as previously described (Taylor et al., 1990). Immunoprecipitation reactions were performed using a rabies G specific monoclonal antibody. Efficient expression of a rabies specific glycoprotein with a molecular weight of approximately 67 kDa was detected with the recombinant ALVAC-RG. No rabies specific products were detected in uninfected cells or cells infected with the parental ALVAC virus.

[0186] Sequential Passaging Experiment. In studies with ALVAC virus in a range of non-avian species no proliferative infection or overt disease was observed (Taylor et al., 1991b). However, in order to establish that neither the parental nor recombinant virus could be adapted to grow in non-avian cells, a sequential passaging experiment was performed.

[0187] The two viruses, ALVAC and ALVAC-RG, were inoculated in 10 sequential blind passages in three cell substrates:

[0188] (1) Primary chick embryo fibroblast (CEF) cells produced from 11 day old white leghorn embryos;

[0189] (2) Vero cells—a continuous line of African Green monkey kidney cells (ATCC # CCL81); and

[0190] (3) MRC-5 cells—a diploid cell line derived from human fetal lung tissue (ATCC # CCL171).

The initial inoculation was performed at an m.o.i. of 0.1 pfu per cell using three 60 mm dishes of each cell substrate containing 2×10⁶ cells per dish. One dish was inoculated in the presence of 40 µg/ml of Cytosine arabinoside (Ara C), an inhibitor of DNA replication. After an absorption period of 1 hour at 37° C., the inoculum was removed and the monolayer washed to remove unabsorbed virus. At this time the medium was replaced with 5 ml of EMEM+2% NBSCS on two dishes (samples t0 and t7) and 5 ml of EMEM+2% NBSCS containing 40 µg/ml Ara C on the third (sample t7A). Sample t0 was frozen at -70° C. to provide an indication of the residual input virus. Samples t7 and t7A were incubated at 37° C. for 7 days, after which time the contents were harvested and the cells disrupted by indirect sonication.

[0191] One ml of sample t7 of each cell substrate was inoculated undiluted onto three dishes of the same cell substrate (to provide samples t0, t7 and t7A) and onto one dish of primary CEF cells. Samples t0, t7 and t7A were treated as for passage one. The additional inoculation on CEF cells was included to provide an amplification step for more sensitive detection of virus which might be present in the non-avian cells.

[0192] This procedure was repeated for 10 (CEF and MRC-5) or 8 (Vero) sequential blind passages. Samples were then frozen and thawed three times and assayed by titration on primary CEF monolayers.

[0193] Virus yield in each sample was then determined by plaque titration on CEF monolayers under agarose. Summarized results of the experiment are shown in Tables 1 and 2.

[0194] The results indicate that both the parental ALVAC and the recombinant ALVAC-RG are capable of sustained replication on CEF monolayers with no loss of titer. In Vero cells, levels of virus fell below the level of detection after 2 passages for ALVAC and 1 passage for ALVAC-RG. In MRC-5 cells, a similar result was evident, and no virus was detected after 1 passage. Although the results for only four passages are shown in Tables 1 and 2 the series was continued for 8 (Vero) and 10 (MRC-5) passages with no detectable adaptation of either virus to growth in the non-avian cells.

[0195] In passage 1 relatively high levels of virus were present in the t7 sample in MRC-5 and Vero cells. However this level of virus was equivalent to that seen in the t0 sample and the t7A sample incubated in the presence of Cytosine arabinoside in which no viral replication can occur. This demonstrated that the levels of virus seen at 7 days in non-avian cells represented residual virus and not newly replicated virus.

[0196] In order to make the assay more sensitive, a portion of the 7 day harvest from each cell substrate was inoculated onto a permissive CEF monolayer and harvested at cytopathic effect (CPE) or at 7 days if no CPE was evident. The results of this experiment are shown in Table 3. Even after amplification through a permissive cell substrate, virus was only detected in MRC-5 and Vero cells for two additional passages. These results indicated that under the conditions used, there was no adaptation of either virus to growth in Vero or MRC-5 cells.

[0197] Inoculation of Macaques. Four HIV seropositive macaques were initially inoculated with ALVAC-RG as described in Table 4. After 100 days these animals were re-inoculated to determine a booster effect, and an additional seven animals were inoculated with a range of doses. Blood was drawn at appropriate intervals and sera analyzed, after heat inactivation at 56° C. for 30 minutes, for the presence of anti-rabies antibody using the Rapid Fluorescent Focus Inhibition Assay (Smith et al., 1973).

[0198] Inoculation of Chimpanzees. Two adult male chimpanzees (50 to 65 kg weight range) were inoculated intramuscularly or subcutaneously with 1×10^7 pfu of vCP65. Animals were monitored for reactions and bled at regular intervals for analysis for the presence of anti-rabies antibody with the RFFI test (Smith et al., 1973). Animals were re-inoculated with an equivalent dose 13 weeks after the initial inoculation.

[0199] Inoculation of Mice. Groups of mice were inoculated with 50 to 100 μ l of a range of dilutions of different batches of vCP65. Mice were inoculated in the footpad. On day 14, mice were challenged by intracranial inoculation of from 15 to 43 mouse LD₅₀ of the virulent CVS strain of rabies virus. Survival of mice was monitored and a protective dose 50% (PD₅₀) calculated at 28 days post-inoculation.

[0200] Inoculation of Dogs and Cats. Ten beagle dogs, 5 months old, and 10 cats, 4 months old, were inoculated subcutaneously with either 6.7 or 7.7 log₁₀ TCID₅₀ of ALVAC-RG. Four dogs and four cats were not inoculated. Animals were bled at 14 and 28 days post-inoculation and anti-rabies antibody assessed in an RFFI test. The animals receiving 6.7 log₁₀ TCID₅₀ of ALVAC-RG were challenged at 29 days post-vaccination with 3.7 log₁₀ mouse LD₅₀ (dogs) or 4.3 log₁₀ mouse LD₅₀ (cats) of the NYGS rabies virus challenge strain.

[0201] Inoculation of Squirrel Monkeys. Three groups of four squirrel monkeys (*Saimiri sciureus*) were inoculated with one of three viruses (a) ALVAC, the parental canarypox virus, (b) ALVAC-RG, the recombinant expressing the rabies G glycoprotein or (c) vCP37, a canarypox recombinant expressing the envelope glycoprotein of feline leukemia virus. Inoculations were performed under ketamine anaesthesia. Each animal received at the same time: (1) 20 μ l instilled on the surface of the right eye without scarification; (2) 100 μ l as several droplets in the mouth; (3) 100 μ l in each of two intradermal injection sites in the shaven skin of the external face of the right arm; and (4) 100 μ l in the anterior muscle of the right thigh.

[0202] Four monkeys were inoculated with each virus, two with a total of 5.0 log₁₀ pfu and two with a total of 7.0 log₁₀ pfu. Animals were bled at regular intervals and sera analyzed for the presence of antirabies antibody using an RFFI test (Smith et al., 1973). Animals were monitored daily for reactions to vaccination. Six months after the initial inoculation the four monkeys receiving ALVAC-RG, two monkeys initially receiving vCP37, and two monkeys initially receiving ALVAC, as well as one naive monkey were inoculated with 6.5 log₁₀ pfu of ALVAC-RG subcutaneously. Sera were monitored for the presence of rabies neutralizing antibody in an RFFI test (Smith et al., 1973).

[0203] Inoculation of Human Cell Lines with ALVAC-RG. In order to determine whether efficient expression of a foreign gene could be obtained in non-avian cells in which the virus does not productively replicate, five cell types, one avian and four non-avian, were analyzed for virus yield, expression of the foreign rabies G gene and viral specific DNA accumulation. The cells inoculated were:

[0204] (a) Vero, African Green monkey kidney cells, ATCC # CCL81;

[0205] (b) MRC-5, human embryonic lung, ATCC # CCL 171;

[0206] (c) WISH human amnion, ATCC # CCL 25;

[0207] (d) Detroit-532, human foreskin, Down's syndrome, ATCC # CCL 54; and

[0208] (e) Primary CEF cells.

[0209] Chicken embryo fibroblast cells produced from 11 day old white leghorn embryos were included as a positive control. All inoculations were performed on preformed monolayers of 2×10^6 cells as discussed below.

A. Methods for DNA Analysis.

[0210] Three dishes of each cell line were inoculated at 5 pfu/cell of the virus under test, allowing one extra dish of each cell line un-inoculated. One dish was incubated in the presence of 40 μ g/ml of cytosine arabinoside (Ara C). After an adsorption period of 60 minutes at 37° C., the inoculum was removed and the monolayer washed twice to remove unadsorbed virus. Medium (with or without Ara C) was then replaced. Cells from one dish (without Ara C) were harvested as a time zero sample. The remaining dishes were incubated at 37° C. for 72 hours, at which time the cells were harvested and used to analyze DNA accumulation. Each sample of 2×10^6 cells was resuspended in 0.5 ml phosphate buffered saline (PBS) containing 40 mM EDTA and incubated for 5 minutes at 37° C. An equal volume of 1.5% agarose prewarmed at 42° C. and containing 120 mM EDTA was added to the cell suspension and gently mixed. The suspension was transferred to an agarose plug mold and allowed to harden for at least 15 min. The agarose plugs were then removed and incubated for 12-16 hours at 50° C. in a volume of lysis buffer (1% sarkosyl, 100 μ g/ml proteinase K, 10 mM Tris HCl pH 7.5, 200 mM EDTA) that completely covers the plug. The lysis buffer was then replaced with 5.0 ml sterile 0.5×TBE (44.5 mM Tris-borate, 44.5 mM boric acid, 0.5 mM EDTA) and equilibrated at 4° C. for 6 hours with 3 changes of TBE buffer. The viral DNA within the plug was fractionated from cellular RNA and DNA using a pulse field electrophoresis system. Electrophoresis was performed for 20 hours at 180 V with a ramp of 50-90 sec at 15° C. in 0.5×TBE. The DNA was run with lambda DNA molecu-

lar weight standards. After electrophoresis the viral DNA band was visualized by staining with ethidium bromide. The DNA was then transferred to a nitrocellulose membrane and probed with a radiolabelled probe prepared from purified ALVAC genomic DNA.

B. Estimation of Virus Yield.

[0211] Dishes were inoculated exactly as described above, with the exception that input multiplicity was 0.1 pfu/cell. At 72 hours post infection, cells were lysed by three successive cycles of freezing and thawing. Virus yield was assessed by plaque titration on CEF monolayers.

C. Analysis of Expression of Rabies G Gene.

[0212] Dishes were inoculated with recombinant or parental virus at a multiplicity of 10 pfu/cell, allowing an additional dish as an uninfected virus control. After a one hour absorption period, the medium was removed and replaced with methionine free medium. After a 30 minute period, this medium was replaced with methionine-free medium containing 25 uCi/ml of ³⁵S-Methionine. Infected cells were labelled overnight (approximately 16 hours), then lysed by the addition of buffer A lysis buffer. Immunoprecipitation was performed as previously described (Taylor et al., 1990) using a rabies G specific monoclonal antibody.

[0213] Results: Estimation of Viral Yield. The results of titration for yield at 72 hours after inoculation at 0.1 pfu per cell are shown in Table 5. The results indicate that while a productive infection can be attained in the avian cells, no increase in virus yield can be detected by this method in the four non-avian cell systems.

[0214] Analysis of Viral DNA Accumulation. In order to determine whether the block to productive viral replication in the non-avian cells occurred before or after DNA replication, DNA from the cell lysates was fractionated by electrophoresis, transferred to nitrocellulose and probed for the presence of viral specific DNA. DNA from uninfected CEF cells, ALVAC-RG infected CEF cells at time zero, ALVAC-RG infected CEF cells at 72 hours post-infection and ALVAC-RG infected CEF cells at 72 hours post-infection in the presence of 40 pg/ml of cytosine arabinoside all showed some background activity, probably due to contaminating CEF cellular DNA in the radiolabelled ALVAC DNA probe preparation. However, ALVAC-RG infected CEF cells at 72 hours post-infection exhibited a strong band in the region of approximately 350 kbp representing ALVAC-specific viral DNA accumulation. No such band is detectable when the culture is incubated in the presence of the DNA synthesis inhibitor, cytosine arabinoside. Equivalent samples produced in Vero cells showed a very faint band at approximately 350 kbp in the ALVAC-RG infected Vero cells at time zero. This level represented residual virus. The intensity of the band was amplified at 72 hours post-infection indicating that some level of viral specific DNA replication had occurred in Vero cells which had not resulted in an increase in viral progeny. Equivalent samples produced in MRC-5 cells indicated that no viral specific DNA accumulation was detected under these conditions in this cell line. This experiment was then extended to include additional human cell lines, specifically WISH and Detroit-532 cells. ALVAC infected CEF cells served as a positive control. No viral specific DNA accumulation was detected in either WISH or Detroit cells inoculated with ALVAC-RG. It should be noted that the limits of detection of

this method have not been fully ascertained and viral DNA accumulation may be occurring, but at a level below the sensitivity of the method. Other experiments in which viral DNA replication was measured by ³H-thymidine incorporation support the results obtained with Vero and MRC-5 cells.

[0215] Analysis of Rabies Gene Expression. To determine if any viral gene expression, particularly that of the inserted foreign gene, was occurring in the human cell lines even in the absence of viral DNA replication, immunoprecipitation experiments were performed on ³⁵S-methionine labelled lysates of avian and non-avian cells infected with ALVAC and ALVAC-RG. The results of immunoprecipitation using a rabies G specific monoclonal antibody illustrated specific immunoprecipitation of a 67 kDa glycoprotein in CEF, Vero and MRC-5, WISH and Detroit cells infected with ALVAC-RG. No such specific rabies gene products were detected in any of the uninfected and parentally infected cell lysates.

[0216] The results of this experiment indicated that in the human cell lines analyzed, although the ALVAC-RG recombinant was able to initiate an infection and express a foreign gene product under the transcriptional control of the H6 early/late vaccinia virus promoter, the replication did not proceed through DNA replication, nor was there any detectable viral progeny produced. In the Vero cells, although some level of ALVAC-RG specific DNA accumulation was observed, no viral progeny was detected by these methods. These results would indicate that in the human cell lines analyzed the block to viral replication occurs prior to the onset of DNA replication, while in Vero cells, the block occurs following the onset of viral DNA replication.

[0217] In order to determine whether the rabies glycoprotein expressed in ALVAC-RG was immunogenic, a number of animal species were tested by inoculation of the recombinant. The efficacy of current rabies vaccines is evaluated in a mouse model system. A similar test was therefore performed using ALVAC-RG. Nine different preparations of virus (including one vaccine batch (J) produced after 10 serial tissue culture passages of the seed virus) with infectious titers ranging from 6.7 to 8.4 log₁₀ TCID₅₀ per ml were serially diluted and 50 to 100 µl of dilutions inoculated into the footpad of four to six week old mice. Mice were challenged 14 days later by the intracranial route with 300 µl of the CVS strain of rabies virus containing from 15 to 43 mouse LD₅₀ as determined by lethality titration in a control group of mice. Potency, expressed as the PD₅₀ (Protective dose 50%), was calculated at 14 days post-challenge. The results of the experiment are shown in Table 6. The results indicated that ALVAC-RG was consistently able to protect mice against rabies virus challenge with a PD₅₀ value ranging from 3.33 to 4.56 with a mean value of 3.73 (STD 0.48). As an extension of this study, male mice were inoculated intracranially with 50 µl of virus containing 6.0 log₁₀ TCID₅₀ of ALVAC-RG or with an equivalent volume of an uninfected cell suspension. Mice were sacrificed on days 1, 3 and 6 post-inoculation and their brains removed, fixed and sectioned. Histopathological examination showed no evidence for neurovirulence of ALVAC-RG in mice.

[0218] In order to evaluate the safety and efficacy of ALVAC-RG for dogs and cats, a group of 14, 5 month old beagles and 14, 4 month old cats were analyzed. Four animals in each species were not vaccinated. Five animals received 6.7 log₁₀ TCID₅₀ subcutaneously and five animals received 7.7 log₁₀ TCID₅₀ by the same route. Animals were bled for analysis for anti-rabies antibody. Animals receiving no inoculation or 6.7 log₁₀ TCID₅₀ of ALVAC-RG were challenged at 29 days post-vaccination with 3.7 log₁₀ mouse LD₅₀ (dogs, in the temporal muscle) or 4.3 log₁₀ mouse LD₅₀ (cats, in the

neck) of the NYGS rabies virus challenge strain. The results of the experiment are shown in Table 7.

[0219] No adverse reactions to inoculation were seen in either cats or dogs with either dose of inoculum virus. Four of 5 dogs immunized with $6.7 \log_{10}$ TCID₅₀ had antibody titers on day 14 post-vaccination and all dogs had titers at 29 days. All dogs were protected from a challenge which killed three out of four controls. In cats, three of five cats receiving $6.7 \log_{10}$ TCID₅₀ had specific antibody titers on day 14 and all cats were positive on day 29 although the mean antibody titer was low at 2.9 IU. Three of five cats survived a challenge which killed all controls. All cats immunized with $7.7 \log_{10}$ TCID₅₀ had antibody titers on day 14 and at day 29 the Geometric Mean Titer was calculated as 8.1 International Units.

[0220] The immune response of squirrel monkeys (*Saimiri sciureus*) to inoculation with ALVAC, ALVAC-RG and an unrelated canarypox virus recombinant was examined. Groups of monkeys were inoculated as described above and sera analyzed for the presence of rabies specific antibody. Apart from minor typical skin reactions to inoculation by the intradermal route, no adverse reactivity was seen in any of the monkeys. Small amounts of residual virus were isolated from skin lesions after intradermal inoculation on days two and four post-inoculation only. All specimens were negative on day seven and later. There was no local reaction to intramuscular injection. All four monkeys inoculated with ALVAC-RG developed anti-rabies serum neutralizing antibodies as measured in an RFFI test. Approximately six months after the initial inoculation all monkeys and one additional naive monkey were re-inoculated by the subcutaneous route on the external face of the left thigh with $6.5 \log_{10}$ TCID₅₀ of ALVAC-RG. Sera were analyzed for the presence of anti-rabies antibody. The results are shown in Table 8.

[0221] Four of the five monkeys naive to rabies developed a serological response by seven days post-inoculation with ALVAC-RG. All five monkeys had detectable antibody by 11 days post-inoculation. Of the four monkeys with previous exposure to the rabies glycoprotein, all showed a significant increase in serum neutralization titer between days 3 and 7 post-vaccination. The results indicate that vaccination of squirrel monkeys with ALVAC-RG does not produce adverse side-effects and a primary neutralizing antibody response can be induced. An anamnestic response is also induced on re-vaccination. Prior exposure to ALVAC or to a canarypox recombinant expressing an unrelated foreign gene does not interfere with induction of an anti-rabies immune response upon re-vaccination.

[0222] The immunological response of HIV-2 seropositive macaques to inoculation with ALVAC-RG was assessed. Animals were inoculated as described above and the presence of anti-rabies serum neutralizing antibody assessed in an RFFI test. The results, shown in Table 9, indicated that HIV-2 positive animals inoculated by the subcutaneous route developed anti-rabies antibody by 11 days after one inoculation. An anamnestic response was detected after a booster inoculation given approximately three months after the first inoculation. No response was detected in animals receiving the recombinant by the oral route. In addition, a series of six animals were inoculated with decreasing doses of ALVAC-RG given by either the intra-muscular or subcutaneous routes. Five of the six animals inoculated responded by 14 days post-vaccination with no significant difference in antibody titer.

[0223] Two chimpanzees with prior exposure to HIV were inoculated with $7.0 \log_{10}$ pfu of ALVAC-RG by the subcutaneous or intra-muscular route. At 3 months post-inoculations both animals were re-vaccinated in an identical fashion. The results are shown in Table 10.

[0224] No adverse reactivity to inoculation was noted by either intramuscular or subcutaneous routes. Both chimpanzees responded to primary inoculation by 14 days and a strongly rising response was detected following re-vaccination.

TABLE 1

Sequential Passage of ALVAC in Avian and non-Avian Cells.				
		CEF	Vero	MRC5
Pass 1				
Sample	t0 ^a	2.4	3.0	2.6
	t7 ^b	7.0	1.4	0.4
	t7A ^c	1.2	1.2	0.4
Pass 2				
Sample	t0	5.0	0.4	N.D. ^d
	t7	7.3	0.4	N.D.
	t7A	3.9	N.D.	N.D.
Pass 3				
Sample	t0	5.4	0.4	N.D.
	t7	7.4	N.D.	N.D.
	t7A	3.8	N.D.	N.D.
Pass 4				
Sample	t0	5.2	N.D.	N.D.
	t7	7.1	N.D.	N.D.
	t7A	3.9	N.D.	N.D.

^aThis sample was harvested at zero time and represents the residual input virus. The titer is expressed as $\log_{10}$ pfu per ml.

^bThis sample was harvested at 7 days post-infection.

^cThis sample was inoculated in the presence of 40 μ g/ml of Cytosine arabinoside and harvested at 7 days post infection.

^dNot detectable

TABLE 2

Sequential Passage of ALVAC-RG in Avian and non-Avian Cells				
		CEF	Vero	MRC-5
Pass 1				
Sample	t0 ^a	3.0	2.9	2.9
	t7 ^b	7.1	1.0	1.4
	t7A ^c	1.8	1.4	1.2
Pass 2				
Sample	t0	5.1	0.4	0.4
	t7	7.1	N.D. ^d	N.D.
	t7A	3.8	N.D.	N.D.
Pass 3				
Sample	t0	5.1	0.4	N.D.
	t7	7.2	N.D.	N.D.
	t7A	3.6	N.D.	N.D.
Pass 4				
Sample	t0	5.1	N.D.	N.D.
	t7	7.0	N.D.	N.D.
	t7A	4.0	N.D.	N.D.

^aThis sample was harvested at zero time and represents the residual input virus. The titer is expressed as $\log_{10}$ pfu per ml.

^bThis sample was harvested at 7 days post-infection.

^cThis sample was inoculated in the presence of 40 μ g/ml of Cytosine arabinoside and harvested at 7 days post-infection.

^dNot detectable.

TABLE 3

Amplification of residual virus by passage in CEF cells				
		CEF	Vero	MRC-5
a) ALVAC				
Pass	2 ^a	7.0 ^b	6.0	5.2
	3	7.5	4.1	4.9
	4	7.5	N.D. ^c	N.D.
	5	7.1	N.D.	N.D.
b) ALVAC-RG				
Pass	2 ^a	7.2	5.5	5.5
	3	7.2	5.0	5.1
	4	7.2	N.D.	N.D.
	5	7.2	N.D.	N.D.

^aPass 2 represents the amplification in CEF cells of the 7 day sample from Pass 1.

^bTiter expressed as log₁₀ pfu per ml

^cNot Detectable

TABLE 4

Schedule of inoculation of rhesus macaques with ALVAC-RG (vCP65)		
Animal	Inoculation	
176L	Primary:	1 × 10 ⁸ pfu of vCP65 orally in TANG
	Secondary:	1 × 10 ⁷ pfu of vCP65 plus 1 × 10 ⁷ pfu of vCP82 ^a by SC route
185 L	Primary:	1 × 10 ⁸ pfu of vCP65 orally in Tang
	Secondary:	1 × 10 ⁷ pfu of vCP65 plus 1 × 10 ⁷ pfu of vCP82 by SC route
177 L	Primary:	5 × 10 ⁷ pfu SC of vCP65 by SC route
	Secondary:	1 × 10 ⁷ pfu of vCP65 plus 1 × 10 ⁷ pfu of vCP82 by SC route
186L	Primary:	5 × 10 ⁷ pfu of vCP65 by SC route
	Secondary:	1 × 10 ⁷ pfu of vCP65 plus 1 × 10 ⁷ pfu of vCP82 by SC route
178L	Primary:	1 × 10 ⁷ pfu of vCP65 by SC route
182L	Primary:	1 × 10 ⁷ pfu of VCP65 by IM route
179L	Primary:	1 × 10 ⁶ pfu of vCP65 by SC route
183L	Primary:	1 × 10 ⁶ pfu of vCP65 by IM route
180L	Primary:	1 × 10 ⁶ pfu of vCP65 by SC route
184L	Primary:	1 × 10 ⁵ pfu of vCP65 by IM route
187L	Primary	1 × 10 ⁷ pfu of vCP65 orally

^avCP82 is a canarypox virus recombinant expressing the measles virus fusion and hemagglutinin genes.

TABLE 5

Analysis of yield in avian and non-avian cells inoculated with ALVAC-RG			
Cell Type	Sample Time		
	t0	t72	t72A ^b
Expt 1			
CEF	3.3 ^a	7.4	1.7
Vero	3.0	1.4	1.7
MRC-5	3.4	2.0	1.7
Expt 2			
CEF	2.9	7.5	<1.7
WISH	3.3	2.2	2.0
Detroit-532	2.8	1.7	<1.7

^aTiter expressed as log₁₀ pfu per ml

^bCulture incubated in the presence of 40 µg/ml of Cytosine arabinoside

TABLE 6

Potency of ALVAC-RG as tested in mice		
Test	Challenge Dose ^a	PD ₅₀ ^b
Initial seed	43	4.56
Primary seed	23	3.34
Vaccine Batch H	23	4.52
Vaccine Batch I	23	3.33
Vaccine Batch K	15	3.64
Vaccine Batch L	15	4.03
Vaccine Batch M	15	3.32
Vaccine Batch N	15	3.39
Vaccine Batch J	23	3.42

^aExpressed as mouse LD₅₀

^bExpressed as log₁₀ TCID₅₀

TABLE 7

Efficacy of ALVAC-RG in dogs and cats				
Dose	Dogs		Cats	
	Antibody ^a	Survival ^b	Antibody	Survival
6.7	11.9	5/5	2.9	3/5
7.7	10.1	N.T.	8.1	N.T.

^aAntibody at day 29 post inoculation expressed as the geometric mean titer in International Units.

^bExpressed as a ratio of survivors over animals challenged

TABLE 8

Anti-rabies serological response of Squirrel monkeys inoculated with canarypox recombinants								
Monkey Previous		Rabies serum-neutralizing antibody ^a						
#	Exposure	-196 ^b	0	3	7	11	21	28
22	ALVAC ^c	NT ^g	<1.2	<1.2	<1.2	2.1	2.3	2.2
51	ALVAC ^c	NT	<1.2	<1.2	1.7	2.2	2.2	2.2
39	vCP37 ^d	NT	<1.2	<1.2	1.7	2.1	2.2	N.T. ^g
55	vCP37 ^d	NT	<1.2	<1.2	1.7	2.2	2.1	N.T.
37	ALVAC-RG ^e	2.2	<1.2	<1.2	3.2	3.5	3.5	3.2
53	ALVAC-RG ^e	2.2	<1.2	<1.2	3.6	3.6	3.6	3.4
38	ALVAC-RG ^f	2.7	<1.7	<1.7	3.2	3.8	3.6	N.T.
54	ALVAC-RG ^f	3.2	<1.7	<1.5	3.6	4.2	4.0	3.6
57	None	NT	<1.2	<1.2	1.7	2.7	2.7	2.3

^aAs determined by RFFI test on days indicated and expressed in International Units

^bDay -196 represents serum from day 28 after primary vaccination

^cAnimals received 5.0 log₁₀ TCID₅₀ of ALVAC

^dAnimals received 5.0 log₁₀ TCID₅₀ of vCP37

^eAnimals received 5.0 log₁₀ TCID₅₀ of ALVAC-RG

^fAnimals received 7.0 log₁₀ TCID₅₀ of ALVAC-RG

^gNot tested.

TABLE 9

Inoculation of rhesus macaques with ALVAC-RG ^a											
Days post-Inoculation	Route of Primary Inoculation										
	or/Tang	SC	SC	SC	IM	SC	IM	SC	IM	OR	
	176L ^b	185L	177L	186L	178L	182L	179L	183L	180L	184L	187L ^b
-84	—	—	—	—	—	—	—	—	—	—	—
-9	—	—	—	—	—	—	—	—	—	—	—
3	—	—	—	—	—	—	—	—	—	—	—
6	—	—	±	±	—	—	—	—	—	—	—
11	—	—	16 ^d	128	—	—	—	—	—	—	—
19	—	—	32	128	—	—	—	—	—	—	—
35	—	—	32	512	—	—	—	—	—	—	—
59	—	—	64	256	—	—	—	—	—	—	—
75	—	—	64	128	—	—	—	—	—	—	—
99 ^c	—	—	64	256	—	—	—	—	—	—	—
2	—	—	32	256	—	—	—	—	—	—	—
6	—	—	512	512	—	—	—	—	—	—	—
15	16	16	512	512	64	32	64	128	32	—	—
29	16	32	256	256	64	64	32	128	32	—	—
55	—	32	—	—	—	32	—	32	16	—	—
57	16	—	128	128	16	—	16	—	—	—	—

^aSee Table 9 for schedule of inoculations.

^bAnimals 176L and 185L received 8.0 log₁₀ pfu by the oral route in 5 ml Tang. Animal 187L received 7.0 log₁₀ pfu by oral route not in Tang.

^cDay of re-vaccination for animals 176L, 185L, 177L and 186L by S.C. route, and primary vaccination for animals 178L, 182L, 179L, 183L, 180L, 184L and 187L.

^dTiters expressed as reciprocal of last dilution showing inhibition of fluorescence in an RFFI test.

TABLE 10

Inoculation of chimpanzees with ALVAC-RG		
Weeks post-Inoculation	Animal 431 I.M.	Animal 457 S.C.
0	<8 ^a	<8
1	<8	<8
2	8	32
4	16	32
8	16	32
12 ^b /0	16	8
13/1	128	128
15/3	256	512
20/8	64	128
26/12	32	128

^aTiter expressed as reciprocal of last dilution showing inhibition of fluorescence in an RFFI test

^bDay of re-inoculation

Example 10

Immunization of Humans Using Canarypox Expressing Rabies Glycoprotein (ALVAC-RG; vCP65)

[0225] ALVAC-RG (vCP65) was Generated as Described in Example 9 and FIGS. 9A and 9B. For scaling-up and vaccine manufacturing ALVAC-RG (vCP65) was grown in primary CEF derived from specified pathogen free eggs. Cells were infected at a multiplicity of 0.1 and incubated at 37° C. for three days.

[0226] The vaccine virus suspension was obtained by ultrasonic disruption in serum free medium of the infected cells; cell debris were then removed by centrifugation and filtration. The resulting clarified suspension was supplemented with lyophilization stabilizer (mixture of amino-acids), dispensed in single dose vials and freeze dried. Three batches of

decreasing titer were prepared by ten-fold serial dilutions of the virus suspension in a mixture of serum free medium and lyophilization stabilizer, prior to lyophilization.

[0227] Quality control tests were applied to the cell substrates, media and virus seeds and final product with emphasis on the search for adventitious agents and innocuity in laboratory rodents. No undesirable trait was found.

[0228] Preclinical data. Studies in vitro indicated that VERO or MRC-5 cells do not support the growth of ALVAC-RG (vCP65); a series of eight (VERO) and 10 (MRC) blind serial passages caused no detectable adaptation of the virus to grow in these non avian lines. Analyses of human cell lines (MRC-5, WISH, Detroit 532, HEL, HNK or EBV-transformed lymphoblastoid cells) infected or inoculated with ALVAC-RG (vCP65) showed no accumulation of virus specific DNA suggesting that in these cells the block in replication occurs prior to DNA synthesis. Significantly, however, the expression of the rabies virus glycoprotein gene in all cell lines tested indicating that the abortive step in the canarypox replication cycle occurs prior to viral DNA replication.

[0229] The safety and efficacy of ALVAC-RG (vCP65) were documented in a series of experiments in animals. A number of species including canaries, chickens, ducks, geese, laboratory rodents (suckling and adult mice), hamsters, guinea-pigs, rabbits, cats and dogs, squirrel monkeys, rhesus macaques and chimpanzees, were inoculated with doses ranging from 10⁵ to 10⁸ pfu. A variety of routes were used, most commonly subcutaneous, intramuscular and intradermal but also oral (monkeys and mice) and intracerebral (mice).

[0230] In canaries, ALVAC-RG (vCP65) caused a "take" lesion at the site of scarification with no indication of disease or death. Intradermal inoculation of rabbits resulted in a typical poxvirus inoculation reaction which did not spread and healed in seven to ten days. There was no adverse side effects

due to canarypox in any of the animal tests. Immunogenicity was documented by the development of anti-rabies antibodies following inoculation of ALVAC-RG (vCP65) in rodents, dogs, cats, and primates, as measured by Rapid Fluorescent Focus Inhibition Test (RFFIT). Protection was also demonstrated by rabies virus challenge experiments in mice, dogs, and cats immunized with ALVAC-RG (vCP65).

[0231] Volunteers. Twenty-five healthy adults aged 20-45 with no previous history of rabies immunization were enrolled. Their health status was assessed by complete medical histories, physical examinations, hematological and blood chemistry analyses. Exclusion criteria included pregnancy, allergies, immune depression of any kind, chronic debilitating disease, cancer, injection of immunoglobins in the past three months, and seropositivity to human immunodeficiency virus (HIV) or to hepatitis B virus surface antigen.

[0232] Study design. Participants were randomly allocated to receive either standard Human Diploid Cell Rabies Vaccine (HDC) batch no E0751 (Pasteur Merieux Serums & Vaccine, Lyon, France) or the study vaccine ALVAC-RG (vCP65).

[0233] The trial was designated as a dose escalation study. Three batches of experimental ALVAC-RG (vCP65) vaccine were used sequentially in three groups of volunteers (Groups A, B and C) with two week intervals between each step. The concentration of the three batches was $10^{3.5}$, $10^{4.5}$, $10^{5.5}$ Tissue Culture Infectious Dose (TCID₅₀) per dose, respectively.

[0234] Each volunteer received two doses of the same vaccine subcutaneously in the deltoid region at an interval of four weeks. The nature of the injected vaccine was not known by the participants at the time of the first injection but was known by the investigator.

[0235] In order to minimize the risk of immediate hypersensitivity at the time of the second injection, the volunteers of Group B allocated to the medium dose of experimental vaccine were injected 1 h previously with the lower dose and those allocated to the higher dose (Group C) received successively the lower and the medium dose at hourly intervals.

[0236] Six months later, the recipients of the highest dosage of ALVAC-RG (vCP65) (Group C) and HDC vaccine were offered a third dose of vaccine; they were then randomized to receive either the same vaccine as previously or the alternate vaccine. As a result, four groups were formed corresponding to the following immunization scheme: 1. HDC, HDC-HDC; 2. HDC, HDC-ALVAC-RG (vCP65); 3. ALVAC-RG (vCP65), ALVAC-RG (vCP65)-HDC; 4. ALVAC-RG (vCP65), ALVAC-RG (vCP65), ALVAC-RG (vCP65).

[0237] Monitoring of Side Effects. All subjects were monitored for 1 h after injection and re-examined every day for the next five days. They were asked to record local and systemic reactions for the next three weeks and were questioned by telephone two times a week.

[0238] Laboratory Investigators. Blood specimens were obtained before enrollment and two, four and six days after each injection. Analysis included complete blood cell count, liver enzymes and creatine kinase assays.

[0239] Antibody assays. Antibody assays were performed seven days prior to the first injection and at days 7, 28, 35, 56, 173, 187 and 208 of the study.

[0240] The levels of neutralizing antibodies to rabies were determined using the Rapid Fluorescent Focus Inhibition test (RFFIT) (Smith et al., 1973). Canarypox antibodies were measured by direct ELISA. The antigen, a suspension of purified canarypox virus disrupted with 0.1% Triton X100,

was coated in microplates. Fixed dilutions of the sera were reacted for two hours at room temperature and reacting antibodies were revealed with a peroxidase labelled anti-human IgG goat serum. The results are expressed as the optical density read at 490 nm.

[0241] Analysis. Twenty-five subjects were enrolled and completed the study. There were 10 males and 15 females and the mean age was 31.9 (21 to 48). All but three subjects had evidence of previous smallpox vaccination; the three remaining subjects had no typical scar and vaccination history. Three subjects received each of the lower doses of experimental vaccine ($10^{3.5}$ and $10^{4.5}$ TCID₅₀), nine subjects received $10^{5.5}$ TCID₅₀ and ten received the HDC vaccine.

[0242] Safety (Table 11). During the primary series of immunization, fever greater than 37.7° C. was noted within 24 hours after injection in one HDC recipient (37.8° C.) and in one vCP65 $10^{5.5}$ TCID₅₀ recipient (38° C.). No other systemic reaction attributable to vaccination was observed in any participant.

[0243] Local reactions were noted in 9/10 recipients of HDC vaccine injected subcutaneously and in 0/3, 1/3 and 9/9 recipients of vCP65 $10^{3.5}$, $10^{4.5}$, $10^{5.5}$ TCID₅₀, respectively.

[0244] Tenderness was the most common symptoms and was always mild. Other local symptoms included redness and induration which were also mild and transient. All symptoms usually subsided within 24 hours and never lasted more than 72 hours.

[0245] There was no significant change in blood cell counts, liver enzymes or creatine kinase values.

[0246] Immune Responses; Neutralizing Antibodies to Rabies (Table 12). Twenty eight days after the first injection all the HDC recipients had protective titers (≥ 0.5 IU/ml). By contrast none in groups A and B ($10^{3.5}$ and $10^{4.5}$ TCID₅₀) and only 2/9 in group C ($10^{5.5}$ TCID₅₀) ALVAC-RG (vCP65) recipients reached this protective titer.

[0247] At day 56 (i.e. 28 days after the second injection) protective titers were achieved in 0/3 of Group A, 2/3 of Group B and 9/9 of Group C recipients of ALVAC-RG (vCP65) vaccine and persisted in all 10 HDC recipients.

[0248] At day 56 the geometric mean titers were 0.05, 0.47, 4.4 and 11.5 IU/ml in groups A, B, C and HDC respectively.

[0249] At day 180, the rabies antibody titers had substantially decreased in all subjects but remained above the minimum protective titer of 0.5 IU/ml in 5/10 HDC recipients and in 5/9 ALVAC-RG (vCP65) recipients; the geometric mean titers were 0.51 and 0.45 IU/ml in groups HDC and C, respectively.

[0250] Antibodies to the Canarypox virus (Table 13). The pre-immune titers observed varied widely with titers varying from 0.22 to 1.23 O.D. units despite the absence of any previous contact with canary birds in those subjects with the highest titers. When defined as a greater than two-fold increase between preimmunization and post second injection titers, a seroconversion was obtained in 1/3 subjects in group B and in 9/9 subjects in group C whereas no subject seroconverted in groups A or HDC.

[0251] Booster Injection. The vaccine was similarly well tolerated six months later, at the time of the booster injection: fever was noted in 2/9 HDC booster recipients and in 1/10 ALVAC-RG (vCP65) booster recipients. Local reactions were present in 5/9 recipients of HDC booster and in 6/10 recipients of the ALVAC-RG (vCP65) booster.

[0252] Observations. FIGS. 13A-13D show graphs of rabies neutralizing antibody titers (Rapid Fluorescent Focus

Inhibition Test or RFFIT, IU/ml): Booster effect of HDC and vCP65 ($10^{5.5}$ TCID₅₀) in volunteers previously immunized with either the same or the alternate vaccine. Vaccines were given at days 0, 28 and 180. Antibody titers were measured at days 0, 7, 28, 35, 56, 173, and 187 and 208.

[0253] As shown in FIGS. 13A to 13D, the booster dose given resulted in a further increase in rabies antibody titers in every subject whatever the immunization scheme. However, the ALVAC-RG (vCP65) booster globally elicited lower immune responses than the HDC booster and the ALVAC-RG (vCP65), ALVAC-RG (vCP65)-ALVAC-RG (vCP65) group had significantly lower titers than the three other groups. Similarly, the ALVAC-RG (vCP65) booster injection resulted in an increase in canarypox antibody titers in 3/5 subjects who had previously received the HDC vaccine and in all five subjects previously immunized with ALVAC-RG (vCP65).

[0254] In general, none of the local side effects from administration of vCP65 was indicative of a local replication of the virus. In particular, lesions of the skin such as those observed after injection of vaccine were absent. In spite of the apparent absence of replication of the virus, the injection resulted in the volunteers generating significant amounts of antibodies to both the canarypox vector and to the expressed rabies glycoprotein.

[0255] Rabies neutralizing antibodies were assayed with the Rapid Fluorescent Focus Inhibition Test (RFFIT) which is known to correlate well with the sero neutralization test in mice. Of 9 recipients of $10^{5.5}$ TCID₅₀, five had low level responses after the first dose. Protective titers of rabies antibodies were obtained after the second injection in all recipients of the highest dose tested and even in 2 of the 3 recipients of the medium dose. In this study, both vaccines were given subcutaneously as usually recommended for live vaccines, but not for the inactivated HDC vaccine. This route of injection was selected as it best allowed a careful examination of the injection site, but this could explain the late appearance of antibodies in HDC recipients: indeed, none of the HDC recipients had an antibody increase at day 7, whereas, in most studies where HDC vaccine is given intramuscularly a significant proportion of subjects do (Klietmann et al., Int'l Green Cross—Geneva, 1981; Kuwert et al., Int'l Green Cross—Geneva, 1981). However, this invention is not necessarily limited to the subcutaneous route of administration.

[0256] The GMT (geometric mean titers) of rabies neutralizing antibodies was lower with the investigational vaccine than with the HDC control vaccine, but still well above the minimum titer required for protection. The clear dose effect response obtained with the three dosages used in this study suggest that a higher dosage might induce a stronger response. Certainly from this disclosure the skilled artisan can select an appropriate dosage for a given patient.

[0257] The ability to boost the antibody response is another important result of this Example; indeed, an increase in rabies antibody titers was obtained in every subject after the 6 month dose whatever the immunization scheme, showing that pre-existing immunity elicited by either the canarypox vector or the rabies glycoprotein had no blocking effect on the booster with the recombinant vaccine candidate or the conventional HDC rabies vaccine. This contrasts findings of others with vaccinia recombinants in humans that immune response may be blocked by pre-existing immunity (Cooney et al.; Etinger et al.).

[0258] Thus, this Example clearly demonstrates that a non-replicating poxvirus can serve as an immunizing vector in humans, with all of the advantages that replicating agents confer on the immune response, but without the safety problem created by a fully permissive virus.

TABLE 11

vCP65 dosage (TCID ₅₀)	Reactions in the 5 days following vaccination							
	10 ^{3.5}		10 ^{4.5}		10 ^{5.5}		H D C control	
	1st	2nd	1st	2nd	1st	2nd	1st	2nd
No. vaccinees	3	3	3	3	9	9	10	10
temp >37.7° C.	0	0	0	0	0	1	1	0
soreness	0	0	1	1	6	8	8	6
redness	0	0	0	0	0	4	5	4
induration	0	0	0	0	0	4	5	4

TABLE 12

No. TCID ₅₀ /dose		Rabies neutralizing antibodies (RFFIT; IU/ml) Individual titers and geometric mean titers (GMT)					
		Days					
		0	7	28	35	56	
1	10 ^{3.5}	<0.1	<0.1	<0.1	<0.1	0.2	
3	10 ^{3.5}	<0.1	<0.1	<0.1	<0.1	<0.1	
4	10 ^{3.5}	<0.1	<0.1	<0.1	<0.1	<0.1	
	G.M.T.	<0.1	<0.1	<0.1	<0.1	<0.1	
6	10 ^{4.5}	<0.1	<0.1	<0.1	<0.1	<0.1	
7	10 ^{4.5}	<0.1	<0.1	<0.1	2.4	1.9	
10	10 ^{4.5}	<0.1	<0.1	<0.1	1.6	1.1	
	G.M.T.	<0.1	<0.1	0.1	0.58	0.47	
11	10 ^{5.5}	<0.1	<0.1	1.0	3.2	4.3	
13	10 ^{5.5}	<0.1	<0.1	0.3	6.0	8.8	
14	10 ^{5.5}	<0.1	<0.1	0.2	2.1	9.4	
17	10 ^{5.5}	<0.1	<0.1	<0.1	1.2	2.5	
18	10 ^{5.5}	<0.1	<0.1	0.7	8.3	12.5	
20	10 ^{5.5}	<0.1	<0.1	<0.1	0.3	3.7	
21	10 ^{5.5}	<0.1	<0.1	0.2	2.6	3.9	
23	10 ^{5.5}	<0.1	<0.1	<0.1	1.7	4.2	
25	10 ^{5.5}	<0.1	<0.1	<0.1	0.6	0.9	
	G.M.T.	<0.1	<0.1	0.16	1.9	4.4*	
2	HDC	<0.1	<0.1	0.8	7.1	7.2	
5	HDC	<0.1	<0.1	9.9	12.8	18.7	
8	HDC	<0.1	<0.1	12.7	21.1	16.5	
9	HDC	<0.1	<0.1	6.0	9.9	14.3	
12	HDC	<0.1	<0.1	5.0	9.2	25.3	
15	HDC	<0.1	<0.1	2.2	5.2	8.6	
16	HDC	<0.1	<0.1	2.7	7.7	20.7	
19	HDC	<0.1	<0.1	2.6	9.9	9.1	
22	HDC	<0.1	<0.1	1.4	8.6	6.6	
24	HDC	<0.1	<0.1	0.8	5.8	4.7	
	G.M.T.	<0.1	<0.1	2.96	9.0	11.5*	

*p = 0.007 student t test

TABLE 13

vCP65 dosage		Canarypox antibodies: ELISA Geometric Mean Titers*				
		Days				
		0	7	28	35	56
	TCID ₅₀ /dose					
	10 ^{3.5}	0.69	ND	0.76	ND	0.68
	10 ^{4.5}	0.49	0.45	0.56	0.63	0.87
	10 ^{5.5}	0.38	0.38	0.77	1.42	1.63
	HDC control	0.45	0.39	0.40	0.35	0.39

*optical density at 1/2s dilution

Example 11

Comparison of the LD₅₀ of ALVAC and NYVAC
with Various Vaccinia Virus Strains

[0259] Mice. Male outbred Swiss Webster mice were purchased from Taconic Farms (Germantown, N.Y.) and maintained on mouse chow and water ad libitum until use at 3 weeks of age ("normal" mice). Newborn outbred Swiss Webster mice were of both sexes and were obtained following timed pregnancies performed by Taconic Farms. All newborn mice used were delivered within a two day period.

[0260] Viruses. ALVAC was derived by plaque purification of a canarypox virus population and was prepared in primary chick embryo fibroblast cells (CEF). Following purification by centrifugation over sucrose density gradients, ALVAC was enumerated for plaque forming units in CEF cells. The WR(L) variant of vaccinia virus was derived by selection of large plaque phenotypes of WR (Panicali et al., 1981). The Wyeth New York State Board of Health vaccine strain of vaccinia virus was obtained from Pharmaceuticals Calf Lymph Type vaccine Dryvax, control number 302001B. Copenhagen strain vaccinia virus VC-2 was obtained from Institut Merieux, France. Vaccinia virus strain NYVAC was derived from Copenhagen VC-2. All vaccinia virus strains except the Wyeth strain were cultivated in Vero African green monkey kidney cells, purified by sucrose gradient density centrifugation and enumerated for plaque forming units on Vero cells. The Wyeth strain was grown in CEF cells and enumerated for plaque forming units in CEF cells.

[0261] Inoculations. Groups of 10 normal mice were inoculated intracranially (ic) with 0.05 ml of one of several dilutions of virus prepared by 10-fold serially diluting the stock preparations in sterile phosphate-buffered saline. In some instances, undiluted stock virus preparation was used for inoculation.

[0262] Groups of 10 newborn mice, 1 to 2 days old, were inoculated ic similarly to the normal mice except that an injection volume of 0.03 ml was used.

[0263] All mice were observed daily for mortality for a period of 14 days (newborn mice) or 21 days (normal mice) after inoculation. Mice found dead the morning following inoculation were excluded due to potential death by trauma.

[0264] The lethal dose required to produce mortality for 50% of the experimental population (LD₅₀) was determined by the proportional method of Reed and Muench.

[0265] Comparison of the LD₅₀ of ALVAC and NYVAC with Various Vaccinia Virus Strains for Normal, Young Outbred Mice by the ic Route. In young, normal mice, the virulence of NYVAC and ALVAC were several orders of magnitude lower than the other vaccinia virus strains tested (Table 14). NYVAC and ALVAC were found to be over 3,000 times less virulent in normal mice than the Wyeth strain; over 12,500 times less virulent than the parental VC-2 strain; and over 63,000,000 times less virulent than the WR(L) variant. These results would suggest that NYVAC is highly attenuated compared to other vaccinia strains, and that ALVAC is generally nonvirulent for young mice when administered intracranially, although both may cause mortality in mice at extremely high doses (3.85×10⁸ PFUs, ALVAC and 3×10⁸ PFUs, NYVAC) by an undetermined mechanism by this route of inoculation.

[0266] Comparison of the LD₅₀ of ALVAC and NYVAC with Various Vaccinia Virus Strains for Newborn Outbred Mice by the ic Route. The relative virulence of 5 poxvirus

strains for normal, newborn mice was tested by titration in an intracranial (ic) challenge model system (Table 15). With mortality as the endpoint, LD₅₀ values indicated that ALVAC is over 100,000 times less virulent than the Wyeth vaccine strain of vaccinia virus; over 200,000 times less virulent than the Copenhagen VC-2 strain of vaccinia virus; and over 25,000,000 times less virulent than the WR-L variant of vaccinia virus. Nonetheless, at the highest dose tested, 6.3×10⁷ PFUs, 100% mortality resulted. Mortality rates of 33.3% were observed at 6.3×10⁶ PFUs. The cause of death, while not actually determined, was not likely of toxicological or traumatic nature since the mean survival time (MST) of mice of the highest dosage group (approximately 6.3 LD₅₀) was 6.7±1.5 days. When compared to WR(L) at a challenge dose of 5 LD₅₀, wherein MST is 4.8±0.6 days, the MST of ALVAC challenged mice was significantly longer (P=0.001).

[0267] Relative to NYVAC, Wyeth was found to be over 15,000 times more virulent; VC-2, greater than 35,000 times more virulent; and WR(L), over 3,000,000 times more virulent. Similar to ALVAC, the two highest doses of NYVAC, 6×10⁶ and 6×10⁷ PFUs, caused 100% mortality. However, the MST of mice challenged with the highest dose, corresponding to 380 LD₅₀, was only 2 days (9 deaths on day 2 and 1 on day 4). In contrast, all mice challenged with the highest dose of WR-L, equivalent to 500 LD₅₀, survived to day 4.

TABLE 14

Calculated 50% Lethal Dose for mice by various vaccinia virus strains and for canarypox virus (ALVAC) by the ic route.	
POXVIRUS STRAIN	CALCULATED LD ₅₀ (PFUs)
WR(L)	2.5
VC-2	1.26 × 10 ⁴
WYETH	5.00 × 10 ⁴
NYVAC	1.58 × 10 ⁸
ALVAC	1.58 × 10 ⁸

TABLE 15

Calculated 50% Lethal Dose for newborn mice by various vaccinia virus strains and for canarypox virus (ALVAC) by the ic route.	
POXVIRUS STRAIN	CALCULATED LD ₅₀ (PFUs)
WR(L)	0.4
VC-2	0.1
WYETH	1.6
NYVAC	1.58 × 10 ⁶
ALVAC	1.00 × 10 ⁷

Example 12

Evaluation of NYVAC (vP866) and NYVAC-RG
(vP879)

[0268] Immunoprecipitations. Preformed monolayers of avian or non-avian cells were inoculated with 10 pfu per cell of parental NYVAC (vP866) or NYVAC-RG (vP879) virus. The inoculation was performed in EMEM free of methionine and supplemented with 2% dialyzed fetal bovine serum. After a one hour incubation, the inoculum was removed and the medium replaced with EMEM (methionine free) containing 20 µCi/ml of ³⁵S-methionine. After an overnight incubation

of approximately 16 hours, cells were lysed by the addition of Buffer A (1% Nonidet P-40, 10 mM Tris pH7.4, 150 mM NaCl, 1 mM EDTA, 0.01% sodium azide, 500 units per ml of aprotinin, and 0.02% phenyl methyl sulfonyl fluoride). Immunoprecipitation was performed using a rabies glycoprotein specific monoclonal antibody designated 24-3F10 supplied by Dr. C. Trinarchi, Griffith Laboratories, New York State Department of Health, Albany, N.Y., and a rat anti-mouse conjugate obtained from Boehringer Mannheim Corporation (Cat. #605-500). Protein A Sepharose CL-48 obtained from Pharmacia LKB Biotechnology Inc., Piscataway, N.J., was used as a support matrix. Immunoprecipitates were fractionated on 10% polyacrylamide gels according to the method of Dreyfuss et al. (1984). Gels were fixed, treated for fluorography with 1M Na-salicylate for one hour, and exposed to Kodak XAR-2 film to visualize the immunoprecipitated protein species.

[0269] Sources of Animals. New Zealand White rabbits were obtained from Hare-Marland (Hewitt, N.J.). Three week old male Swiss Webster outbred mice, timed pregnant female Swiss Webster outbred mice, and four week old Swiss Webster nude ($nu^{+}nu^{+}$) mice were obtained from Taconic Farms, Inc. (Germantown, N.Y.). All animals were maintained according to NIH guidelines. All animal protocols were approved by the institutional IACUC. When deemed necessary, mice which were obviously terminally ill were euthanized.

[0270] Evaluation of Lesions in Rabbits. Each of two rabbits was inoculated intradermally at multiple sites with 0.1 ml of PBS containing 10^4 , 10^5 , 10^6 , 10^7 , or 10^8 pfu of each test virus or with PBS alone. The rabbits were observed daily from day 4 until lesion resolution. Indurations and ulcerations were measured and recorded.

[0271] Virus Recovery from Inoculation Sites. A single rabbit was inoculated intradermally at multiple sites of 0.1 ml of PBS containing 10^6 , 10^7 , or 10^8 pfu of each test virus or with PBS alone. After 11 days, the rabbit was euthanized and skin biopsy specimens taken from each of the inoculation sites were aseptically prepared by mechanical disruption and indirect sonication for virus recovery. Infectious virus was assayed by plaque titration on CEF monolayers.

[0272] Virulence in Mice. Groups of ten mice, or five in the nude mice experiment, were inoculated ip with one of several dilutions of virus in 0.5 ml of sterile PBS. Reference is also made to Example 11.

[0273] Cyclophosphamide (CY) Treatment. Mice were injected by the ip route with 4 mg (0.02 ml) of CY (SIGMA) on day -2, followed by virus injection on day 0. On the following days post infection, mice were injected ip with CY: 4 mg on day 1; 2 mg on days 4, 7 and 11; 3 mg on days 14, 18, 21, 25 and 28. Immunosuppression was indirectly monitored by enumerating white blood cells with a Coulter Counter on day 11. The average white blood cell count was 13,500 cells per μ l for untreated mice ($n=4$) and 4,220 cells per μ l for CY-treated control mice ($n=5$).

[0274] Calculation of LD_{50} . The lethal dose required to produce 50% mortality (LD_{50}) was determined by the proportional method of Reed and Muench (Reed and Muench 1938).

[0275] Potency Testing of NYVAC-RG in Mice. Four to six week old mice were inoculated in the footpad with 50 to 100 μ l of a range of dilutions ($2.0-8.0 \log_{10}$ tissue culture infective dose 50% ($TCID_{50}$)) of either VV-RG (Kieny et al., 1984), ALVAC-RG (Taylor et al., 1991b), or the NYVAC-RG. Each

group consisted of eight mice. At 14 days post-vaccination, the mice were challenged by intracranial inoculation with 15 LD_{50} of the rabies virus CVS strain (0.03 ml). On day 28, surviving mice were counted and protective does 50% (PD_{50}) calculated.

[0276] Derivation of NYVAC (vP866). The NYVAC strain of vaccinia virus was generated from VC-2, a plaque cloned isolate of the COPENHAGEN vaccine strain. To generate NYVAC from VC-2, eighteen vaccinia ORFs, including a number of viral functions associated with virulence, were precisely deleted in a series of sequential manipulations as described earlier in this disclosure. These deletions were constructed in a manner designed to prevent the appearance of novel unwanted open reading frames. FIG. 10 schematically depicts the ORFs deleted to generate NYVAC. At the top of FIG. 10 is depicted the HindIII restriction map of the vaccinia virus genome (VC-2 plaque isolate, COPENHAGEN strain). Expanded are the six regions of VC-2 that were sequentially deleted in the generation of NYVAC. The deletions were described earlier in this disclosure (Examples 1 through 6). Below such deletion locus is listed the ORFs which were deleted from that locus, along with the functions or homologies and molecular weight of their gene products.

[0277] Replication Studies of NYVAC and ALVAC on Human Tissue Cell Lines. In order to determine the level of replication of NYVAC strain of vaccinia virus (vP866) in cells of human origin, six cell lines were inoculated at an input multiplicity of 0.1 pfu per cell under liquid culture and incubated for 72 hours. The COPENHAGEN parental clone (VC-2) was inoculated in parallel. Primary chick embryo fibroblast (CEF) cells (obtained from 10-11 day old embryonated eggs of SPF origin, Spafas, Inc., Storrs, Conn.) were included to represent a permissive cell substrate for all viruses. Cultures were analyzed on the basis of two criteria: the occurrence of productive viral replication and expression of an extrinsic antigen.

[0278] The replication potential of NYVAC in a number of human derived cells are shown in Table 16. Both VC-2 and NYVAC are capable of productive replication in CEF cells, although NYVAC with slightly reduced yields. VC-2 is also capable of productive replication in the six human derived cell lines tested with comparable yields except in the EBV transformed lymphoblastoid cell line JT-1 (human lymphoblastoid cell line transformed with Epstein-Barr virus, see Rickinson et al., 1984). In contrast, NYVAC is highly attenuated in its ability to productively replicate in any of the human derived cell lines tested. Small increases of infectious virus above residual virus levels were obtained from NYVAC-infected MRC-5 (ATCC #CCL171, human embryonic lung origin), DETROIT 532 (ATCC #CCL54, human foreskin, Downs Syndrome), HEL 299 (ATCC #CCL137, human embryonic lung cells) and HNK (human neonatal kidney cells, Whittaker Bioproducts, Inc. Walkersville, Md., Cat #70-151) cells. Replication on these cell lines was significantly reduced when compared to virus yields obtained from NYVAC-infected CEF cells or with parental VC-2 (Table 16). It should be noted that the yields at 24 hours in CEF cells for both NYVAC and VC-2 is equivalent to the 72-hour yield. Allowing the human cell line cultures to incubate an additional 48 hours (another two viral growth cycles) may, therefore, have amplified the relative virus yield obtained.

[0279] Consistent with the low levels of virus yields obtained in the human-derived cell lines, MRC-5 and DETROIT 532, detectable but reduced levels of NYVAC-

specific DNA accumulation were noted. The level of DNA accumulation in the MRC-5 and DETROIT 532 NYVAC-infected cell lines relative to that observed in NYVAC-infected CEF cells paralleled the relative virus yields. NYVAC-specific viral DNA accumulation was not observed in any of the other human-derived cells.

[0280] An equivalent experiment was also performed using the avipox virus, ALVAC. The results of virus replication are also shown in Table 16. No progeny virus was detectable in any of the human cell lines consistent with the host range restriction of canarypox virus to avian species. Also consistent with a lack of productive replication of ALVAC in these human-derived cells is the observation that no ALVAC-specific DNA accumulation was detectable in any of the human-derived cell lines.

[0281] Expression of Rabies Glycoprotein by NYVAC-RG (vP879) in Human Cells. In order to determine whether efficient expression of a foreign gene could be obtained in the absence of significant levels of productive viral replication, the same cell lines were inoculated with the NYVAC recombinant expressing the rabies virus glycoprotein (vP879, Example 7) in the presence of ^{35}S -methionine. Immunoprecipitation of the rabies glycoprotein was performed from the radiolabelled culture lysate using a monoclonal antibody specific for the rabies glycoprotein. Immunoprecipitation of a 67 kDa protein was detected consistent with a fully glycosylated form of the rabies glycoprotein. No serologically crossreactive product was detected in uninfected or parental NYVAC infected cell lysates. Equivalent results were obtained with all other human cells analyzed.

[0282] Inoculations on the Rabbit Skin. The induction and nature of skin lesions on rabbits following intradermal (id) inoculations has been previously used as a measure of pathogenicity of vaccinia virus strains (Buller et al., 1988; Child et al., 1990; Fenner, 1958; Flexner et al., 1987; Ghendon and Chemos 1964). Therefore, the nature of lesions associated with id inoculations with the vaccinia strains WR (ATCC #VR119 plaque purified on CV-1 cells, ATCC #CCL70, and a plaque isolate designated L variant, ATCC #VR2035 selected, as described in Panicali et al., 1981)), WYETH (ATCC #VR325 marketed as DRYVAC by Wyeth Laboratories, Marietta, Pa.), COPENHAGEN (VC-2), and NYVAC was evaluated by inoculation of two rabbits (A069 and A128). The two rabbits displayed different overall sensitivities to the viruses, with rabbit A128 displaying less severe reactions than rabbit A069. In rabbit A128, lesions were relatively small and resolved by 27 days post-inoculation. On rabbit A069, lesions were intense, especially for the WR inoculation sites, and resolved only after 49 days. Intensity of the lesions was also dependent on the location of the inoculation sites relative to the lymph drainage network. In particular, all sites located above the backspine displayed more intense lesions and required longer times to resolve the lesions located on the flanks. All lesions were measured daily from day 4 to the disappearance of the last lesion, and the means of maximum lesion size and days to resolution were calculated (Table 17). No local reactions were observed from sites injected with the control PBS. Ulcerative lesions were observed at sites injected with WR, VC-2 and WYETH vaccinia virus strains. Significantly, no induration or ulcerative lesions were observed at sites of inoculation with NYVAC.

[0283] Persistence of Infectious Virus at the Site of Inoculation. To assess the relative persistence of these viruses at the site of inoculation, a rabbit was inoculated intradermally at

multiple sites with 0.1 ml PBS containing 10^6 , 10^7 or 10^8 pfu of VC-2, WR, WYETH or NYVAC. For each virus, the 10^7 pfu dose was located above the backspine, flanked by the 10^6 and 10^8 doses. Sites of inoculation were observed daily for 11 days. WR elicited the most intense response, followed by VC-2 and WYETH (Table 18). Ulceration was first observed at day 9 for WR and WYETH and day 10 for VC-2. Sites inoculated with NYVAC or control PBS displayed no induration or ulceration. At day 11 after inoculation, skin samples from the sites of inoculation were excised, mechanically disrupted, and virus was titrated on CEF cells. The results are shown in Table 18. In no case was more virus recovered at this timepoint than was administered. Recovery of vaccinia strain, WR, was approximately 10^6 pfu of virus at each site irrespective of amount of virus administered. Recovery of vaccinia strains WYETH and VC-2 was 10^3 to 10^4 pfu regardless of amount administered. No infectious virus was recovered from sites inoculated with NYVAC.

[0284] Inoculation of Genetically or Chemically Immune Deficient Mice. Intraperitoneal inoculation of high doses of NYVAC (5×10^8 pfu) or ALVAC (10^9 pfu) into nude mice caused no deaths, no lesions, and no apparent disease through the 100 day observation period. In contrast, mice inoculated with WR (10^3 to 10^4 pfu), WYETH (5×10^7 or 5×10^8 pfu) or VC-2 (10^4 to 10^9 pfu) displayed disseminated lesions typical of poxviruses first on the toes, then on the tail, followed by severe orchitis in some animals. In mice infected with WR or WYETH, the appearance of disseminated lesions generally led to eventual death, whereas most mice infected with VC-2 eventually recovered. Calculated LD_{50} values are given in Table 19.

[0285] In particular, mice inoculated with VC-2 began to display lesions on their toes (red papules) and 1 to 2 days later on the tail. These lesions occurred between 11 and 13 days post-inoculation (pi) in mice given the highest doses (10^9 , 10^8 , 10^7 and 10^6 pfu), on day 16 pi in mice given 10^5 pfu and on day 21 pi in mice given 10^4 pfu. No lesions were observed in mice inoculated with 10^3 and 10^2 pfu during the 100 day observation period. Orchitis was noticed on day 23 pi in mice given 10^9 and 10^8 pfu, and approximately 7 days later in the other groups (10^7 to 10^4 pfu). Orchitis was especially intense in the 10^9 and 10^8 pfu groups and, although receding, was observed until the end of the 100 day observation period. Some pox-like lesions were noticed on the skin of a few mice, occurring around 30-35 days pi. Most pox lesions healed normally between 60-90 days pi. Only one mouse died in the group inoculated with 10^9 pfu (Day 34 pi) and one mouse died in the group inoculated with 10^8 pfu (Day 94 pi). No other deaths were observed in the VC-2 inoculated mice.

[0286] Mice inoculated with 10^4 pfu of the WR strain of vaccinia started to display pox lesions on Day 17 pi. These lesions appeared identical to the lesions displayed by the VC-2 injected mice (swollen toes, tail). Mice inoculated with 10^3 pfu of the WR strain did not develop lesions until 34 days pi. Orchitis was noticed only in the mice inoculated with the highest dose of WR (10^4 pfu). During the latter stages of the observation period, lesions appeared around the mouth and the mice stopped eating. All mice inoculated with 10^4 pfu of WR died or were euthanized when deemed necessary between 21 days and 31 days pi. Four out of the 5 mice injected with 10^3 pfu of WR died or were euthanized when deemed necessary between 35 days and 57 days pi. No deaths were observed in mice inoculated with lower doses of WR (1 to 100 pfu).

[0287] Mice inoculated with the WYETH strain of vaccinia virus at higher doses (5×10^7 and 5×10^8 pfu) showed lesions on toes and tails, developed orchitis, and died. Mice injected with 5×10^6 pfu or less of WYETH showed no signs of disease or lesions.

[0288] As shown in Table 19, CY-treated mice provided a more sensitive model for assaying poxvirus virulence than did nude mice. LD₅₀ values for the WR, WYETH, and VC-2 vaccinia virus strains were significantly lower in this model system than in the nude mouse model. Additionally, lesions developed in mice injected with WYETH, WR and VC-2 vaccinia viruses, as noted below, with higher doses of each virus resulting in more rapid formation of lesions. As was seen with nude mice, CY-treated mice injected with NYVAC or ALVAC did not develop lesions. However, unlike nude mice, some deaths were observed in CY-treated mice challenged with NYVAC or ALVAC, regardless of the dose. These random incidences are suspect as to the cause of death.

[0289] Mice injected with all doses of WYETH (9.5×10^4 to 9.5×10^9 pfu) displayed pox lesions on their tail and/or on their toes between 7 and 15 days pi. In addition, the tails and toes were swollen. Evolution of lesions on the tail was typical of pox lesions with formation of a papule, ulceration and finally formation of a scab. Mice inoculated with all doses of VC-2 (1.65×10^5 to 1.65×10^9) also developed pox lesions on their tails and/or their toes analogous to those of WYETH injected mice. These lesions were observed between 7-12 days post inoculation. No lesions were observed on mice injected with lower doses of WR virus, although deaths occurred in these groups.

[0290] Potency Testing of NYVAC-RG. In order to determine that attenuation of the COPENHAGEN strain of vaccinia virus had been effected without significantly altering the ability of the resulting NYVAC strain to be a useful vector, comparative potency tests were performed. In order to monitor the immunogenic potential of the vector during the sequential genetic manipulations performed to attenuate the virus, a rabiesvirus glycoprotein was used as a reporter extrinsic antigen. The protective efficacy of the vectors expressing the rabies glycoprotein gene was evaluated in the standard NIH mouse potency test for rabies (Seligmann, 1973). Table 20 demonstrates that the PD₅₀ values obtained with the highly attenuated NYVAC vector are identical to those obtained using a COPENHAGEN-based recombinant containing the rabies glycoprotein gene in the tk locus (Kieny et al., 1984) and similar to PD₅₀ values obtained with ALVAC-RG, a canarypox based vector restricted to replication to avian species.

[0291] Observations. NYVAC, deleted of known virulence genes and having restricted in vitro growth characteristics, was analyzed in animal model systems to assess its attenuation characteristics. These studies were performed in comparison with the neurovirulent vaccinia virus laboratory strain, WR, two vaccinia virus vaccine strains, WYETH (New York City Board of Health) and COPENHAGEN (VC-2), as well as with a canarypox virus strain, ALVAC (See also Example 11). Together, these viruses provided a spectrum of relative pathogenic potentials in the mouse challenge model and the rabbit skin model, with WR being the most virulent strain, WYETH and COPENHAGEN (VC-2) providing previously utilized attenuated vaccine strains with documented characteristics, and ALVAC providing an example of a poxvirus whose replication is restricted to avian species. Results from these in vivo analyses clearly demonstrate the highly

attenuated properties of NYVAC relative to the vaccinia virus strains, WR, WYETH and COPENHAGEN (VC-2) (Tables 14-20). Significantly, the LD₅₀ values for NYVAC were comparable to those observed with the avian host restricted avipoxvirus, ALVAC. Deaths due to NYVAC, as well as ALVAC, were observed only when extremely high doses of virus were administered via the intracranial route (Example 11, Tables 14, 15, 19). It has not yet been established whether these deaths were due to nonspecific consequences of inoculation of a high protein mass. Results from analyses in immunocompromised mouse models (nude and CY-treated) also demonstrate the relatively high attenuation characteristics of NYVAC, as compared to WR, WYETH and COPENHAGEN strains (Tables 17 and 18). Significantly, no evidence of disseminated vaccinia infection or vaccinal disease was observed in NYVAC-inoculated animals or ALVAC-inoculated animals over the observation period. The deletion of multiple virulence-associated genes in NYVAC shows a synergistic effect with respect to pathogenicity. Another measure of the innocuity of NYVAC was provided by the intradermal administration on rabbit skin (Tables 17 and 18). Considering the results with ALVAC, a virus unable to replicate in nonavian species, the ability to replicate at the site of inoculation is not the sole correlate with reactivity, since intradermal inoculation of ALVAC caused areas of induration in a dose dependent manner. Therefore, it is likely that factors other than the replicative capacity of the virus contribute to the formation of the lesions. Deletion of specific virulence-associated genes in NYVAC prevents lesion occurrence.

[0292] Together, the results in this Example and in foregoing Examples, including Example 11, demonstrate the highly attenuated nature of NYVAC relative to WR, and the previously utilized vaccinia virus vaccine strains, WYETH and COPENHAGEN. In fact, the pathogenic profile of NYVAC, in the animal model systems tested, was similar to that of ALVAC, a poxvirus known to productively replicate only in avian species. The apparently restricted capacity of NYVAC to productively replicate on cells derived from humans (Table 16) and other species, including the mouse, swine, dog and horse, provides a considerable barrier that limits or prevents potential transmission to unvaccinated contacts or to the general environment in addition to providing a vector with reduced probability of dissemination within the vaccinated individual.

[0293] Significantly, NYVAC-based vaccine candidates have been shown to be efficacious. NYVAC recombinants expressing foreign gene products from a number of pathogens have elicited immunological responses towards the foreign gene products in several animal species, including primates. In particular, a NYVAC-based recombinant expressing the rabies glycoprotein was able to protect mice against a lethal rabies challenge. The potency of the NYVAC-based rabies glycoprotein recombinant was comparable to the PD₅₀ value for a COPENHAGEN-based recombinant containing the rabies glycoprotein in the tk locus (Table 20). NYVAC-based recombinants have also been shown to elicit measles virus neutralizing antibodies in rabbits and protection against pseudorabies virus and Japanese encephalitis virus challenge in swine. The highly attenuated NYVAC strain confers safety advantages with human and veterinary applications (Tartaglia et al., 1992). Furthermore, the use of

NYVAC as a general laboratory expression vector system may greatly reduce the biological hazards associated with using vaccinia virus.

[0294] By the following criteria, the results of this Example and the Examples herein, including Example 11, show NYVAC to be highly attenuated: a) no detectable induration or ulceration at site of inoculation (rabbit skin); b) rapid clearance of infectious virus from intradermal site of inoculation (rabbit skin); c) absence of testicular inflammation (nude mice); d) greatly reduced virulence (intracranial challenge, both three-week old and newborn mice); e) greatly reduced pathogenicity and failure to disseminate in immunodeficient subjects (nude and cyclophosphamide treated mice); and f) dramatically reduced ability to replicate on a variety of human tissue culture cells. Yet, in spite of being highly attenuated, NYVAC, as a vector, retains the ability to induce strong immune responses to extrinsic antigens.

TABLE 16

Replication of COPENHAGEN (VC-2), NYVAC and ALVAC in avian or human derived cell lines					
Cells	Hours post-infection	Yield ^a			% Yield
		VC-2	NYVAC	ALVAC	
CEF	0	3.8 ^b	3.7	4.5	25
	24	8.3	7.8	6.6	
	48	8.6	7.9	7.7	
	72	8.3	7.7	7.5	
	72A ^c	<1.4	1.8	3.1	
MRC-5	0	3.8	3.8	4.7	0.25
	72	7.2	4.6	3.8	
	72A	2.2	2.2	3.7	
	72A	2.2	2.2	3.7	
WISH*	0	3.4	3.4	4.3	0.0004
	72	7.6	2.2	3.1	
	72A	— ^d	1.9	2.9	
DETROIT	0	3.8	3.7	4.4	1.6
	72	7.2	5.4	3.4	
	72A	1.7	1.7	2.9	
HEL	0	3.8	3.5	4.3	0.125
	72	7.5	4.6	3.3	
	72A	2.5	2.1	3.6	
JT-1	0	3.1	3.1	4.1	0.039
	72	6.5	3.1	4.2	
	72A	2.4	2.1	4.4	
HNK	0	3.8	3.7	4.7	0.079
	72	7.6	4.5	3.6	
	72A	3.1	2.7	3.7	

^aYield of NYVAC at 72 hours post-infection expressed as a percentage of yield of VAC-2 after 72 hours on the same cell line.

^bTiter expressed as LOG₅₀ pfu per ml.

^cSample was incubated in the presence of 40 g/ml of cytosine arabinoside.

^dNot determined.

*ATCC #CCL25 Human amnionic cells.

TABLE 17

Induration and ulceration at the site of intradermal inoculation of the rabbit skin					
VIRUS	DOSE ^a	INDURATION		ULCERATION	
		Size ^b	Days ^c	Size	Days
WR	10 ⁴	386	30	88	30
	10 ⁵	622	35	149	32
	10 ⁶	1057	34	271	34
	10 ⁷	877	35	204	35
	10 ⁸	581	25	88	26

TABLE 17-continued

Induration and ulceration at the site of intradermal inoculation of the rabbit skin					
VIRUS	DOSE ^a	INDURATION		ULCERATION	
		Size ^b	Days ^c	Size	Days
WYETH	10 ⁴	32	5	— ^d	—
	10 ⁵	116	15	—	—
	10 ⁶	267	17	3	15
	10 ⁷	202	17	3	24
	10 ⁸	240	29	12	31
VC-2	10 ⁴	64	7	—	—
	10 ⁵	86	8	—	—
	10 ⁶	136	17	—	—
	10 ⁷	167	21	6	10
	10 ⁸	155	32	6	8
NYVAC	10 ⁴	—	—	—	—
	10 ⁵	—	—	—	—
	10 ⁶	—	—	—	—
	10 ⁷	—	—	—	—
	10 ⁸	—	—	—	—

^apfu of indicated vaccinia virus in 0.1 ml PBS inoculated intradermally into one site.

^bmean maximum size of lesions (mm²)

^cmean time after inoculation for complete healing of lesion.

^dno lesions discernable.

TABLE 18

Persistence of poxviruses at the site of intradermal inoculation		
Virus	Inoculum Dose	Total Virus Recovered
WR	8.0 ^a	6.14
	7.0	6.26
	6.0	6.21
WYETH	8.0	3.66
	7.0	4.10
	6.0	3.59
VC-2	8.0	4.47
	7.0	4.74
	6.0	3.97
NYVAC	8.0	0
	7.0	0
	6.0	0

^aexpressed as log₁₀ pfu.

TABLE 19

Virulence studies in immunocompromised mice		
Poxvirus Strain	LD ₅₀ ^a	
	Nude mice	Cyclophosphamide treated mice
WR	422	42
VC-2	>10 ⁹	<1.65 × 10 ⁵
WYETH	1.58 × 10 ⁷	1.83 × 10 ⁶
NY VAC	>5.50 × 10 ⁸	7.23 × 10 ⁸
ALVAC	>10 ⁹	≥5.00 × 10 ^{8b}

^aCalculated 50% lethal dose (pfu) for nude or cyclophosphamide treated mice by the indicated vaccinia viruses and for ALVAC by intraperitoneal route.

^b5 out of 10 mice died at the highest dose of 5 × 10⁸ pfu.

TABLE 20

Comparative efficacy of NYVAC-RG and ALVAC-RG in mice	
Recombinant	PD ₅₀ ^a
VV-RG	3.74
ALVAC-RG	3.86
NYVAC-RG	3.70

^aFour to six week old mice were inoculated in the footpad with 50-100 µl of a range of dilutions (2.0-8.0 log₁₀ tissue culture infection dose 50% (TCID₅₀) of either the VV-RG (Kieny et al., 1984), ALVAC-RG (vCP65) or NYVAC-RG (vP879). At day 14, mice of each group were challenged by intracranial inoculation of 30 µl of a live CVS strain rabies virus corresponding to 15 lethal dose 50% (LD₅₀) per mouse. At day 28, surviving mice were counted and a protective dose 50% (PD₅₀) was calculated.

Example 13

Construction of TROVAC Recombinants Expressing the Hemagglutinin Glycoproteins of Avian Influenza Viruses

[0295] This Example describes the development of fowlpox virus recombinants expressing the hemagglutinin genes of three serotypes of avian influenza virus.

[0296] Cells and Viruses. Plasmids containing cDNA clones of the H4, H5 and H7 hemagglutinin genes were obtained from Dr. Robert Webster, St. Jude Children's Research Hospital, Memphis, Tenn. The strain of FPV designated FP-1 has been described previously (Taylor et al., 1988a, b). It is a vaccine strain useful in vaccination of day old chickens. The parental virus strain Duvette was obtained in France as a fowlpox scab from a chicken. The virus was attenuated by approximately 50 serial passages in chicken embryonated eggs followed by 25 passages on chick embryo fibroblast (CEF) cells. This virus was obtained in September 1980 by Rhone Merieux, Lyon, France, and a master viral seed established. The virus was received by Virogenetics in September 1989, where it was subjected to four successive plaque purifications. One plaque isolate was further amplified in primary CEF cells and a stock virus, designated as TROVAC, was established. The stock virus used in the in vitro recombination test to produce TROVAC-AIH5 (vFP89) and TROVAC-AIH4 (vFP92) had been further amplified through 8 passages in primary CEF cells. The stock virus used to produce TROVAC-AIH7 (vFP100) had been further amplified through 12 passages in primary CEF cells.

[0297] Construction of Fowlpox Insertion Plasmid at F8 Locus. Plasmid pRW731.15 contains a 10 kbp PvuII-PvuII fragment cloned from TROVAC genomic DNA. The nucleotide sequence was determined on both strands for a 3659 bp PvuII-EcoRV fragment. This sequence is shown in FIG. 11 (SEQ ID NO:67). The limits of an open reading frame designated in this laboratory as F8 were determined within this sequence. The open reading frame is initiated at position 495 and terminates at position 1887. A deletion was made from position 779 to position 1926, as described below.

[0298] Plasmid pRW761 is a sub-clone of pRW731.15 containing a 2430 bp EcoRV-EcoRV fragment. Plasmid pRW761 was completely digested with XbaI and partially digested with SspI. A 3700 bp XbaI-SspI band was isolated and ligated with the annealed double-stranded oligonucleotides JCA017 (SEQ ID NO:37) and JCA018 (SEQ ID NO:38).

JCA017 (SEQ ID NO: 37)

5' CTAGACACTTTATGTTTTTAAATATCCGGTCTTAAAGCTTCCCGGG

GATCCTTATACGGGAATAAT 3'

JCA018 (SEQ ID NO: 38)

5' ATTATTCCTCCGTATAAGGATCCCCGGGAAGCTTTTAAAGCCGGATA

TTAAAAACATAAAGTGT 3'

[0299] The plasmid resulting from this ligation was designated pJCA002. Plasmid pJCA004 contains a non-pertinent gene linked to the vaccinia virus H6 promoter in plasmid pJCA002. The sequence of the vaccinia virus H6 promoter has been previously described (Taylor et al., 1988a, b; Guo et al. 1989; Perkus et al., 1989). Plasmid pJCA004 was digested with EcoRV and BamHI which deletes the non-pertinent gene and a portion of the 3' end of the H6 promoter. Annealed oligonucleotides RW178 (SEQ ID NO:48) and RW179 (SEQ ID NO:49) were cut with EcoRV and BamHI and inserted between the EcoRV and BamHI sites of JCA004 to form pRW846.

RW178 (SEQ ID NO: 48):

5' TCATTATCGCGATATCCGTGTTAACTAGCTAGCTAATTTTATTCCC

GGGATCCTTATCA 3'

RW179 (SEQ ID NO: 49):

5' GTATAAGGATCCCGGAATAAAATAGCTAGCTAGTTAACACGGAT

ATCGCGATAATGA 3'

Plasmid pRW846 therefore contains the H6 promoter 5' of EcoRV in the de-ORFed F8 locus. The HincII site 3' of the H6 promoter in pRW846 is followed by translation stop codons, a transcriptional stop sequence recognized by vaccinia virus early promoters (Yuen et al., 1987) and a SmaI site.

[0300] Construction of Fowlpox Insertion Plasmid at F7 Locus. The original F7 non-de-ORFed insertion plasmid, pRW731.13, contained a 5.5 kb FP genomic PvuII fragment in the PvuII site of pUC9. The insertion site was a unique HincII site within these sequences. The nucleotide sequence shown in FIG. 12 (SEQ ID NO:68) was determined for a 2356 bp region encompassing the unique HincII site. Analysis of this sequence revealed that the unique HincII site (FIG. 12, underlined) was situated within an ORF encoding a polypeptide of 90 amino acids. The ORF begins with an ATG at position 1531 and terminates at position 898 (positions marked by arrows in FIG. 12).

[0301] The arms for the de-ORFed insertion plasmid were derived by PCR using pRW731.13 as template. A 596 bp arm (designated as HB) corresponding to the region upstream from the ORF was amplified with oligonucleotides F73PH2 (SEQ ID NO:50) (5'-GACAATCTAAGTCCTATATTAGAC-3') and F73PB (SEQ ID NO:51) (5'-GGATTTTATAGGTAGACAC-3'). A 270 bp arm (designated as EH) corresponding to the region downstream from the ORF was amplified using oligonucleotides F75PE (SEQ ID NO:52) (5'-TCATCGTCTTCATCATCG-3') and F73PH1 (SEQ ID NO:53) (5'-GTCTTAACTTATTGTAAAGGTATACCTG-3').

[0302] Fragment EH was digested with EcoRV to generate a 126 bp fragment. The EcoRV site is at the 3'-end and the 5'-end was formed, by PCR, to contain the 3' end of a HincII site. This fragment was inserted into pBS-SK (Stratagene, La Jolla, Calif.) digested with HincII to form plasmid pF7D1.

The sequence was confirmed by dideoxynucleotide sequence analysis. The plasmid pF7D1 was linearized with *Apa*I, blunt-ended using T4 DNA polymerase, and ligated to the 596 bp HB fragment. The resultant plasmid was designated as pF7D2. The entire sequence and orientation were confirmed by nucleotide sequence analysis.

[0303] The plasmid pF7D2 was digested with *Eco*RV and *Bgl*II to generate a 600 bp fragment. This fragment was inserted into pBS-SK that was digested with *Apa*I, blunt-ended with T4 DNA polymerase, and subsequently digested with *Bam*HI. The resultant plasmid was designated as pF7D3. This plasmid contains an HB arm of 404 bp and a EH arm of 126 bp.

[0304] The plasmid pF7D3 was linearized with *Xho*I and blunt-ended with the Klenow fragment of the *E. coli* DNA polymerase in the presence of 2 mM dNTPs. This linearized plasmid was ligated with annealed oligonucleotides F7MCSB (SEQ ID NO:54) (5'-AACGATTAGTTAGTTAC-TAAAGCTTGCTGTCAGCCCGGGTTTTT-TATTAGTTTAGTT AGTC-3') and F7MCSA (SEQ ID NO:55) (5'-GACTAACTAACTAATAAAAAA-CCCGGGCTGCAGCAAGCTTTTTGTAACTAACTAATCGTT-3'). This was performed to insert a multiple cloning region containing the restriction sites for *Hind*III, *Pst*I and *Sma*I between the EH and HB arms. The resultant plasmid was designated as pF7DO.

[0305] Construction of Insertion Plasmid for the H4 Hemagglutinin at the F8 Locus. A cDNA copy encoding the avian influenza H4 derived from A/Ty/Min/833/80 was obtained from Dr. R. Webster in plasmid pTM4H833. The plasmid was digested with *Hind*III and *Nru*I and blunt-ended using the Klenow fragment of DNA polymerase in the presence of dNTPs. The blunt-ended 2.5 kbp *Hind*III-*Nru*I fragment containing the H4 coding region was inserted into the *Hinc*II site of pIBI25 (International Biotechnologies, Inc., New Haven, Conn.). The resulting plasmid pRW828 was partially cut with *Ban*II, the linear product isolated and recut with *Hind*III. Plasmid pRW828 now with a 100 bp *Hind*III-*Ban*II deletion was used as a vector for the synthetic oligonucleotides RW152 (SEQ ID NO:56) and RW153 (SEQ ID NO:57). These oligonucleotides represent the 3' portion of the H6 promoter from the *Eco*RV site and align the ATG of the promoter with the ATG of the H4 cDNA.

RW152 (SEQ ID NO: 56):
5' GCACGGAACAAAGCTTATCGCATATCCGTTAAGTTTGTATCGTAAT
GCTATCAATCACGATTCTGTTCTGCTCATAGCAGAGGGCTCATCTCAGA
AT 3'

RW153 (SEQ ID NO: 57):
5' ATTCTGAGATGAGCCCTCTGCTATGAGCAGGAACAGAATCGTGATTG
ATAGCATTACGATACAACTTAACGGATATCGGATAAGCTTTGTTCCGT
GC 3'

[0306] The oligonucleotides were annealed, cut with *Ban*II and *Hind*III and inserted into the *Hind*III-*Ban*II deleted pRW828 vector described above. The resulting plasmid pRW844 was cut with *Eco*RV and *Dra*I and the 1.7 kbp fragment containing the 3' H6 promoted H4 coding sequence was inserted between the *Eco*RV and *Hinc*II sites of pRW846 (described previously) forming plasmid pRW848. Plasmid

pRW848 therefore contains the H4 coding sequence linked to the vaccinia virus H6 promoter in the de-ORFed F8 locus of fowlpox virus.

[0307] Construction of Insertion Plasmid for H5 Hemagglutinin at the F8 Locus. A cDNA clone of avian influenza H5 derived from A/Turkey/Ireland/1378/83 was received in plasmid pTH29 from Dr. R. Webster. Synthetic oligonucleotides RW10 (SEQ ID NO:58) through RW13 (SEQ ID NO:61) were designed to overlap the translation initiation codon of the previously described vaccinia virus H6 promoter with the ATG of the H5 gene. The sequence continues through the 5' *Sall* site of the H5 gene and begins again at the 3' H5 *Dra*I site containing the H5 stop codon.

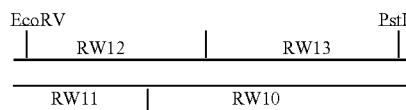
RW10 (SEQ ID NO: 58):
5' GAAAAATTTAAAGTCGACCTGTTTTGTGAGTTGTTGCGTGGTAAC
CAATGCAAATCTGGTCACT 3'

RW11 (SEQ ID NO: 59):
5' TCTAGCAAGACTGACTATTGCAAAAAGAAGCACTATTTCTCCATTA
CGATACAACTTAACGGAT 3'

RW12 (SEQ ID NO: 60):
5' ATCCGTTAAGTTTGTATCGTAATGGAGGAAATAGTGCTTCTTTTGC
AATAGTCAGTCTTGCTAGAAAGTGACCAATTTGCATTGGT 3'

RW13 (SEQ ID NO:61):
5' TACCACGCAAACTCAACAAACAGGTCGACTTTAAATTTTCTG
CA 3'

[0308] The oligonucleotides were annealed at 95° C. for three minutes followed by slow cooling at room temperature. This results in the following double strand structure with the indicated ends.



[0309] Cloning of oligonucleotides between the *Eco*RV and *Pst*I sites of pRW742B resulted in pRW744. Plasmid pRW742B contains the vaccinia virus H6 promoter linked to a non-pertinent gene inserted at the *Hinc*II site of pRW731.15 described previously. Digestion with *Pst*I and *Eco*RV eliminates the non-pertinent gene and the 3'-end of the H6 promoter. Plasmid pRW744 now contains the 3' portion of the H6 promoter overlapping the ATG of avian influenza H5. The plasmid also contains the H5 sequence through the 5' *Sall* site and the 3' sequence from the H5 stop codon (containing a *Dra*I site). Use of the *Dra*I site removes the H5 3' non-coding end. The oligonucleotides add a transcription termination signal recognized by early vaccinia virus RNA polymerase (Yuen et al., 1987). To complete the H6 promoted H5 construct, the H5 coding region was isolated as a 1.6 kbp *Sall*-*Dra*I fragment from pTH29. Plasmid pRW744 was partially digested with *Dra*I, the linear fragment isolated, recut with *Sall* and the plasmid now with eight bases deleted between *Sall* and *Dra*I was used as a vector for the 1.6 kbp pTH29 *Sall* and *Dra*I fragment. The resulting plasmid pRW759 was cut with *Eco*RV and *Dra*I. The 1.7 kbp PRW759 *Eco*RV-*Dra*I fragment containing the 3' H6 promoter and the H5 gene was

inserted between the EcoRV and HincII sites of pRW846 (previously described). The resulting plasmid pRW849 contains the H6 promoted avian influenza virus H5 gene in the de-ORFed F8 locus.

[0310] Construction of Insertion Vector for H7 Hemagglutinin at the F7 Locus. Plasmid pCVH71 containing the H7 hemagglutinin from A/CK/VIC/1/85 was received from Dr. R. Webster. An EcoRI-BamHI fragment containing the H7 gene was blunt-ended with the Klenow fragment of DNA polymerase and inserted into the HincII site of pIBI25 as pRW827. Synthetic oligonucleotides RW165 (SEQ ID NO:62) and RW166 (SEQ ID NO:63) were annealed, cut with HincII and StyI and inserted between the EcoRV and StyI sites of pRW827 to generate pRW845.

RW165 (SEQ ID NO: 62):
 5' GTACAGGTCGACAAGCTTCCCGGGTATCGCGATATCCGTTAAGTTTG
 TATCGTAATGAATACTCAAATCTAATACTCACTCTTGTGGCAGCCATTC
 ACACAAATGCAGACAAAATCTGCCTTGGACATCAT 3'

RW166 (SEQ ID NO: 63):
 5' ATGATGTCCAAGGCAGATTTGTCTGCATTGTGTGAATGGCTGCCA
 CAAGAGTGAGTATTAGAATTTGAGTATTCATTACGATACAACTTAACGG
 ATATCGCGATACCCGGGAAGCTTGTGCGACCTGTAC 3'

[0311] Oligonucleotides RW165 (SEQ ID NO:62) and RW166 (SEQ ID NO:63) link the 3' portion of the H6 promoter to the H7 gene. The 3' non-coding end of the H7 gene was removed by isolating the linear product of an ApaLI digestion of pRW845, recutting it with EcoRI, isolating the largest fragment and annealing with synthetic oligonucleotides RW227 (SEQ ID NO:64) and RW228 (SEQ ID NO:65). The resulting plasmid was pRW854.

RW227 (SEQ ID NO: 64):
 5' ATAACATGCGGTGCACATTGTATATAAGTTAACGAATTCGAAGTC
 AAGC 3'

RW228 (SEQ ID NO: 65):
 5' GCTTGACTTGAATTCGTTAACTTATATACAAATGGTGCACCGCATG
 TTAT 3'

The stop codon of H7 in pRW854 is followed by an HpaI site. The intermediate H6 promoted H7 construct in the de-ORFed F7 locus (described below) was generated by moving the pRW854 EcoRV-HpaI fragment into pRW858 which had been cut with EcoRV and blunt-ended at its PstI site. Plasmid pRW858 (described below) contains the H6 promoter in an F7 de-ORFed insertion plasmid.

[0312] The plasmid pRW858 was constructed by insertion of an 850 bp SmaI/HpaI fragment, containing the H6 promoter linked to a non-pertinent gene, into the SmaI site of pF7DO described previously. The non-pertinent sequences were excised by digestion of pRW858 with EcoRV (site 24 bp upstream of the 3'-end of the H6 promoter) and PstI. The 3.5 kb resultant fragment was isolated and blunt-ended using the Klenow fragment of the *E. coli* DNA polymerase in the presence of 2 mM dNTPs. This blunt-ended fragment was ligated to a 1700 bp EcoRV/HpaI fragment derived from pRW854 (described previously). This EcoRV/HpaI fragment contains

the entire AIV HA (H7) gene juxtaposed 3' to the 3'-most 24 bp of the VV H6 promoter. The resultant plasmid was designated pRW861.

[0313] The 126 bp EH arm (defined previously) was lengthened in pRW861 to increase the recombination frequency with genomic TROVAC DNA. To accomplish this, a 575 bp AccI/SnaBI fragment was derived from pRW 731.13 (defined previously). The fragment was isolated and inserted between the AccI and NaeI sites of pRW861. The resultant plasmid, containing an EH arm of 725 bp and a HB arm of 404 bp flanking the AIV H7 gene, was designated as pRW869. Plasmid pRW869 therefore consists of the H7 coding sequence linked at its 5' end to the vaccinia virus H6 promoter. The left flanking arm consists of 404 bp of TROVAC sequence and the right flanking arm of 725 bp of TROVAC sequence which directs insertion to the de-ORFed F7 locus.

[0314] Development of TROVAC-Avian Influenza Virus Recombinants. Insertion plasmids containing the avian influenza virus HA coding sequences were individually transfected into TROVAC infected primary CEF cells by using the calcium phosphate precipitation method previously described (Panicali et al., 1982; Piccini et al., 1987). Positive plaques were selected on the basis of hybridization to HA specific radiolabelled probes and subjected to sequential rounds of plaque purification until a pure population was achieved. One representative plaque was then amplified to produce a stock virus. Plasmid pRW849 was used in an in vitro recombination test to produce recombinant TROVAC-AIH5 (vFP89) expressing the H5 hemagglutinin. Plasmid pRW848 was used to produce recombinant TROVAC-AIH4 (vFP92) expressing the H4 hemagglutinin. Plasmid pRW869 was used to produce recombinant TROVAC-AIH7 (vFP100) expressing the H7 hemagglutinin.

[0315] Immunofluorescence. In influenza virus infected cells, the HA molecule is synthesized and glycosylated as a precursor molecule at the rough endoplasmic reticulum. During passage to the plasma membrane it undergoes extensive post-translational modification culminating in proteolytic cleavage into the disulphide linked HA₁ and HA₂ subunits and insertion into the host cell membrane where it is subsequently incorporated into mature viral envelopes. To determine whether the HA molecules produced in cells infected with the TROVAC-AIV recombinant viruses were expressed on the cell surface, immunofluorescence studies were performed. Indirect immunofluorescence was performed as described (Taylor et al., 1990). Surface expression of the H5 hemagglutinin in TROVAC-AIH5, H4 hemagglutinin in TROVAC-AIH4 and H7 hemagglutinin in TROVAC-AIH7 was confirmed by indirect immunofluorescence. Expression of the H5 hemagglutinin was detected using a pool of monoclonal antibodies specific for the H5HA. Expression of the H4HA was analyzed using a goat monospecific anti-H4 serum. Expression of the H7HA was analyzed using a H7 specific monoclonal antibody preparation.

[0316] Immunoprecipitation. It has been determined that the sequence at and around the cleavage site of the hemagglutinin molecule plays an important role in determining viral virulence since cleavage of the hemagglutinin polypeptide is necessary for virus particles to be infectious. The hemagglutinin proteins of the virulent H5 and H7 viruses possess more than one basic amino acid at the carboxy terminus of HA1. It

is thought that this allows cellular proteases which recognize a series of basic amino acids to cleave the hemagglutinin and allow the infectious virus to spread both in vitro and in vivo. The hemagglutinin molecules of H4 avirulent strains are not cleaved in tissue culture unless exogenous trypsin is added.

[0317] In order to determine that the hemagglutinin molecules expressed by the TROVAC recombinants were authentically processed, immunoprecipitation experiments were performed as described (Taylor et al., 1990) using the specific reagents described above.

[0318] Immunoprecipitation analysis of the H5 hemagglutinin expressed by TROVAC-AIH5 (vFP89) showed that the glycoprotein is evident as the two cleavage products HA₁ and HA₂ with approximate molecular weights of 44 and 23 kDa, respectively. No such proteins were precipitated from uninfected cells or cells infected with parental TROVAC. Similarly immunoprecipitation analysis of the hemagglutinin expressed by TROVAC-AIH7 (vFP100) showed specific precipitation of the HA₂ cleavage product. The HA₁ cleavage product was not recognized. No proteins were specifically precipitated from uninfected CEF cells or TROVAC infected CEF cells. In contrast, immunoprecipitation analysis of the expression product of TROVAC-AIH4 (vFP92) showed expression of only the precursor protein HA₀. This is in agreement with the lack of cleavage of the hemagglutinins of avirulent subtypes in tissue culture. No H4 specific proteins were detected in uninfected CEF cells or cells infected with TROVAC. Generation of recombinant virus by recombination, in situ hybridization of nitrocellulose filters and screening for B-galactosidase activity are as previously described (Panicali et al., 1982; Perkus et al., 1989).

Example 14

Generation of an ALVAC Recombinant Expressing HIV1 gag (+pro) (IIIB), gp120 (MN) (+transmembrane) Epitopes

[0319] A plasmid, pHXB2D, containing HIV1 (IIIB) cDNA sequence (Ratner et al, 1985), was obtained from Robert Gallo (NCI, NIH). The sequence encoding the 5'-end of the gag gene was cloned between vaccinia virus tk flanking arms. This was accomplished by cloning the 1,625 bp BglII fragment of pHXB2D, containing the 5'-end of the gag gene, into the 4,075 bp BglII fragment of pSD542VCVQ. The plasmid generated by this manipulation is called pHIVG2.

[0320] The 3'-end of the gag gene was then cloned into pHIVG2. This was accomplished by cloning a 280 bp ApaI-BamHI PCR fragment, containing the 3'-end of the gag gene, into the 5,620 bp ApaI-BamHI fragment of pHIVG2. (This PCR fragment was generated from the plasmid, pHXB2D, with the oligonucleotide primers, HIVP5 (SEQ ID NO:69; 5'-TGTGGCAAAGAAGGGC-3') and HIVP6 (SEQ ID NO:70; 5'-TTGGATCCTTATTGTGACGAGGGGTC-3').) The plasmid generated by this manipulation is called pHIVG3.

[0321] The I3L promoter was then cloned upstream of the gag gene. This was accomplished by cloning the oligonucleotides, HIVL17 (SEQ ID NO:71; 5'-GATCT-TGAGATAAAGTGAAAATATATATCAT-TATATTACAAAGTACAATTATTTA GGTTTAATCATGGGTGCGAGAGCGTCAG-TATTAAGCGGGGAGAATTAGAT-3') and HIVL18 (SEQ

ID NO:72; 5'-CGATCTAATTCTCCCCCGCTTAATACT-GACGCTCT CGCACCCATGATTAAACCTAAATAAT-TGTACTTTGTAATATAATGATATATATTTTCACTTT ATCTCAA-3'), encoding the vaccinia virus I3L promoter and the 5'-end of the gag gene, into the 5,540 bp partial BglII-ClaI fragment of pHIVG3. The plasmid generated by this manipulation is called pHIVG4.

[0322] The portion of the gag gene encoding p24, p2, p7 and p6 was then eliminated. This was accomplished by cloning the oligonucleotides, HIVL19 (SEQ ID NO:73; 5'-CT-GACACAGG ACACAGCAATCAGGTCAGCCAAAAT-TACTAATTTTATCTCGAGGTCGACAGGACCCG-3') and HIVL20 (SEQ ID NO:74; 5'-GATCCGGGTCCTGTC-GACCTCGAGATAAAAA TTAGTAATTTTGGCTGAC-CTGATTGCTGTGTCCTGTGTCAG-3'), into the 4,450 bp partial PvuII-BamHI fragment of pHIVG4. The plasmid generated by this manipulation is called pHIVG5.

[0323] The remainder of the gag gene, as well as the pol gene, was then cloned downstream of the p17 "gene". This was accomplished by cloning the 4,955 bp ClaI-SalI fragment of pHXB2D, containing most of the gag gene and all of the pol gene, into the 4,150 bp ClaI-SalI fragment of pHIVG5. The plasmid generated by this manipulation is called pHIVG6.

[0324] Extraneous 3'-noncoding sequence was then eliminated. This was accomplished by cloning a 360 bp AflII-BamHI PCR fragment, containing the 3'-end of the pol gene, into the 8,030 bp AflII-BamHI fragment of pHIVG6. (This PCR fragment was generated from the plasmid, pHXB2D, with the oligonucleotide primers, HIVP7 (SEQ ID NO:75; 5'-AAG AAAATTATAGGAC-3') and HIVP8 (SEQ ID NO:76; 5'-TTGGATCCC TAATCCTCATCCTGT-3').) The plasmid generated by this manipulation is called pHIVG7.

[0325] The I3L-promoted gag and pol genes were then cloned between canary pox C3 flanking arms. This was accomplished by cloning the 4,360 bp partial BglII-BamHI fragment of pHIVG7, containing the I3L-promoted gag and pol genes, into the BamHI site of pVQH6CP3L. The plasmid generated by this manipulation is called pHIVGE14.

[0326] The H6-promoted HIV1gp120(MN) (+transmembrane) "gene" (Gurgo et al, 1988) was then cloned into pHIVGE14. This was accomplished by cloning the 1,700 bp NruI-SmaI fragment of pC5HIVMN120T, containing the gp120(+transmembrane) "gene", into the 11,400 bp NruI-SmaI fragment of pHIVGE14. The plasmid generated by this manipulation is called pHIVGE14T.

[0327] Most of the pol gene was then removed. This was accomplished by cloning a 540 bp ApaI-BamHI PCR fragment, containing the 3'-end of the HIV1 protease "gene", into the 10,000 bp ApaI-BamHI fragment of pHIVGE14T. (This PCR fragment was generated from the plasmid, pHIVG7, with the oligonucleotide primers, HIVP5 and HIVP37 (SEQ ID NO:77; 5'-AAAGGATCCCCCGGGTTAAAAATT-TAAAGTGCAACC-3').) This manipulation removes most of the pol gene, but leaves the protease "gene" intact. The plasmid generated by this manipulation is called pHIV32. The DNA sequence of pHIV32 (SEQ ID NOS: 78 and 79) is shown in FIGS. 14A-14C which shows the nucleotide sequence of the H6-promoted HIV1gp120(+transmembrane) gene and the I3L-promoted HIV1gag(+pro) gene contained in pHIV32:

<u>gag (+pro) and gp120 (+transmembrane)</u>			
FEATURES	From	To/Span	Description
frag	1	56	C3 flanking arm
frag	162	76 (C)	HIV1 (IIIB) env transmembrane region
frag	1728	163 (C)	HIV1 (MM) gp120 gene
frag	1853	1729 (C)	vaccinia H6 promoter
frag	1925	1983	vaccinia I3L promoter
frag	1984	3746	HIV1 (IIB) gag/pro gene
frag	3753	3808	C3 flanking arm

[0328] The DNA sequence of the ALVAC C3 flanking arm (SEQ ID NOS: 80 and 81) is shown in FIGS. 15A-F. FIGS. 15A to 15F show the nucleotide sequence of the C3 locus in pVQH6CP3L:

<u>C3 LOCUS pVQH6CP3L</u>			
FEATURES	From	To/Span	Description
frag	1	1460	C3 flanking arm
frag	1461	1501	Cloning sites
frag	1630	1502	H6 promoter
frag	1717	4291	C3 flanking arm

[0329] pHIV32 was used in vitro recombination with ALVAC as the rescuing virus to yield vCP205.

[0330] vCP205 (ALVAC-MN120TMG) was deposited on Mar. 6, 1997 under the terms of the Budapest Treaty with the American Type Culture Collection (ATCC), P.O. Box 1549, Manassas, Va. 20108 USA under ATCC accession number VR-2557.

Example 15

Generation of an ALVAC Recombinant Expressing HIV1 gag (+pro) (IIIB), gp120 (MN) (+transmembrane) and 2 nef (BRU) Epitopes

[0331] Expression cassettes encoding two nef CTL epitopes, CTL1 (amino acids 66-147) and CTL2 (amino acids 182-206) (Wain-Hobson et al, 1985; Nixon and McMichael, 1991), were then inserted into vCP205. The insertion plasmid, p2-60-HIV.3, containing the nef CTL epitopes, was generated by the following procedure. The I3L-promoted CTL2 epitope was cloned into pBSH6. This was accomplished by cloning a 255 bp PCR HindIII-XhoI fragment, containing the I3L-promoted CTL2 epitope, into the 3,100 bp HindIII-XhoI fragment of pBSH6. (The 255 bp PCR fragment was generated by the following procedure. A 216 bp PCR fragment, containing the I3L-promoter and the 5'-end of the CTL2 epitope, was generated from the plasmid, pMPI3H, with the oligonucleotide primers, VQPCR13 (SEQ ID NO: 82; 5'-ATCATCAAGCTTAATTAATTAGTTATTA-GACAAGGTGAAAACGAACTATTTGTAGCTT AAT-TATTAGACATCATGCAGTGGTTAAAC-3') and I3PCRCTL (SEQ ID NO: 83; 5'-CTAGCTACGTGAT-GAAATGCTAATCTAGAATCAAATCTC-CACTCCATGATTAAACCTAA ATAATTGTAC-3'). This 216 bp PCR fragment was then used as a template in a second PCR reaction with the oligonucleotide primers, VQPCR13

and CTLPCR (SEQ ID NO: 84; 5'-GAATTCCTCGAG-GATCCTCTAGATTAAACAATTTT-TAAAATATTCAGGATGTAATTCTCT AGCTACGTGAT-GAAATGC-3'), to generate the PCR fragment, containing the I3L-promoted CTL2 epitope, that was digested with HindIII and XhoI and cloned into pBSH6). The plasmid generated by this manipulation is called p2-60-HIV.1.

[0332] The H6-promoted CTL1 epitope was then cloned into p2-60-HIV.1. This was accomplished by cloning a 290 bp NruI-EcoRI fragment, containing the H6-promoted CTL1 epitope, into the 3,300 bp NruI-EcoRI fragment of p2-60-HIV.1. (The 290 bp NruI-EcoRI fragment was generated by the following procedure. A 195 bp PCR fragment, containing the H6-promoter and the 5'-end of the CTL1 epitope, was generated from the plasmid, pH6T2, with the oligonucleotide primers, H6PCR1 (SEQ ID NO: 85; 5'-ACTACTAAGCT-TCTTTATTCTATACTTAAAAAGTG-3') and NCCPCR1 (SEQ ID NO: 86; 5'-CAGCTGCTTTGTAAAGTCATTG-GTCTTAAAGGTACTTGAGGTGTTACTG-GAAAACCTACC ATTACGATACAAACTTAACG-GATATCGCG-3'). This 195 bp PCR fragment and the oligonucleotides, NCC174A (SEQ ID NO: 87; 5'-ACTTACAAAGCAGCTGTAGATCTTTCT-CACTTTTTTAAAAGAAAAAGGAGGTTTAGAAGG GCTAATTCATTCTCAACGAAGACAA-GATATCTTGATTGTGG-3') and NCC174B (SEQ ID NO: 88; 5'-CCACAAATCAAGAATATCTTGTCTTCGT-TGAGAATGAATTAGCCCTTCTAAACCTCCTT TTTCTTTTAAAAAGTGAGAAAGATCTA-CAGCTGCTTTGTAAAGT-3'), were then used as templates in a second PCR reaction with the oligonucleotide primers, H6PCR1 and NCCPCR2 (SEQ ID NO: 89; 5'-CTGCCAAT-CAGGAAAATATCCTTGTGTAT-GATAAATCCACAAATCAAGAATATC-3'). The resulting 317 bp PCR fragment, containing the H6-promoter and most of the CTL1 epitope, and the oligonucleotides, NCC291A (SEQ ID NO: 90; 5'-GGATATTTTCCTGATTGGCAGAAT-TACACACCAGGACCAGGAGTCAGATACCCATTAAC CTTTGTTGGTGCTACAAGC-3') and NCC291B (SEQ ID NO: 91; 5'-GCTTGTAGCACCAACCAAAGGT-TAATGGGTATCTGACTCCTGGTCCTGGT-GTGTAATC TGCCAATCAGGAAAATATCC-3'), were then used as templates in a third PCR reaction with the oligonucleotide primers, H6PCR1 and NCCPCR3 (SEQ ID NO: 92; 5'-ACTACTGAATTCTCGAGAAAATTATGG-TACTAGCTTGTAGCACCAACC-3'), to generate the PCR fragment, containing the H6-promoted CTL1 epitope, that was digested with NruI and EcoRI and cloned into p2-60-HIV.1) The plasmid generated by this manipulation is called p2-60-HIV.2.

[0333] The I3L-promoted CTL2 and H6-promoted CTL1 epitopes were then cloned between canarypox C6 flanking arms. This was accomplished by cloning the 640 bp XhoI fragment of p2-60-HIV.2, containing the two (2) nef CTL epitopes, into the XhoI site of pC6L. The plasmid generated by this manipulation is called p2-60-HIV.3. The DNA sequence of p2-60-HIV.3 (SEQ ID NOS: 93-96) is shown in FIG. 16. FIG. 16 shows the nucleotide sequence of the I3L-promoted nef CTL2 epitope and H6-promoted nef CTL1 epitope contained in p2-60-HIV.3:

NEF CTL epitopes			
FEATURES	From	To/Span	Description
frag	1	51	C6 Left Arm
pept	175	98	(C) nef CTL2
frag	275	176	(C) I3L promoter
frag	337	460	H6 promoter
pept	461	709	1 nef CTL1
frag	751	801	C6 Right Arm

[0334] The DNA sequence of the ALVAC C6 flanking arm (SEQ ID NOS: 97 and 98) is shown in FIGS. 17A-C. FIG. 17A to 17C show the nucleotide sequence of the C6 locus in pC6L:

C6 LOCUS pC6L			
FEATURES	From	To/Span	Description
frag	1	381	C6 flanking arm
frag	382	447	Cloning sites
frag	448	1615	C6 flanking arm

[0335] p2-60HIV.3 was used in in vitro recombination experiments with vCP205 as the rescuing virus to yield vCP264.

Example 16

Generation of an ALVAC Recombinant Expressing HIV1 gag (+pro) (IIIB), gp120 (MN) (+transmembrane) and 2 nef (BRU) and 3 pol (IIIB) CTL Epitope Containing Regions

[0336] Expression cassettes encoding three (3) pol CTL epitopes, poll (amino acids 172-219), pol2 (amino acids 325-383) and pol3 (amino acids 461-519) (Ratner et al, 1985; Nixon and McMichael, 1991), were then inserted into vCP264. The insertion plasmid, pC5POLT5A, containing the three (3) pol CTL epitopes, was generated by cloning a 948 bp XhoI-BamHI fragment, containing the H6-promoted poll epitope, the I3L-promoted pol2 epitope and the 42K-promoted pol3 epitope, into the 2,940 bp XhoI-BamHI fragment of PBSK⁺. (The 948 bp XhoI-BamHI fragment was generated by the following procedure. A 183 bp PCR fragment, containing the poll epitope, was generated from the plasmid, pHXB2D, with the oligonucleotide primers, P1A (SEQ ID NO: 99; 5'-TTTGTATCGTAATGATTGAGACTGTAC-CAGTAAAATTAAAGCC-3') and P1B (SEQ ID NO: 100; 5'-GGGCTGCAGGAATTCTAATCAATTAAG-GCCCAATTTTGAATTTCCCTTCCTTTTCC ATCTCTG-3'). A 224 bp PCR fragment, containing the pol2 epitope, was generated from the plasmid, pHXB2D, with the oligonucleotide primers, P2A (SEQ ID NO: 101; 5'-ACAAAGTACAATTATTAGGTTTAAT-CATGGCAATATTCCAAAGTAGCATGAC-3') and P2B (SEQ ID NO: 102; 5'-ATCATCCTCGAGAAAAATTAGG-TAAGTCCCCACCTCAACAGATG-3'). A 236 bp PCR fragment, containing the pol3 epitope, was generated from the plasmid, pHXB2D, with the oligonucleotide primers, P3A (SEQ ID NO: 103; 5'-AAAATATATAATTA-

CAATATAAAATGCCACTAACAGAAGAAG-CAGAGCTAGAACTGGC-3') and P3B (SEQ ID NO: 104; 5'-ATCATCTCTAGACTCGAGGATCCAT-AAAAATTATCCTGTTTTTCAGATTTTAAATGGCT C-3'). A 340 bp PCR fragment, containing the I3L and H6 promoters (in a head-to-head configuration) was generated from the plasmid, p2-60-HIV.2, with the oligonucleotide primers, P2IVH (SEQ ID NO: 105; 5'-GTCATGC-TACTTTTGAATATTGCCATGATTAAAC-CTAATAATTGTACTTTG-3,) and IVHP1 (SEQ ID NO: 106; 5'-TTTAATTTTACTGGTACAGTCTCAAT-CATTACGATACAAACTTAAACGGATATCGCG-3'). A 168 bp PCR fragment, containing the 42K promoter, was generated from the plasmid, pVQ42KTh4.1, with the oligonucleotide primers, EPS42K (SEQ ID NO: 107; 5'-AATTGATTGAATTCCTGCAGCCCGGGTCAAAAAATATAAATG-3') and 42 KP3B (SEQ ID NO: 108; 5'-CCAGTTCTAGCTCTGCTTCTTCTGT-TAGTGGCATTATATTGTAATTATATATTTTC-3'). A 511 bp PCR fragment, containing the H6 promoter and I3L-promoted pol2 epitope, was generated by using the 224 bp PCR fragment, containing the pol2 epitope, and the 340 bp PCR fragment, containing the I3L and H6 promoters, as templates in a PCR reaction with the oligonucleotide primers, P2B and IVHP1. A 347 bp PCR fragment, containing the 42K-promoted pol3 epitope, was generated by using the 168 bp PCR fragment, containing the 42K promoter, and the 236 bp PCR fragment, containing the pol3 epitope, as templates in a PCR reaction with the oligonucleotide primers, IPS42K and P3B. A 506 bp PCR fragment, containing the poll epitope and the 42K-promoted pol3 epitope, was generated by using the 183 bp PCR fragment, containing the poll epitope, and the 347 bp PCR fragment, containing the 42K-promoted pol3 epitope, as templates in a PCR reaction with the oligonucleotide primers, P1A and P3B. A 977 bp PCR fragment, containing the H6-promoted poll epitope, the I3L-promoted pol2 epitope and the 42K-promoted pol3 epitope, was generated by using the 511 bp PCR fragment, containing the H6 promoter and I3L-promoted pol2 epitope, and the 506 bp PCR fragment, containing the poll epitope and 42K-promoted pol3 epitope, as templates in a PCR reaction with the oligonucleotide primers, P2B and P3B. The 977 bp PCR fragment was then digested with XhoI and BamHI and cloned into the 2,940 bp XhoI-BamHI fragment of pBSK⁺.) The plasmid generated by this manipulation is called pBSPOLT5.

[0337] Nucleotide sequence analysis of pBSPOLT5 indicated that there was an error in the pol2 epitope. In order to correct this mistake, the 948 bp XhoI-BamHI fragment, containing the H6-promoted poll epitope, the I3L-promoted pol2 epitope and the 42K-promoted pol3 epitope, was used as a template in a PCR reaction with the oligonucleotide primers, 13PCR1 (SEQ ID NO: 109; 5'-ATCATCGGATCCAAGCT-TACATCATGCAGTGG-3') and FIXPOL2 (SEQ ID NO: 110; 5'-ATCATCCTCGAGCTAATTCAATTAGGTTG-TAAGTCCCCACCTCAAC-3'). The resulting PCR fragment, containing the corrected I3L-promoted pol2 epitope, was digested with HindIII and XhoI and cloned into the 3,650 bp HindIII-XhoI fragment of pBSPOLT5. The plasmid generated by this manipulation is called pBSPOLT5A.

[0338] The H6-promoted poll epitope, I3L-promoted pol2 epitope and 42K-promoted pol3 epitope was then cloned between canary pox C5 flanking arms. This was accomplished by cloning the 897 bp BamHI-XhoI fragment of pBSPOLT5A, containing the H6-promoted poll epitope, the

I3L-promoted pol2 epitope and the 42K-promoted pol3 epitope, into the 4,675 bp BamHI-XhoI fragment of pNC5L-SP5. The plasmid generated by this manipulation is called pC5POLT5A. The DNA sequence of pC5POLT5A (SEQ ID NOS: 111-115) is shown in FIGS. 18A-B. FIGS. 18A to 18B shows the nucleotide sequence of the I3L-promoted pol2 epitope, H6-promoted pol1 epitope and 42K-promoted pol3 epitope contained in pC5POLT5A:

POL CTL epitopes			
FEATURES	From	To/Span	Description
frag	1	50	C5 Left Arm
pept	272	92 (C)	POL 2
frag	372	273 (C)	I3L promoter
frag	377	500	H6 promoter
pept	501	647 1	POL1
frag	676	782	—42K promoter
pept	783	962 1	POL 3
frag	986	1035	C5 Right Arm

[0339] The DNA sequence of the ALVAC C5 flanking arm (SEQ ID NOS: 116 and 117) is shown in FIGS. 19A-C. FIGS. 19A to 19C show the nucleotide sequence of the C5 locus in pNC5L-SP5:

C5 LOCUS pNC5L-SP5			
FEATURES	From	To/Span	Description
frag	1	1549	C5 flanking arm
frag	1550	1637	Cloning sites
frag	1638	2049	C5 flanking arm

[0340] pC5POLT5A was used in in vitro recombination experiments with vCP264 as the rescuing virus to yield vCP300.

Example 17

Restriction and Immunoprecipitation Analyses

[0341] Restriction enzyme analysis was performed to confirm that the HIV1 sequences in vCP300 are in the proper loci. ALVAC, vCP205, vCP264 and vCP300 DNA were digested with HindIII, PstI or XhoI and the resultant fragments fractionated on an agarose gel. When the sizes of the resulting fragments were compared, it was determined that, as expected, the gag(+pro) and gp120(+transmembrane) genes were inserted into the C3 locus, the nef epitopes were inserted into the C6 locus and the pol epitopes were inserted into the C5 locus.

[0342] Immunoprecipitation analysis was performed to determine whether vCP300 expresses authentic HIV1 gag and gp120(+transmembrane) gene products. HeLa cell monolayers were either mock infected or infected at an m.o.i. of 10 pfu/cell with ALVAC or vCP300. Following an hour adsorption period, the inoculum was aspirated and the cells were overlaid with 2 mls of modified Eagle's medium (minus methionine) containing 2% fetal bovine serum and [³⁵S]-methionine (20 µCi/ml). Cells were harvested at 18 hrs post-infection by the addition of 1 ml 3× buffer A (3% NP-40, 30 mM Tris (pH7.4), 3 mM EDTA, 0.03% Na Azide and 0.6

mg/ml PMSF) and 50 µl aprotinin, with subsequent scraping of the cell monolayers. Lysates from the infected cells were analyzed for HIV1gag and gp120(+transmembrane) gene expression using serum from HIV1-seropositive individuals (obtained from New York State Department of Health). The sera was bound to Protein A-sepharose in an overnight incubation at 4° C. Following this incubation period, the material was washed 4× with 1× buffer A. Lysates, precleared with normal human sera and protein A-sepharose, were then incubated overnight at 4° C. with the HIV1-seropositive human sera bound to protein A-sepharose. After the overnight incubation period, the samples were washed 4× with 1× buffer A and 2× with a LiCl₂/urea buffer. Precipitated proteins were dissociated from the immune complexes by the addition of 2× Laemmli's buffer (125 mM Tris (pH6.8), 4% SDS, 20% glycerol, 10% 2-mercaptoethanol) and boiling for 5 min. Proteins were fractionated on a 10% Dreyfuss gel system (Dreyfuss et al., 1984), fixed and treated with 1M Na-salicylate for fluorography. This analysis indicated that HIV1gag and gp120(+transmembrane) gene products were precipitated from vCP300-infected cells, but were not precipitated from mock infected or ALVAC-infected cells.

[0343] Expression of the nef and pol epitopes in vCP300-infected cells has not been confirmed because no epitope specific serological reagents are yet available. Nucleotide sequence analysis, however, has confirmed that the nef and pol sequences cloned into vCP300 are correct. PCR fragments, containing the nef and pol expression cassettes, were generated from vCP300 DNA. Nucleotide sequence analysis of these fragments indicated that the nef and pol sequences are correct. vCP205 expresses the same cell surface-associated form of HIV1 gp120 as expressed by vCP300. The immunogenicity of this gene product, as expressed by vCP205, has been assayed in small laboratory animals.

Example 18

Immunogenicity Studies

[0344] Groups of two rabbits or guinea pigs were inoculated intramuscularly (im) with 10⁸ pfu of ALVAC, vCP205, or with 0.1 mg of peptide CLTB-36 (GPKEP-FRDYVDRFYKNKRKRIHIGPGRFYTTKN) (SEQ ID NOS: 118) adjuvanted with 0.05 mg of QS-21 according to the schedule below (Table 21).

TABLE 21

Immunization schedule for rabbits and guinea pigs inoculated with ALVAC, vCP205, or with peptide CLTB-36 in QS-21.				
INOCULATION				
GROUP	WEEK 0	WEEK 4	WEEK 8	
1	ALVAC	ALVAC	CLTB-36/QS-21	
2	vCP205	vCP205	vCP205	
3	vCP205	vCP205	CLTB-36/QS-21	
4	CLTB-36/QS-21	CLTB-36/QS-21	CLTB-36/QS-21	

[0345] Each rabbit and guinea pig was bled prior to the first inoculation and at 2-week intervals following the first inoculation through week 14. Serum was prepared from each blood sample and stored at -70° C. until use. Each serum was tested for antibody responses to recombinant HIV MN/BRU hybrid gp160 or to 25-mer synthetic HIV MN gp120 V3 loop

(American Bio-Technologies, Inc. Cambridge, Mass., product # 686010) by kinetics enzyme-linked immunosorbent assay (KELISA).

[0346] Rabbits immunized with vCP205 (Group 2) produced the highest levels of anti-gp160 antibodies (FIG. 20). Rabbits were immunized according to the schedule in Table 21 (arrows in FIG. 20) and bled at 2 week intervals. Each serum was diluted 1:100 in dilution buffer and tested for reactivity with purified recombinant HIV MN/BRU gp160 using a kinetics ELISA. Both rabbits in this group began producing gp160 reactive antibodies after a single inoculation. Boosting with subsequent inoculations produced only minor increases in antibody levels. Rabbits inoculated twice with vCP205 and boosted with peptide CLTB-36 in QS-21 adjuvant (Group 3) apparently failed to make anti-gp160 antibodies when compared to control rabbits (Group 1). Of the rabbits immunized three times with peptide CLTB-36 in QS-21, only one responded by generating gp160-specific antibodies. The one responsive rabbit (A353) began producing gp160 antibodies only after the third immunization.

[0347] Rabbits immunized only with peptide CLTB-36 would not be expected to generate broadly reactive gp160-specific antibodies since the peptide contains only a small portion of the envelope glycoprotein, the V3 loop. Thus, sera were tested for reactivity to a peptide containing 25 amino acids of the HIV MN V3 loop (FIG. 21). Rabbits were immunized according to the schedule in Table 21 (arrows in FIG. 22) and bled at 2 week intervals. Each serum was diluted 1:100 in dilution buffer and tested for reactivity with a 25-mer synthetic peptide representing the HIV MN gp120 V3 loop (CNKRKRIHIGPGRAFYTTKNIIGTIC; (SEQ ID NO: 119) American Bio-Technologies, Inc. Cambridge, Mass., product # 686010) using a kinetics ELISA. As before, the highest V3 antibody responses were found in the sera of rabbits inoculated three times with vCP205. Two inoculations with vCP205 followed by peptide CLTB-36 in QS-21 produced anti-V3 antibody responses, but not as high as Group 2 rabbits. Also, as before, only one rabbit responded to three inoculations with peptide CLTB-36 in QS-21.

[0348] Guinea pigs in all groups, including one animal in Group 1, produced antibodies that reacted with HIV gp160 (FIG. 22). Guinea pigs were immunized according to the schedule in Table 21 (arrows in FIG. 22) and bled at 2 week intervals. Each serum was diluted 1:100 in dilution buffer and tested for reactivity with purified recombinant HIV MN/BRU gp160 using a kinetics ELISA. The single animal in Group 1 that responded did so only after inoculation with peptide CLTB-36 in QS-21 adjuvant. Antibody levels in the sera of all guinea pigs in Groups 2, 3, and 4 were similar. Most of the guinea pigs responded to a single inoculation by producing gp160 antibodies.

[0349] Similar results were seen using a HIV MN V3 25-mer peptide as the KELISA antigen (FIG. 23). Guinea pigs were immunized according to the schedule in Table 21 (arrows in FIG. 23) and bled at 2 week intervals. Each serum was diluted 1:100 in dilution buffer and tested for reactivity with a 25-mer synthetic peptide representing the HIV MN gp120 V3 loop (CNKRKRIHIGPGRAFYTTKNIIGTIC (SEQ ID NO: 120) American Bio-Technologies, Inc. Cambridge, Mass., product # 686010) using a kinetics ELISA. A single inoculation of peptide CLTB-36 in QS-21 elicited V3 antibody responses which were boosted by second and third inoculations. Two inoculations with vCP205 were necessary

to induce V3 antibody responses which was boosted to higher levels by the third inoculation of vCP205 or CLTB-36 in QS-21.

[0350] Expression and immunogenicity of the Nef and Pol CTL epitopes expressed by vCP300 is demonstrated by the following in vitro assays. Fresh PBMC samples were derived from HIV-seropositive individuals. Twenty-percent of these cells were inoculated with vCP300 at an m.o.i. of 10. Two hours post-infection the cells were washed and mixed with autologous, uninoculated PBMCs at a ratio of uninoculated/inoculated of 10:1. (Seeding density equaled 1.5×10^6 cells/ml). On day 0, exogenous IL-7 was added at a final concentration of 1000 U/ml. On day three, the addition of an exogenous source of IL-7 and IL-2 was added at a final concentration of 1000 U/ml and 220 U/ml, respectively. After 12 days in culture, the in vitro stimulated cell population was used in a standard ^{51}Cr -release assay using autologous Epstein-Barr virus-transformed B cells infected with vaccinia virus (WR) recombinants expressing HIV-1 proteins as targets. The results from assays obtained using an Effector/Target (E/T) cell ratio of 20:1 are shown in FIGS. 24 and 25 and expressed as percent specific lysis. The combined results demonstrate the ability of vCP300-infected PBMCs to stimulate HIV-1, Env-, Gag-, Pol-, and Nef-specific cytolytic activity. Further, abrogation of the cytolytic activities by anti-CD8 monoclonal antibodies demonstrates that the nature of the cell mediating the cytolytic activities are classical CD8⁺ CTLs.

[0351] In summary, the inoculation of rabbits and guinea pigs with the HIV ALVAC recombinant canarypox virus, vCP205, elicited antibodies to the HIV envelope glycoprotein and a region of the HIV envelope glycoprotein associated with neutralization of HIV, the gp120 V3 loop region. The expression and immunogenicity of the vCP300 expressed Env, Gag, Pol and Nef encoded products is demonstrated by the in vitro stimulation of CD8⁺ CTLs from seropositive individuals. Thus, vCP205 and vCP300 and precursors to these recombinants and expression products and DNA from these recombinants are useful, as described above.

Example 19

Generation of vCP1307; an ALVAC Recombinant
Expressing a Form of HIV1 gp120+TM with 2
ELDKWA Epitopes Inserted into the gp120 V3 Loop

[0352] vCP1307, an ALVAC recombinant expressing HIV1 gp120+TM with 2 ELDKWA epitopes from HIV1 gp41 inserted into the gp120 V3 loop region, was generated by the following procedure. The sequence encoding part of the ELDKWA elements and V3 loop was cloned into pBSK+ (Stratagene, LaJolla, Calif.). This was accomplished by cloning a 225 bp EcoRI-SacI-digested PCR fragment, containing part of the ELDKWA-V3 loop sequence, into the 2,900 bp EcoRI-SacI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pBSHIVMN120T, with the primers, HIVP72 (SEQ ID NO: 121; 5'-TTATTACCATTC-CAAGTACTATT-3') and HIVP74 (SEQ ID NO: 122) 5'-TCTGTACAAATTAATTGTACAAGAC-CCAACTACGAGCTCGACAAATGGGC-CCATATAGGACC AGGGAGAGAATTG-GATAAGTGGGCGAATATAATAGGAAGTATAAGAC-3').) The plasmid generated by this manipulation is called pHIV55.

[0353] pBSHIVMN120T, a plasmid containing the H6-promoted HIV1 gp120+TM gene, was generated by the following procedure. A plasmid, pMN1.8-9, containing a cDNA copy of the HIV1 (MN) env gene, was obtained from Marvin Reitz (NCI, NIH). An early transcription termination signal sequence, T₅NT, in the env gene was modified. This was accomplished by cloning a 1,100 bp KpnI-EcoRI-di-

gested PCR fragment, containing the T₅NT-modified 5'-end of the env gene, into the 2,900 bp KpnI-EcoRI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIVMN6 (SEQ ID NO: 123; 5'-GGGTTATTAATGATCTGTAG-3') and HIV3B2 (SEQ ID NO: 124; 5'-GAATTACAGTAGAAGAAATCCCTCCACAATAAAAC-3').) The plasmid generated by this manipulation is called pBSMIDMN.

[0354] The T₅NT-modified 5'-end of the env gene was then cloned upstream to the rest of the env gene. This was accomplished by cloning the 1,025 bp KpnI-EcoRI fragment of pBSMIDMN, containing the T₅NT-modified 5'-end of the env gene, into the 4,300 bp KpnI-EcoRI fragment of pBS3MN. (pBS3MN was generated by cloning a 430 bp EcoRI-SacI-digested PCR fragment, containing a central portion of the env gene, and a 1,050 bp SacI-XbaI-digested PCR fragment, containing the 3'-end of the env gene, into the 2,900 bp EcoRI-XbaI fragment of pBSK+. The 430 bp PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIV3B1 (SEQ ID NO: 125; 5'-GTTT-TAATTGTGGAGGGGAATCTTCTACTGTAATTC-3') and HIVMN4 (SEQ ID NO: 126; 5'-ATCATCGAGCTC-CTATCGTGCTC-3'). The 1,050 bp PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIVMN5 (SEQ ID NO: 127; 5'-ATCATCGAGCTCTGTTCCTTGGGTTCTTAG-3') and HIVMN3P (SEQ ID NO: 128; 5'-ATCATCTCTA-GAATAAAAATTATAGCAAAGCCCTTCCAAGCC-3').) The plasmid generated by this manipulation is called pBSMID3MN.

[0355] The H6 promoter (Perkus et al., 1989) was then cloned upstream to the env gene. This was accomplished by cloning the 320 bp KpnI fragment of pH6IIBE, containing the H6 promoter linked to the 5'-end of the HIV1 (IIB) env gene, and the 2,450 bp KpnI-XbaI fragment of pBSMID3MN, containing the bulk of the HIV1 (MN) env gene, into the 2,900 bp KpnI-XbaI fragment of pBSK+. The plasmid generated by this manipulation is called pH6HMNE.

[0356] The sequence encoding gp41 was then replaced with the sequence encoding the HIV1 env transmembrane (TM) region. This was accomplished by cloning a 480 bp EcoRI-XbaI-digested PCR fragment, containing the 3'-end of the gp120 gene and the HIV1 env transmembrane region, into the 4,200 bp EcoRI-XbaI fragment of pH6HMNE. (This PCR fragment was generated from the PCR fragment, PCR-MN11, and oligonucleotides, HIVTM1 (SEQ ID NO: 129; 5'-TTATTCATAATGATAGTAGGAGGCTTGG-TAGGTTTAAGAATAGTTTTTGCTGTACTCTCTGT AGTGAATAGAGTTAGGCAGGGATAA-3') and HIVTM2 (SEQ ID NO: 130; 5'-TTATCCCTGCCTAACTCTATTACATACAGAGAGTACAGCAAAAACCTATTCT-TAAACCTACCA AGCCTCCTACTATCATTATGAATAA-3'), with the oligonucleotides, HIV3B1 (SEQ ID NO: 125) and HIVTM3 (SEQ ID NO: 131; 5'-ATCATCTCTA-GAATAAAAATTATCCCTGCCTAACTCTATTAC-3').) PCR-MN11 was generated from the plasmid, pH6HMNE, with the oligonucleotides, HIV3B1 (SEQ ID NO: 125) and HIVMN18 (SEQ ID NO: 132; 5'-GCCTCCTACTATCAT-TATGAATAATCTTTTTTCTCTCTG-3').) The plasmid generated by this manipulation is called pBSHIVMN120T.]

[0357] Another part of the sequence encoding the ELDKWA epitopes and V3 loop was then cloned into pBSK+. This was accomplished by cloning a 300 bp HindIII-SacI-digested PCR fragment, containing part of the

ELDKWA-V3 loop sequence, into the 2,900 bp HindIII-SacI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pBSHIVMN120T, with the primers, HIVP69 (SEQ ID NO: 133; 5'-TGATAGTACCAGCTATAGGT-TGAT-3') and HIVP75 (SEQ ID NO: 134; 5'-TTTGTC-GAGCTCGTAGTTGGGTCTTGTACAATT-3').) The plasmid generated by this manipulation is called pHIV56.

[0358] The ELDKWA-V3 loop sequences from pHIV55 and pHIV56 were then cloned into the H6-promoted gp120+TM gene. This was accomplished by cloning the 225 bp EcoRI-SacI fragment of pHIV55 and the 300 bp HindIII-SacI fragment of pHIV56, containing the ELDKWA-V3 loop sequences, into the 4,300 bp EcoRI-HindIII fragment of pBSHIVMN120T. The plasmid generated by this manipulation is called pHIV57.

[0359] The H6-promoted gp120+TM construct containing the ELDKWA epitopes was then cloned between C5 flanking arms. This was accomplished by cloning the 1,700 bp NruI-XbaI fragment of pHIV57, containing the H6-promoted gp120+TM (with ELDKWA epitopes) gene, into the 4,700 bp NruI-XbaI fragment of pSIVGC15. (pSIVGC15 contains the H6-promoted SIV env gene cloned between C5 flanking arms.) The plasmid generated by this manipulation is called pHIV59. The DNA sequence of the H6-promoted gp120+TM (with ELDKWA epitopes) gene in pHIV59 is shown in FIG. 26. pHIV59 was used in in vitro recombination experiments with ALVAC as the rescuing virus to yield vCP1307.

[0360] FACS analysis was performed to determine whether HIV1 gp120+TM (with ELDKWA epitopes) was expressed on the surface of vCP1307-infected cells. 5×10⁶ HeLa-S3 cells in S-MEM (Sigma M-8028 Joklik suspension media) were infected at an m.o.i. of 5 pfu/cell with ALVAC, vP1286 (a WR recombinant expressing HIV1 gp120+TM) or vCP1307. Following a 60 minute adsorption period at 37° C., the cells were washed with 10 mls of S-MEM and centrifuged at 1,000 RPM for 5 minutes. The samples were then resuspended in 1 ml of S-MEM, transferred to 5 ml Sarsted tubes and placed on a rotator at 37° C. After 18 hours, 200 ul aliquots (1×10⁶ cells) were placed in polypropylene tubes and washed with 3 mls of PBS-CMF (with 0.2% Na₂S₂O₃+0.2% BSA). The supernatant was then decanted and the pellet was resuspended in 100 ul of a 1:100 dilution of sera from HIV1-seropositive humans (obtained from the New York State Dept. of Health) or a 1:100 dilution of a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (obtained from Viral Testing Systems Corp., Houston, Tex.). The samples were incubated at 4° C. for 60 minutes, washed two times with PBS-CMF (with 0.2% Na₂S₂O₃+0.2% BSA) and centrifuged at 1,000 RPM for 5 minutes. The supernatant was decanted and the pellet was resuspended in a 1:100 dilution of goat anti-human FITC (obtained from Boehringer Mannheim). The samples were incubated at 4° C. for 30 minutes, washed twice with PBS-CMF (with 0.2% Na₂S₂O₃+0.2% BSA) and analyzed on a Facscan flow cytometer. A gene product containing the ELDKWA epitope was expressed at low levels on the surface of vCP1307-infected cells, but was not expressed on the surface of ALVAC-infected or vP1286-infected cells (FIG. 27, lower panel). A gene product reactive with the HIV1-seropositive sera was expressed on the surface of vP1286-infected cells and vCP1307-infected cells, but was not expressed on the surface of ALVAC-infected cells (FIG. 27, upper panel). These results indicate that the ELDKWA epitope of the HIV1 gp120+TM (with ELDKWA epitopes) gene product is expressed on the surface of vCP1307-infected

cells, consistent with the fact that a portion of the V3 loop of this gene product has been replaced with ELDKWA epitopes.

[0361] Immunoprecipitation analysis was performed to determine whether vCP1307 expresses a form of gp120+TM which contains an immunogenic ELDKWA epitope. HeLa cell monolayers were infected at an m.o.i. of 10 pfu/cell with ALVAC (the parental virus), vP1286 (a WR recombinant expressing HIV1 gp120+TM) or vCP1307. Following an hour adsorption period, the inoculum was removed and the cells were overlaid with 2 mls of modified Eagle's medium (minus cysteine and methionine) containing 2% dialyzed fetal bovine serum and [³⁵S]-TRANS label (30 µCi/ml). The lysates were harvested at 18 hrs post-infection by addition of 1 ml 3× buffer A (450 mM NaCl, 3% NP-40, 30 mM Tris (pH=7.4), 3 mM EDTA, 0.03% Na-Azide and 0.6 mg/ml PMSF) and analyzed for expression of 1) the ELDKWA epitope, using a 1:100 dilution of a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (obtained from Viral Testing Systems Corp., Houston, Tex.) and 2) HIV1 gene products, using a 1:100 dilution of sera from HIV1-seropositive humans (obtained from the New York State Dept. of Health). Lysates, precleared with normal human sera and a protein A-sepharose complex, were incubated overnight at 4° C. with an IAM41-2F5-protein A-sepharose complex or an HIV1-seropositive sera-protein A-sepharose complex. The samples were washed 4× with 1× buffer A and 2× with a LiCl₂/urea buffer. Precipitated proteins were dissociated from the immune complexes by the addition of 2× Laemmli's buffer (125 mM Tris (pH=6.8), 4% SDS, 20% glycerol, 10% 2-mercaptoethanol) and boiling for 5 min. Proteins were fractionated on an SDS-polyacrylamide gel, fixed and treated with 1 M Na-salicylate for fluorography. Proteins of the appropriate size were precipitated with the monoclonal antibody to the ELDKWA epitope from vCP1307-infected cells, but were not precipitated from ALVAC-infected cells or vP1286-infected cells. Furthermore, proteins of the appropriate size were precipitated with the human HIV1-seropositive sera from vP1286-infected cells and vCP1307-infected cells, but were not precipitated from ALVAC-infected cells. These results indicate that vCP1307 expresses a form of gp120+TM which contains an antigenic ELDKWA epitope.

Example 20

Generation of vP1313; a NYVAC Recombinant
Expressing a Form of HIV1 gp120+TM with 2
ELDKWA Epitopes Inserted into the gp120 V3 Loop

[0362] vP1313, a NYVAC recombinant expressing HIV1 gp120+TM with 2 ELDKWA epitopes from HIV1 gp41 inserted into the gp120 V3 loop, was generated by the following procedure. The sequence encoding part of the ELDKWA epitopes and V3 loop was cloned into pBSK+. This was accomplished by cloning a 225 bp EcoRI-SacI-digested PCR fragment, containing part of the ELDKWA-V3 loop sequence, into the 2,900 bp EcoRI-SacI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pBSHIVMN120T, with the primers, HIVP72 (SEQ ID NO: 144; 5'-TTATTACCAATTCCAAGTACTATT-3') and HIVP74 (SEQ ID NO: 145; 5'-TCTGTACAAATTAATTGTACAA-GACCCAACTACGAGCTCGACAAATGGGC-CCATATAGGACC AGGGAGAGAATTG-

GATAAGTGGGCGAATATAATAGGAAGTATAAGAC-3').) The plasmid generated by this manipulation is called pHIV55.

[0363] pBSHIVMN120T, a plasmid containing the H6-promoted HIV1 gp120+TM gene, was generated by the following procedure. A plasmid, pMN1.8-9, containing a cDNA copy of the HIV1 (MN) env gene, was obtained from Marvin Reitz (NCI, NIH). An early transcription termination signal sequence, T₅NT, in the env gene was modified. This was accomplished by cloning a 1,100 bp KpnI-EcoRI-digested PCR fragment, containing the T₅NT-modified 5'-end of the env gene, into the 2,900 bp KpnI-EcoRI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIVMN6 (SEQ ID NO: 146; 5'-GGGTTATTAATGATCTGTAG-3') and HIV3B2 (SEQ ID NO: 124; 5'-GAATTACAGTAGAAGAAATCCCTCCACAATTAAC-3').) The plasmid generated by this manipulation is called pBSMIDMN.

[0364] The T₅NT-modified 5'-end of the env gene was then cloned upstream to the rest of the env gene. This was accomplished by cloning the 1,025 bp KpnI-EcoRI fragment of pBSMIDMN, containing the T₅NT-modified 5'-end of the env gene, into the 4,300 bp KpnI-EcoRI fragment of pBS3MN. (pBS3MN was generated by cloning a 430 bp EcoRI-SacI-digested PCR fragment, containing a central portion of the env gene, and a 1,050 bp SacI-XbaI-digested PCR fragment, containing the 3'-end of the env gene, into the 2,900 bp EcoRI-XbaI fragment of pBSK+. The 430 bp PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIV3B1 (SEQ ID NO: 125; 5'-GTTT-TAATTGTGGAGGGGAATTCTTCTACTGTAATTC-3') and HIVMN4 (SEQ ID NO: 126; 5'-ATCATCGAGCTC-CTATCGCTGCTC-3'). The 1,050 bp PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIVMN5 (SEQ ID NO: 127; 5'-ATCATCGAGCTCTGTTCTTGGGTTCTTAG-3') and HIVMN3P (SEQ ID NO: 128; 5'-ATCATCTCTA-GAATAAAATTATAGCAAAGCCCTTTCCAAGCC-3').) The plasmid generated by this manipulation is called pBSMID3MN.

[0365] The H6 promoter was then cloned upstream to the env gene. This was accomplished by cloning the 320 bp KpnI fragment of pH6IIBE, containing the H6 promoter linked to the 5'-end of the HIV1 (IIBE) env gene, and the 2,450 bp KpnI-XbaI fragment of pBSMID3MN, containing the bulk of the HIV1 (MN) env gene, into the 2,900 bp KpnI-XbaI fragment of pBSK+. The plasmid generated by this manipulation is called pH6HMNE.

[0366] The sequence encoding gp41 was then replaced with the sequence encoding the HIV1 env transmembrane (TM) region. This was accomplished by cloning a 480 bp EcoRI-XbaI-digested PCR fragment, containing the 3'-end of the gp120 gene and the HIV1 env transmembrane region, into the 4,200 bp EcoRI-XbaI fragment of pH6HMNE. (This PCR fragment was generated from the PCR fragment, PCR-MN11, and oligonucleotides, HIVTM1 (SEQ ID NO: 129; 5'-TTATTCATAATGATAGTAGGAGGCTTGG-TAGGTTTAAGAATAGTTTGTCTGTAATCTCTGT AGTGAATAGAGTTAGGCAGGGATAA-3') and HIVTM2 (SEQ ID NO: 130; 5'-TTATCCCTGCCTAATCTATTAC-TACAGAGAGTACAGCAAAAACTATTCT-TAAACCTACCA AGCCTCCTACTATCATTATGAATAA-3'), with the oligonucleotides, HIV3B1 (SEQ ID NO: 125) and HIVTM3 (SEQ ID NO: 131; 5'-ATCATCTCTA-

GAATAAAAATTATCCCTGCCTAACTCTATTCAC-3'). PCR-MN11 was generated from the plasmid, pH6HME, with the oligonucleotides, HIV3B1 (SEQ ID NO: 125) and HIVMN18 (SEQ ID NO: 132; 5'-GCCTCTACTATCAT-TATGAATAATCTTTTTTCTCTCTG-3').) The plasmid generated by this manipulation is called pBSHIVMN120T.] [0367] Another part of the sequence encoding the ELDKWA epitopes and V3 loop was then cloned into pBSK+. This was accomplished by cloning a 300 bp HindIII-SacI-digested PCR fragment, containing part of the ELDKWA-V3 loop sequence, into the 2,900 bp HindIII-SacI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pBSHIVMN120T, with the primers, HIVP69 (SEQ ID NO: 133; 5'-TGATAGTACCAGCTATAGGT-TGAT-3') and HIVP75 (SEQ ID NO: 134; 5'-TTTGTC-GAGCTCGTAGTTGGGTCTTGTACAATT-3').) The plasmid generated by this manipulation is called pHIV56.

[0368] The ELDKWA-V3 loop sequences from pHIV55 and pHIV56 were then cloned into the H6-promoted gp120+TM gene. This was accomplished by cloning the 225 bp EcoRI-SacI fragment of pHIV55 and the 300 bp HindIII-SacI fragment of pHIV56, containing the ELDKWA-V3 loop sequences, into the 4,300 bp EcoRI-HindIII fragment of pBSHIVMN120T. The plasmid generated by this manipulation is called pHIV57.

[0369] The H6-promoted gp120+TM construct containing the ELDKWA epitopes was then cloned between C5 flanking arms. This was accomplished by cloning the 1,700 bp NruI-XbaI fragment of pHIV57, containing the H6-promoted gp120+TM (with ELDKWA epitopes) gene, into the 4,700 bp NruI-XbaI fragment of pSIVGC15. (pSIVGC15 contains the H6-promoted SIV env gene cloned between C5 flanking arms) The plasmid generated by this manipulation is called pHIV59.

[0370] The H6-promoted gp120+TM (with ELDKWA epitopes) gene was then cloned between I4L flanking arms. This was accomplished by cloning the 1,850 bp BamHI-SmaI fragment of pHIV59, containing the H6-promoted gp120+TM (with ELDKWA epitopes) gene, into the 3,600 bp BamHI-SmaI fragment of pSD550VC. The plasmid generated by this manipulation is called pHIV60. The DNA sequence of the H6-promoted gp120+TM (with ELDKWA epitopes) gene in pHIV60 is shown in FIG. 28.

[0371] pHIV60 was used in in vitro recombination experiments with NYVAC as the rescuing virus to yield vP1313.

[0372] FACS analysis was performed to determine whether HIV1 gp120+TM (with ELDKWA epitopes) was expressed on the surface of vP1313-infected cells. 5×10^6 HeLa-S3 cells in S-MEM (Sigma M-8028 Joklik suspension media) were infected at an m.o.i. of 5 pfu/cell with NYVAC, vP1286 (a WR recombinant expressing HIV1 gp120+TM) or vP1313. Following a 60 minute adsorption period at 37° C., the cells were washed with 10 mls of S-MEM and centrifuged at 1,000 RPM for 5 minutes. The samples were then resuspended in 1 ml of S-MEM, transferred to 5 ml Sarstedt tubes and placed on a rotator at 37° C. After 18 hours, 200 μ l aliquots (1×10^6 cells) were placed in polypropylene tubes and washed with 3 mls of PBS-CMF (with 0.2% NaN₃+0.2% BSA). The supernatant was then decanted and the pellet was resuspended in 100 μ l of a 1:100 dilution of sera from HIV1-seropositive humans (obtained from the New York State Dept. of Health), or a 1:100 dilution of a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (obtained from Viral Testing Systems Corp. Houston, Tex.). The samples were

incubated at 4° C. for 60 minutes, washed two times with PBS-CMF (with 0.2% NaN₃+0.2% BSA) and centrifuged at 1,000 RPM for 5 minutes. The supernatant was decanted and the pellet was resuspended in a 1:100 dilution of goat anti-human FITC (obtained from Boehringer Mannheim). The samples were incubated at 4° C. for 30 minutes, washed twice with PBS-CMF (with 0.2% NaN₃+0.2% BSA) and analyzed on a Facscan flow cytometer. A gene product containing the ELDKWA epitope was expressed on the surface of vP1313-infected cells, but was not expressed on the surface of NYVAC-infected or vP1286-infected cells (FIG. 29, lower panel). A gene product reactive with the HIV1-seropositive sera was expressed on the surface of vP1286-infected cells and vP1313-infected cells, but was not expressed on the surface of NYVAC-infected cells (FIG. 29, upper panel). These results indicate that the ELDKWA epitope of the HIV1 gp120+TM (with ELDKWA epitopes) gene product is expressed on the surface of vP1313-infected cells, consistent with the fact that a portion of the V3 loop of this gene product has been replaced with ELDKWA epitopes.

[0373] Immunoprecipitation analysis was performed to determine: whether vP1313 expresses a form of gp120+TM which contains an immunogenic ELDKWA epitope. HeLa cell monolayers were infected at an m.o.i. of 10 pfu/cell with NYVAC (the parental virus), vP1286 (a WR recombinant expressing HIV1 gp120+TM) or vP1313. Following an hour adsorption period, the inoculum was removed and the cells were overlaid with 2 mls of modified Eagle's medium (minus cysteine and methionine) containing 2% dialyzed fetal bovine serum and [³⁵S]-TRANS label (30 μ Ci/ml). The lysates were harvested at 18 hrs post-infection by addition of 1 ml 3 $\times$ buffer A (450 mM NaCl, 3% NP-40, 30 mM Tris (pH=7.4), 3 mM EDTA, 0.03% Na-Azide and 0.6 mg/ml PMSF) and analyzed for expression of 1) the ELDKWA epitope, using a 1:100 dilution of a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (obtained from Viral Testing Systems Corp., Houston, Tex.) and 2) HIV1 gene products, using a 1:100 dilution of sera from HIV1-seropositive humans (obtained from the New York State Dept. of Health). Lysates, precleared with normal human sera and a protein A-sepharose complex, were incubated overnight at 4° C. with an IAM41-2F5-protein A-sepharose complex or an HIV1-seropositive sera-protein A-sepharose complex. The samples were washed 4 $\times$ with 1 $\times$ buffer A and 2 $\times$ with a LiCl₂/urea buffer. Precipitated proteins were dissociated from the immune complexes by the addition of 2 $\times$ Laemmli's buffer (125 mM Tris (pH=6.8), 4% SDS, 20% glycerol, 10% 2-mercaptoethanol) and boiling for 5 min. Proteins were fractionated on an SDS-polyacrylamide gel, fixed and treated with 1 M Na-salicylate for fluorography. Proteins of the appropriate size were precipitated with the monoclonal antibody to the ELDKWA epitope from vP1313-infected cells, but were not precipitated from NYVAC-infected cells or vP1286-infected cells. Furthermore, proteins of the appropriate size were precipitated with the human HIV1-seropositive sera from vP1286-infected cells and vP1313-infected cells, but were not precipitated from NYVAC-infected cells. These results indicate that vP1313 expresses a form of gp120+TM which contains an immunogenic ELDKWA epitope.

Example 21

Generation of vP1319; a COPAK Recombinant
Expressing a Form of HIV1 gp120+TM with 2
ELDKWA Epitopes Inserted into the gp120 V3 Loop

[0374] vP1319, a COPAK recombinant expressing HIV1 gp120+TM with 2 ELDKWA epitopes from HIV1 gp41

inserted into the gp120 V3 loop, was generated by the following procedure. The sequence encoding part of the ELDKWA epitopes and V3 loop was cloned into pBSK+. This was accomplished by cloning a 225 bp EcoRI-SacI-digested PCR fragment, containing part of the ELDKWA-V3 loop sequence, into the 2,900 bp EcoRI-SacI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pBSHIVMN120T, with the primers, HIVP72 (SEQ ID NO: 121; 5'-TTATTACCAATCCAGTACTATT-3') and HIVP74 (SEQ ID NO: 122; 5'-TCTGTACAAATTAATTGTACAA-GACCCAACTACGAGCTCGACAAATGGGC-CCATATAGGACC AGGGAGAGAATTG-GATAAGTGGGCGAATATAATAGGAACATAAGAC-3').) The plasmid generated by this manipulation is called pHIV55. pBSHIVMN120T, a plasmid containing the H6-promoted HIV1 gp120+TM gene, was generated by the following procedure. A plasmid, pMN1.8-9, containing a cDNA copy of the HIV1 (MN) env gene, was obtained from Marvin Reitz (NCI, NIH). An early transcription termination signal sequence, T₃NT, in the env gene was modified. This was accomplished by cloning a 1,100 bp KpnI-EcoRI-digested PCR fragment, containing the T₃NT-modified 5'-end of the env gene, into the 2,900 bp KpnI-EcoRI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIVMN6 (SEQ ID NO: 123; 5'-GGGTATTATTAATGATCTGTAG-3') and HIV3B2 (SEQ ID NO: 124; 5'-GAATTACAGTAGAAGAAATCCCTCCACAATTAAC-3').) The plasmid generated by this manipulation is called pBSMIDMN.

[0375] The T₃NT-modified 5'-end of the env gene was then cloned upstream to the rest of the env gene. This was accomplished by cloning the 1,025 bp KpnI-EcoRI fragment of pBSMIDMN, containing the T₃NT-modified 5'-end of the env gene, into the 4,300 bp KpnI-EcoRI fragment of pBS3MN. (pBS3MN was generated by cloning a 430 bp EcoRI-SacI-digested PCR fragment, containing a central portion of the env gene, and a 1,050 bp SacI-XbaI-digested PCR fragment, containing the 3'-end of the env gene, into the 2,900 bp EcoRI-XbaI fragment of pBSK+. The 430 bp PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIV3B1 (SEQ ID NO: 125; 5'-GTTT-TAATTGTGGAGGGGAATCTTCTACTGTAATTC-3') and HIVMN4 (SEQ ID NO: 126; 5'-ATCATCGAGCTC-CTATCGCTGCTC-3'). The 1,050 bp PCR fragment was generated from the plasmid, pMN1.8-9, with the oligonucleotides, HIVMN5 (SEQ ID NO: 127; 5'-ATCATCGAGCTCTGTTCTTGGGTTCTTAG-3') and HIVMN3P (SEQ ID NO: 128; 5'-ATCATCTCTA-GAATAAAAATTATAGCAAAGCCCTTCCAAGCC-3').) The plasmid generated by this manipulation is called pBSMID3MN.

[0376] The H6 promoter was then cloned upstream to the env gene. This was accomplished by cloning the 320 bp KpnI fragment of pH6IIIBE, containing the H6 promoter linked to the 5'-end of the HIV1 (IIIB) env gene, and the 2,450 bp KpnI-XbaI fragment of pBSMID3MN, containing the bulk of the HIV1 (MN) env gene, into the 2,900 bp KpnI-XbaI fragment of pBSK+. The plasmid generated by this manipulation is called pH6HMNE.

[0377] The sequence encoding gp41 was then replaced with the sequence encoding the HIV1 env transmembrane (TM) region. This was accomplished by cloning a 480 bp EcoRI-XbaI-digested PCR fragment, containing the 3'-end of the gp120 gene and the HIV1 env transmembrane region, into

the 4,200 bp EcoRI-XbaI fragment of pH6HMNE. (This PCR fragment was generated from the PCR fragment, PCR-MN11, and oligonucleotides, HIVTM1 (SEQ ID NO: 129; 5'-TTATTCATAATGATAGTAGGAGGCTTGG-TAGGTTTAAAGAATAGTTTTTGTCTACTCTCTGT AGTGAATAGAGTTAGGCAGGGATAA-3') and HIVTM2 (SEQ ID NO: 130; 5'-TTATCCCTGCCTAACTCTATTAC-TACAGAGAGTACAGCAAAAACTATTCT-TAAACCTACCA AGCCTCCTACTATCATTATGAATAA-3'), with the oligonucleotides, HIV3B1 (SEQ ID NO: 125) and HIVTM3 (SEQ ID NO: 131; 5'-ATCATCTCTA-GAATAAAAATTATCCCTGCCTAACTCTATTAC-3').) PCR-MN11 was generated from the plasmid, pH6HMNE, with the oligonucleotides, HIV3B1 (SEQ ID NO: 125) and HIVMN18 (SEQ ID NO: 132; 5'-GCCTCCTACTATCAT-TATGAATAATCTTTTTTCTCTCTG-3').) The plasmid generated by this manipulation is called pBSHIVMN120T.

[0378] Another part of the sequence encoding the ELDKWA epitopes and V3 loop was then cloned into pBSK+. This was accomplished by cloning a 300 bp HindIII-SacI-digested PCR fragment, containing part of the ELDKWA-V3 loop sequence, into the 2,900 bp HindIII-SacI fragment of pBSK+. (This PCR fragment was generated from the plasmid, pBSHIVMN120T, with the primers, HIVP69 (SEQ ID NO: 133; 5'-TGATAGTACCAGCTATAGGT-TGAT-3') and HIVP75 (SEQ ID NO: 134; 5'-TTTGTC-GAGCTCGTAGTTGGGTCTTGTACAATT-3').) The plasmid generated by this manipulation is called pHIV56.

[0379] The ELDKWA-V3 loop sequences from pHIV55 and pHIV56 were then cloned into the H6-promoted gp120+TM gene. This was accomplished by cloning the 225 bp EcoRI-SacI fragment of pHIV55 and the 300 bp HindIII-SacI fragment of pHIV56, containing the ELDKWA-V3 loop sequences, into the 4,300 bp EcoRI-HindIII fragment of pBSHIVMN120T. The plasmid generated by this manipulation is called pHIV57.

[0380] The H6-promoted gp120+TM construct containing the ELDKWA epitopes was then cloned between C5 flanking arms. This was accomplished by cloning the 1,700 bp NruI-XbaI fragment of pHIV57, containing the H6-promoted gp120+TM (with ELDKWA epitopes) gene, into the 4,700 bp NruI-XbaI fragment of pSIVGC15. (pSIVGC15 contains the H6-promoted SIV env gene cloned between C5 flanking arms.) The plasmid generated by this manipulation is called pHIV59.

[0381] The H6-promoted gp120+TM (with ELDKWA epitopes) gene was then cloned between COPAK flanking arms. This was accomplished by cloning the 1,850 bp BamHI-SmaI fragment of pHIV59, containing the H6-promoted gp120+TM (with ELDKWA epitopes) gene, into the 4,600 bp BamHI-SmaI fragment of pSD553VC. The plasmid generated by this manipulation is called pHIV61. The DNA sequence of the H6-promoted gp120+TM (with ELDKWA epitopes) gene in pHIV61 is shown in FIG. 30.

[0382] pHIV61 was used in in vitro recombination experiments with COPAK as the rescuing virus to yield vP1319.

[0383] FACS analysis was performed to determine whether HIV1 gp120+TM (with ELDKWA epitopes) was expressed on the surface of vP1319-infected cells. 5×10^6 HeLa-S3 cells in S-MEM (Sigma M-8028 Joklik suspension media) were infected at an m.o.i. of 5 pfu/cell with WR, vP1286 (a WR recombinant expressing HIV1 gp120+TM) or vP1319. Following a 60 minute adsorption period at 37°C., the cells were washed with 10 mls of S-MEM and centrifuged at 1,000 RPM

for 5 minutes. The samples were then resuspended in 1 ml of S-MEM, transferred to 5 ml Sarstedt tubes and placed on a rotator at 37° C. After 18 hours, 200 μ l aliquots (1×10^6 cells) were placed in polypropylene tubes and washed with 3 mls of PBS-CMF (with 0.2% NaN_3 +0.2% BSA). The supernatant was then decanted and the pellet was resuspended in 100 μ l of a 1:100 dilution of sera from HIV1-seropositive humans (obtained from the New York State Dept. of Health), a 1:500 dilution of a mouse monoclonal antibody specific for the HIV1 (MN) V3 loop, 50.1 (obtained from M. Robert-Guroff, NCI, NIH.) or a 1:100 dilution of a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (obtained from Viral Testing Systems Corp., Houston, Tex.). The samples were incubated at 4° C. for 60 minutes, washed two times with PBS-CMF (with 0.2% NaN_3 +0.2% BSA) and centrifuged at 1,000 RPM for 5 minutes. The supernatant was decanted and the pellet was resuspended in a 1:100 dilution of goat anti-human FITC or goat anti-mouse FITC (obtained from Boehringer Mannheim). The samples were incubated at 4° C. for 30 minutes, washed twice with PBS-CMF (with 0.2% NaN_3 +0.2% BSA) and analyzed on a Facscan flow cytometer. A gene product containing the ELDKWA epitope was expressed on the surface of vP1319-infected cells, but was not expressed on the surface of WR-infected cells or vP1286-infected cells (FIG. 31, middle panel). A gene product containing the V3 loop was expressed on the surface of vP1286-infected cells, but was not expressed on the surface of WR-infected cells or vP1319-infected cells (FIG. 31, lower panel). A gene product reactive with the HIV1-seropositive sera was expressed on the surface of vP1286-infected cells and vP1319-infected cells, but was not expressed on the surface of WR-infected cells (FIG. 31, upper panel). This analysis indicated that 1) the ELDKWA epitope of the HIV1 gp120+TM (with ELDKWA epitopes) gene product is expressed on the surface of vP1319-infected cells and 2) the gene product expressed on the surface of vP1319-infected cells does not contain a wild-type V3 loop, consistent with the fact that the V3 loop of this gene product has been replaced with ELDKWA epitopes.

[0384] Immunoprecipitation analysis was performed to determine whether vP1319 expresses a form of gp120+TM which contains an immunogenic ELDKWA epitope. HeLa cell monolayers were infected at an m.o.i. of 10 pfu/cell with NYVAC (the parental virus), vP1286 (a WR recombinant expressing HIV1 gp120+TM) or vP1319. Following an hour adsorption period, the inoculum was removed and the cells were overlaid with 2 mls of modified Eagle's medium (minus cysteine and methionine) containing 2% dialyzed fetal bovine serum and [^{35}S]-TRANS label (30 $\mu\text{Ci/ml}$). The lysates were harvested at 18 hrs post-infection by addition of 1 ml 3 $\times$ buffer A (450 mM NaCl, 3% NP-40, 30 mM Tris (pH=7.4), 3 mM EDTA, 0.03% Na-Azide and 0.6 mg/ml PMSF) and analyzed for expression of 1) the ELDKWA epitope, using a 1:100 dilution of a human monoclonal antibody specific for the ELDKWA epitope, IAM41-2F5 (obtained from Viral Testing Systems Corp., Houston, Tex.) and 2) HIV1 gene products, using a 1:100 dilution of sera from HIV1-seropositive humans (obtained from the New York State Dept. of Health). Lysates, precleared with normal human sera and a protein A-sepharose complex, were incubated overnight at 4° C. with an IAM41-2F5-protein A-sepharose complex or an HIV1-seropositive sera-protein A-sepharose complex. The samples were washed 4 $\times$ with 1 $\times$ buffer A and 2 $\times$ with a LiCl_2 /urea buffer. Precipitated proteins

were dissociated from the immune complexes by the addition of 2 $\times$ Laemmli's buffer (125 mM Tris (pH=6.8), 4% SDS, 20% glycerol, 10% 2-mercaptoethanol) and boiling for 5 min. Proteins were fractionated on an SDS-polyacrylamide gel, fixed and treated with 1 M Na-salicylate for fluorography. Proteins of the appropriate size were precipitated with the monoclonal antibody to the ELDKWA epitope from vP1319-infected cells, but were not precipitated from NYVAC-infected cells or vP1286-infected cells. Furthermore, proteins of the appropriate size were precipitated with the human HIV1-seropositive sera from vP1286-infected cells and vP1319-infected cells, but were not precipitated from NYVAC-infected cells. These results indicate that vP1319 expresses a form of gp120+TM which contains an immunogenic ELDKWA epitope.

[0385] Since vCP1307, vP1313 and vP1319 each express the ELDKWA epitope in an immunogenic configuration, these recombinants have numerous utilities, as do the expression products, antibodies elicited thereby, and DNA from these recombinants, as discussed above.

Example 22

Inocuity and the Immunogenicity of vCP205 in Macaques Inoculated by Intramuscular Route

Experimental Animals:

[0386] Species: *Macaca fascicularis* (adult, wild caught)

Number: 8

Sex: Males

[0387] Origin: Mauritius Island considered free of Herpes B, Filovirus and Tuberculosis. Previous history: polio experiments.

Diet and drinking water: Commercial diet and fruits; tap water ad libitum.

[0388] Four male *Cynomolgus* macaques were inoculated five times, at one month intervals, with one dose of ALVAC-HIV (vCP205) (containing $10^{5.8}$ TCID $_{50}$ /dose) by intramuscular route. The injections caused neither symptoms nor lesions. Body weight of monkeys was not altered by the injections. Four control animals were injected with placebo. (Mixture of DMEM-F12 medium (25%), Lactoglutamate (25%) and freeze-drying substrate (50%)). General condition was monitored daily and injection sites were observed on days 1, 2, 3, 4 and 7 after each inoculation. Body weights were recorded once a week.

[0389] Blood samples were collected in EDTA blood collection Vacutainer® tubes (Becton-Dickinson, Meyland, France) for hematological analyses, in lithium-heparin microvette CB 100 tubes (Sarstedt, Nümbrecht, Germany) for biochemical analysis and in tubes with serum separator SST Vacutainer® tubes (Becton-Dickinson, Meylan, France) for serological analyses (MON:TSA.034.00). Samplings were done on days 0, 3, 7, 14, 28, 31, 35, 42, 56, 59, 63, 70, 84, 87, 91, 98, 112, 115, 119, 126 and 140. Anesthesia (Ketamine, 20 mg/kg, intramuscular) was used for clinical examinations and blood sampling.

[0390] Hematological and biochemical analysis were carried out with the VET TEST 8008 Apparatus. Anti-HIV gp160, p24 proteins and V3 peptide antibodies were titered according to an ELISA technique. Maxisorp F96 NUNC

plates wells were coated for 1 hour at 37° C., with one of the following antigens diluted in 0.1 M carbonate buffer, pH 9.6:

[0391] 130 ng per well of purified gp160 MN/BRU (from recombinant vaccinia containing 30% of cleaved gp160 and no α_2 macroglobulin),

[0392] 200 ng of V3MN peptide,

[0393] 130 ng of purified "p24" HIV (*E. coli*, P25 LAI isolate, batch 672C1, Transgene).

[0394] All incubations were carried out in a final volume of 100 μ l, followed by 3 washings performed with phosphate buffered saline, pH 7.1-0.1% Tween 20. Plates were blocked for 1 hour at 37° C. with 150 μ l of phosphate buffered saline pH 7.1-0.05% Tween 20-5% (W/V) powdered skim milk (Gloria).

[0395] Serial threefold dilutions of the sera, ranging from 1/50 to 1/12150, in phosphate buffered saline—0.05% Tween 20-5% (W/V) powdered skim milk, were added to the wells and incubated for 90 min at 37° C.

[0396] After washing, anti-monkey IgG peroxidase conjugate (Cappel, goat IgG fraction), diluted 1/3000 in phosphate buffered saline—0.5% Tween 20-5% powdered skim milk, was added and the plates incubated for another 90 min at 37° C. The plates, washed four times, were incubated in the dark for 30 min at room temperature with the substrate O-phenylenediamine dihydrochloride (Sigma tablets). The substrate was used at the concentration of 1.5 mg/ml in 0.05 M phosphate citrate buffer, pH 5.0 containing 0.03 containing 0.03% sodium perborate (Sigma capsules).

[0397] The reactions were stopped with 50 μ l of 4N H₂SO₄. The optical density was measured at 490-650 nm with an automatic plate reader (Vmax, Molecular Devices). The antibody titers were calculated according to the formula:

$$\text{Titer} = \log \frac{OD_{490-650} \times 10}{1/\text{dilution}} \quad (OD \text{ value range: } 0.2 \text{ to } 1)$$

[0398] Neutralizing antibody assay determines the dilution of serum that prevents the development of syncytia in 50% of microwells infected with 10 TCID₅₀ of HIV MN. The MN strain was obtained from F. Barre-Sinoussi and propagated in CEM clone 166 cells.

[0399] Sera were decplemented and twofold serial dilutions in RPMI beginning 1/10 were prepared. Equal volumes of serum dilution and HIV suspension (500 μ l each) were mixed and incubated for 2 h at 37° C. The HIV suspension had been adjusted to contain 10² to 10^{2.5} TCID₅₀ per ml.

[0400] Prior to use, indicator CEMss cells were plated in microwells coated with poly-L-lysine, and incubated for 1 h at 37° C. Culture medium was removed and replaced with the virus/serum mixtures (100 μ l/well, 6 wells per dilution). After 1 h incubation at 37° C. culture medium was added to each well and the plates were incubated at 37° C. All incubations were in a CO₂ 5% incubator.

[0401] Seven and 14 days later, the cultures were examined under the microscope and wells showing syncytia were recorded. Neutralizing 50% titer was computed according to SPEARMAN and KÄRBER and expressed as the log₁₀ of the end-point. As a confirmation, supernatants of the cultures were collected on day seven, pooled for each dilution and assayed for RT activity. Each assay includes an infectivity titration of the virus suspension, titration of antibody in a reference serum and a set of uninfected microwells as negative controls.

[0402] Results:

[0403] A majority of the parameters selected to monitor hematological and biochemical status varied within normal limits, including: erythrocyte number, mean corpuscle volume, hematocrite, creatinin and alanine aminotransferase.

[0404] Some variations were seen, which cannot be attributed to the repeated immunizations with ALVAC-HIV (vCP205): i) unexplained lymphocytosis on weeks 8 and 9 in both the test and the control groups; ii) a decreased level of hemoglobin in both groups on weeks 17 and 20 and in control groups; iii) a decreased level of hemoglobin in both groups on weeks 17 and 20 and in controls on week 9; iv) erratic high values of the aspartate aminotransferase in two control monkeys and last; iv) irregular trombocytes counts caused by microcoagulation of some specimens.

[0405] The anti-HIV immune response induced by vCP205 was assessed by ELISA tests using purified gp160 MN/BRU (from recombinant vaccinia), V3MN synthetic peptide and p24 (from *E. coli*, LAI isolate). All the animals developed antibodies against gp160 and V3, and 2/4 against p24. The positive anti-HIV immune response usually appeared after 2, or maximum, 3 injections. Subsequent vCP205 inoculations mainly maintained (sometimes slightly increased) the antibody levels and improved homogeneity of the response between macaques. Highest antibody titers were usually observed two weeks after each inoculation, followed by a decrease until the next booster. Neutralizing antibodies against HIV/MN were detectable in all immunized monkeys.

[0406] Clinical observation: neither erythema nor edema were reported at the site of inoculation. Body weights were stable in control monkeys and in ALVAC-HIV (vCP205) recipients (FIG. 32).

[0407] Hematological analyses: Leucocyte counts were greatly modified in both control and tested animals on weeks 8 and 9 with formula inversion (FIG. 33a). This fact, noted in both groups, is without correlation with the viral injections.

[0408] Erythrocyte number, corpuscle mean volume and hematocrite varied within normal limits but hemoglobin showed some discrepancy on weeks 9, 17 and 20 in controls and on weeks 17 and 20 in animals inoculated with ALVAC-HIV (vCP205) (FIGS. 33b and c). Thrombocytes values varied depending on the sampling quality (microcoagulation) (FIG. 33c).

[0409] Biochemical analyses: Creatinin and ALAT (SGP-Transaminase) did not vary significantly after the reiterated inoculations FIGS. 34 and 36). The AST (SGOTransaminase) values presented variations particularly important in control monkeys #3 and 2 respectively on week 5 and 8-9 (FIG. 35).

[0410] Serological analyses (considering the ELISA titers of the negative control group of macaques sera, the negative detection threshold of the serological response was considered to be, in log₁₀: 1.56±0.24, 1.92±0.12 and 2.18±0.34, for gp160, V3 and p24 respectively): gp160 and V3 specific response (FIGS. 37a-37b, 38a-38b): the kinetics of antibody of gp160 was similar to that to V3. The magnitude of the latter was slightly weaker (mean titer at week 20 of 4.37 versus 8.84).

[0411] Two injections were necessary to induce a detectable immune response. Three monkeys showed a maximum response after the second injection; the fourth one required

three (gp160) or four (V3) injections to do so. During the four week interval between injections, antibody titers consistently increased then faded, to be boosted by the next inoculation. While there were significant individual differences in the responses to the initial injections, the responses leveled out as the experiment progressed.

[0412] p24 a specific response (FIGS. 37c, 38c): a response was observed for 2 macaques (macaques 5 and 7) out of 4 after respectively 2 and 3 injections of vCP205. This is in contrast with a guinea-pig test in which no anti-p24 antibodies were detected in any inoculated animal groups. As with anti-gp160 and anti-V3 antibodies, titers fluctuated up and down between injections and individual differences progressively disappeared. Unlike that of gp160 and V3, the anti-p24 antibody profile did not reach a plateau.

[0413] Neutralizing antibody: as shown in FIG. 39, all four monkeys with vCP205 developed detectable levels of neutralizing antibody against HIV (MN). One of them tested positive after one injection, two after the second injection and the last one required five administrations. It is noteworthy that the latter animal also showed the slowest kinetics of ELISA antibody. The levels of neutralizing activity are relatively modest (1/10 to 1/30 in arithmetical expression) and, likewise ELISA measurements, went up and down in the intervals between injections.

[0414] Effect of a late boost with the proteins gp160 and p24: The four monkeys were boosted 7 weeks post the last injection of vCP205 with 200 µg of gp160 and 200 µg of p24 proteins in incomplete Freund's adjuvant (Montanide ISA51) to raise hyperimmune reference sera; this caused a pronounced increase (at least 10-fold) in antibody titers, suggesting that the plateau seen in the ELISA analysis were not the limit of response.

[0415] The immunization regimen induced high levels of binding antibody to gp160 MN/BRU and V3 MN peptide, and low but definite neutralizing antibody. Serological results showed higher antibody levels than those observed in macaques inoculated with ALVAC-HIV (vCP125) and one booster (instead of two) was sufficient to obtain a good anamnestic type response. This Example shows that vCP205 and expression products thereof, antibodies therefrom, and DNA from vCP205, can be used as described above.

Example 23

Inocuity and Immunogenicity of vCP300 In Macaques

Experimental Animals:

[0416] Species: *Macaca fascicularis*

Number: 8

Sex: Males

[0417] Origin: Mauritius Island considered without Herpes B, Filovirus and tuberculosis.

[0418] Four male *Cynomolgus* macaques were immunized five times, at one month intervals, with one dose of ALVAC-HIV (vCP300) (containing $10^{6.16}$ TCID₅₀/dose) by intramuscular route. Four control animals were injected with placebo.

As a sixth injection, all the animals received ALVAC-HIV (vCP300) by intravenous route. The regimen was as follows:

Group #1

Product: Placebo

[0419] Route: Intramuscular alternately in the left or right deltoid muscle

Volume: 1 ml

[0420] Number of injections: 5 (on weeks 0, 4, 8, 12 and 16).

Group #2

Product: ALVAC-HIV

[0421] Route: Intramuscular alternately in the left or right deltoid muscle.

Volume: 1 ml.

Dose: $10^{6.16}$ TCID₅₀.

[0422] Number of injections: 5 (on weeks 0, 4, 8, 12 and 16).

Groups #1 and #2

[0423] On week 20

Product: ALVAC-HIV (vCP300)

Route: Intravenous

Volume: 1 ml

Dose: $10^{6.16}$ TCID₅₀.

[0424] Number of injections: 1.

[0425] Clinical observations: Injection site was observed on days 1, 2, 3, 4 and 7 following each inoculation. Animals were weighed once a week. Samplings: Blood samples were taken under ketamin anesthesia from the femoral vein. Blood was collected in the following order in Vacutainer tubes (Becton Dickinson, Meylan, France):

- 1) 1.8 ml in 0.129M buffered sodium citrated tube (prothrombine).
- 2) 1 ml in 5 mg sodium fluoride and 4 mg potassium oxalate tube (glucose).
- 3) 2 ml in 0.17M EDTA K₃ tube (hematological analyses).
- 4) 2 to 3 ml in tubes for serum separation with inert barrier material and clot activator (biochemical and serological analyses).

[0426] Samplings were done on days 0, 3, 7, 14, 28, 31, 35, 42, 56, 59, 63, 70, 84, 87, 91, 98, 112, 119, 126, 140 and 143.

[0427] Dosages:

[0428] Hematological analyses included: blood counts and differential leucocyte counts, hemoglobin, thrombocytes, prothrombin, reticulocytes and sedimentation rate.

[0429] Biochemical analyses included: sodium, potassium, glucose, alkaline phosphatases, cholesterol, total proteins and electrophoresis, transaminases SGOT and SGPT.

[0430] Serological analyses: Anti-HIV gp160 glycoprotein, p24 protein, V3 peptide and nef protein antibodies were titrated according to a modification of the ELISA technique:

[0431] Maxisorp F96 NUNC plates wells were coated for 1 hour at 37° C., then overnight at 4° C., with one of the following antigens diluted in 0.1 M carbonate buffer, pH 9.6:

[0432] 130 ng per well of purified gp160 MN/BRU (from recombinant vaccinia VVTG 5156),

[0433] 200 ng of V3MN peptide,

[0434] 130 ng of purified p24 HIV (*E. coli*, p25 LAI isolate, batch 672C1, Transgene).

[0435] All incubations were carried out in a final volume of 100 μ l, followed by 3 washings performed with phosphate buffered saline, pH 7.1-0.1% Tween 20. Plates were blocked for 1 hour at 37° C. with 150 μ l of phosphate buffered saline pH 7.1-0.05% Tween 20-5% (W/V) powdered skim milk (Gloria). Serial threefold dilutions of the sera, ranging from 1/50 to 1/12150 or 1/500 to 1/121500, in phosphate buffered saline—0.05% Tween 20-5% (W/V) powdered skim milk, were added to the wells and incubated for 90 min. at 37° C.

[0436] After washing, anti-monkey IgG peroxidase conjugate (Cappel, goat IgG fraction), diluted 1/3000 in phosphate buffered saline—0.05% Tween 20-5% powdered skim milk, was added and the plates incubated for another 90 min. at 37° C. The plates, washed four times, were incubated in the dark for 30 min. at room temperature with the substrate O-phenylenediamine dihydrochloride (Sigma tablets), the substrate was used at the concentration of 1.5 mg/ml in 0.05 M phosphate citrate buffer, pH 5.0 containing 0.03% sodium perborate (Sigma capsules). The reactions were stopped with 50 μ l of 4N H₂SO₄.

[0437] The optical density was measured at 490-650 nm with an automatic plate reader (Vmax, Molecular Devices). The blanks were subtracted and the values of the duplicates averaged. The antibody titers were calculated for the OD value range of 0.2 to 1.2, from the regression curve of a standard anti-gp160 and anti-p24 hyperimmune serum of guinea-pig which was present on each ELISA plate. The titer of the standard serum had been previously determined according to the formula:

$$\text{Titer} = \log \frac{OD_{490-650} \times 10}{1/\text{dilution}} \quad (\text{OD value range: 0.2 to 1.2})$$

[0438] Since no standard monkey anti-nef serum was available, the determination of anti-nef antibodies was performed by including in the test a reference monoclonal mouse antibody (anti-nef HIV1 ALI, MATG0020, Transgene) as an internal positive control. Anti-mouse IgG peroxidase conjugate (Amersham) diluted 1/5000, was then used and sera titers were calculated using the formula mentioned above.

[0439] Results:

[0440] The injections caused neither symptoms nor lesions. Body weight of monkeys was not altered by the injections. Hematological parameters did not vary significantly and biochemical analyses showed no alteration of kidneys and liver functions.

[0441] Hematological results: Variations, when present, were similar in pattern and in range in the placebo and in the vaccinee groups.

[0442] Individual WBC counts varied within normal limits. Differential WBC counts often showed a diminution of lymphocytes 3 days after the blood samplings (FIG. 40). Erythrocyte counts, hematocrit and hemoglobin transiently decreased after each blood sampling contrary to reticulocyte counts which increased regularly after the puncture (FIGS. 41a, 41b, 41c). Mean corpuscle volume was stable in all the animals except an increase on day 140. Thrombocyte counts showed some variations (FIG. 41) but prothrombin level was

stable (FIG. 42). There was no sign of anemia in either group. Sedimentation rate was 1 mm after one hour in all the samples.

[0443] Biochemical results: For a better interpretation of the variations observed, a standard serum (pool of 18 macaque sera) was analyzed at the beginning (Std a) and at the end (Std p) of each series of samples to be tested.

[0444] Cholesterol values varied in the same way in controls and in test group (FIGS. 43a and 43b).

[0445] Sodium and potassium were stable after all the injections but, as for total proteins and glucose, there was a great rising on day 140. On that day, blood specimens were drawn prior to the intravenous injection without anesthesia (so that clinical reactions could be monitored without interference); the change observed in several biological parameters was likely due to the stress associated with handling and sampling in the absence of anesthesia (FIGS. 43a and 43b). Electrophoresis profiles (data not shown) were very similar in all the samples. Creatinine, bilirubin, glutamic oxaloacetic and glutamic pyruvic transaminases and alkaline phosphatases varied within normal limits and always in the same direction in both control and test groups (FIGS. 43c and 43d). Kidneys and liver functions were therefore not affected by the inoculations of ALVAV-HIV (vCP300).

[0446] Serological results: Two (macaques # 6, 7, 8) or three (macaque #5) injections were necessary to induce detectable anti-gp160 and anti-V3 responses (FIG. 44a, 44b, 45a, 45b). Two weeks after the second injection, these responses were variable between animals (anti-gp160 titers fluctuating between 2 to 4.6 logs). This response heterogeneity was smoothed out by the third injection. The subsequent intramuscular injections mainly maintained or increased the titers which reached around 4.3 and 3.6 for respectively anti-gp160 and anti-V3 antibodies after the fourth to fifth injection. Detectable anti-p24 antibodies (FIGS. 46a, 46b) were observed after three (macaques # 6, 8) to four (macaque #7) or five (macaque 5) vCP300 intramuscular injections. The animals with the highest anti-gp160/V3 titers exhibited the highest anti-p24 ($\approx$ 4.3 on week 18 post-primoinmunization). None of the animals raised anti-nef antibodies (FIG. 47a, 47b).

[0447] The immune response induced by vCP300 was assessed by analyzing in ELISA the anti-HIV-1 gp160, V3, p24 and nef sera antibodies.

[0448] All the animals developed antibodies against gp160, V3 and p24: significant anti-gp160 or V3 responses were obtained after 2 or at most 3 intramuscular injections. Subsequent inoculations maintained or increased the antibody levels. Anti-p24 responses were detected after 3 to 5 injections and each inoculation of vCP300 increased the levels. No anti-nef antibodies could be detected in any of the animals.

[0449] The highest antibody titers were usually observed two weeks after each intramuscular injection, followed by a decrease until the next boost.

[0450] These serological results are very close to those obtained with ALVAC-HIV (vCP205) which expressed the same proteins but no CTL epitopes. Two minor differences can be pointed out in this example with vCP300: slightly lower anti-gp160/V3 antibody titers ($\approx$ 0.2 to 0.5 log), and higher anti-p24 responses (all macaques positive, higher sera titers). Because of the individual variations between animals, these differences were not deemed significant. No indication of hypersensitivity was seen following intravenous inoculation. No side effects were recorded. This regimen induced

high levels of binding antibodies to gp160 (though lower than with vCP205), V3 and p24 antigens. This Example shows that vCP300 and expression products thereof, antibodies therefrom, and DNA from vCP300 can be used as described above.

[0451] Having thus described in detail preferred embodiments of the present invention, it is to be understood that the invention defined by the appended claims is not to be limited by particular details set forth in the above description as many apparent variations thereof are possible without departing from the spirit or scope thereof.

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SD22mer

<400> SEQUENCE: 6

cgattactat gaaggatccg tt 22

<210> SEQ ID NO 7
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
SD20mer

<400> SEQUENCE: 7

taatgatact tcctaggcaa 20

<210> SEQ ID NO 8
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
SD42mer

<400> SEQUENCE: 8

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<210> SEQ ID NO 9
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
SD40mer

<400> SEQUENCE: 9
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<210> SEQ ID NO 10
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as HEM5

<400> SEQUENCE: 10
gatccgaatt ctagct 16

<210> SEQ ID NO 11
<211> LENGTH: 12
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as HEM6

<400> SEQUENCE: 11
gcttaagatc ga 12

<210> SEQ ID NO 12
<211> LENGTH: 75
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as ATI3

<400> SEQUENCE: 12
tatgagtaac ttaactcttt tgtaattaa aagtatattc aaaaaataag ttatataaat 60
agatctgaat tcggtt 75

<210> SEQ ID NO 13
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as ATI4

<400> SEQUENCE: 13
actcattgaa ttgagaaaac aattaatttt catataagtt ttttattcaa tatatttattc 60
tagacttaag caa 73

<210> SEQ ID NO 14
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
MPSYN177

<400> SEQUENCE: 14

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aaaatgggcg tggattgtta actttatata acttattttt tgaatatac 49

<210> SEQ ID NO 15
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
MPSYN59

<400> SEQUENCE: 15

acacgaatga ttttctaaag tatttggaaa gttttatagg tagttgatag aacaaaatac 60

ataattt 67

<210> SEQ ID NO 16
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
MPSYN62

<400> SEQUENCE: 16

tgtgcttact aaaagatttc ataaaccttt caaaatatcc atcaactatc t 51

<210> SEQ ID NO 17
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
MPSYN60

<400> SEQUENCE: 17

tgtaaaaata aatcactttt tatactaaga tctcccgggc tgcagc 46

<210> SEQ ID NO 18
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
MPSYN61

<400> SEQUENCE: 18

tgttttatgt attaaaaacat ttttathtag tgaaaaatat gattctagag ggcccgacgt 60

cgccgg 66

<210> SEQ ID NO 19
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
MPSYN82

<400> SEQUENCE: 19

tttctgtata ttgcaacaa tttagatctt actcaaaata tgtaacaata 50

<210> SEQ ID NO 20
<211> LENGTH: 44
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as
MPSYN233

<400> SEQUENCE: 20

tgtcatttaa cactatactc atattaataa aaataatatt tatt 44

<210> SEQ ID NO 21
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as 518A1

<400> SEQUENCE: 21

gactcctgagt accttgtaat ataatgatat atattttcac tttatctcat ttgagaataa 60
aaagatctta gg 72

<210> SEQ ID NO 22
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as 518A2

<400> SEQUENCE: 22

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tagaatcctt aa 72

<210> SEQ ID NO 23
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as 518B1

<400> SEQUENCE: 23

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tagcgtacta gg 72

<210> SEQ ID NO 24
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as 518B2

<400> SEQUENCE: 24

gtctagaggg cccttttttt aataaattga aaagtaatta tcctaaact gcatactacg 60
catgacctt aa 72

<210> SEQ ID NO 25
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as VQ1A

<400> SEQUENCE: 25

gggagatctc tcgagctgca gggcgccgga tcctttttct 40

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<210> SEQ ID NO 26
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as VQ1B

<400> SEQUENCE: 26

ccctctagag agctcgacgt cccgcggcct aggaaaaaga 40

<210> SEQ ID NO 27
<211> LENGTH: 59
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE75

<400> SEQUENCE: 27

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<210> SEQ ID NO 28
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE76

<400> SEQUENCE: 28

cgggatcctg gtagaagatc tggagcccat tacgatacaa acttaacgga tatcg 55

<210> SEQ ID NO 29
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE42

<400> SEQUENCE: 29

aattcgagct ccccggg 17

<210> SEQ ID NO 30
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE43

<400> SEQUENCE: 30

cccggggagc tcg 13

<210> SEQ ID NO 31
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 31

ctttttataa aaagttaact acgtag 26

<210> SEQ ID NO 32
<211> LENGTH: 34

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE167

<400> SEQUENCE: 32
gatacctacgt agttaacttt ttataaaaag agct 34

<210> SEQ ID NO 33
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE182

<400> SEQUENCE: 33
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<210> SEQ ID NO 34
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE183

<400> SEQUENCE: 34
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<210> SEQ ID NO 35
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE162

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aagcttg 67

<210> SEQ ID NO 36
<211> LENGTH: 67
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as CE163

<400> SEQUENCE: 36
aattcaagct tataaaaatt aaatcccatc atccttgaga atctcaacta gtaaaggaac 60
gatacctg 67

<210> SEQ ID NO 37
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Double-stranded oligonucleotide referred to
as JCA017

<400> SEQUENCE: 37
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ggaataat 68

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<210> SEQ ID NO 38
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Double-stranded oligonucleotide referred to as JCA018

<400> SEQUENCE: 38

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<210> SEQ ID NO 39
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Replacement sequence for bases from 167 through position 455 of 880 bp canarypox PvuII fragment

<400> SEQUENCE: 39

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<210> SEQ ID NO 40
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW145

<400> SEQUENCE: 40

actctcaaaa gcttcccgga aattctagct agctagtttt tataaa 46

<210> SEQ ID NO 41
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW146

<400> SEQUENCE: 41

gatctttata aaaactagct agctagaatt cccgggaagc ttttgagagt 50

<210> SEQ ID NO 42
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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as Oligonucleotide A

<400> SEQUENCE: 42

ctgaaattat ttcattatcg cgatatccgt taagtttgta tcgtaatggt tcctcaggct 60
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<210> SEQ ID NO 43
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as Oligonucleotide B

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<400> SEQUENCE: 43

cattacgata caaacttaac ggatatcgcg ataatgaaat aatttcag 48

<210> SEQ ID NO 44

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as Oligonucleotide
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<400> SEQUENCE: 44

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gcttagatct cag 73

<210> SEQ ID NO 45

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as Oligonucleotide
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<400> SEQUENCE: 45

ctgagatcta agcttgctcg ggatcgtgta aataggaat tccccaaac a 51

<210> SEQ ID NO 46

<211> LENGTH: 45

<212> TYPE: DNA

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<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as Oligonucleotide
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<400> SEQUENCE: 46

caacggaaaa accagaagggtgtacaaacag gagagcctga ggaac 45

<210> SEQ ID NO 47

<211> LENGTH: 11

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pRW824 sequence of BamHI followed by SmaI

<400> SEQUENCE: 47

ggatccccgg g 11

<210> SEQ ID NO 48

<211> LENGTH: 60

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as RW178

<400> SEQUENCE: 48

tcattatcgc gatatccgtg ttaactagct agctaatttt tattcccggtg atccttatca 60

<210> SEQ ID NO 49

<211> LENGTH: 60

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as RW179

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<400> SEQUENCE: 49

gtataaggat cccgggaata aaaattagct agctagttaa cacggatatc gcgataatga 60

<210> SEQ ID NO 50

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as F73PH2

<400> SEQUENCE: 50

gacaatctaa gtcctatatt agac 24

<210> SEQ ID NO 51

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as F73PB

<400> SEQUENCE: 51

ggatttttag gtagacac 18

<210> SEQ ID NO 52

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as F75PE

<400> SEQUENCE: 52

tcacgtctt catcatcg 18

<210> SEQ ID NO 53

<211> LENGTH: 29

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<223> OTHER INFORMATION: Oligonucleotide referred to as F73PH1

<400> SEQUENCE: 53

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<210> SEQ ID NO 54

<211> LENGTH: 61

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as F7MCSB

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<210> SEQ ID NO 55

<211> LENGTH: 60

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as F7MCSA

<400> SEQUENCE: 55

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gactaactaa ctaataaaaa acccgggctg cagcaagctt tttgtaacta actaatcggt 60

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW152

<400> SEQUENCE: 56

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<210> SEQ ID NO 57
<211> LENGTH: 99
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW153

<400> SEQUENCE: 57

attctgagat gagccctctg ctatgagcag gaacagaatc gtgattgata gcattacgat 60

acaaacttaa cggatatcgc gataagcttt gttccgtgc 99

<210> SEQ ID NO 58
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW10

<400> SEQUENCE: 58

gaaaaattta aagtcgacct gttttgttga gttgtttgcg tggtaaccaa tgcaaatctg 60

gtcact 66

<210> SEQ ID NO 59
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<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW11

<400> SEQUENCE: 59

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acggat 66

<210> SEQ ID NO 60
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW12

<400> SEQUENCE: 60

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<210> SEQ ID NO 61
<211> LENGTH: 49

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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW13

<400> SEQUENCE: 61
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<210> SEQ ID NO 62
<211> LENGTH: 132
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW165

<400> SEQUENCE: 62
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<210> SEQ ID NO 63
<211> LENGTH: 132
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW166

<400> SEQUENCE: 63
atgatgtcca aggcagattt tgtctgcatt tgtgtgaatg gctgccaca gagtgagtat 60
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gtcgacctgt ac 132

<210> SEQ ID NO 64
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW227

<400> SEQUENCE: 64
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<210> SEQ ID NO 65
<211> LENGTH: 51
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide referred to as RW228

<400> SEQUENCE: 65
gcttgacttg gaattcgta acttatatac aaatggtgca ccgcatgtta t 51

<210> SEQ ID NO 66
<211> LENGTH: 3209
<212> TYPE: DNA
<213> ORGANISM: Canarypox virus

<400> SEQUENCE: 66
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ctaaagataa tcttattaaa aaaaaataat atcacgttta gtaatattaa aatatattaa	2640
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tcaaatctt attgacatca agttagattg tgaaatgag attatgaaat taaggaatac	2760
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aaattctttt caaggattca ataataaatt gccttacgag attcagtaca ttatactgga	3000
gaatcttaat aacctgaac taaaaaaaaa tttagataat atacattaaa aaggtaataa	3060
gatcatctgt tattataagc aaagatgctt gttgccaata atatacaaca ggtatttgtt	3120
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<210> SEQ ID NO 67

<211> LENGTH: 3659

<212> TYPE: DNA

<213> ORGANISM: Fowlpox virus

<400> SEQUENCE: 67

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aaaatgattt ttacaaaaat acctataaga acaataaaaa tataattaca ttacggaaa	420
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agttatataa aaacatgatt agccccaat cggatgaaaa tataaaagat gttgagaatt	540
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caaaagtagt attatactgg atgttttag atcaacgtgt acaagataat tgggctttaa	660
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cagaatttcc tgtgttcgt aaacatccat acgggtccatt ttctatatct attgcaaac	1140
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acattccagt gtaattattg aggtcaaagc tagtaactta atagatgaca ggacagctg 3659

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<210> SEQ ID NO 68
<211> LENGTH: 2356
<212> TYPE: DNA
<213> ORGANISM: Fowlpox virus

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<400> SEQUENCE: 68

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ctgatatttc tgaatatttc tgaatatttc atgttactta cttactccta tcttagacga 180
taataaaaatt cgaggcgtaa tatgttttcc caaatatttg aaattcttat acgtatcggc 240
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attatatatg aagaaa 2356

<210> SEQ ID NO 69
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as HIVP5

<400> SEQUENCE: 69

tgtggcaag aagggc 16

<210> SEQ ID NO 70
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as HIVP6

<400> SEQUENCE: 70

ttggatcctt attgtgacga ggggtc 26

<210> SEQ ID NO 71
<211> LENGTH: 106
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVL17

<400> SEQUENCE: 71

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aatcatgggt gcgagagcgt cagtattaag cgggggagaa ttgat 106

<210> SEQ ID NO 72
<211> LENGTH: 104
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVL18

<400> SEQUENCE: 72

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ttgtactttg taatataatg atatataatt tcaactttatc tcaa 104

<210> SEQ ID NO 73
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVL19

<400> SEQUENCE: 73

ctgacacagg acacagcaat caggtcagcc aaaattacta atttttatct cgaggctgac 60
aggacccg 68

<210> SEQ ID NO 74
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVL20

<400> SEQUENCE: 74

gatccggggtc ctgtcgacct cgagataaaa attagtaatt ttggctgacc tgattgctgt 60
gtcctgtgtc ag 72

<210> SEQ ID NO 75
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as HIVP7

<400> SEQUENCE: 75

aagaaaatta taggac 16

<210> SEQ ID NO 76
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as HIVP8

<400> SEQUENCE: 76

ttggatccct aatcctcacc ctgt 24

<210> SEQ ID NO 77
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as HIVP37

<400> SEQUENCE: 77

aaaggatccc ccgggttaaa aatttaaagt gcaacc 36

<210> SEQ ID NO 78
<211> LENGTH: 3807
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32,
coding strand

<400> SEQUENCE: 78

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tattcttaaa cctaccaagc ctctactat cattatgaat aatctttttt ctctctgcac 180

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<210> SEQ ID NO 79

<211> LENGTH: 3808

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: DNA sequence of plasmid referred to as pHIV32,
template strand

<400> SEQUENCE: 79

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ataagaattt ggatggttcg gaggatgata gtaatactta ttagaaaaaa gagagacgtg 180
gtgagaagag aaacggaacc acccagcatg aggattacca agttaacaat gatgaaatat 240
aaatatatta agtgaagagg ttaacaggga gtatagagga ggaggtccag acttctagag 300
ccacagcaag cacaggcaca ggaatggtgg tagagaacaa ttatcatcgg gacattataa 360
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<210> SEQ ID NO 80

<211> LENGTH: 4291

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Nucleotide sequence of C3 locus of ALVAC in the plasmid, pVQH6CP3L, coding strand

<400> SEQUENCE: 80

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<210> SEQ ID NO 81

<211> LENGTH: 4291

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Nucleotide sequence of C3 locus of ALVAC in the plasmid, pVQH6CP3L, template strand

<400> SEQUENCE: 81

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<210> SEQ ID NO 82
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as VQPCR13

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<400> SEQUENCE: 82

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<210> SEQ ID NO 83
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as I3PCRCTL

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<400> SEQUENCE: 83

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<210> SEQ ID NO 84
<211> LENGTH: 77
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as CTLPCR

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<400> SEQUENCE: 84

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<210> SEQ ID NO 85

<211> LENGTH: 35

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as H6PCR1

<400> SEQUENCE: 85

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<210> SEQ ID NO 86

<211> LENGTH: 88

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as NCCPCR1

<400> SEQUENCE: 86

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<210> SEQ ID NO 87

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide referred to as NCC174A

<400> SEQUENCE: 87

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<210> SEQ ID NO 88

<211> LENGTH: 102

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<223> OTHER INFORMATION: Oligonucleotide referred to as NCC174B

<400> SEQUENCE: 88

ccacaaatca agaatatctt gtcttctgtg agaatgaatt agcccttcta aacctccttt 60

ttcttttaaa aagttagaaaa gatctacagc tgctttgtaa gt 102

<210> SEQ ID NO 89

<211> LENGTH: 54

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as NCCPCR2

<400> SEQUENCE: 89

ctgccaatca ggaaaatatc cttgtgtatg ataaatccac aaatcaagaa tatc 54

<210> SEQ ID NO 90

<211> LENGTH: 79

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as NCC291A

<400> SEQUENCE: 90

ggatattttc ctgattggca gaattacaca ccaggaccag gagtcagata cccattaacc 60
tttggttggt gctacaagc 79

<210> SEQ ID NO 91
<211> LENGTH: 79
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as NCC291B

<400> SEQUENCE: 91

gcttgtagca ccaaccaaag gttaatgggt atctgactcc tggctctggt gtgtaattct 60
gccaatcagg aaaatatcc 79

<210> SEQ ID NO 92
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as NCCPCR3

<400> SEQUENCE: 92

actactgaat tctcgagaaa aattatggta ctactgtgta gcaccaacc 49

<210> SEQ ID NO 93
<211> LENGTH: 801
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DNA sequence of the plasmid, p2-60-HIV.3,
coding strand

<400> SEQUENCE: 93

agtacaataa aaagtattaa ataaaaatc ttacttacga aaaaatgact aattagctat 60
aaaaacccgg gctgcagctc gaggatcctc tagattaaca atttttaaaa tattcaggat 120
gtaattctct agctacgtga tgaaatgcta atctagaatc aaatctccac tccatgatta 180
aacctaaata attgtacttt gtaatatata gatatatatt ttcactttat ctcatttgag 240
aataaaaatg tttttgttta accactgcat gatgtctaata taattaagct acaaatagtt 300
tcgttttcac cttgtctaata aactaatata ttaagcttct ttattctata cttaaaaagt 360
gaaaataaat acaaagggtc ttgagggttg tgttaaatg aaagcgagaa ataatacata 420
attatttcat tatcgcgata tccgttaagt ttgtatcgta atggtagggt ttccagtaac 480
acctcaagta cctttaagac caatgactta caaagcagct gtagatcttt ctcacttttt 540
aaaagaaaaa ggagggttag aagggttaata tcattctcaa cgaagacaag atattcttga 600
tttggtgatt tatcatcac aaggatattt tctgtattgg cagaattaca caccaggacc 660
aggagtcaga taccattata cctttggttg gtgctacaag ctagtacat aatttttctc 720
gaggaattct ttttattgat taactagtca aatgagtata tataaattgaa aaagtaaaat 780
ataaatcata taataatgaa a 801

<210> SEQ ID NO 94

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<211> LENGTH: 801
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DNA sequence of the plasmid, p2-60-HIV.3,
template strand

<400> SEQUENCE: 94

tcattgttatt ttccataatt tatttttatg aatgaatgct tttttactga ttaatcgata 60
tttttgggcc cgacgtcgag ctccctaggag atctaattgt taaaaatttt ataagtccta 120
cattaagaga tcgatgcact actttacgat tagatccttag ttttagagggtg aggtactaat 180
ttggatttat taacatgaaa cattatatta ctatatataa aagtgaataa gagtaaaactc 240
ttatttttac aaaaacaaat tgggtgacgta ctacagatta attaattcga tgtttatcaa 300
agcaaaagtg gaacagatta ttgattaatt aattcgaaga aataagatat gaatttttca 360
cttttattta tgtttccaag aactcccaac acaatttaac tttcgcctctt tattagtatt 420
taataaagta atagcgctat aggcaattca aacatagcat taccatccaa aaggtcattg 480
tggagttcat ggaaattctg gttactgaat gtttcgctga catctagaaa gagtgaaaaa 540
ttttcttttt cctccaaatc ttcccagatta agtaagagtt gcttctgttc tataagaact 600
aaacacctaa atagtatgtg ttcctataaa aggactaacc gtcttaattgt gtggctcctgg 660
tcctcagtct atgggtaatt ggaaaccaac cacgatgttc gatcatggta ttaaaaagag 720
ctccttaaga aaaataacta attgatcagt ttactcatat atattaactt tttcatttta 780
tatttagtat attattactt t 801

<210> SEQ ID NO 95
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Human immunodeficiency virus type 1

<400> SEQUENCE: 95

Cys Asn Lys Phe Tyr Glu Pro His Leu Glu Arg Ala Val His His Phe
1 5 10 15
Ala Leu Arg Ser Asp Phe Arg Trp Glu Met Pro
20 25

<210> SEQ ID NO 96
<211> LENGTH: 83
<212> TYPE: PRT
<213> ORGANISM: Human immunodeficiency virus type 1

<400> SEQUENCE: 96

Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
1 5 10 15
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
20 25 30
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
35 40 45
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
50 55 60
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
65 70 75 80
Leu Val Pro

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<210> SEQ ID NO 97
<211> LENGTH: 1615
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence of the ALVAC C6 locus in the plasmid, pC6L, coding strand

<400> SEQUENCE: 97

gagctcgcgg ccgcctatca aaagtcttaa tgagttaggt gtagatagta tagatattac 60
tacaaaaggta ttcataatttc ctatcaattc taaagtagat gatattaata actcaaagat 120
gatgatagta gataatagat acgctcatat aatgactgca aatttggacg gttcacattt 180
taatcatcac gcgttcataa gtttcaactg catagatcaa aatctcacta aaaagatagc 240
cgatgtattt gagagagatt ggacatctaa ctacgctaaa gaaattacag ttataaataa 300
tacataatgg attttgttat catcagttat atttaacata agtacaataa aaagtattaa 360
ataaaaatac ttacttacga aaaaatgact aattagctat aaaaaccggg gctgcagctc 420
gaggaattct ttttattgat taactagtca aatgagtata tataattgaa aaagtaaaat 480
ataaatcata taataatgaa acgaaatatc agtaatagac aggaactggc agattcttct 540
tctaatagaag taagtactgc taaatctcca aaattagata aaaatgatac agcaaataca 600
gcttcattca acgaattacc ttttaatttt ttcagacaca ccttattaca aactaactaa 660
gtcagatgat gagaaagtaa atataaattt aacttatggg tataatataa taaagattca 720
tgatattaat aatttactta acgatgttaa tagacttatt ccatcaacc cttcaaacct 780
ttctggatat tataaaatac cagttaatga tattaaaata gattgtttaa gagatgtaaa 840
taattatttg gaggtaaagg atataaaatt agtctatctt tcacatggaa atgaattacc 900
taatattaat aattatgata ggaatttttt aggatttaca gctgttatat gtatcaacaa 960
tacaggcaga tctatggtta tggtaaaaca ctgtaacggg aagcagcatt ctatggtaac 1020
tggectatgt ttaatagcca gatcatttta ctctataaac attttaccac aaataatagg 1080
atcctctaga tatttaatat tatatctaac aacaacaaaa aaatttaacg atgtatggcc 1140
agaagtattt tctactaata aagataaaga tagtctatct tatctacaag atatgaaaga 1200
agataatcat ttagtagtag ctactaatat ggaaagaaat gtatacaaaa acgtggaagc 1260
ttttatatta aatagcatat tactagaaga tttaaaatct agacttagta taacaaaaca 1320
gttaaatgcc aatatcgatt ctatatttca tcataacagt agtacattaa tcagtgatat 1380
actgaaacga tctacagact caactatgca aggaataagc aatatgcaa ttatgtctaa 1440
tattttaact ttagaactaa aacgttctac caatactaaa aataggatac gtgataggct 1500
gttaaaagct gcaataaata gtaaggatgt agaagaaata ctttgttcta taccttcgga 1560
ggaaagaact ttagaacaac ttaagtttaa tcaaacttgt atttatgaag gtacc 1615

<210> SEQ ID NO 98
<211> LENGTH: 1615
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence of the ALVAC C6 locus in the plasmid, pC6L, template strand

<400> SEQUENCE: 98

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ctcgagcgcc ggcggatagt tttcagaatt actcaatcca catctatcat atctataatg	60
atgtttccat aagtataaag gatagttaag atttcatcta ctataattat tgagtttcta	120
ctactatcat ctattatcta tgcgagtata ttactgacgt ttaaacctgc caagtgtaaa	180
attagtagtg cgcaagtatt caaagttgac gtatctagtt ttagagtgat ttttctatcg	240
gctacataaa ctctctctaa cctgtagatt gatgcgattt ctttaatgtc aatatttatt	300
atgtattacc taaaacaata gtagtcaata taaattgtat tcatgttatt tttcataatt	360
tatttttatg aatgaatgct tttttactga ttaatcgata tttttgggcc cgacgtcgag	420
ctccttaaga aaaataacta attgatcagt ttactcatat atattaactt tttcatttta	480
tatttagtat attattactt tgctttatag tcattatctg tccttgaccg tctaagaaga	540
agattacttc attcatgacg atttagaggt tttaatctat ttttactatg tcgtttatgt	600
cgaagtaagt tgcttaatgg aaaattaaaa aagtctgtgt ggaataatgt ttgattgatt	660
cagtctacta ctctttcatt tatattttaa ttgaataccc atattatatt atttctaagt	720
actataatta ttaaataaat tgctacaatt atctgaataa ggtagtggg gaagtttggga	780
aagacctata atattttatg gtcaattact ataattttat ctaacaaatt ctctacattt	840
attaataaac ctccattttc tatattttta tcagatagaa agtgtacctt tacttaatgg	900
attataatta ttaatactat ccttaaaaaa tcctaaatgt cgacaatata catagttgtt	960
atgtccgtct agataccaat accattttgt gacattgcc ttcgtcgtaa gataccattg	1020
accggataca aattatcggt ctagtaaaat gagatatttg taaaatgggtg tttattatcc	1080
taggagatct ataaattata atatagattg ttgttgtttt tttaaattgc tacataccgg	1140
tcttcataaa agatgattat ttctatttct atcagataga atagatgttc tatactttct	1200
tctattagta aatcatcatc gatgattata cctttcttta catatgtttt tgcaccttcg	1260
aaaaataat ttatcgata atgatcttct aaattttaga tctgaatcat attgttttgt	1320
caatttacgg ttatagctaa gatataaagt agtattgtca tcatgtaatt agtcaactata	1380
tgactttgct agatgtctga gttgatacgt tccttattcg ttatacgggt aatacagatt	1440
ataaaattga aatcttgatt ttgcaagatg gttatgattt ttatcctatg cactatccga	1500
caattttcga cgttatttat cattcctaca tcttctttat gaaacaagat atggaagcct	1560
cctttcttga aatcttggtg aattcaaatt agtttgaaca taaatacttc catgg	1615

<210> SEQ ID NO 99
 <211> LENGTH: 43
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide primer referred to as P1A

<400> SEQUENCE: 99

tttgtatcgt aatgattgag actgtaccag taaaattaaa gcc	43
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<210> SEQ ID NO 100
 <211> LENGTH: 66
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide primer referred to as P1B

<400> SEQUENCE: 100

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gggctgcagg aattctaatac aattaaggcc caatttttga aattttccct tccttttcca 60

tctctg 66

<210> SEQ ID NO 101

<211> LENGTH: 53

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as P2A

<400> SEQUENCE: 101

acaaagtaca attatttagg tttaatcatg gcaatattcc aaagtagcat gac 53

<210> SEQ ID NO 102

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as P2B

<400> SEQUENCE: 102

atcatcctcg agaaaaatta ggtaagtccc cacctcaaca gatg 44

<210> SEQ ID NO 103

<211> LENGTH: 58

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as P3A

<400> SEQUENCE: 103

aaaatatata attacaatat aaaatgccac taacagaaga agcagagcta gaactggc 58

<210> SEQ ID NO 104

<211> LENGTH: 60

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as P3B

<400> SEQUENCE: 104

atcatctcta gactcgagga tccataaaaa ttatcctggt ttcagatttt taaatggctc 60

<210> SEQ ID NO 105

<211> LENGTH: 52

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as P2IVH

<400> SEQUENCE: 105

gtcatgctac ttttgaatat tgccatgatt aaacctaaat aattgtactt tg 52

<210> SEQ ID NO 106

<211> LENGTH: 56

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Oligonucleotide primer referred to as IVHP1

<400> SEQUENCE: 106

tttaatttta ctggtacagt ctcaatcatt acgatacaaa cttaacggat atcgcg 56

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<210> SEQ ID NO 107
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as EPS42K

<400> SEQUENCE: 107
aattgattag aattcctgca gcccggtca aaaaaatata aatg 44

<210> SEQ ID NO 108
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as 42KP3B

<400> SEQUENCE: 108
ccagttctag ctctgcttct tctgttagtg gcattttata ttgtaattat atattttc 58

<210> SEQ ID NO 109
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as I3PCR1

<400> SEQUENCE: 109
atcatcgat ccaagcttac atcatgcagt gg 32

<210> SEQ ID NO 110
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide primer referred to as FIXPOL2

<400> SEQUENCE: 110
atcatcctcg agctattcaa ttaggttgta agtccccacc tcaac 45

<210> SEQ ID NO 111
<211> LENGTH: 1035
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DNA sequence of the plasmid, pC5POLT5A, coding strand

<400> SEQUENCE: 111
ttagaaatta tgcattttag atctttataa gcggccgtga ttaactagtc ataaaaaccc 60
gggatcgatt ctagactcga gctattcaat taggttgtaa gtccccacct caacagatgt 120
tgtctcagct cctctatttt tgttctatgc tgcctatttt ctaagtcaga tctacatac 180
aaatcatcca tgtattgata gataactatg tctggatttt gttttctaaa aggctctaag 240
atttttgtca tgctactttg gaatattgcc atgattaaac ctaaataatt gtactttgta 300
atataatgat atatattttc actttatctc atttgagaat aaaaatgttt ttgtttaacc 360
actgcatgat gtaagcttct ttattctata cttaaaaagt gaaaataaat acaaaggttc 420
ttgaggggtg tgtaaaattg aaagcgagaa ataatacataa attatttcat tatcgcgata 480
tccgttaagt ttgtatcgta atgattgaga ctgtaccagt aaaattaaag ccaggaatgg 540

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atggcccaaa agttaaacaa tggccattga cagaagaaaa aataaaagca ttagtagaaa    600
tttgtacaga gatggaaaag gaagggaaaaa tttcaaaaat tgggccttaa ttgattagaa    660
ttcctgcagc ccagggtcaaa aaaatataaa tgattcacca tctgatagaa aaaaaattta    720
ttgggaagaa tatgataata ttttgggatt tcaaaattga aaatatataa ttacaatata    780
aaatgccact aacagaagaa gcagagctag aactggcaga aaacagagag attctaaaag    840
aaccagtaca tggagtgtat tatgacccat caaaagactt aatagcagaa atacagaagc    900
aggggcaagg ccaatggaca tatcaaatTT atcaagagcc atttaaaaat ctgaaaacag    960
gataattttt atggatcctt tttatagcta attagtcacg tacctttgag agtaccactt   1020
cagctacctc ctttg                                     1035

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<210> SEQ ID NO 112
<211> LENGTH: 1035
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DNA sequence of the plasmid, pC5POLT5A,
        template strand

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<400> SEQUENCE: 112
aatctttaat acgtaaaatc tagaaatatt cgccggcact aattgatcag tatttttggg    60
ccctagctaa gatctgagct cgataagtta atccaacatt caggggtgga gttgtctaca   120
acagagtcga ggagataaaa acaagatacg acgggataaa gattcagtct aggatgtatg   180
tttagtaggt acataactat ctattgatac agacctaaaa caaaagattt tccgagattc   240
taaaaacagt acgatgaaac cttataacgg tactaatttg gatttattaa catgaaacat   300
tatattacta tatataaaag tgaaatagag taaactctta tttttacaaa aacaaattgg   360
tgacgtacta cattcgaaga aataagatat gaatttttca cttttattta tgtttccaag   420
aactcccaac acaatttaac ttctgctctt tattagtatt taataaagta atagcgctat   480
aggcaattca aacatagcat tactaactct gacatggtea ttttaatttc ggtccttacc   540
taccgggttt tcaatttgtt accggtaact gtcttctttt ttattttcgt aatcatcttt   600
aaacatgtct ctaccttttc cttccctttt aaagttttta acccggaatt aactaatctt   660
aaggacgtcg ggtccagttt ttttatattt actaagtggg agactatctt ttttttaaT   720
aacccttctt atactattat aaaaccctaa agttttaact tttatatatt aatgttatat   780
tttacggtga ttgtcttctt cgtctcgatc ttgaccgtct tttgtctctc taagattttc   840
ttggtcatgt acctcacata atactgggta gttttctgaa ttatcgtctt tatgtcttcg   900
tccccgttcc ggttacctgt atagtttaaa tagttctcgg taaattttta gacttttgtc   960
ctattaaaaa tacctaggaa aaatatcgat taatcagtgc atggaaactc tcatggtgaa  1020
gtcgatggag gaaac                                     1035

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<210> SEQ ID NO 113
<211> LENGTH: 60
<212> TYPE: PRT
<213> ORGANISM: Human immunodeficiency virus type 1

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<400> SEQUENCE: 113

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Thr Thr Leu Gly Trp Arg Leu Leu His Gln Arg Leu Glu Glu Ile Lys
1           5           10          15

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Thr Arg His Gln Gly Ile Glu Leu Asp Ser Gly Val Tyr Leu Asp Asp
 20 25 30
 Met Tyr Gln Tyr Ile Val Ile Asp Pro Asn Gln Lys Arg Phe Pro Glu
 35 40 45
 Leu Ile Lys Thr Met Ser Ser Gln Phe Ile Ala Met
 50 55 60

<210> SEQ ID NO 114
 <211> LENGTH: 49
 <212> TYPE: PRT
 <213> ORGANISM: Human immunodeficiency virus type 1
 <400> SEQUENCE: 114

Met Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro
 1 5 10 15
 Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val
 20 25 30
 Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly
 35 40 45
 Pro

<210> SEQ ID NO 115
 <211> LENGTH: 59
 <212> TYPE: PRT
 <213> ORGANISM: Human immunodeficiency virus type 1
 <400> SEQUENCE: 115

Met Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu
 1 5 10 15
 Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp
 20 25 30
 Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln
 35 40 45
 Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr
 50 55

<210> SEQ ID NO 116
 <211> LENGTH: 2049
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Nucleotide sequence of the ALVAC C5 locus of
 the plasmid, pNC5L-SP5, coding strand

<400> SEQUENCE: 116
 gaattgcggc cgctgaatgt taaatgttat actttggatg aagctataaa tatgcattgg 60
 aaaaataatc catttaaaga aaggattcaa atactacaaa acctaagcga taatatgtta 120
 actaagctta ttcttaacga cgctttaaat atacacaaat aaacataatt tttgtataac 180
 ctaacaaata actaaacat aaaaataata aaaggaaatg taatatcgta attattttac 240
 tcaggaatgg ggtaaataat ttatatcacg tgtatatcta tactgttatc gtatactctt 300
 tacaattact attacgaata tgcaagagat aataagatta cgtattttaag agaactctgt 360
 catgataatt gggtagcaca tagtgataaa tgctatttcg catcgttaca taaagtcagt 420
 tggaaagatg gatttgacag atgtaactta ataggtgcaa aaatgttaaa taacagcatt 480

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ctatcggaag ataggatacc agttatatta tacaaaaatc actggttga taaaacagat	540
tctgcaatat tcgtaaaaga tgaagattac tgcgaatttg taaactatga caataaaaag	600
ccatttatct caacgacatc gtgtaattct tccatgtttt atgtatgtgt ttcagatatt	660
atgagattac tataaacttt ttgtatactt atattccgta aactatatta atcatgaaga	720
aaatgaaaa gtatagaagc tgttcacgag cgggtgttga aaacaacaaa attatacatt	780
caagatggct tacatatagc tctgtgaggc tatcatggat aatgacaatg catctctaaa	840
taggtttttg gacaatggat tcgaccctaa cacggaatat ggtactctac aatctcctct	900
tgaaatggct gtaatgttca agaataccga ggctataaaa atcttgatga ggtatggagc	960
taaaacctgta gttactgaat gcacaacttc ttgtctgcat gatcgggtgt tgagagacga	1020
ctacaaaata gtgaaagatc tgttgaagaa taactatgta aacaatgttc tttacagcgg	1080
aggctttact cctttgtgtt tggcagctta ccttaacaaa gttaatttgg ttaaacttct	1140
attggctcat tcggcgagtg tagatatctt aaacacggat cggttaactc ctctacatat	1200
agccgtatca aataaaaatt taacaatggt taaacttcta ttgaacaaag gtgctgatac	1260
tgacttgctg gataacatgg gacgtactcc tttaatgac gctgtacaat ctggaaatat	1320
tgaaatatgt agcacactac ttaaaaaaaa taaaatgtcc agaactggga aaaattgatc	1380
ttgccagctg taattcatgg tagaaaagaa gtgctcaggc tacttttcaa caaaggagca	1440
gatgtaaact acatctttga aagaaatgga aaatcatata ctgttttga attgattaaa	1500
gaaagtact ctgagacaca aaagaggtag ctgaagtggc actctcaaag gtacgtgact	1560
aattagctat aaaaaggatc cgggtaccctc gagtctagaa tcgatcccg gtttttatga	1620
ctagttaatc acggccgctt ataaagatct aaaatgcata atttctaat aatgaaaaaa	1680
aagtacatca tgagcaacgc gttagtatat tttacaatgg agattaacgc tctataccgt	1740
tctatgttta ttgattcaga tgatgtttta gaaaagaaag ttattgaata tgaaaacttt	1800
aatgaagatg aagatgacga cgatgattat tgttgtaaat ctgttttaga tgaagaagat	1860
gacgcgctaa agtatactat ggttacaaag tataagtcta tactactaat ggcgacttgt	1920
gcaagaaggt atagtatagt gaaaatgttg ttagattatg attatgaaaa accaaataaa	1980
tcagatccat atctaaaggt atctccttgg cacataatct catctattcc tagtttagaa	2040
tacctgcag	2049

<210> SEQ ID NO 117

<211> LENGTH: 2049

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: DNA sequence of the ALVAC C5 locus in the plasmid, pCN5L-SP5, template strand

<400> SEQUENCE: 117

cttaacgccg gcgacttaca atttacaata tgaacacctac ttcgatattt atacgtaacc	60
tttttattag gtaaatttct ttcctaagtt tatgatgttt tggattcgct attatacaat	120
tgattcgaat aagaattgct gcgaaattta tatgtgttta tttgtattaa aaacatattg	180
gattgtttat tgattttgta tttttattat tttcctttac attatagcat taataaaatg	240
agtccctacc ccaatttata aatatagtcg acatatagat atgacaatag catatgagaa	300
atgttaatga taatgcttat acgttctcta ttattctaata gcataaattc tcttagaaca	360

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gtactattaa cccatgctgt atcactatctt acgataaagc gtagcaatgt atttcagtca 420
acctttctac ctaaactgtc tacattgaat tatccacgtt tttacaatctt attgtcgtaa 480
gatagccttc taccctatgg tcaatataat atgttttttag tgaccaacct attttgtcta 540
agacgttata agcattttct acttctaatac acgcttaaac atttgatact gttatttttc 600
ggtaaataga gttgctgtag cacattaaga aggtacaaaa tacatacaca aagtctataa 660
tactctaata atatttgaaa aacatatgaa tataaggcat ttgatataat tagtacttct 720
tttacttttt catatcttcg acaagtgtc gccacaact tttgttgtt taatatgtaa 780
gtttaccga atgtatatgc agacactccg atagtaccta ttactgttac gtagagattt 840
atccaaaaac ctgttaccta agctgggatt gtgccttata ccatgagatg ttagaggaga 900
actttaccga cattacaagt tcttatggct ccgatatctt tagaactact ccatacctcg 960
atttggacat caatgactta cgtgttgaag aacagacgta ctacgccaca actctctgct 1020
gatgttttat cactttctag acaacttctt attgatacat ttgttacaag aaatgtcgcc 1080
tccgaaatga ggaaacacaa accgtcgaat ggaattgttt caattaaacc aatttgaaga 1140
taaccgagta agccgcctac atctataaag tttgtgccta gccaatgag gagatgtata 1200
tcggcatagt ttatttttaa attgttacca atttgaagat aacttgtttc cagcactatg 1260
actgaacgac ctattgtacc ctgcatgagg aaattactag cgacatgtta gacctttata 1320
actttataca tcgtgtgatg aatttttttt attttacagg tcttgaccct ttttaactag 1380
aacggtcgac attaagtacc atcttttctt cagcagtcct atgaaaagtt gtttcctcgt 1440
ctacatttga ttagaaaact ttctttacct tttagtatat gacaaaacct taactaattt 1500
ctttcaatga gactctgtgt tttctccatc gacttcacca tgagagtctc catgcactga 1560
ttaatcgata tttttctag gccatgggag ctcagatctt agctagggcc caaaaatact 1620
gatcaattag tgccggcgaa tattttctaga ttttacgtat taaagattta ttactttttt 1680
ttcatgtagt actcgttgcg caatcatata aaatgttacc tctaattgcg agatatggca 1740
agatacaaat aactaagtct actacaaaat cttttctttc aataacttat acttttgaaa 1800
ttactcttac ttctactgct gctactaata acaacattta gacaaaatct acttcttcta 1860
ctgcgcgatt tcatatgata ccaatgttct atattcagat atgatgatta ccgctgaaca 1920
cgttcttcca tatcatatca cttttacaac aatctaatac taactacttt tggtttattt 1980
agtctaggta tagatttcca tagaggaaac gtgtattaaa gtagataagg atcaaatctt 2040
atggacgtc 2049

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<210> SEQ ID NO 118

<211> LENGTH: 34

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Peptide referred to as CLTB-36, which is a small portion of the HIV1 gp120 envelope glycoprotein, the V3 loop.

<400> SEQUENCE: 118

Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Asn
1 5 10 15

Lys Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr
20 25 30

-continued

Lys Asn

<210> SEQ ID NO 119
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic peptide representing the HIV MN
gp120 V3 loop

<400> SEQUENCE: 119

Cys Asn Lys Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala Phe Tyr
1 5 10 15

Thr Thr Lys Asn Ile Ile Gly Thr Ile Cys
20 25

<210> SEQ ID NO 120
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic peptide representing HIV MN gp120
V3 loop

<400> SEQUENCE: 120

Cys Asn Lys Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala Phe Tyr
1 5 10 15

Thr Thr Lys Asn Ile Ile Gly Thr Ile Cys
20 25

<210> SEQ ID NO 121
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer referred to as HIVP72

<400> SEQUENCE: 121

ttattaccat tccaagtact att 23

<210> SEQ ID NO 122
<211> LENGTH: 109
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer referred to as HIVP74

<400> SEQUENCE: 122

tctgtacaaa ttaattgtac aagacccaac tacgagctcg acaaatgggc ccatatagga 60

ccaggagag aattggataa gtgggcgaat ataataggaa ctataagac 109

<210> SEQ ID NO 123
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVMN6

<400> SEQUENCE: 123

gggttattaa tgatctgtag 20

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<210> SEQ ID NO 124
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIV3B2

<400> SEQUENCE: 124
gaattacagt agaagaattc ccctccacaa ttaaaac 37

<210> SEQ ID NO 125
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIV3B1

<400> SEQUENCE: 125
gttttaattg tggaggggaa ttcttctact gtaattc 37

<210> SEQ ID NO 126
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVMN4

<400> SEQUENCE: 126
atcatcgagc tcctatcgct gctc 24

<210> SEQ ID NO 127
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVMN5

<400> SEQUENCE: 127
atcatcgagc tctgttcctt gggttcttag 30

<210> SEQ ID NO 128
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVMN3P

<400> SEQUENCE: 128
atcatctcta gaataaaaat tatagcaaag ccttttccaa gcc 43

<210> SEQ ID NO 129
<211> LENGTH: 87
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVTM1

<400> SEQUENCE: 129
ttattcataa tgatagtagg aggcttgga ggtttaagaa tagtttttgc tgtactctct 60
gtagtgaata gagttaggca gggataa 87

<210> SEQ ID NO 130
<211> LENGTH: 87

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVTM2

<400> SEQUENCE: 130

ttatccctgc ctaactctat tcactacaga gactacagca aaaactattc ttaaacctac      60
caagcctcct actatcatta tgaataa                                           87

<210> SEQ ID NO 131
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVTM3

<400> SEQUENCE: 131

atcatctcta gaataaaaaat tatccctgcc taactctatt cac                        43

<210> SEQ ID NO 132
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide referred to as HIVMN18

<400> SEQUENCE: 132

gcctcctact atcattatga ataatctttt ttctctctg                             39

<210> SEQ ID NO 133
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer referred to as HIVP69

<400> SEQUENCE: 133

tgatagtacc agctataggt tgat                                             24

<210> SEQ ID NO 134
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer referred to as HIVP75

<400> SEQUENCE: 134

ttgtcgagc tcgtagttgg gtcttgtaga att                                    33

<210> SEQ ID NO 135
<211> LENGTH: 2020
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DNA sequence of the H6-promoted HIV1 gp120 +
      TM (with ELDKWA epitopes) gene between C5 flanking arms, coding
      strand

<400> SEQUENCE: 135

agaaagttac tctgagacac aaaagaggta gctgaagtgg tactctcaaa ggtacgtgac      60
taattagcta taaaaaggat cggggttaat taattagtca tcaggcaggg cgagaacgag      120
actatctgct cgtaattaa ttagagcttc tttattctat acttaaaaaa tgaaaataaa      180

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tacaaagggt cttgagggtt gtgttaaatt gaaagcgaga aataatcata aattatttca	240
ttatcgcgat atgcgttaag tttgtatcgt atatgaaaga gcagaagaca gtggcaatga	300
gagtgaagga gaaatatcag cacttgtgga gatgggggtg gagatggggc accatgctcc	360
ttgggatgtt gatgatctgt agtgctacag aaaaattgtg ggtcacagtc tattatgggg	420
tacctgtgtg gaaagaagca accaccactc tttttgtgc atcagatgct aaagcatatg	480
atacagaggt acataatgtt tgggccacac atgcctgtgt acccacagac cccaaccac	540
aagaagtaga attggtaaat gtgacagaaa attttaacat gtggaaaaat aacatggtag	600
aacagatgca tgaggatata atcagtttat gggatcaaag cctaaagcca tgtgtaaaat	660
taaccccact ctgtgttact ttaaattgca ctgatttgag gaatactact aataccaata	720
atagtactgc taataacaat agtaatagcg agggaacaat aaagggagga gaaatgaaaa	780
actgctcttt caatatcacc acaagcataa gagataagat gcagaaagaa tatgcacttc	840
tttataaact tgatatagta tcaataaata atgatatgac cagctatagg ttgataagtt	900
gtaatacctc agtcattaca caagcttgtc caaagatata ctttgagcca attcccatat	960
actattgtgc cccggctggt tttgcgattc taaagtgtaa cgataaaaag ttcagtggaa	1020
aaggatcatg taaaaatgtc agcacagtac aatgtacaca tggaattagg ccagtagtat	1080
caactcaact gctgttaaat ggcagtctag cagaagaaga ggtagtaatt agatctgaga	1140
atttcaatga taatgctaaa accatcatag tacatctgaa tgaatctgta caaattaatt	1200
gtacaagacc caactacgag ctcgacaaat gggcccatat aggaccaggg agagaattgg	1260
ataagtgggc gaataataa ggaactataa gacaagcaca ttgtaacatt agtagagcaa	1320
aatggaatga cactttaaga cagatagtta gcaaattaaa agaacaattt aagaataaaa	1380
caatagtctt taatcaatcc tcaggagggg acccagaaat tgtaatgcac agttttaatt	1440
gtggagggga attcttctac tgtaattcat caccactgtt taatagtact tggaatggta	1500
ataaactttg gaataatact acagggtcaa ataacaatat cacacttcaa tgcaaaataa	1560
aacaaattat aaacatgtgg caggaagtag gaaaagcaat atatgcccct ccatttgaag	1620
gacaaattag atgttcatca aatattacag ggctactatt aacaagagat ggtggtaagg	1680
acacggacac gaacgacacc gagatcttca gacctggagg aggagatatg agggacaatt	1740
ggagaagtga attatataaa tataaagtag taacaattga accattagga gtagcaccca	1800
ccaaggcaaa gagaagagtg gtgcagagag aaaaaagatt attcataatg atagtaggag	1860
gcttggtagg tttaagaata gtttttgctg tactctctgt agtgaataga gttaggcagg	1920
gataattttt attctagaat cgatcccggt tttttatgac tagttaatca cggccgtta	1980
taaagatcta aaatgcataa tttctaaata atgaaaaaaa	2020

<210> SEQ ID NO 136

<211> LENGTH: 2020

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: DNA sequence of the H6-promoted HIV1 gp120 +
 TM (with ELDKWA epitopes) gene between C5 flanking arms, template
 strand

<400> SEQUENCE: 136

tctttcaatg agactctgtg ttttctccat cgacttcacc atgagagttt ccatgcactg	60
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attaatcgat atttttcccta ggccaatta attaatcagt agtccgtccc gctcttgctc 120
tgatagacga gcaattaatt aatctcgaag aaataagata tgaatttttc acttttatTT 180
atgtttccaa gaactcccaa cacaatttaa ctttcgctct ttattagtat ttaataaagt 240
aatagcgcta tacgcaattc aaacatagca tatactttct cgtcttctgt caccgttact 300
ctcacttcct ctttatagtc gtgaacacct ctacccccac ctctaccccg tggtagcagg 360
aacctacaa ctactagaca tcacgatgtc tttttaacac ccagtgtcag ataatacccc 420
atggacacac ctttcttcgt tgggtggtgag ataaaacacg tagtctacga tttcgtatac 480
tatgtctcca tgtattacaa acccggtgtg tacggacaca tgggtgtctg gggttgggtg 540
ttcttcatct taaccattta cactgtcttt taaaattgta caccttttta ttgtaccatc 600
ttgtctacgt actcctatat tagtcaaata ccctagtttc ggatttcggg acacatttta 660
attgggggtga gacacaatga aatttaacgt gactaaactc cttatgatga ttatggttat 720
tatcatgacg attattgtta tcattatcgc tcccttgta tttccctcct ctttactttt 780
tgacgagaaa gttatagtgg tgttcgtatt ctctattcta cgtctttctt atacgtgaag 840
aaatatttga actatatcat agttatttat tactatcatg gtcgatatcc aactattcaa 900
cattatggag tcagtaatgt gttcgaacag gtttctatag gaaactcggg taagggtatg 960
tgataacacg gggccgacca aaacgctaag atttcacatt gctatttttc aagtcacctt 1020
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gttgagttga cgacaattta ccgtcagatc gtcttcttct ccatcattaa tctagactct 1140
taaaagtact attacgattt tggtagtata atgtagactt acttagacat gtttaattaa 1200
catgttctcg gttgatgctc gagctgttta cccgggtata tcttggtccc tctcttaacc 1260
tattcacccg cttatattat ccttgatatt ctgttcgtgt aacattgtaa tcatctcggt 1320
ttaccttact gtgaaattct gtctatcaat cgtttaattt tcttggtaaa ttcttatttt 1380
gttatcagaa attagttagg agtctctccc tgggtcttta acattacgtg tcaaaattaa 1440
cacctccctc taagaagatg acattaagta gtggtgacaa attatcatga acctaccat 1500
tattatgaac cttattatga tgteccagtt tattgttata gtgtgaagtt acgttttatt 1560
ttgtttaata tttgtacacc gtccctcatc cttttcgta tatacgggga gggtaacttc 1620
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tgtgctgtgt cttgctgtgg ctctagaagt ctggacctcc tcctctatac tcctgttaa 1740
cctcttctact taatatattt atatttcac atgtttaact tggtaactct catcgtgggt 1800
ggttccggtt ctcttctcac cacgtctctc ttttttctaa taagtattac tatcatctc 1860
cgaaccatcc aaattcttat caaaaacgac atgagagaca tcacttatct caatccgtcc 1920
ctattaaaaa taagatctta gctagggccc aaaaatactg atcaattagt gccggcgaat 1980
atttctagat tttacgtatt aaagatttat tacttttttt 2020

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<210> SEQ ID NO 137

<211> LENGTH: 551

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: HIV1 gp120 + TM (with ELDKWA epitopes)
expressed by vCP1307-infected cells

Met 1	Lys	Glu	Gln	Lys 5	Thr	Val	Ala	Met	Arg 10	Val	Lys	Glu	Lys	Tyr 15	Gln
His	Leu	Trp	Arg 20	Trp	Gly	Trp	Arg	Trp 25	Gly	Thr	Met	Leu	Leu 30	Gly	Met
Leu	Met	Ile 35	Cys	Ser	Ala	Thr	Glu 40	Lys	Leu	Trp	Val 45	Thr	Val	Tyr	Tyr
Gly	Val 50	Pro	Val	Trp	Lys 55	Glu	Ala	Thr	Thr	Thr	Leu 60	Phe	Cys	Ala	Ser
Asp 65	Ala	Lys	Ala	Tyr 70	Asp	Thr	Glu	Val	His	Asn 75	Val	Trp	Ala	Thr	His
Ala	Cys	Val	Pro	Thr 85	Asp	Pro	Asn	Pro	Gln 90	Glu	Val	Glu	Leu	Val 95	Asn
Val	Thr	Glu	Asn 100	Phe	Asn	Met	Trp	Lys 105	Asn	Asn	Met	Val	Glu 110	Gln	Met
His	Glu	Asp 115	Ile	Ile	Ser	Leu	Trp 120	Asp	Gln	Ser	Leu	Lys 125	Pro	Cys	Val
Lys	Leu 130	Thr	Pro	Leu	Cys	Val 135	Thr	Leu	Asn	Cys	Thr 140	Asp	Leu	Arg	Asn
Thr 145	Thr	Asn	Thr	Asn 150	Asn	Ser	Thr	Ala	Asn	Asn 155	Asn	Ser	Asn	Ser	Glu 160
Gly	Thr	Ile	Lys 165	Gly	Gly	Glu	Met	Lys 170	Asn	Cys	Ser	Phe	Asn	Ile 175	Thr
Thr	Ser	Ile	Arg 180	Asp	Lys	Met	Gln	Lys 185	Glu	Tyr	Ala	Leu	Leu 190	Tyr	Lys
Leu	Asp	Ile 195	Val	Ser	Ile	Asn	Asn 200	Asp	Ser	Thr	Ser	Tyr 205	Arg	Leu	Ile
Ser	Cys 210	Asn	Thr	Ser	Val	Ile 215	Thr	Gln	Ala	Cys	Pro 220	Lys	Ile	Ser	Phe
Glu 225	Pro	Ile	Pro	Ile	His 230	Tyr	Cys	Ala	Pro	Ala 235	Gly	Phe	Ala	Ile	Leu 240
Lys	Cys	Asn	Asp 245	Lys	Lys	Phe	Ser	Gly 250	Lys	Gly	Ser	Cys	Lys	Asn 255	Val
Ser	Thr	Val	Gln 260	Cys	Thr	His	Gly	Ile 265	Arg	Pro	Val	Val 270	Ser	Thr	Gln
Leu	Leu	Leu 275	Asn	Gly	Ser	Leu	Ala 280	Glu	Glu	Glu	Val 285	Val	Ile	Arg	Ser
Glu 290	Asn	Phe	Asn	Asp	Asn	Ala 295	Lys	Thr	Ile	Ile	Val 300	His	Leu	Asn	Glu
Ser 305	Val	Gln	Ile	Asn 310	Cys	Thr	Arg	Pro	Asn	Tyr 315	Glu	Leu	Asp	Lys	Trp 320
Ala	His	Ile	Gly 325	Pro	Gly	Arg	Glu	Leu	Asp 330	Lys	Trp	Ala	Asn	Ile	Ile 335
Gly	Thr	Ile	Arg 340	Gln	Ala	His	Cys	Asn 345	Ile	Ser	Arg	Ala	Lys 350	Trp	Asn
Asp	Thr	Leu 355	Arg	Gln	Ile	Val	Ser 360	Lys	Leu	Lys	Glu	Gln 365	Phe	Lys	Asn
Lys 370	Thr	Ile	Val	Phe	Asn 375	Gln	Ser	Ser	Gly	Gly	Asp 380	Pro	Glu	Ile	Val
Met 385	His	Ser	Phe	Asn 390	Cys	Gly	Gly	Glu	Phe	Phe 395	Tyr	Cys	Asn	Ser	Ser 400

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Pro Leu Phe Asn Ser Thr Trp Asn Gly Asn Asn Thr Trp Asn Asn Thr
 405 410 415

Thr Gly Ser Asn Asn Asn Ile Thr Leu Gln Cys Lys Ile Lys Gln Ile
 420 425 430

Ile Asn Met Trp Gln Glu Val Gly Lys Ala Ile Tyr Ala Pro Pro Ile
 435 440 445

Glu Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr
 450 455 460

Arg Asp Gly Gly Lys Asp Thr Asp Thr Asn Asp Thr Glu Ile Phe Arg
 465 470 475 480

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
 485 490 495

Tyr Lys Val Val Thr Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
 500 505 510

Lys Arg Arg Val Val Gln Arg Glu Lys Arg Leu Phe Ile Met Ile Val
 515 520 525

Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val Val
 530 535 540

Asn Arg Val Arg Gln Gly Asn
 545 550

<210> SEQ ID NO 138

<211> LENGTH: 2028

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Nucleotide sequence of H6-promoted HIV1 gp120
 + TM (with ELDKWA epitopes) gene between I4L flanking arms,
 coding strand.

<400> SEQUENCE: 138

tactttgtaa tataatgata tatattttca ctttatctca tttgagaata aaaagatcac	60
aaaaattaac taatcaggat cggggttaat taattagtca tcaggcaggg cgagaacgag	120
actatctgct cgtaaatata ttagagcttc tttattctat acttaaaaag tgaaaataaa	180
tacaaagggt cttgagggtt gtgttaaatt gaaagcgaga aataatcata aattatttca	240
ttatcgcat atgcgttaag tttgtatcgt atatgaaaga gcagaagaca gtggcaatga	300
gagtgaagga gaaatatcag cacttggtga gatgggggtg gagatggggc accatgctcc	360
ttgggatgtt gatgatctgt agtgctacag aaaaattgtg ggtcacagtc tattatgggg	420
tacotgtgtg gaaagaagca accaccactc tattttgtgc atcagatgct aaagcatatg	480
atacagaggt acataatgtt tgggccacac atgcctgtgt acccacagac cccaaccac	540
aagaagtaga attggtaaat gtgacagaaa attttaacat gtggaaaaat aacatggtag	600
aacagatgca tgaggatata atcagtttat gggatcaaag cctaaagcca tgtgtaaaat	660
taacccact ctgtgttact ttaaattgca ctgatttgag gaatactact aataccaata	720
atagtactgc taataacaat agtaatagcg aggaacaat aaaggaggga gaaatgaaaa	780
actgtctttt caatatcacc acaagcataa gagataagat gcagaaagaa tatgcacttc	840
tttataaact tgatatagta tcaataaata atgatatgac cagctatagg ttgataagtt	900
gtaatacctc agtcattaca caagcttgtc caaagatata ctttgagcca attccatac	960
actattgtgc cccggctggt ttgctgattc taaagtgtaa cgataaaaag ttcagtggaa	1020

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```

aaggatcatg taaaaatgtc agcacagtac aatgtacaca tggaattagg ccagtagtat 1080
caactcaact gctgttaaat ggcagtctag cagaagaaga ggtagtaatt agatctgaga 1140
atttcaatga taatgctaaa accatcatag tacatctgaa tgaatctgta caaattaatt 1200
gtacaagacc caactacgag ctgcacaaat gggcccatat aggaccaggg agagaattgg 1260
ataagtgggc gaataataa ggaactataa gacaagcaca ttgtaacatt agtagagcaa 1320
aatggaatga cactttaaga cagatagtta gcaaattaaa agaacaattt aagaataaaa 1380
caatagtctt taatcaatcc tcaggagggg acccagaaat tgtaatgcac agttttaatt 1440
gtggagggga attcttctac tgtaattcat caccactgtt taatagtact tggaatggta 1500
ataatacttg gaataatact acagggtcaa ataacaatat cacacttcaa tgcaaaataa 1560
aacaatttat aaacatgtgg caggaagtag gaaaagcaat atatgccctt cccattgaag 1620
gacaatttag atgttcacaa aatattacag ggctactatt aacaagagat ggtggtaagg 1680
acacggacac gaacgacacc gagatcttca gacctggagg aggagatatg agggacaatt 1740
ggagaagtga attatataaa tataaagtag taacaattga accattagga gtagcaccca 1800
ccaaggcaaa gagaagatgt gtgcagagag aaaaaagatt attcataatg atagtaggag 1860
gcttggtagg ttaagaata gtttttgctg tactctctgt agtgaataga gttaggcagg 1920
gataattttt attctagaat cgatcccggt agatcttagc taactgattt ttctgggaaa 1980
aaaattattt aacttttcat taatagggat ttgacgtatg tagcgtac 2028

```

<210> SEQ ID NO 139

<211> LENGTH: 2028

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Nucleotide sequence of H6-promoted HIV1 gp120
+ TM (with ELDKWA epitopes) gene between I4L flanking arms,
template strand

<400> SEQUENCE: 139

```

atgaaacatt atattactat atataaaagt gaaatagagt aaactcttat ttttctagt 60
tttttaattg attagtccca ggcccaatta attaatcagt agtccgtccc gctcttgctc 120
tgatagacga gcaattaatt aatctcgaag aaataagata tgaatttttc acttttat 180
atgtttccaa gaactcccaa cacaatttaa ctttcgctct ttattagtat ttaataaagt 240
aatagcgcta tacgcaatcc aaacatagca tatactttct cgtcttctgt caccgttact 300
ctcacttcct ctttatagtc gtgaacacct ctacccccac ctctaccccg tggtagcagg 360
aacctacaaa ctactagaca tcacgatgtc tttttaacac ccagtgtcag ataatacccc 420
atggacacac ctttctctgt tgggtgtgag ataaaacacg tagtctacga tttcgtatac 480
tatgtctcca tgtattacaa acccgggtgtg tacggacaca tgggtgtctg gggttgggtg 540
ttcttcatct taaccattta cactgtcttt taaaattgta caccttttta ttgtaccatc 600
ttgtctacgt actcctatat tagtcaaata ccttagtttc ggatttcggg acacatttta 660
attgggggtg gacacaatga aatttaacgt gactaaactc cttatgatga ttatggttat 720
tatcatgacg attattgtta tcattatcgc tcccttggtt tttccctcct ctttactttt 780
tgacgagaaa gttatagtgg tgttcgtatt ctctattceta cgtctttctt atacgtgaag 840
aatattttga actatatcat agttatttat tactatcatg gtcgatatcc aactattcaa 900

```

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```

cattatggag tcagtaatgt gttcgaacag gtttctatag gaaactcggg taagggtatg    960
tgataacacg gggccgacca aaacgctaag atttcacatt gctatTTTTc aagtcacctt    1020
ttcctagtag atttttacag tcgtgtcatg ttacatgtgt accttaatcc ggcatcata    1080
gttgagttga cgacaattta ccgtcagatc gtcttcttct ccatacattaa tctagactct    1140
taaagttact attacgattt tggtagtata atgtagactt acttagacat gtttaattaa    1200
catgttctgg gttgatgctc gagctgttta cccgggtata tcctgggcc tctcttaacc    1260
tattcacccg cttatattat ccttgatatt ctgttcgtgt aacattgtaa tcatctcgtt    1320
ttaccttact gtgaaattct gtctatcaat cgtttaattt tcttgtaaaa tctttatttt    1380
gttatcagaa attagttagg agtcctcccc tgggtcttta acattacgtg tcaaaattaa    1440
cacctccccc taagaagatg acattaagta gtggtgacaa attatcatga accttaccat    1500
tattatgaac cttattatga tgtcccagtt tattgttata gtgtgaagtt acgtttttatt    1560
ttgtttaata tttgtacacc gtccttcac cttttcgtta tatacgggga gggtaacttc    1620
ctgtttaate tacaagtagt ttataatgtc ccgatgataa ttgttctcta ccaccattcc    1680
tgtgcctgtg cttgtctgtg ctctagaagt ctggacctcc tcctctatac tcctgttaa    1740
cctcttcaact taatatattt atatttcac attgttaact tggtaatcct catcgtgggt    1800
ggttccggtt ctcttctcac cactctctc tttttctaa taagtattac tatcatcctc    1860
cgaaccatcc aaattcttat caaaaacgac atgagagaca tcacttatct caatccgtcc    1920
ctattaataa taagatctta gctagggccc tctagaatcg attgactaaa aagacccttt    1980
ttttaataaa ttgaaaagta attatcccta aactgcatac atcgcatg    2028

```

```

<210> SEQ ID NO 140
<211> LENGTH: 550
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HIV1 gp120 + TM (with ELDKWA epitopes)
        expressed by vP1313-infected cells

```

```

<400> SEQUENCE: 140

```

```

Met Lys Glu Gln Lys Thr Val Ala Met Arg Val Lys Glu Lys Tyr Gln
 1             5             10            15

His Leu Trp Arg Trp Gly Trp Arg Trp Gly Thr Met Leu Leu Gly Met
 20            25            30

Leu Met Ile Cys Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr
 35            40            45

Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser
 50            55            60

Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His
 65            70            75            80

Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val Glu Leu Val Asn
 85            90            95

Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met Val Glu Gln Met
100           105           110

His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val
115           120           125

Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr Asp Leu Arg Asn
130           135           140

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Thr	Thr	Asn	Thr	Asn	Asn	Ser	Thr	Ala	Asn	Asn	Asn	Ser	Asn	Ser	Glu
145					150					155					160
Gly	Thr	Ile	Lys	Gly	Gly	Glu	Met	Lys	Asn	Cys	Ser	Phe	Asn	Ile	Thr
			165						170					175	
Thr	Ser	Ile	Arg	Asp	Lys	Met	Gln	Lys	Glu	Tyr	Ala	Leu	Leu	Tyr	Lys
			180					185					190		
Leu	Asp	Ile	Val	Ser	Ile	Asn	Asn	Asp	Ser	Thr	Ser	Tyr	Arg	Leu	Ile
	195					200						205			
Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Ile	Ser	Phe
	210					215					220				
Glu	Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu
225					230					235					240
Lys	Cys	Asn	Asp	Lys	Lys	Phe	Ser	Gly	Lys	Gly	Ser	Cys	Lys	Asn	Val
			245						250					255	
Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln
			260					265					270		
Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser
	275					280						285			
Glu	Asn	Phe	Asn	Asp	Asn	Ala	Lys	Thr	Ile	Ile	Val	His	Leu	Asn	Glu
	290					295					300				
Ser	Val	Gln	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Tyr	Glu	Leu	Asp	Lys	Trp
305					310					315					320
Ala	His	Ile	Gly	Pro	Gly	Arg	Glu	Leu	Asp	Lys	Trp	Ala	Asn	Ile	Ile
			325					330						335	
Gly	Thr	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Ser	Arg	Ala	Lys	Trp	Asn
			340					345					350		
Asp	Thr	Leu	Arg	Gln	Ile	Val	Ser	Lys	Leu	Lys	Glu	Gln	Phe	Lys	Asn
	355						360					365			
Lys	Thr	Ile	Val	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val
	370					375					380				
Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Ser	Ser
385					390					395					400
Pro	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Asn	Asn	Thr	Trp	Asn	Asn	Thr
			405					410						415	
Thr	Gly	Ser	Asn	Asn	Ile	Thr	Leu	Gln	Cys	Lys	Ile	Lys	Gln	Ile	
			420				425					430			
Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Ile	Tyr	Ala	Pro	Pro	Ile
	435						440					445			
Glu	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr
	450					455					460				
Arg	Asp	Gly	Gly	Lys	Asp	Thr	Asp	Thr	Asn	Asp	Thr	Glu	Ile	Phe	Arg
465					470					475					480
Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys
				485				490						495	
Tyr	Lys	Val	Val	Thr	Ile	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	Ala
			500					505					510		
Lys	Arg	Arg	Val	Val	Gln	Arg	Glu	Lys	Arg	Leu	Phe	Ile	Met	Ile	Val
	515						520					525			
Gly	Gly	Leu	Val	Gly	Leu	Arg	Ile	Val	Phe	Ala	Val	Leu	Ser	Val	Val
	530					535					540				

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Asn Arg Val Arg Gln Gly
545 550

<210> SEQ ID NO 141
<211> LENGTH: 2060
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: H6-promoted HIV1 gp120 + TM (with ELDKWA epitopes) gene between A24R and K1L flanking arms, coding sequence

<400> SEQUENCE: 141

```

ataaaccatt agataaagtt gatctcaagc gctcttttct ggtgtaataa aaattaatta      60
attactcgag ggtaccggat cggggttaat taattagtca tcaggcaggg cgagaacgag      120
actatctgct cgtaataata ttagagcttc tttattctat acttaaaaag tgaataataa      180
tacaaagggt cttgagggtt gtgttaaatt gaaagcgaga aataatcata aattatttca      240
ttatcgcat atgcgttaag tttgtatcgt atatgaaaga gcagaagaca gtggcaatga      300
gagtgaagga gaaatatcag cacttggtga gatgggggtg gagatggggc accatgctcc      360
ttgggatgtt gatgatctgt agtgctacag aaaaattgtg ggtcacagtc tattatgggg      420
tacctgtgtg gaaagaagca accaccactc tttttgtgc atcagatgct aaagcatatg      480
atacagaggt acataatgtt tgggccacac atgcctgtgt acccacagac cccaaccac      540
aagaagtaga attggtaaat gtgacagaaa attttaacat gtggaaaaat aacatggtag      600
aacagatgca tgaggatata atcagtttat gggatcaaag cctaaagcca tgtgtaaaat      660
taacccact ctgtgttact ttaaattgca ctgatttgag gaatactact aataccaata      720
atagtactgc taataacaat agtaatagcg agggaacaat aaaggaggga gaaatgaaaa      780
actgctcttt caatatcacc acaagcataa gagataagat gcagaaagaa tatgcacttc      840
ttataaaact tgatatagta tcaataaata atgatagtac cagctatagg ttgataagtt      900
gtaataacct agtcattaca caagcttgtc caaagatata ctttgagcca attccatac      960
actattgtgc cccggctggt tttgcgattc taaagtgtaa cgataaaaag ttcagtggaa     1020
aaggatcatg taaaatgtc agcacagtac aatgtacaca tggaattagg ccagtagtat     1080
caactcaact gctgtttaat ggcagtctag cagaagaaga ggtagtaatt agatctgaga     1140
atttcaatga taatgctaaa accatcatag tacatctgaa tgaatctgta caaattaatt     1200
gtacaagacc caactacgag ctcgacaaat gggcccatat aggaccaggg agagaattgg     1260
ataagtgggc gaataataa ggaactataa gacaagcaca ttgtaacatt agtagagcaa     1320
aatggaatga cactttaaga cagatagtta gcaaattaaa agaacaattt aagaataaaa     1380
caatagtctt taatcaatcc tcaggagggg acccagaaat tgtaatgcac agttttaatt     1440
gtggagggga attctctac tgtaattcat caccactggt taatagtact tggaatggta     1500
ataaactctg gaataatact acagggtcaa ataacaatat cacacttcaa tgcaaaataa     1560
aacaatttat aaacatgtgg cagggaagtag gaaaagcaat atatgccctt ccattgaag     1620
gacaatttag atgttcatca aatattacag ggctactatt aacaagagat ggtggttaag     1680
acacggacac gaacgacacc gagatcttca gacctggagg aggagatatg agggacaatt     1740
ggagaagtga attatataaa tataaagtag taacaattga accattagga gtagcaccca     1800
ccaaggcaaa gagaagagtg gtgcagagag aaaaaagatt attcataatg atagtaggag     1860

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gcttggtagg tttaagaata gtttttgctg tactctctgt agtgaataga gttaggcagg 1920
gataatTTTT attcgagaat cgatcccggg aatcgattcg cgatagctga ttagtTTTTg 1980
ttaacaaaaa tgtgggagaa tctaattagt tttcttttac acaattgacg tacatgagtc 2040
tgagttcctt gtttttgcta 2060

```

<210> SEQ ID NO 142

<211> LENGTH: 2060

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: H6-promoted HIV1 gp120 + TM (with ELDKWA epitopes) gene between A24R and K1L flanking arms, template strand

<400> SEQUENCE: 142

```

tatttggtaa tctatttcaa ctagagttcg cgagaaaaga ccacattatt tttaattaat 60
taatgagctc ccattggccta ggcccaatta attaatcagt agtccgtccc gctcttgcctc 120
tgatagacga gcaattaatt aatctogaag aaataagata tgaatttttc acttttattt 180
atgtttccaa gaactcccaa cacaatttaa ctttcgctct ttattagtat ttaataaagt 240
aatagcgcta tacgcaattc aaacatagca tatactttct cgtcttctgt caccgttact 300
ctcacttcct ctttatagtc gtgaacacct ctacccccac ctctaccccg tggtagcagg 360
aaccctacaa ctactagaca tcacgatgtc tttttaacac ccagtgtcag ataatacccc 420
atggacacac ctttcttcgt tgggtgtgag ataaaacacg tagctacga ttctgtatac 480
tatgtctcca tgtattacaa acccggtgtg tacggacaca tgggtgtctg ggggtgggtg 540
ttcttcatct taaccattta cactgtcttt taaaattgta caccttttta ttgtaccatc 600
ttgtctacgt actcctatat tagtcaaata ccctagtttc ggatttcggt acacatttta 660
attgggggtga gacacaatga aatttaacgt gactaaactc cttatgatga ttatggttat 720
tatcatgacg attattgtta tcattatcgc tcccttgta tttccctcct ctttactttt 780
tgacgagaaa gttatagtgg tgttcgtatt ctctattcta cgtctttctt atacgtgaag 840
aaatatttga actatatcat agttatttat tactatcatg gtcgatatcc aactattcaa 900
cattatggag tcagtaattgt gttcgaacag gtttctatag gaaactcggg taagggtatg 960
tgataaacac gggccgacca aaacgctaag atttcacatt gctatttttc aagtcacctt 1020
ttcctagtag atttttacag tcgtgtcatg ttacatgtgt acctaatcc ggctcatcata 1080
gttgagttga cgacaattta ccgtcagatc gtcttcttct ccatcattaa tctagactct 1140
taaaagtact attacgattt tggtagtata atgtagactt acttagacat gtttaattaa 1200
catgttctgg gttgatgctc gagctgttta cccgggtata tcctggtecc tctcttaacc 1260
tattcacccg cttatattat ccttgatatt ctgttcgtgt aacattgtaa tcatctcggt 1320
ttaccttact gtgaaattct gtctatcaat cgtttaattt tcttgtaaaa ttcttatttt 1380
gttatcagaa attagttagg agtcctcccc tgggtcttta acattacgtg tcaaaattaa 1440
cacctccctc taagaagatg acattaagta gtggtgacaa attatcatga accttaccat 1500
tattatgaac cttattatga tgtcccagtt tattgttata gtgtgaagtt acgtttttatt 1560
ttgtttaata ttgtacacc gtccttcac cttttcgtta tatacgggga gggtaacttc 1620
ctgtttaatc tacaagtagt ttataatgtc ccgatgataa ttgttctcta ccaccattcc 1680
tgtgcctgtg cttgtgtggt ctctagaagt ctggacctcc tcctctatac tccctgttaa 1740

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cctcttcaact taatatattt atatttcac attgttaact tggtaaccc catcgtaggt 1800
ggttcggttt ctcttctcac cacgtctctc ttttttctaa taagtattac tatcctctc 1860
cgaaccatcc aaattcttat caaaaacgac atgagagaca tcacttatct caatccgtcc 1920
ctattaaaaa taagatctta gctagggccc ttagctaagc gctatcgact aatcaaaaac 1980
aattgttttt acaccctctt agattaatca aaaagaaatg tgttaactgc atgtactcag 2040
actcaaggaa caaaaacgat 2060

```

```

<210> SEQ ID NO 143
<211> LENGTH: 551
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HIV1 gp120 + TM (with ELDKWA epitopes)
        expressed by vP1319 infected cells

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```

<400> SEQUENCE: 143

```

```

Met Lys Glu Gln Lys Thr Val Ala Met Arg Val Lys Glu Lys Tyr Gln
 1             5             10             15
His Leu Trp Arg Trp Gly Trp Arg Trp Gly Thr Met Leu Leu Gly Met
          20             25             30
Leu Met Ile Cys Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr
          35             40             45
Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser
          50             55             60
Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His
 65             70             75             80
Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val Glu Leu Val Asn
          85             90             95
Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met Val Glu Gln Met
          100            105            110
His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val
          115            120            125
Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr Asp Leu Arg Asn
          130            135            140
Thr Thr Asn Thr Asn Asn Ser Thr Ala Asn Asn Asn Ser Asn Ser Glu
          145            150            155            160
Gly Thr Ile Lys Gly Gly Glu Met Lys Asn Cys Ser Phe Asn Ile Thr
          165            170            175
Thr Ser Ile Arg Asp Lys Met Gln Lys Glu Tyr Ala Leu Leu Tyr Lys
          180            185            190
Leu Asp Ile Val Ser Ile Asn Asn Asp Ser Thr Ser Tyr Arg Leu Ile
          195            200            205
Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Ile Ser Phe
          210            215            220
Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu
          225            230            235            240
Lys Cys Asn Asp Lys Lys Phe Ser Gly Lys Gly Ser Cys Lys Asn Val
          245            250            255
Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln
          260            265            270
Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser

```

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275	280	285
Glu Asn Phe Asn Asp Asn Ala Lys Thr Ile Ile Val His Leu Asn Glu 290 295 300		
Ser Val Gln Ile Asn Cys Thr Arg Pro Asn Tyr Glu Leu Asp Lys Trp 305 310 315 320		
Ala His Ile Gly Pro Gly Arg Glu Leu Asp Lys Trp Ala Asn Ile Ile 325 330 335		
Gly Thr Ile Arg Gln Ala His Cys Asn Ile Ser Arg Ala Lys Trp Asn 340 345 350		
Asp Thr Leu Arg Gln Ile Val Ser Lys Leu Lys Glu Gln Phe Lys Asn 355 360 365		
Lys Thr Ile Val Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val 370 375 380		
Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Ser 385 390 395 400		
Pro Leu Phe Asn Ser Thr Trp Asn Gly Asn Asn Thr Trp Asn Asn Thr 405 410 415		
Thr Gly Ser Asn Asn Asn Ile Thr Leu Gln Cys Lys Ile Lys Gln Ile 420 425 430		
Ile Asn Met Trp Gln Glu Val Gly Lys Ala Ile Tyr Ala Pro Pro Ile 435 440 445		
Glu Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr 450 455 460		
Arg Asp Gly Gly Lys Asp Thr Asp Thr Asn Asp Thr Glu Ile Phe Arg 465 470 475 480		
Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys 485 490 495		
Tyr Lys Val Val Thr Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala 500 505 510		
Lys Arg Arg Val Val Gln Arg Glu Lys Arg Leu Phe Ile Met Ile Val 515 520 525		
Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val Val 530 535 540		
Asn Arg Val Arg Gln Gly Asn 545 550		

<210> SEQ ID NO 144
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Primer referred to as HIVP72

<400> SEQUENCE: 144

ttattaccat tccaagtact att

23

<210> SEQ ID NO 145
 <211> LENGTH: 109
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Primer referred to as HIVP74

<400> SEQUENCE: 145

tctgtacaaa ttaattgtac aagacccaac tacgagctcg acaaatgggc ccatatagga

60

-continued

ccagggagag aattggataa gtggcgcaat ataataggaa ctataagac 109

<210> SEQ ID NO 146
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide referred to as HIVMN6

<400> SEQUENCE: 146

gggttattaa tgatctgtag 20

<210> SEQ ID NO 147
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Human immunodeficiency virus type 1

<400> SEQUENCE: 147

Glu Leu Asp Lys Trp Ala
 1 5

<210> SEQ ID NO 148
 <211> LENGTH: 4
 <212> TYPE: PRT
 <213> ORGANISM: Human immunodeficiency virus type 1

<400> SEQUENCE: 148

Leu Asp Lys Trp
 1

<210> SEQ ID NO 149
 <211> LENGTH: 5
 <212> TYPE: PRT
 <213> ORGANISM: Newcastle disease virus

<400> SEQUENCE: 149

Arg Arg Gln Arg Arg
 1 5

1-35. (canceled)

36. A protein having an amino acid sequence comprising the amino acid sequence of HIV1 gp120, wherein the amino acid sequence of the gp120 is modified so as to contain an epitope not naturally occurring in HIV1 gp120.

37. The protein of claim **36**, wherein the epitope is a B-cell epitope.

38. The protein of claim **36**, wherein the amino acid sequence of the gp120 is modified in the V3 loop so as to contain the epitope.

39. The protein of claim **38**, wherein the epitope is a B-cell epitope.

40. The protein of claim **38**, wherein the epitope is ELDKWA or LDKW.

41. The protein of claim **36**, wherein the amino acid sequence of the gp120 is modified to contain at least one of HIV1gag(+ pro) (IIIB), gp120(MN) (+ transmembrane), nef (BRU)CTL, pol(IIIB)CTL, and ELDKWA or LDKW epitopes.

42. The protein of claim **41**, wherein the amino acid sequence of the gp120 is modified in the V3 loop to contain the epitope.

43. The protein of claim **38**, comprising the amino acid sequence identified as SEQ ID NO: 137, SEQ ID NO: 140 or SEQ ID NO: 143.

44. The protein having the amino acid sequence identified as SEQ ID NO: 137, SEQ ID NO: 140 or SEQ ID NO: 143.

45. A nucleic acid molecule comprising a nucleic acid sequence which encodes the protein of claim **36**.

46. A nucleic acid molecule comprising a nucleic acid sequence which encodes the protein of claim **37**.

47. A nucleic acid molecule comprising a nucleic acid sequence which encodes the protein of claim **38**.

48. A nucleic acid molecule comprising a nucleic acid sequence which encodes the protein of claim **39**.

49. A nucleic acid molecule comprising a nucleic acid sequence which encodes the protein of claim **40**.

50. A nucleic acid molecule comprising a nucleic acid sequence which encodes the protein of claim **41**.

51. A nucleic acid molecule comprising a nucleic acid sequence which encodes the protein of claim **42**.

52. A nucleic acid molecule comprising the nucleic acid sequence which encodes the amino acid sequence identified as SEQ ID NO: 137, SEQ ID NO: 140 or SEQ ID NO: 143.

53. The nucleic acid molecule of claim **52** selected from the group consisting of the nucleic acid molecules identified as SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 139, SEQ ID NO: 141 and SEQ ID NO: 142.

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