

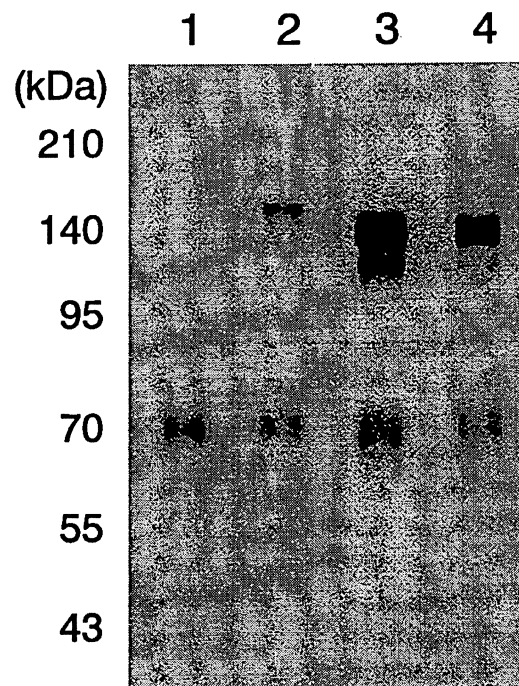
Fig.1

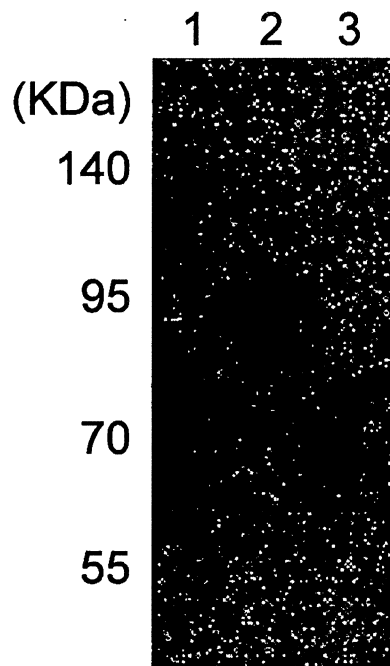
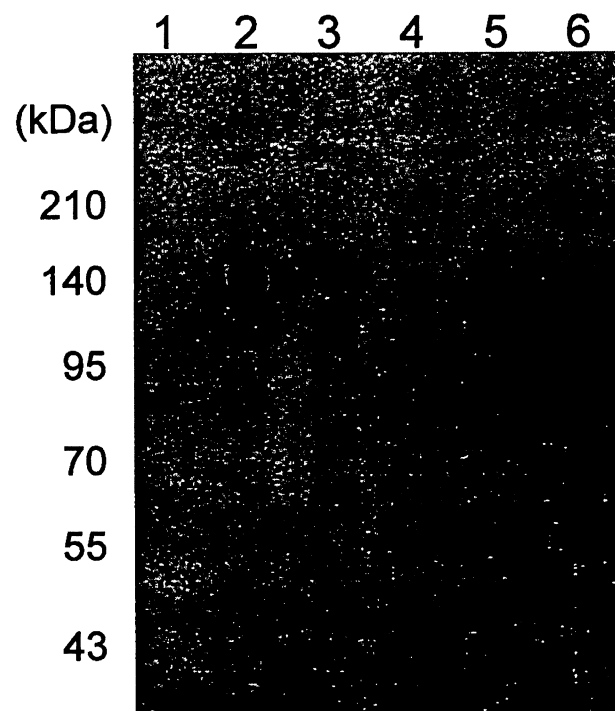
Fig.2(A)**Fig.2(B)**

Fig.3

(A)



(B)

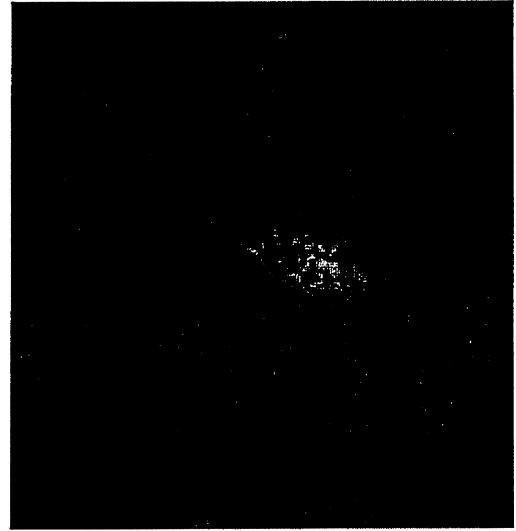


Fig.4(A)

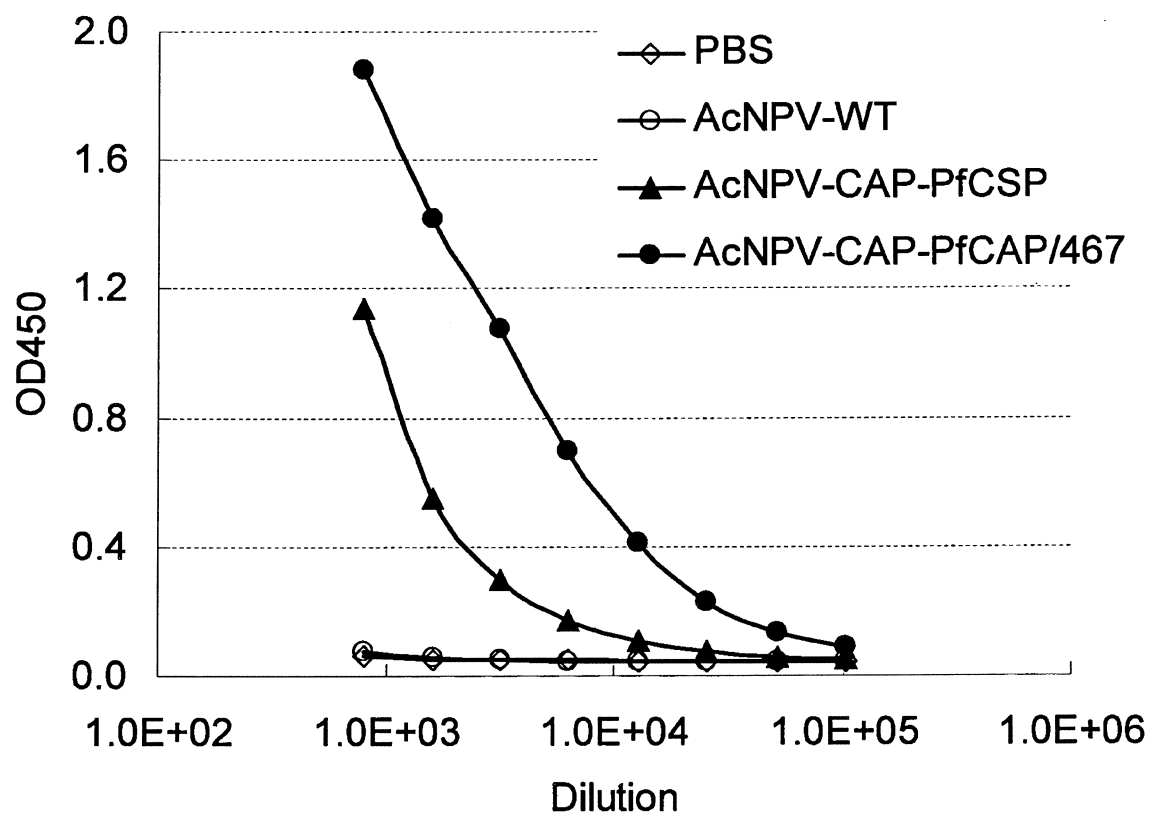


Fig.4(B)

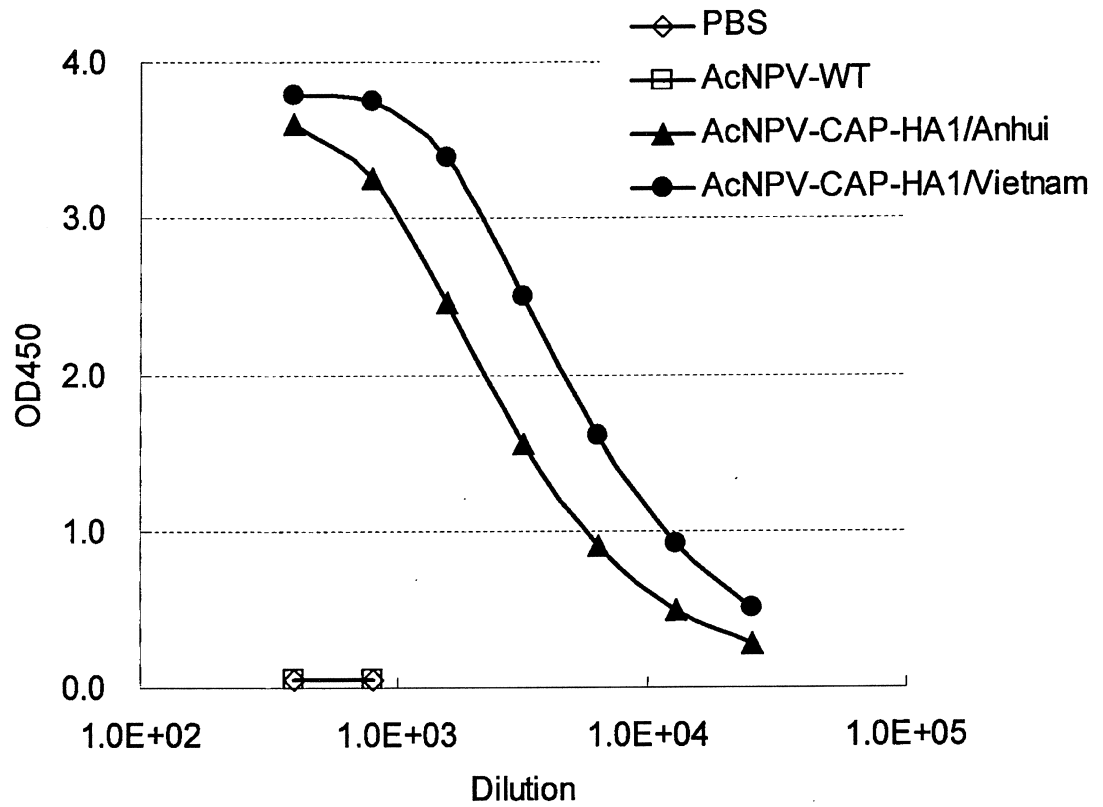


Fig.5

No.	Virus Name	Mammalian Cell Promoter	Viral Promoter	Antigen ORF	ORF size (a.a.)	Fusion Protein	ORF size (a.a.)	Antigen + Membran protein (a.a.)	Total ORF size (a.a.)
1	CAP-HA1/Anhul	CAG	Polyhedrin	Anhul (17-345)	329	gp64 (21-512)	492	821	847
2	CAP-HA1/Anhul/272	CAG	Polyhedrin	Anhul (17-345)	329	gp64 (272-512)	241	570	596
3	CAP-HA1/Anhul/467	CAG	Polyhedrin	Anhul (17-345)	329	gp64 (467-512)	46	375	401
4	CAP-HA1/Vietnam	CAG	Polyhedrin	Vietnam (17-346)	330	gp64 (21-512)	492	822	848
5	CAP-HA1/Vietnam/51	CAG	Polyhedrin	Vietnam (17-346)	330	gp64 (51-512)	462	792	818
6	CAP-HA1/Vietnam/101	CAG	Polyhedrin	Vietnam (17-346)	330	gp64 (101-512)	412	742	768
7	CAP-HA1/Vietnam/154	CAG	Polyhedrin	Vietnam (17-346)	330	gp64 (154-512)	359	689	715
8	CAP-HA1/Vietnam/201	CAG	Polyhedrin	Vietnam (17-346)	330	gp64 (201-512)	312	642	668
9	CAP-HA1/Vietnam/272	CAG	Polyhedrin	Vietnam (17-346)	330	gp64 (272-512)	241	571	597
10	CAP-HA1/Vietnam/467	CAG	Polyhedrin	Vietnam (17-346)	330	gp64 (467-512)	46	376	402
11	CAP-AH1/345	CAG	Polyhedrin	Anhul GD (1-345)	345	gp64 (21-512)	492	837	863
12	CAP-AH1/345/467	CAG	Polyhedrin	Anhul GD (1-345)	345	gp64 (467-512)	46	391	417
13	CAP-AH1/410	CAG	Polyhedrin	Anhul GD (17-410)	394	gp64 (21-512)	492	886	912
14	CAP-AH1/410/467	CAG	Polyhedrin	Anhul GD (17-410)	394	gp64 (467-512)	46	440	466
15	CAP-AH1/473	CAG	Polyhedrin	Anhul GD (17-473)	457	gp64 (21-512)	492	949	975
16	CAP-AH1/473/467	CAG	Polyhedrin	Anhul GD (17-473)	457	gp64 (467-512)	46	503	529
17	CAP-AH1/520	CAG	Polyhedrin	Anhul GD (17-520)	504	gp64 (21-512)	492	996	1022
18	CAP-AH1/520/467	CAG	Polyhedrin	Anhul GD (17-520)	504	gp64 (467-512)	46	550	576
19	CAP-VN1/345	CAG	Polyhedrin	Vietnam GD (17-346)	330	gp64 (21-512)	492	822	848
20	CAP-VN1/345/467	CAG	Polyhedrin	Vietnam GD (17-346)	330	gp64 (467-512)	46	376	402
21	CAP-VN1/410	CAG	Polyhedrin	Vietnam GD (17-410)	394	gp64 (21-512)	492	866	912
22	CAP-VN1/410/467	CAG	Polyhedrin	Vietnam GD (17-410)	394	gp64 (467-512)	46	440	466
23	CAP-VN1/473	CAG	Polyhedrin	Vietnam GD (17-473)	457	gp64 (21-512)	492	949	975
24	CAP-VN1/473/467	CAG	Polyhedrin	Vietnam GD (17-473)	457	gp64 (467-512)	46	503	529
25	CAP-VN1/520	CAG	Polyhedrin	Vietnam GD (17-520)	504	gp64 (21-512)	492	996	1022
26	CAP-VN1/520/467	CAG	Polyhedrin	Vietnam GD (17-520)	504	gp64 (467-512)	46	550	576
27	CAP-PCSP	CAG	Polyhedrin	PCSP (19-373)	355	gp64 (21-512)	492	847	873
28	CAP-PCSP/167	CAG	Polyhedrin	PCSP (19-373)	355	gp64 (467-512)	46	596	622
29	CAP-PCSP/167	CAG	Polyhedrin	PCSP (19-373)	355	gp64 (21-512)	46	401	427
30	CAP-PCSP/A361E	CAG	Polyhedrin	PCSP (19-373)/A361E	355	gp64 (21-512)	492	847	873
31	CAP-PCSP/A361E/272	CAG	Polyhedrin	PCSP (19-373)/A361E	355	gp64 (272-512)	241	596	622
32	CAP-PCSP/A361E/467	CAG	Polyhedrin	PCSP (19-373)/A361E	355	gp64 (467-512)	46	401	427
33	CAP-PCSP-76	CAG	Polyhedrin	PCSP (76-373)	298	gp64 (21-512)	492	790	816
34	CAP-PCSP-76/467	CAG	Polyhedrin	PCSP (76-373)	298	gp64 (467-512)	46	344	370
35	CAP-PCSP+209	CAG	Polyhedrin	PCSP+209-373	165	gp64 (21-512)	492	657	683
36	CAP-PCSP+209/467	CAG	Polyhedrin	PCSP+209-373	165	gp64 (467-512)	46	211	237
37	CAP-PCSP+76/209	CAG	Polyhedrin	PCSP+76-128 + 209-373	218	gp64 (21-512)	492	710	736
38	CAP-PCSP+76/209/467	CAG	Polyhedrin	PCSP+76-128 + 209-373	218	gp64 (467-512)	46	264	290
39	CAP-CO/167	CAG	Polyhedrin	PCSP GD (1-397)	397	gp64 (21-512)	492	889	915
40	CAP-CO/167	CAG	Polyhedrin	PCSP GD (1-397)	397	gp64 (467-512)	46	443	469
41	CAP-CO/19	CAG	Polyhedrin	PCSP GD (19-373)	355	gp64 (21-512)	492	847	873
42	CAP-CO/19/467	CAG	Polyhedrin	PCSP GD (19-373)	355	gp64 (467-512)	46	401	427
43	CAP-CO/76	CAG	Polyhedrin	PCSP GD (76-373)	298	gp64 (21-512)	492	790	816
44	CAP-CO/76/467	CAG	Polyhedrin	PCSP GD (76-373)	298	gp64 (467-512)	46	344	370
45	CAP-CO/205	CAG	Polyhedrin	PCSP GD (205-373)	169	gp64 (21-512)	492	661	687
46	CAP-CO/205/467	CAG	Polyhedrin	PCSP GD (205-373)	169	gp64 (467-512)	46	215	241
47	CAP-HA1/Anhul	CAG	vp39p	Vietnam (17-346)	330	gp64 (21-512)	492	822	848
48	CAP-HA1/Anhul	CAG	gp64p	Vietnam (17-346)	330	gp64 (21-512)	492	822	848
49	CAP39-PCSP/A361E	CAG	vp39p	PCSP (19-373)/A361E	355	gp64 (21-512)	492	847	873
50	CAP64-PCSP/A361E	CAG	gp64p	PCSP (19-373)/A361E	355	gp64 (21-512)	492	847	873
51	CAP-CO/167/VS	CAG	Polyhedrin	PCSP GD (1-397)	397	VS/G (458-549)	92	489	515
52	CAP-CO/18/VS	CAG	Polyhedrin	PCSP GD (19-373)	355	VS/G (458-549)	92	447	473
53	CAP-CO/76/VS	CAG	Polyhedrin	PCSP GD (76-373)	298	VS/G (458-549)	92	390	416
54	CAP-CO/205/VS	CAG	Polyhedrin	PCSP GD (205-373)	169	VS/G (458-549)	92	261	287
55	Dual-PCSP-PCSP-gp64	CMV	Polyhedrin	Ph25 (23-171) + PCSP (19-373)	504	gp64 (21-512)	492	996	1099
56	Dual-PCSP-PCSP-gp64	CMV	Polyhedrin	Ph25 (1587-1682) + PCSP (19-373)	451	gp64 (21-512)	492	943	1024

SEQUENCE LISTING

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OTSUKA PHARMACEUTICAL CO., LTD.

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<151> 2007-08-07

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2/38

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3/38

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5/38

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6/38

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7/38

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8/38

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9/38

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10/38

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11/38

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 accgtcactc atgcgcaaga tttttggag aagacacaca acgggaagct ctgcgatctg 180
 gatgggggtga agcctctgat tctcgggac tgctccgtgg cgggggtggtt gcttggcaac 240
 cctatgtgtg atgagttcat caacgtgcct gaatggtctt atattgtgga aaaagcgaat 300
 cccgctaacg acctttgta ccttggtaac ttcaacgatt acgaagaact caaacacctc 360
 ctcagcagaa tcaatcactt cgaaaaaata cagattattc ccaaatcttc ctggtccgac 420
 catgaggcat ccagcggagt atcaagtga tgcccgtagc agggcactcc ctcatttttc 480
 cgcaacgtgg tgtggtgat caagaaaaat aacacttatt cgaccatcaa gagaagctac 540
 aacaacacta accaggagga cctgttgatc ctttggggca tacatcatag caacgacgog 600
 gcagaacaga ccaagcttta ccagaacctt acaacatata tcagcgtggg caccagtact 660
 cttaatcaac ggttggtgcc caagatcgct acaaggagta aggtgaatgg gcagagcggg 720
 cgaatggatt tcttctggac cattcttaaa ccaatgacg ctataaactt tgagagcaac 780
 ggcaacttta ttgccccga atatgcatac aagattgtga agaagggtga cagcgccatt 840
 gtaaaaagcg aggtggagta cggtaattgt aacacaaagt gccaaacacc tatagggggc 900
 attaatagct caatgccttt ccacaacatt caccactga ctatcggtga atgccccaaa 960
 tacgtgaagt caaacaact ggtactggca acagggtcc ggaattctcc cctgcgcgag 1020
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 ggcatgtag acggatggtg tgggtatcat catagtaacg aacagggtac cggctacgcg 1140
 gccgataagg agtcaacca gaaggcaatt gacggcgtca caataaggt caactccata 1200
 attgataaaa tgaacacca gttcgaggcc gtagggcgcg aatttaacaa cctcgaaaga 1260

12/38

aggatcgaga acctgaataa gaagatggag gatgggttcc tcgacgttg gacttataat 1320
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 aaaaatctgt atgataaagt gcgccttcaa ctgagagaca acgccaagga actcgggaac 1440
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 acttatgact acccacaata ctctgaggaa gcccgactga agcgagagga aattagtgt 1560
 gtgaagctgg aaagcatcgg aacctatcaa attttgagta ttactotac agtggaagc 1620
 tcactggcgc ttgcaatcat ggtggctggc cttagcttgt ggatgtgctc caatggaagc 1680
 ttgcagtgcc gaattgcat c 1701

<210> 46
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer AH17-F

<400> 46
 gactctgcag gatcagatct gtattgggta cc 32

<210> 47
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer AH345-R

<400> 47
 cgatcccggg ctctctttct cctccgctcg c 31

<210> 48
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer AH410-R

<400> 48
 cgatcccggg cggcctcgaa ctgggtgttc att 33

<210> 49
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer AH473-R

<400> 49
 cgatcccggg cgtctctgag ttgaaggcgc ac 32

13/38

<210> 50
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer AH520-R

<400> 50
 cgatcccggg caccactaat ttcctctcgc ttc 33

<210> 51
 <211> 1704
 <212> DNA
 <213> influenza virus

<400> 51
 atggagaaaa ttgtcctgct gttcgtatt gtttcctgg ttaaatccga tcagatctgt 60
 atcggatata acgcgaataa tagcacagag caagtggata ccattatgga aaagaatgtg 120
 actgtgaccc acgctcagga cattctggag aaaaagcaca acggaaaatt gtgcgacctt 180
 gatggggtga agccattgat tctgagagac tgctctgtgg ctggatggct gctggggaac 240
 cctatgtgcg atgagttcat taatgttccc gagtggctct acatagtcca aaaggctaatt 300
 cctgtcaatg atctttgcta ccttggggat ttaatagaat atgaggagct gaaacatttg 360
 ttgagtagaa tcaaccactt tgagaaaatc cagatcatcc ccaagagttc ctggtcatct 420
 catgaagcaa gccttggtgt gagctcagcc tgcccttata aaggcaaata cagcttcttt 480
 cggaacgtgg tctggctcat caagaaaaat tcaacctata cgactatcaa gagatcctat 540
 aacaacacaa atcaggagga tctgttgga ctgtggggca tccaccatcc taacgatgca 600
 gcagagcaga ccaagctcta ccagaaccca actacctaca tctccgttgg aactagcaca 660
 ctgaaccaga gatttgtacc tagaattgct acccgatcca aagtcaatgg ccagtccgga 720
 agaatggaat tcttctggac aattctgaaa cccaatgacg ccattaattt cgagtcaaac 780
 ggcaatttca ttgtccaga gtatgcttac aagatcgtga aaaagggtga tagtacaatt 840
 atgaagagtg agttggagta cggcaactgc aatacaaaat gtcaaacacc catgggcgct 900
 atcaattcat ccatgccttt ccacaatac caccocctta ctatcggaga gtgccgaag 960
 tatgtcaagt ccaacaggct ggtcctggca actggactgc ggaatagccc gcaacgcgaa 1020
 cggaggagga aaaagcgggg actgtttgga gctattgcag gcttcatcga aggtggttgg 1080
 caggcatggt tggacggtt gtatgggtat catcactcca acgaacaggg gagcggttat 1140
 gccgcagaca aagagtcaac tcagaaggca attgatggag ttacaaacaa agtgaatagc 1200
 attatcgaca aatgaatac gcagtttgag gctgtcggcc gcgagttcaa taatctggag 1260
 cggagaatcg aaaacctgaa caaaaagatg gaggacggct tctggacgt gtggacatat 1320

14/38

aacgcagaac tgctogtget tatggagaat gaacggaccc tcgattttca cgactccaac 1380
 gtaaagaatc tgtatgacaa agtcaggctc cagcttagag ataacgcaa ggaattgggg 1440
 aatggatgtt ttgaattcta ccataagtgc gacaacgagt gcatggagtc cgtaagaaac 1500
 ggaacctatg actatcccca gtactcagag gaggcaagac taaaagaga ggagattagt 1560
 ggtgtgaaac tcgagtccat aggcatttat cagatcctga gtatctactc tacgtggcg 1620
 tcatccctgg ccctggccat catggttgct ggcttgacac tctggatgtg tagtaacggg 1680
 agtctgcaat gcagaatatg tatt 1704

<210> 52
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer VN17-F

<400> 52
 gactctgcag gatcagatct gtatcggata tc 32

<210> 53
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer VN346-R

<400> 53
 cgatcccggg cccgctttt cctcctcctg tcg 33

<210> 54
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer VN410-R

<400> 54
 cgatcccggg cctcaaactg cgtattcatt ttg 33

<210> 55
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer VN473-R

<400> 55
 cgatcccggg ctotaagctg gagcctgact ttgtc 35

15/38

<210> 56
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer VN520-R

<400> 56
 cgatcccggg cactaatctc ctctctttta agtc 34

<210> 57
 <211> 1191
 <212> DNA
 <213> Plasmodium falciparum

<400> 57
 atgatgcgaa aattggccat actgtcagtc agcagcttct tgttcgtgga ggccctgttt 60
 caggaatacc agtgcatagg ttccagctct aatacgcgag ttctgaacga gctgaactac 120
 gataacgcgc gcaccaacct ctacaatgag ctggagatga attactacgg caagcaggag 180
 aattggtact cactcaagaa gaactccaga agtctcgggg agaacgacga cggaataat 240
 gaggacaacg aaaaacttag aaaacccaaa cacaagaaac tgaacaacc tgccgatgtt 300
 aatctgtatc ctaatgcaaa cccaatgtg gacccaatg ctaacccaa cgtcgatccg 360
 aacgcgaacc ctaatgtgga tctaacgcc aatccaaacg ogaatccgaa tgccaacca 420
 aacgccaacc caaacgctaa cccaacgcg aacccaacg ctaatccgaa cgccaatccc 480
 aatgctaato ccaatgcgaa ccctaacgt aatcccaacg caaatccgaa cgcaaaccct 540
 aacgcaaacc ccaatgcaa ccctaacgcc aacccgaatg ccaatcctaa tgtggaccgc 600
 aacgccaatc cgaatgcaaa cccaatgcc aatccaaacg ctaatcctaa cgccaacccc 660
 aacgccaacc ctaatgctaa tccgaatgcg aatccaaatg ctaacccgaa cgctaatoa 720
 aatgcaaato ccaatgcaaa tccaatgcg aacccgaatg ctaacccctaa tgcaaatcct 780
 aatgcaaacc ctaatgcgaa tccaatgca aacccaata agaataatca gggaaatggc 840
 cagggacata atatgcctaa tgaccctaac aggaacgttg atgagaacgc gaatgcgaac 900
 tctgctgtaa agaacaacaa caatgaagag ccctccgata aacatattaa ggagtatctg 960
 aataagatcc agaactcctt gtctaccgaa tgggtcccct gttctgtgac gtgtgtaac 1020
 ggaatccagg taaggatcaa acccggcagt gccacaagc caaaggacga gctcgattac 1080
 gctaatgata ttgaaaagaa aatttgtaag atggagaagt gcagctccgt attcaatgtg 1140
 gtcaacagct caattggcct catcatggtt ctttccttct tgttctctaa t 1191

<210> 58
 <211> 34
 <212> DNA

16/38

<213> Artificial Sequence

<220>

<223> primer PfCSP_opt-f

<400> 58

gactctgcag atgatgcgaa aattggccat actg

34

<210> 59

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer PfCSP_opt-r(397)

<400> 59

cgatcccggg cattgaggaa cagaaaggaa agaaccatg

39

<210> 60

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer PfCSP_opt-f(19)

<400> 60

gactctgcag ctgttcagg aataccagtg ctatgg

36

<210> 61

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> primer PfCSP_opt-r(373)

<400> 61

cgatcccggg ccttctccat cttacaaatt ttctttcaa tatcattagc

50

<210> 62

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer PfCSP_opt-f(76)

<400> 62

gactctgcag gacgacggaa ataatgagga caacg

35

<210> 63

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

17/38

<223> primer PfCSP_opt-f(205)

<400> 63

gactctgcag aatgcaaacc caaatgccaa tccaaacgc

39

<210> 64

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer gp64-p-f

<400> 64

gactcggacc ggccagataa aaataatctt atcaattaag

40

<210> 65

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer gp64-p-r

<400> 65

cgatactagt agcactgagg cttcttatat acccg

35

<210> 66

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer vp39-p-f

<400> 66

gactcggacc gcgtcgtaca aatcgaaata ttgtgtg

38

<210> 67

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer gp64-p-r

<400> 67

cgatactagt gtgattgaga aagaaatctc ttattc

36

<210> 68

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer VSV-G-f

<400> 68

18/38

gactccccgg gcgttcgaac atcctcacat tcaag

35

<210> 69

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer VSV-G-r

<400> 69

gactcactta gtgctttcca agtcggttca tctc

34

<210> 70

<211> 397

<212> PRT

<213> PfCSP protein XP_001351122

<400> 70

Met Met Arg Lys Leu Ala Ile Leu Ser Val Ser Ser Phe Leu Phe Val
1 5 10 15

Glu Ala Leu Phe Gln Glu Tyr Gln Cys Tyr Gly Ser Ser Ser Asn Thr
20 25 30

Arg Val Leu Asn Glu Leu Asn Tyr Asp Asn Ala Gly Thr Asn Leu Tyr
35 40 45

Asn Glu Leu Glu Met Asn Tyr Tyr Gly Lys Gln Glu Asn Trp Tyr Ser
50 55 60

Leu Lys Lys Asn Ser Arg Ser Leu Gly Glu Asn Asp Asp Gly Asn Asn
65 70 75 80

Glu Asp Asn Glu Lys Leu Arg Lys Pro Lys His Lys Lys Leu Lys Gln
85 90 95

Pro Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Val Asp Pro
100 105 110

Asn Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Val Asp Pro
115 120 125

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
130 135 140

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
145 150 155 160

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro

19/38

165

170

175

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
 180 185 190

Asn Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Ala Asn Pro
 195 200 205

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
 210 215 220

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
 225 230 235 240

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
 245 250 255

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
 260 265 270

Asn Lys Asn Asn Gln Gly Asn Gly Gln Gly His Asn Met Pro Asn Asp
 275 280 285

Pro Asn Arg Asn Val Asp Glu Asn Ala Asn Ala Asn Ser Ala Val Lys
 290 295 300

Asn Asn Asn Asn Glu Glu Pro Ser Asp Lys His Ile Lys Glu Tyr Leu
 305 310 315 320

Asn Lys Ile Gln Asn Ser Leu Ser Thr Glu Trp Ser Pro Cys Ser Val
 325 330 335

Thr Cys Gly Asn Gly Ile Gln Val Arg Ile Lys Pro Gly Ser Ala Asn
 340 345 350

Lys Pro Lys Asp Glu Leu Asp Tyr Ala Asn Asp Ile Glu Lys Lys Ile
 355 360 365

Cys Lys Met Glu Lys Cys Ser Ser Val Phe Asn Val Val Asn Ser Ser
 370 375 380

Ile Gly Leu Ile Met Val Leu Ser Phe Leu Phe Leu Asn
 385 390 395

<210> 71

<211> 567

<212> PRT

<213> HA/A/Anhui/1/2005 protein ABD28180

20/38

<400> 71

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
20 25 30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
35 40 45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
50 55 60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65 70 75 80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
85 90 95

Glu Lys Ala Asn Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
130 135 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Thr Pro Ser Phe Phe
145 150 155 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Thr Tyr Pro Thr Ile
165 170 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp
180 185 190

Gly Ile His His Ser Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
195 200 205

Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
210 215 220

Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225 230 235 240

21/38

Arg Met Asp Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
 245 250 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
 260 265 270

Val Lys Lys Gly Asp Ser Ala Ile Val Lys Ser Glu Val Glu Tyr Gly
 275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala Ile Asn Ser Ser
 290 295 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
 305 310 315 320

Tyr Val Lys Ser Asn Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
 325 330 335

Pro Leu Arg Glu Arg Arg Arg Lys Arg Gly Leu Phe Gly Ala Ile Ala
 340 345 350

Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly
 355 360 365

Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu
 370 375 380

Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser Ile
 385 390 395 400

Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe Asn
 405 410 415

Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly
 420 425 430

Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu
 435 440 445

Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr
 450 455 460

Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn
 465 470 475 480

Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser
 485 490 495

22/38

Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg
 500 505 510

Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr
 515 520 525

Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu
 530 535 540

Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser
 545 550 555 560

Leu Gln Cys Arg Ile Cys Ile
 565

<210> 72

<211> 568

<212> PRT

<213> HA/A/Vietnam/1203/2004 protein

AAW80717

<400> 72

Met Glu Lys Ile Val Leu Leu Phe Ala Ile Val Ser Leu Val Lys Ser
 1 5 10 15

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
 20 25 30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
 35 40 45

Leu Glu Lys Lys His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
 50 55 60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
 65 70 75 80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
 85 90 95

Glu Lys Ala Asn Pro Val Asn Asp Leu Cys Tyr Pro Gly Asp Phe Asn
 100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
 115 120 125

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Ser His Glu Ala Ser
 130 135 140

23/38

Leu Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Lys Ser Ser Phe Phe
 145 150 155 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Thr Tyr Pro Thr Ile
 165 170 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
 180 185 190

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
 195 200 205

Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
 210 215 220

Leu Val Pro Arg Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
 225 230 235 240

Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
 245 250 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
 260 265 270

Val Lys Lys Gly Asp Ser Thr Ile Met Lys Ser Glu Leu Glu Tyr Gly
 275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
 290 295 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
 305 310 315 320

Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
 325 330 335

Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly Ala Ile
 340 345 350

Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr
 355 360 365

Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys
 370 375 380

Glu Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser
 385 390 395 400

24/38

Ile Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe
 405 410 415

Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp
 420 425 430

Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
 435 440 445

Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu
 450 455 460

Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly
 465 470 475 480

Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
 485 490 495

Ser Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala
 500 505 510

Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
 515 520 525

Ile Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala
 530 535 540

Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
 545 550 555 560

Ser Leu Gln Cys Arg Ile Cys Ile
 565

<210> 73

<211> 1720

<212> PRT

<213> PfMSP1 protein XP_001352170

<400> 73

Met Lys Ile Ile Phe Phe Leu Cys Ser Phe Leu Phe Phe Ile Ile Asn
 1 5 10 15

Thr Gln Cys Val Thr His Glu Ser Tyr Gln Glu Leu Val Lys Lys Leu
 20 25 30

Glu Ala Leu Glu Asp Ala Val Leu Thr Gly Tyr Ser Leu Phe Gln Lys
 35 40 45

25/38

Glu Lys Met Val Leu Asn Glu Glu Glu Ile Thr Thr Lys Gly Ala Ser
50 55 60

Ala Gln Ser Gly Ala Ser Ala Gln Ser Gly Ala Ser Ala Gln Ser Gly
65 70 75 80

Ala Ser Ala Gln Ser Gly Ala Ser Ala Gln Ser Gly Ala Ser Ala Gln
85 90 95

Ser Gly Thr Ser Gly Pro Ser Gly Pro Ser Gly Thr Ser Pro Ser Ser
100 105 110

Arg Ser Asn Thr Leu Pro Arg Ser Asn Thr Ser Ser Gly Ala Ser Pro
115 120 125

Pro Ala Asp Ala Ser Asp Ser Asp Ala Lys Ser Tyr Ala Asp Leu Lys
130 135 140

His Arg Val Arg Asn Tyr Leu Phe Thr Ile Lys Glu Leu Lys Tyr Pro
145 150 155 160

Glu Leu Phe Asp Leu Thr Asn His Met Leu Thr Leu Cys Asp Asn Ile
165 170 175

His Gly Phe Lys Tyr Leu Ile Asp Gly Tyr Glu Glu Ile Asn Glu Leu
180 185 190

Leu Tyr Lys Leu Asn Phe Tyr Phe Asp Leu Leu Arg Ala Lys Leu Asn
195 200 205

Asp Val Cys Ala Asn Asp Tyr Cys Gln Ile Pro Phe Asn Leu Lys Ile
210 215 220

Arg Ala Asn Glu Leu Asp Val Leu Lys Lys Leu Val Phe Gly Tyr Arg
225 230 235 240

Lys Pro Leu Asp Asn Ile Lys Asp Asn Val Gly Lys Met Glu Asp Tyr
245 250 255

Ile Lys Lys Asn Lys Thr Thr Ile Ala Asn Ile Asn Glu Leu Ile Glu
260 265 270

Gly Ser Lys Lys Thr Ile Asp Gln Asn Lys Asn Ala Asp Asn Glu Glu
275 280 285

Gly Lys Lys Lys Leu Tyr Gln Ala Gln Tyr Asp Leu Ser Ile Tyr Asn

290 295 300

Lys Gln Leu Glu Glu Ala His Asn Leu Ile Ser Val Leu Glu Lys Arg
305 310 315 320

Ile Asp Thr Leu Lys Lys Asn Glu Asn Ile Lys Lys Leu Leu Asp Lys
325 330 335

Ile Asn Glu Ile Lys Asn Pro Pro Pro Ala Asn Ser Gly Asn Thr Pro
340 345 350

Asn Thr Leu Leu Asp Lys Asn Lys Lys Ile Glu Glu His Glu Glu Lys
355 360 365

Ile Lys Glu Ile Ala Lys Thr Ile Lys Phe Asn Ile Asp Ser Leu Phe
370 375 380

Thr Asp Pro Leu Glu Leu Glu Tyr Tyr Leu Arg Glu Lys Asn Lys Lys
385 390 395 400

Val Asp Val Thr Pro Lys Ser Gln Asp Pro Thr Lys Ser Val Gln Ile
405 410 415

Pro Lys Val Pro Tyr Pro Asn Gly Ile Val Tyr Pro Leu Pro Leu Thr
420 425 430

Asp Ile His Asn Ser Leu Ala Ala Asp Asn Asp Lys Asn Ser Tyr Gly
435 440 445

Asp Leu Met Asn Pro His Thr Lys Glu Lys Ile Asn Glu Lys Ile Ile
450 455 460

Thr Asp Asn Lys Glu Arg Lys Ile Phe Ile Asn Asn Ile Lys Lys Lys
465 470 475 480

Ile Asp Leu Glu Glu Lys Asn Ile Asn His Thr Lys Glu Gln Asn Lys
485 490 495

Lys Leu Leu Glu Asp Tyr Glu Lys Ser Lys Lys Asp Tyr Glu Glu Leu
500 505 510

Leu Glu Lys Phe Tyr Glu Met Lys Phe Asn Asn Phe Asn Lys Asp
515 520 525

Val Val Asp Lys Ile Phe Ser Ala Arg Tyr Thr Tyr Asn Val Glu Lys
530 535 540

27/38

Gln Arg Tyr Asn Asn Lys Phe Ser Ser Ser Asn Asn Ser Val Tyr Asn
 545 550 555 560

Val Gln Lys Leu Lys Lys Ala Leu Ser Tyr Leu Glu Asp Tyr Ser Leu
 565 570 575

Arg Lys Gly Ile Ser Glu Lys Asp Phe Asn His Tyr Tyr Thr Leu Lys
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Thr Gly Leu Glu Ala Asp Ile Lys Lys Leu Thr Glu Glu Ile Lys Ser
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Ser Glu Asn Lys Ile Leu Glu Lys Asn Phe Lys Gly Leu Thr His Ser
 610 615 620

Ala Asn Gly Ser Leu Glu Val Ser Asp Ile Val Lys Leu Gln Val Gln
 625 630 635 640

Lys Val Leu Leu Ile Lys Lys Ile Glu Asp Leu Arg Lys Ile Glu Leu
 645 650 655

Phe Leu Lys Asn Ala Gln Leu Lys Asp Ser Ile His Val Pro Asn Ile
 660 665 670

Tyr Lys Pro Gln Asn Lys Pro Glu Pro Tyr Tyr Leu Ile Val Leu Lys
 675 680 685

Lys Glu Val Asp Lys Leu Lys Glu Phe Ile Pro Lys Val Lys Asp Met
 690 695 700

Leu Lys Lys Glu Gln Ala Val Leu Ser Ser Ile Thr Gln Pro Leu Val
 705 710 715 720

Ala Ala Ser Glu Thr Thr Glu Asp Gly Gly His Ser Thr His Thr Leu
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Ser Gln Ser Gly Glu Thr Glu Val Thr Glu Glu Thr Glu Glu Thr Glu
 740 745 750

Glu Thr Val Gly His Thr Thr Thr Val Thr Ile Thr Leu Pro Pro Thr
 755 760 765

Gln Pro Ser Pro Pro Lys Glu Val Lys Val Val Glu Asn Ser Ile Glu
 770 775 780

His Lys Ser Asn Asp Asn Ser Gln Ala Leu Thr Lys Thr Val Tyr Leu
 785 790 795 800

Lys Lys Leu Asp Glu Phe Leu Thr Lys Ser Tyr Ile Cys His Lys Tyr
805 810 815

Ile Leu Val Ser Asn Ser Ser Met Asp Gln Lys Leu Leu Glu Val Tyr
820 825 830

Asn Leu Thr Pro Glu Glu Glu Asn Glu Leu Lys Ser Cys Asp Pro Leu
835 840 845

Asp Leu Leu Phe Asn Ile Gln Asn Asn Ile Pro Ala Met Tyr Ser Leu
850 855 860

Tyr Asp Ser Met Asn Asn Asp Leu Gln His Leu Phe Phe Glu Leu Tyr
865 870 875 880

Gln Lys Glu Met Ile Tyr Tyr Leu His Lys Leu Lys Glu Glu Asn His
885 890 895

Ile Lys Lys Leu Leu Glu Glu Gln Lys Gln Ile Thr Gly Thr Ser Ser
900 905 910

Thr Ser Ser Pro Gly Asn Thr Thr Val Asn Thr Ala Gln Ser Ala Thr
915 920 925

His Ser Asn Ser Gln Asn Gln Gln Ser Asn Ala Ser Ser Thr Asn Thr
930 935 940

Gln Asn Gly Val Ala Val Ser Ser Gly Pro Ala Val Val Glu Glu Ser
945 950 955 960

His Asp Pro Leu Thr Val Leu Ser Ile Ser Asn Asp Leu Lys Gly Ile
965 970 975

Val Ser Leu Leu Asn Leu Gly Asn Lys Thr Lys Val Pro Asn Pro Leu
980 985 990

Thr Ile Ser Thr Thr Glu Met Glu Lys Phe Tyr Glu Asn Ile Leu Lys
995 1000 1005

Asn Asn Asp Thr Tyr Phe Asn Asp Asp Ile Lys Gln Phe Val Lys
1010 1015 1020

Ser Asn Ser Lys Val Ile Thr Gly Leu Thr Glu Thr Gln Lys Asn
1025 1030 1035

Ala Leu Asn Asp Glu Ile Lys Lys Leu Lys Asp Thr Leu Gln Leu
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Ser Phe Asp Leu Tyr Asn Lys Tyr Lys Leu Lys Leu Asp Arg Leu
1055 1060 1065

Phe Asn Lys Lys Lys Glu Leu Gly Gln Asp Lys Met Gln Ile Lys
1070 1075 1080

Lys Leu Thr Leu Leu Lys Glu Gln Leu Glu Ser Lys Leu Asn Ser
1085 1090 1095

Leu Asn Asn Pro His Asn Val Leu Gln Asn Phe Ser Val Phe Phe
1100 1105 1110

Asn Lys Lys Lys Glu Ala Glu Ile Ala Glu Thr Glu Asn Thr Leu
1115 1120 1125

Glu Asn Thr Lys Ile Leu Leu Lys His Tyr Lys Gly Leu Val Lys
1130 1135 1140

Tyr Tyr Asn Gly Glu Ser Ser Pro Leu Lys Thr Leu Ser Glu Val
1145 1150 1155

Ser Ile Gln Thr Glu Asp Asn Tyr Ala Asn Leu Glu Lys Phe Arg
1160 1165 1170

Val Leu Ser Lys Ile Asp Gly Lys Leu Asn Asp Asn Leu His Leu
1175 1180 1185

Gly Lys Lys Lys Leu Ser Phe Leu Ser Ser Gly Leu His His Leu
1190 1195 1200

Ile Thr Glu Leu Lys Glu Val Ile Lys Asn Lys Asn Tyr Thr Gly
1205 1210 1215

Asn Ser Pro Ser Glu Asn Asn Lys Lys Val Asn Glu Ala Leu Lys
1220 1225 1230

Ser Tyr Glu Asn Phe Leu Pro Glu Ala Lys Val Thr Thr Val Val
1235 1240 1245

Thr Pro Pro Gln Pro Asp Val Thr Pro Ser Pro Leu Ser Val Arg
1250 1255 1260

Val Ser Gly Ser Ser Gly Ser Thr Lys Glu Glu Thr Gln Ile Pro
1265 1270 1275

Thr Ser Gly Ser Leu Leu Thr Glu Leu Gln Gln Val Val Gln Leu

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Gln Asn Tyr Asp Glu Glu Asp Asp Ser Leu Val Val Leu Pro Ile		
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Phe Gly Glu Ser Glu Asp Asn Asp Glu Tyr Leu Asp Gln Val Val		
1310	1315	1320
Thr Gly Glu Ala Ile Ser Val Thr Met Asp Asn Ile Leu Ser Gly		
1325	1330	1335
Phe Glu Asn Glu Tyr Asp Val Ile Tyr Leu Lys Pro Leu Ala Gly		
1340	1345	1350
Val Tyr Arg Ser Leu Lys Lys Gln Ile Glu Lys Asn Ile Phe Thr		
1355	1360	1365
Phe Asn Leu Asn Leu Asn Asp Ile Leu Asn Ser Arg Leu Lys Lys		
1370	1375	1380
Arg Lys Tyr Phe Leu Asp Val Leu Glu Ser Asp Leu Met Gln Phe		
1385	1390	1395
Lys His Ile Ser Ser Asn Glu Tyr Ile Ile Glu Asp Ser Phe Lys		
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Leu Leu Asn Ser Glu Gln Lys Asn Thr Leu Leu Lys Ser Tyr Lys		
1415	1420	1425
Tyr Ile Lys Glu Ser Val Glu Asn Asp Ile Lys Phe Ala Gln Glu		
1430	1435	1440
Gly Ile Ser Tyr Tyr Glu Lys Val Leu Ala Lys Tyr Lys Asp Asp		
1445	1450	1455
Leu Glu Ser Ile Lys Lys Val Ile Lys Glu Glu Lys Glu Lys Phe		
1460	1465	1470
Pro Ser Ser Pro Pro Thr Thr Pro Pro Ser Pro Ala Lys Thr Asp		
1475	1480	1485
Glu Gln Lys Lys Glu Ser Lys Phe Leu Pro Phe Leu Thr Asn Ile		
1490	1495	1500
Glu Thr Leu Tyr Asn Asn Leu Val Asn Lys Ile Asp Asp Tyr Leu		
1505	1510	1515

31/38

Ile Asn Leu Lys Ala Lys Ile Asn Asp Cys Asn Val Glu Lys Asp
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Asp Asp Lys Ile Asp Leu Phe Lys Asn Pro Tyr Asp Phe Glu Ala
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Ile Lys Lys Leu Ile Asn Asp Asp Thr Lys Lys Asp Met Leu Gly
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Lys Leu Leu Ser Thr Gly Leu Val Gln Asn Phe Pro Asn Thr Ile
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Ile Ser Lys Leu Ile Glu Gly Lys Phe Gln Asp Met Leu Asn Ile
 1595 1600 1605

Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu Asn Ser Gly
 1610 1615 1620

Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys Leu Leu
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Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn Pro
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Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Thr Cys
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 1670 1675 1680

Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys
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<211> 217

<212> PRT

<213> Pfs25 protein

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<400> 74

32/38

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Gly Phe Leu Ile Gln Met Ser Gly His Leu Glu Cys Lys Cys Glu Asn
35 40 45

Asp Leu Val Leu Val Asn Glu Glu Thr Cys Glu Glu Lys Val Leu Lys
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Cys Asp Glu Lys Thr Val Asn Lys Pro Cys Gly Asp Phe Ser Lys Cys
65 70 75 80

Ile Lys Ile Asp Gly Asn Pro Val Ser Tyr Ala Cys Lys Cys Asn Leu
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Gly Tyr Asp Met Val Asn Asn Val Cys Ile Pro Asn Glu Cys Lys Asn
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Val Thr Cys Gly Asn Gly Lys Cys Ile Leu Asp Thr Ser Asn Pro Val
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Lys Thr Gly Val Cys Ser Cys Asn Ile Gly Lys Val Pro Asn Val Gln
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Asp Gln Asn Lys Cys Ser Lys Asp Gly Glu Thr Lys Cys Ser Leu Lys
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Cys Leu Lys Glu Asn Glu Thr Cys Lys Ala Val Asp Gly Ile Tyr Lys
165 170 175

Cys Asp Cys Lys Asp Gly Phe Ile Ile Asp Asn Glu Ser Ser Ile Cys
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<211> 1704

<212> DNA

<213> HA/A/Anhui/1/2005 gene

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 ccagccaatg acctctgta ccaggggaat tcaacgact atgaagaact gaaacaccta 360
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34/38

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<211> 1707

<212> DNA

<213> HA/A/Vietnam/1203/2004 gene AY818135

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 aataatacca accaagaaga tottttgga ctgtggggga ttcacatcc taatgatgog 600
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<211> 5163

<212> DNA

<213> PfMSP1 gene XM_001352134

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acaggttata gtttatttca aaaggaaaa atggtattaa atgaagaaga aattactaca 180

aaaggtgcaa gtgctcaaag tgggtcaagt gctcaaagt gtgcaagtgc tcaaagtgt 240

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37/38

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38/38

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