Figure 1 1/10

Amino Acid Sequence of STF2.HA1 (VAX125) (SEQ ID 1)

1	AQVINTNSLS	LLTQNNLNKS	QSALGTAIER	LSSGLRINSA	KDDAAGQAIA
51	NRFTANIKGL	TQASRNANDG	ISIAQTTEGA	LNEINNNLQR	VRELAVQSAN
101	STNSQSDLDS	IQAEITQRLN	EIDRVSGQTQ	FNGVKVLAQD	NTLTIQVGAN
151	DGETIDIDLK	QINSQTLGLD	SLNVQKAYDV	KDTAVTTKAY	ANNGTTLDVS
201	GLDDAAIKAA	TGGTNGTASV	TGGAVKFDAD	NNKYFVTIGG	FTGADAAKNG
251	DYEVNVATDG	TVTLAAGATK	TTMPAGATTK	TEVQELKDTP	AVVSADAKNA
301	LIAGGVDATD	ANGAELVKMS	YTDKNGKTIE	GGYALKAGDK	YYAADYDEAT
351	GAIKAKTTSY	TAADGTTKTA	ANQLGGVDGK	TEVVTIDGKT	YNASKAAGHD
401	FKAQPELAEA	AAKTTENPLQ	KIDAALAQVD	ALRSDLGAVQ	NRFNSAITNL
451	GNTVNNLSEA	RSRIEDSDYA	TEVSNMSRAQ	ILQQAGTSVL	AQANQVPQNV
501	LSLLAKGIAP	LQLGNCSVAG	WILGNPECEL	LISRESWSYI	VEKPNPENGT
551	CYPGHFADYE	ELREQLSSVS	SFERFEIFPK	ESSWPNHTTT	GVSASCSHNG
601	ESSFYKNLLW	LTGKNGLYPN	LSKSANNKE	KEVLVLWGVH	HPPNIGDQRA
651	LYHKENAYVS	VVSSHYSRKF	TPEIAKRPKV	RDQEGRINYY	WTLLEPGDTI
701	IFEANGNLIA	PRYAFALSRG	FGSGIINS		

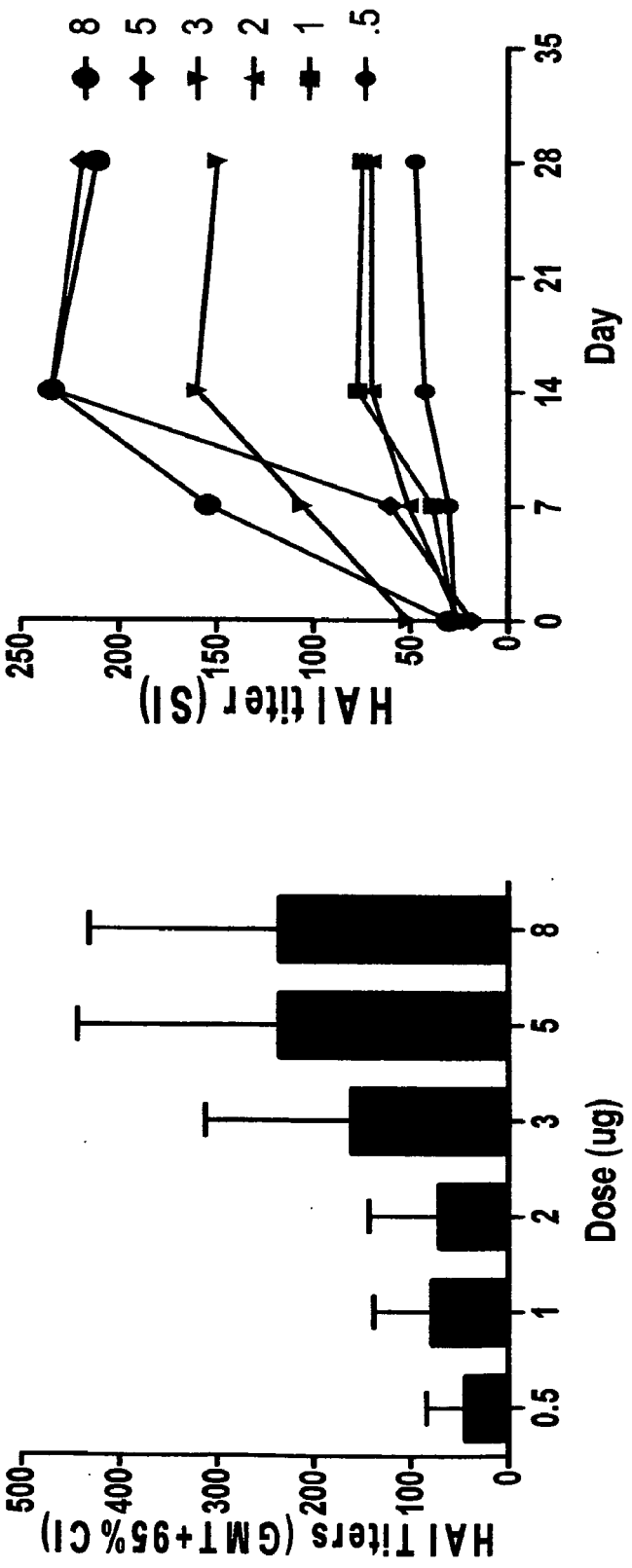

A
HAI Titers (GMT+95% CI)
500
400
300
200
100
0
0.5
1
2
3
5
8
Dose (ug)
B
HAI titer (SI)
250
200
150
100
50
0
0
7
14
21
28
35
Day
8
5
3
2
1
.5

Figure 2

2/10

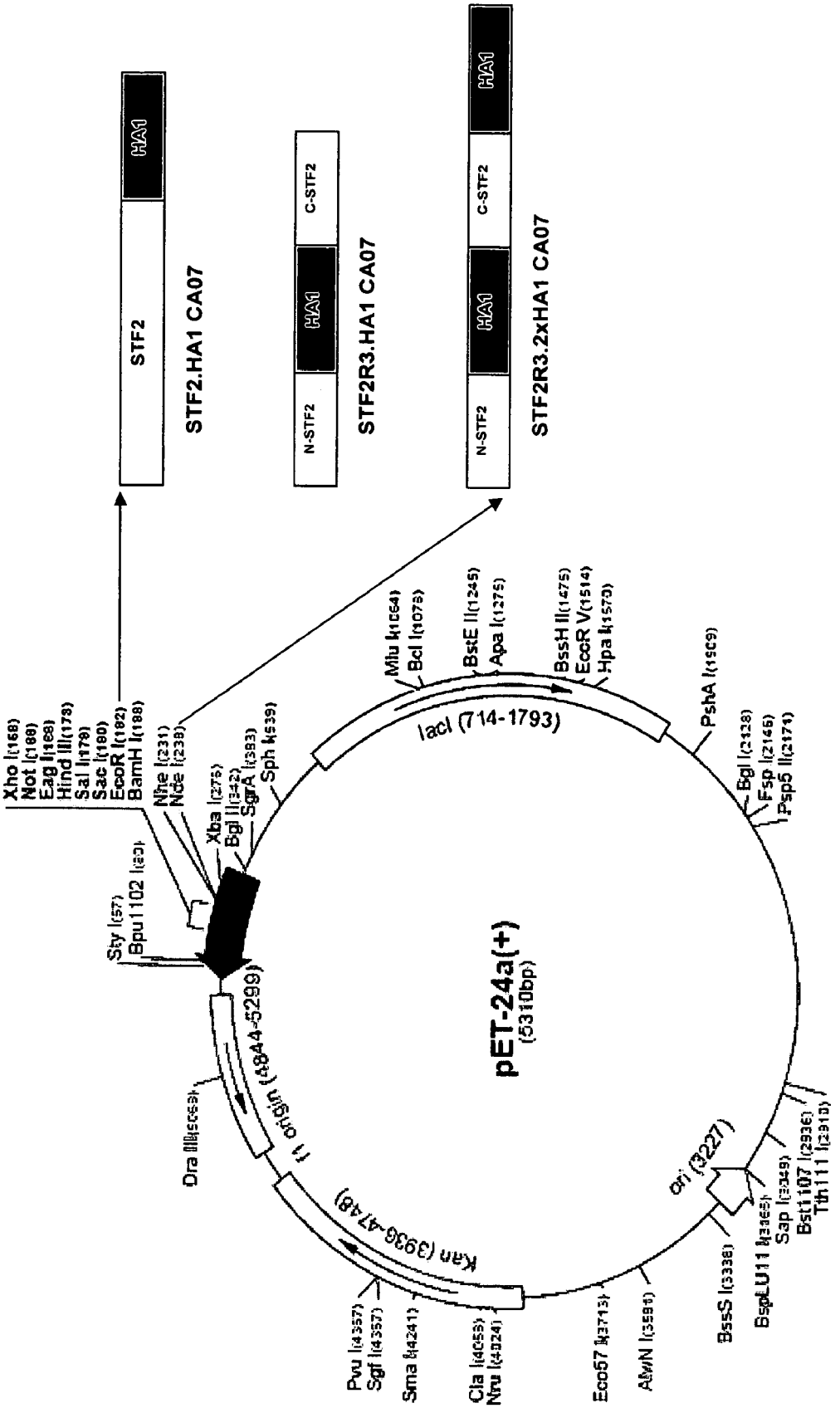

STF2
HA1
STF2.HA1 CA07
N-STF2
HA1
C-STF2
STF2R3.HA1 CA07
N-STF2
HA1
C-STF2
HA1
STF2R3.2xHA1 CA07
pET-24a(+)
(5310bp)
lacI (714-1793)
Kan (3939-4748)
f1 origin (4844-5299)
ori (3227)
Xho I(158)
Not I(168)
Eag I(168)
Hind III(178)
Sal I(179)
Sac I(180)
EcoR I(182)
BamH I(188)
Nhe I(231)
Nde I(238)
Xba I(275)
Bgl II(342)
SgrA I(383)
Sph I(539)
Sty I(57)
Bpu1102 I(63)
Dra III(658)
Pvu I(4357)
Sgf I(4357)
Sma I(4241)
Cla I(4053)
Nru I(4024)
Eco57 I(3713)
AlwN I(3584)
BssS I(3338)
BspLU11 I(3465)
Sap I(3349)
Bst1107 I(2936)
Tth111 I(2918)
Bgl I(2428)
Fsp I(2145)
Psp5 II(2171)
PshA I(1509)
Mlu I(1054)
Bcl I(1078)
BstE II(1245)
Apa I(1275)
BssH II(1475)
EcoR V(1514)
Hpa I(1570)

Figure 3

Figure 4

HL184 STF2.HA1-2 CA7 (CA07 H1N1) (VAX 128A) (SEQ ID 2)

ATGGCACAAGTAATCAACACTAACAGTCTGTCGCTGCTGACCCAGAATAACCTGAACAAATCCCAGTCCGCACTGGG
CACCGCTATCGAGCGTCTGTCTTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGTCAGGCGATTGCTA
ACCGTTTCACCGCGAACATCAAAGGTCTGACTCAGGCTTCCCGTAACGCTAACGACGGTATCTCCATTGCGCAGACC
ACTGAAGGCGCGCTGAACGAAATCAACAACAACCTGCAGCGTGTGCGTGAACTGGCGGTTCAGTCTGCTAACAGCAC
CAACTCCCAGTCTGACCTCGACTCCATCCAGGCTGAAATCACCCAGCGCCTGAACGAAATCGACCGTGTATCCGGCC
AGACTCAGTTCAACGGCGTGAAAGTCCTGGCGCAGGACAACACCCTGACCATCCAGGTTGGCGCCAACGACGGTGAA
ACTATCGATATCGATCTGAAGCAGATCAACTCTCAGACCCTGGGTCTGGACTCACTGAACGTGCAGAAAGCGTATGA
TGTGAAAGATACAGCAGTAACAACGAAAGCTTATGCCAATAATGGTACTACACTGGATGTATCGGGTCTTGATGATG
CAGCTATTAAAGCGGCTACGGGTGGTACGAATGGTACGGCTTCTGTAACCGGTGGTGCGGTTAAATTTGACGCAGAT
AATAACAAGTACTTTGTTACTATTGGTGGCTTTACTGGTGCTGATGCCGCCAAAAATGGCGATTATGAAGTTAACGT
TGCTACTGACGGTACAGTAACCCTTGCGGCTGGCGCAACTAAAACCACAATGCCTGCTGGTGCGACAACTAAAACAG
AAGTACAGGAGTTAAAAGATACACCGGCAGTTGTTTCAGCAGATGCTAAAAATGCCTTAATTGCTGGCGGCGTTGAC
GCTACCGATGCTAATGGCGCTGAGTTGGTCAAAATGTCTTATACCGATAAAAATGGTAAGACAATTGAAGGCGGTTA
TGCGCTTAAAGCTGGCGATAAGTATTACGCCGCAGATTACGATGAAGCGACAGGAGCAATTAAAGCTAAAACTACAA
GTTATACTGCTGCTGACGGCACTACCAAAACAGCGGCTAACCAACTGGGTGGCGTAGACGGTAAAACCGAAGTCGTT
ACTATCGACGGTAAAACCTACAATGCCAGCAAAGCCGCTGGTCATGATTTCAAAGCACAACCAGAGCTGGCGGAAGC
AGCCGCTAAAACCACCGAAAACCCGCTGCAGAAAATTGATGCCGCGCTGGCGCAGGTGGATGCGCTGCGCTCTGATC
TGGGTGCGGTACAAAACCGTTTCAACTCTGCTATCACCAACCTGGGCAATACCGTAAACAATCTGTCTGAAGCGCGT
AGCCGTATCGAAGATTCCGACTACGCGACCGAAGTTTCCAACATGTCTCGCGCGCAGATTCTGCAGCAGGCCGGTAC
TTCCGTTCTGGCGCAGGCTAACCAGGTCCCGCAGAACGTGCTGTCTCTGTTAGCGAGC**GGCGTCGCACCGCTGCATC**
TGGGTAAGTGTAACATTGCTGGTTGGATTCTGGGTAACCCAGAGTGTGAGAGCCTGTCCACCGCGAGCAGCTGGAGC
TATATCGTCGAAACCCCGAGCAGCGACAATGGCACCTGCTATCCTGGCGACTTCATTGATTACGAAGAACTGCGTGA
GCAACTGAGCAGCGTGTCGAGCTTTGAGCGTTTTGAAATCTTCCCGAAAACCAGCAGCTGGCCGAATCATGACAGCA
ATAAGGGTGTCACGGCAGCGTGCCCGCACGCTGGTGCGAAATCCTTTTACAAAAACTTGATTTGGCTGGTGAAGAAA
GGCAATAGCTACCCGAAACTGTCTAAGTCCTACATCAATGATAAGGGTAAAGAAGTTCTGGTTCTGTGGGGCATCCA
CCACCCGAGCACTTCTGCGGATCAACAATCTCTGTACCAGAACGCCGACGCCTACGTTTTCGTTGGCAGCTCCCGTT
ACAGCAAGAAATTCAAACCGGAGATTGCGATTCGCCCGAAGGTCCGTGACCAGGAAGGTCGCATGAACTACTATTGG
ACCCTGGTGGAGCCGGGTGATAAGATCACGTTTGAAGCCACGGGTAACTTGGTGGTTCCGCGCTATGCGTTCGCGAT
GGAGCGTAACGCAGGCAGCGGTATCATCATTTCGTAG (2190 BP)

Figure 5 5/10

HL184 STF2.HA1-2 CA7 (CA07 H1N1) (VAX 128A) (SEQ ID 3)

MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKGLTQASRNANDGISIAQT
TEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRLNEIDRVSGQTQFNGVKVLAQDNTLTIQVGANDGE
TIDIDLKQINSQTLGLDSLNVQKAYDVKDTAVTTKAYANNGTTLDVSGLDDAAIKAATGGTNGTASVTGGAVKFDAD
NNKYFVTIGGFTGADAAKNGDYEVNVATDGTVTLAAGATKTTMPAGATTKTEVQELKDTPAVVSADAKNALIAGGVD
ATDANGAELVKMSYTDKNGKTIEGGYALKAGDKYYAADYDEATGAIKAKTTSYTAADGTTKTAANQLGGVDGKTEVV
TIDGKTYNASKAAGHDFKAQPELAEAAAKTTENPLQKIDAALAQVDALRSDLGAVQNRFNSAITNLGNTVNNLSEAR
SRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLAS**GVAPLHLGKCNIAGWILGNPECESLSTASSWS**
YIVETPSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKK
GNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYW
TLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIIS*

Figure 6

HL185 STF2R3 HA1-2 CA7 (CA07 H1N1) (VAX 128B) (SEQ ID 5)

ATGGCACAAGTAATCAACACTAACAGTCTGTCGCTGCTGACCCAGAATAACCTGAACAAATCCCAGTCCGCACTGGG
CACCGCTATCGAGCGTCTGTCTTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGTCAGGCGATTGCTA
ACCGTTTCACCGCGAACATCAAAGGTCTGACTCAGGCTTCCCGTAACGCTAACGACGGTATCTCCATTGCGCAGACC
ACTGAAGGCGCGCTGAACGAAATCAACAACAACCTGCAGCGTGTGCGTGAACTGGCGGTTCAGTCTGCTAACAGCAC
CAACTCCCAGTCTGACCTCGACTCCATCCAGGCTGAAATCACCCAGCGCCTGAACGAAATCGACCGTGTATCCGGCC
AGACTCAGTTCAACGGCGTGAAAGTCCTGGCGCAGGACAACACCCTGACCATCCAGGTTGGCGCCAACGACGGTGAA
ACTATCGATATCGATCTGAAGCAGATCAACTCTCAGACCCTGGGTCTGGACTCACTGAACGTGCAGAAAGCGTATGA
TGTGAAAGATACAGCAGTAACAACGAAAGCT**GGCGTCGCACCGCTGCATCTGGGTAAGTGTAACATTGCTGGTTGGA**
TTCTGGGTAACCCAGAGTGTGAGAGCCTGTCCACCGCGAGCAGCTGGAGCTATATCGTCGAAACCCCGAGCAGCGAC
AATGGCACCTGCTATCCTGGCGACTTCATTGATTACGAAGAACTGCGTGAGCAACTGAGCAGCGTGTCGAGCTTTGA
GCGTTTTGAAATCTTCCCGAAAACCAGCAGCTGGCCGAATCATGACAGCAATAAGGGTGTCACGGCAGCGTGCCCGC
ACGCTGGTGCGAAATCCTTTTACAAAAACTTGATTTGGCTGGTGAAGAAAGGCAATAGCTACCCGAAACTGTCTAAG
TCCTACATCAATGATAAGGGTAAAGAAGTTCTGGTTCTGTGGGGCATCCACCACCCGAGCACTTCTGCGGATCAACA
ATCTCTGTACCAGAACGCCGACGCCTACGTTTTCGTTGGCAGCTCCCGTTACAGCAAGAAATTCAAACCGGAGATTG
CGATTCGCCCGAAGGTCCGTGACCAGGAAGGTCGCATGAACTACTATTGGACCCTGGTGGAGCCGGGTGATAAGATC
ACGTTTGAAGCCACGGGTAACTTGGTGGTTCCGCGCTATGCGTTCGCGATGGAGCGTAACGCAGGCAGCGGTATCAT
CATTTCGTCAGTTGTTTCAGCAGATGCTAAAAATGCCTTAATTGCTGGCGGCGTTGACGCTACCGATGCTAATGGCG
CTGAGTTGGTCAAAATGTCTTATACCGATAAAAATGGTAAGACAATTGAAGGCGGTTATGCGCTTAAAGCTGGCGAT
AAGTATTACGCCGCAGATTACGATGAAGCGACAGGAGCAATTAAAGCTAAAACCACAAGTTATACTGCTGCTGACGG
CACTACCAAAACAGCGGCTAACCAACTGGGTGGCGTAGACGGTAAAACCGAAGTCGTTACTATCGACGGTAAAACCT
ACAATGCCAGCAAAGCCGCTGGTCATGATTTCAAAGCACAACCAGAGCTGGCGGAAGCAGCCGCTAAAACCACCGAA
AACCCGCTGCAGAAAATTGATGCCGCGCTGGCGCAGGTGGATGCGCTGCGCTCTGATCTGGGTGCGGTACAAAACCG
TTTCAACTCTGCTATCACCAACCTGGGCAATACCGTAAACAATCTGTCTGAAGCGCGTAGCCGTATCGAAGATTCCG
ACTACGCGACCGAAGTTTCCAACATGTCTCGCGCGCAGATTTTGCAGCAGGCCGGTACTTCCGTTCTGGCGCAGGCT
AACCAGGTCCCGCAGAACGTGCTGAGCCTGTTACGT**TAG (1884 bp)**

Figure 7

HL185 STF2R3 HA1-2 CA7 (CA07 H1N1)(VAX 128B) (SEQ ID6)

MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKGLTQASRNANDG
ISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRLNEIDRVSGQTQFNGVKVLAQDN
TLTIQVGANDGETIDIDLKQINSQTLGLDSLNVQKAYDVKDTAVTTKA**GVAPLHLGKCNIAGWILGNPECE**
SLSTASSWSYIVETPSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSWPNHDSNKGVTAACPHA
GAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFVGSSRYSKKF
KPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISSVVSADAKNALIA
GGVDATDANGAELVKMSYTDKNGKTIEGGYALKAGDKYYAADYDEATGAIKAKTTSYTAADGTTKTAANQL
GGVDGKTEVVTIDGKTYNASKAAGHDFKAQPELAEAAAKTTENPLQKIDAALAQVDALRSDLGAVQNRFNS
AITNLGNTVNNLSEARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR*

Figure 8

HL186 STF2R3.2xHA1-2 CA7 (CA07 H1N1)(VAX 128C) (SEQ ID 7)

ATGGCACAAGTAATCAACACTAACAGTCTGTCGCTGCTGACCCAGAATAACCTGAACAAATCCCAGTCCGC
ACTGGGCACCGCTATCGAGCGTCTGTCTTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGTC
AGGCGATTGCTAACCGTTTCACCGCGAACATCAAAGGTCTGACTCAGGCTTCCCGTAACGCTAACGACGGT
ATCTCCATTGCGCAGACCACTGAAGGCGCGCTGAACGAAATCAACAACAACCTGCAGCGTGTGCGTGAACT
GGCGGTTCAGTCTGCTAACAGCACCAACTCCCAGTCTGACCTCGACTCCATCCAGGCTGAAATCACCCAGC
GCCTGAACGAAATCGACCGTGTATCCGGCCAGACTCAGTTCAACGGCGTGAAAGTCCTGGCGCAGGACAAC
ACCCTGACCATCCAGGTTGGCGCCAACGACGGTGAAACTATCGATATCGATCTGAAGCAGATCAACTCTCA
GACCCTGGGTCTGGACTCACTGAACGTGCAGAAAGCGTATGATGTGAAAGATACAGCAGTAACAACGAAAG
CTGGCGTCGCACCGCTGCATCTGGGTAAGTGTAACATTGCTGGTTGGATTCTGGGTAACCCAGAGTGTGAG
AGCCTGTCCACCGCGAGCAGCTGGAGCTATATCGTCGAAACCCCGAGCAGCGACAATGGCACCTGCTATCC
TGGCGACTTCATTGATTACGAAGAACTGCGTGAGCAACTGAGCAGCGTGTCGAGCTTTGAGCGTTTTGAAA
TCTTCCCGAAAACCAGCAGCTGGCCGAATCATGACAGCAATAAGGGTGTCACGGCAGCGTGCCCGCACGCT
GGTGCGAAATCCTTTTACAAAAACTTGATTTGGCTGGTGAAGAAAGGCAATAGCTACCCGAAACTGTCTAA
GTCCTACATCAATGATAAGGGTAAAGAAGTTCTGGTTCTGTGGGGCATCCACCACCCGAGCACTTCTGCGG
ATCAACAATCTCTGTACCAGAACGCCGACGCCTACGTTTTCGTTGGCAGCTCCCGTTACAGCAAGAAATTC
AAACCGGAGATTGCGATTCGCCCGAAGGTCCGTGACCAGGAAGGTCGCATGAACTACTATTGGACCCTGGT
GGAGCCGGGTGATAAGATCACGTTTGAAGCCACGGGTAACTTGGTGGTTCCGCGCTATGCGTTCGCGATGG
AGCGTAACGCAGGCAGCGGTATCATCATTTCGTCAGTTGTTTCAGCAGATGCTAAAAATGCCTTAATTGCT
GGCGGCGTTGACGCTACCGATGCTAATGGCGCTGAGTTGGTCAAAATGTCTTATACCGATAAAAATGGTAA
GACAATTGAAGGCGGTTATGCGCTTAAAGCTGGCGATAAGTATTACGCCGCAGATTACGATGAAGCGACAG
GAGCAATTAAAGCTAAAACTACAAGTTATACTGCTGCTGACGGCACTACCAAAACAGCGGCTAACCAACTG
GGTGGCGTAGACGGTAAAACCGAAGTCGTTACTATCGACGGTAAAACCTACAATGCCAGCAAAGCCGCTGG
TCATGATTTCAAAGCACAACCAGAGCTGGCGGAAGCAGCCGCTAAAACCACCGAAAACCCGCTGCAGAAAA
TTGATGCCGCGCTGGCGCAGGTGGATGCGCTGCGCTCTGATCTGGGTGCGGTACAAAACCGTTTCAACTCT
GCTATCACCAACCTGGGCAATACCGTAAACAATCTGTCTGAAGCGCGTAGCCGTATCGAAGATTCCGACTA
CGCGACCGAAGTTTCCAACATGTCTCGCGCGCAGATTCTGCAGCAGGCCGGTACTTCCGTTCTGGCGCAGG
CTAACCAGGTCCCGCAGAACGTGCTGTCTCTGTTAGCGAGCGGCGTCGCACCGCTGCATCTGGGTAAGTGT
AACATTGCTGGTTGGATTCTGGGTAACCCAGAGTGTGAGAGCCTGTCCACCGCGAGCAGCTGGAGCTATAT
CGTCGAAACCCCGAGCAGCGACAATGGCACCTGCTATCCTGGCGACTTCATTGATTACGAAGAACTGCGTG
AGCAACTGAGCAGCGTGTCGAGCTTTGAGCGTTTTGAAATCTTCCCGAAAACCAGCAGCTGGCCGAATCAT
GACAGCAATAAGGGTGTCACGGCAGCGTGCCCGCACGCTGGTGCGAAATCCTTTTACAAAAACTTGATTTG
GCTGGTGAAGAAAGGCAATAGCTACCCGAAACTGTCTAAGTCCTACATCAATGATAAGGGTAAAGAAGTTC
TGGTTCTGTGGGGCATCCACCACCCGAGCACTTCTGCGGATCAACAATCTCTGTACCAGAACGCCGACGCC
TACGTTTTCGTTGGCAGCTCCCGTTACAGCAAGAAATTCAAACCGGAGATTGCGATTCGCCCGAAGGTCCG
TGACCAGGAAGGTCGCATGAACTACTATTGGACCCTGGTGGAGCCGGGTGATAAGATCACGTTTGAAGCCA
CGGGTAACTTGGTGGTTCCGCGCTATGCGTTCGCGATGGAGCGTAACGCAGGCAGCGGTATCATCATTTCG
TAG (2556 bp)

Figure 9

HL186 STF2R3.2xHA1-2 CA7 (CA07 H1N1) (VAX 128C) (SEQ ID 8)

MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKGLTQASRNANDG
ISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRLNEIDRVSGQTQFNGVKVLAQDN
TLTIQVGANDGETIDIDLKQINSQTLGLDSLNVQKAYDVKDTAVTTKA**GVAPLHLGKCNIAGWILGNPECE**
SLSTASSWSYIVETPSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSWPNHDSNKGVTAACPHA
GAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFVGSSRYSKKF
KPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISSVVSADAKNALIA
GGVDATDANGAELVKMSYTDKNGKTIEGGYALKAGDKYYAADYDEATGAIKAKTTSYTAADGTTKTAANQL
GGVDGKTEVVTIDGKTYNASKAAGHDFKAQPELAEAAAKTTENPLQKIDAALAQVDALRSDLGAVQNRFNS
AITNLGNTVNNLSEARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLAS**GVAPLHLGKC**
NIAGWILGNPECESLSTASSWSYIVETPSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSWPNH
DSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADA
YVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIIS

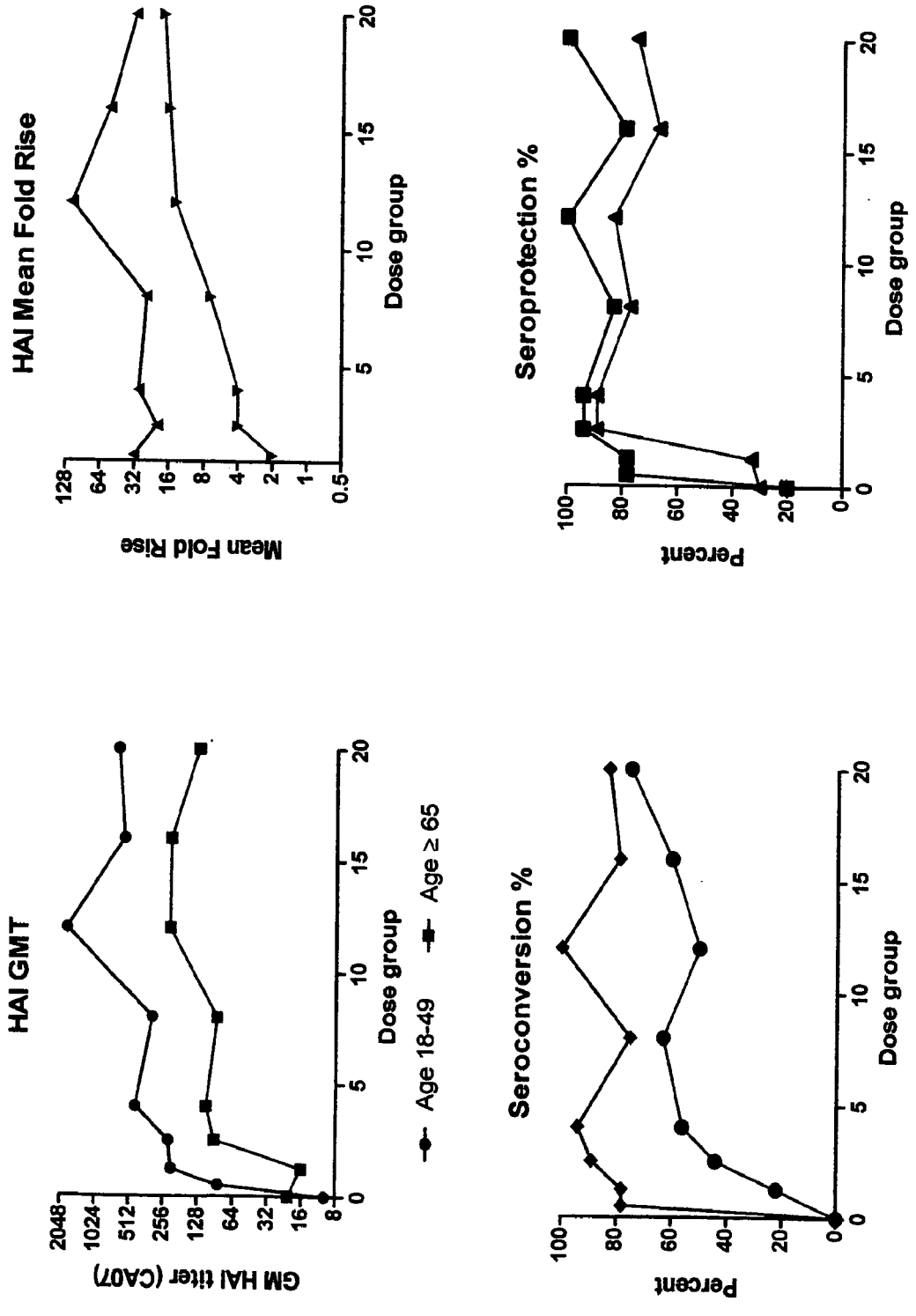

HAI Mean Fold Rise
Mean Fold Rise
128
64
32
16
8
4
2
1
0.5
0
5
10
15
20
Dose group
Seroprotection %
Percent
100
80
60
40
20
0
0
5
10
15
20
Dose group
HAI GMT
GM HAI titer (CA07)
2048
1024
512
256
128
64
32
16
8
0
5
10
15
20
Dose group
Age 18-49
Age ≥ 65
Seroconversion %
Percent
100
80
60
40
20
0
0
5
10
15
20
Dose group

Figure 10