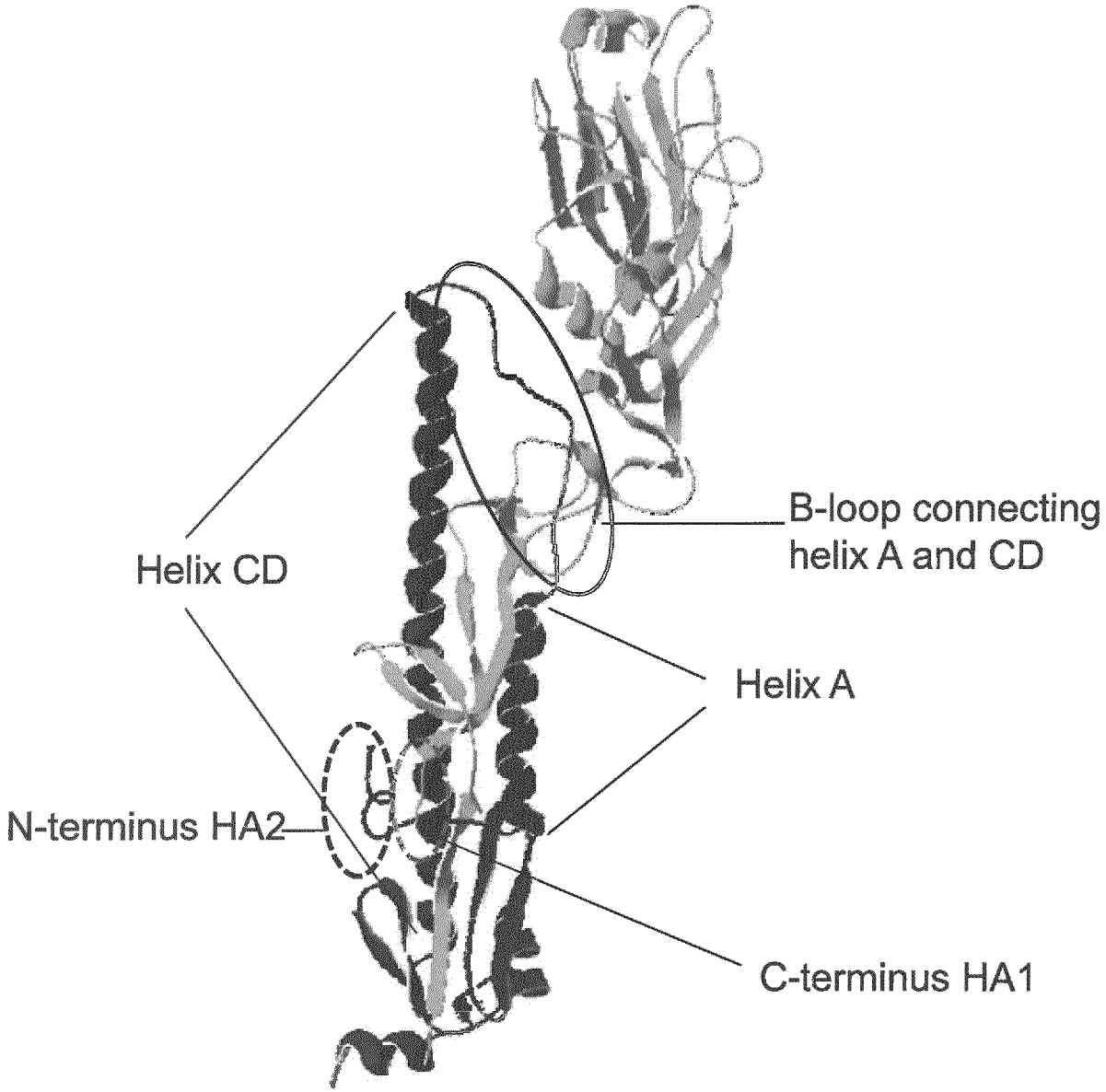

Helix CD
B-loop connecting
helix A and CD
Helix A
N-terminus HA2
C-terminus HA1

Fig. 1

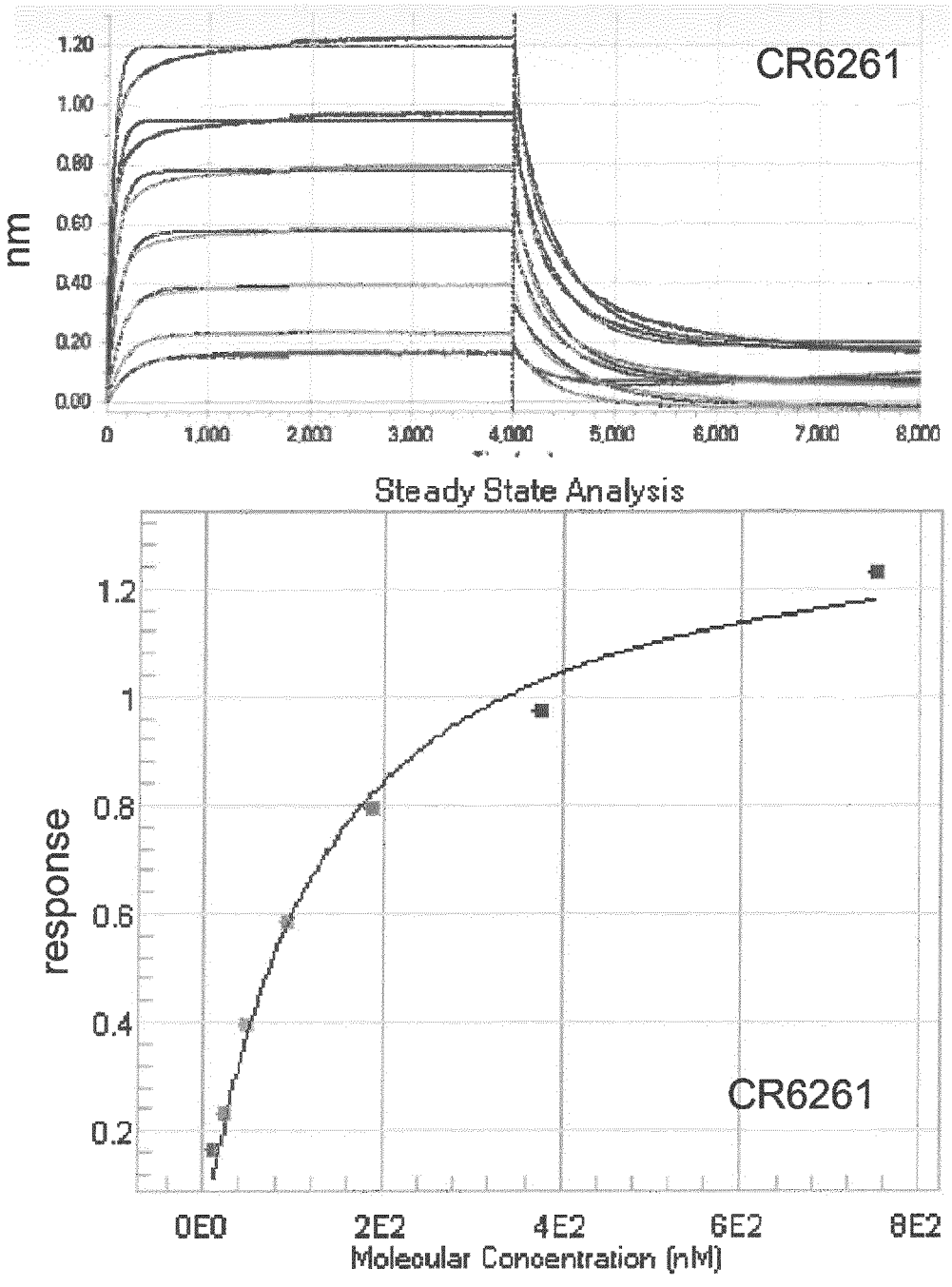


Fig.2A s127H1 SEQ ID NO: 66

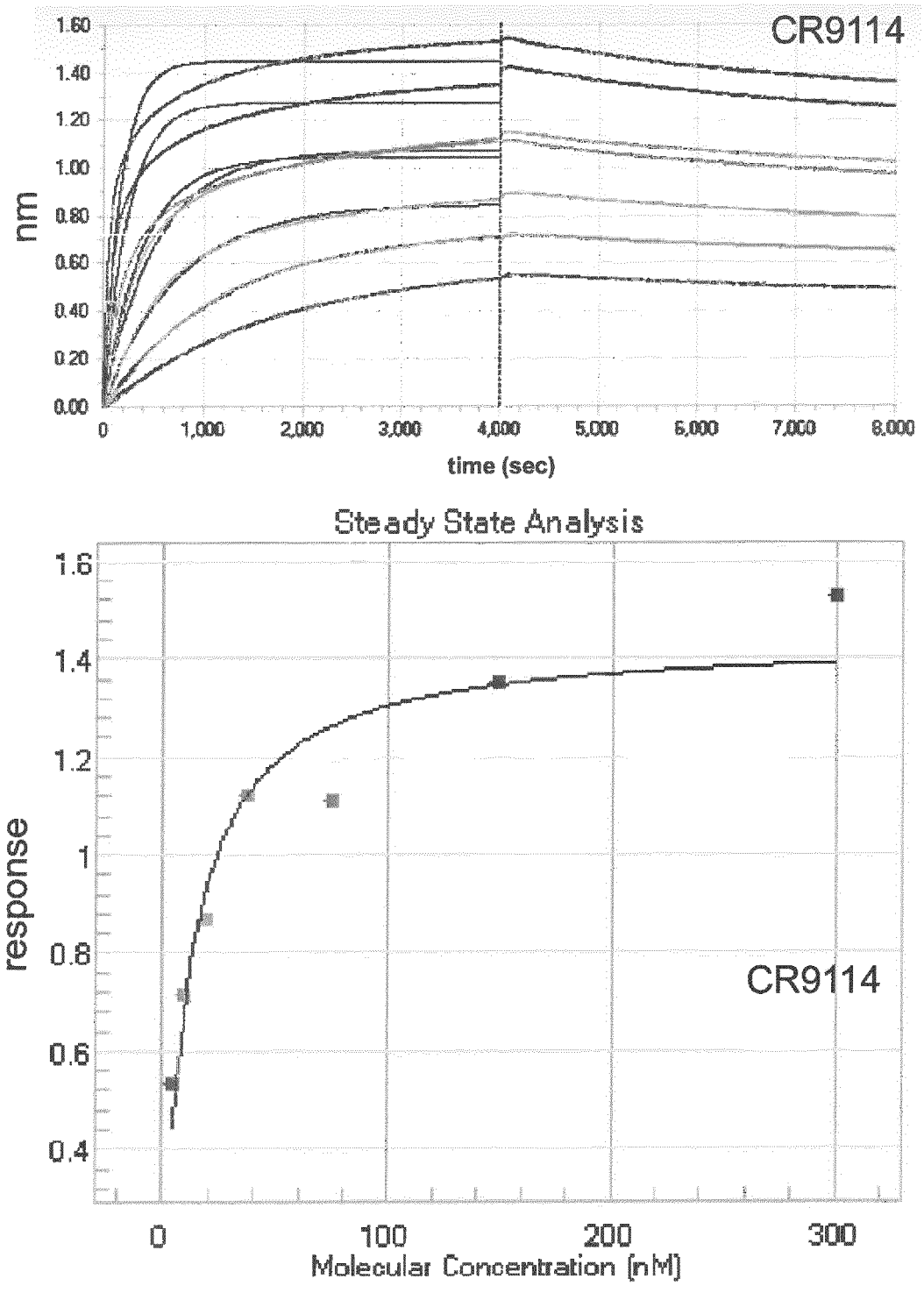


Fig.2A - continued s127H1 SEQ ID NO: 66

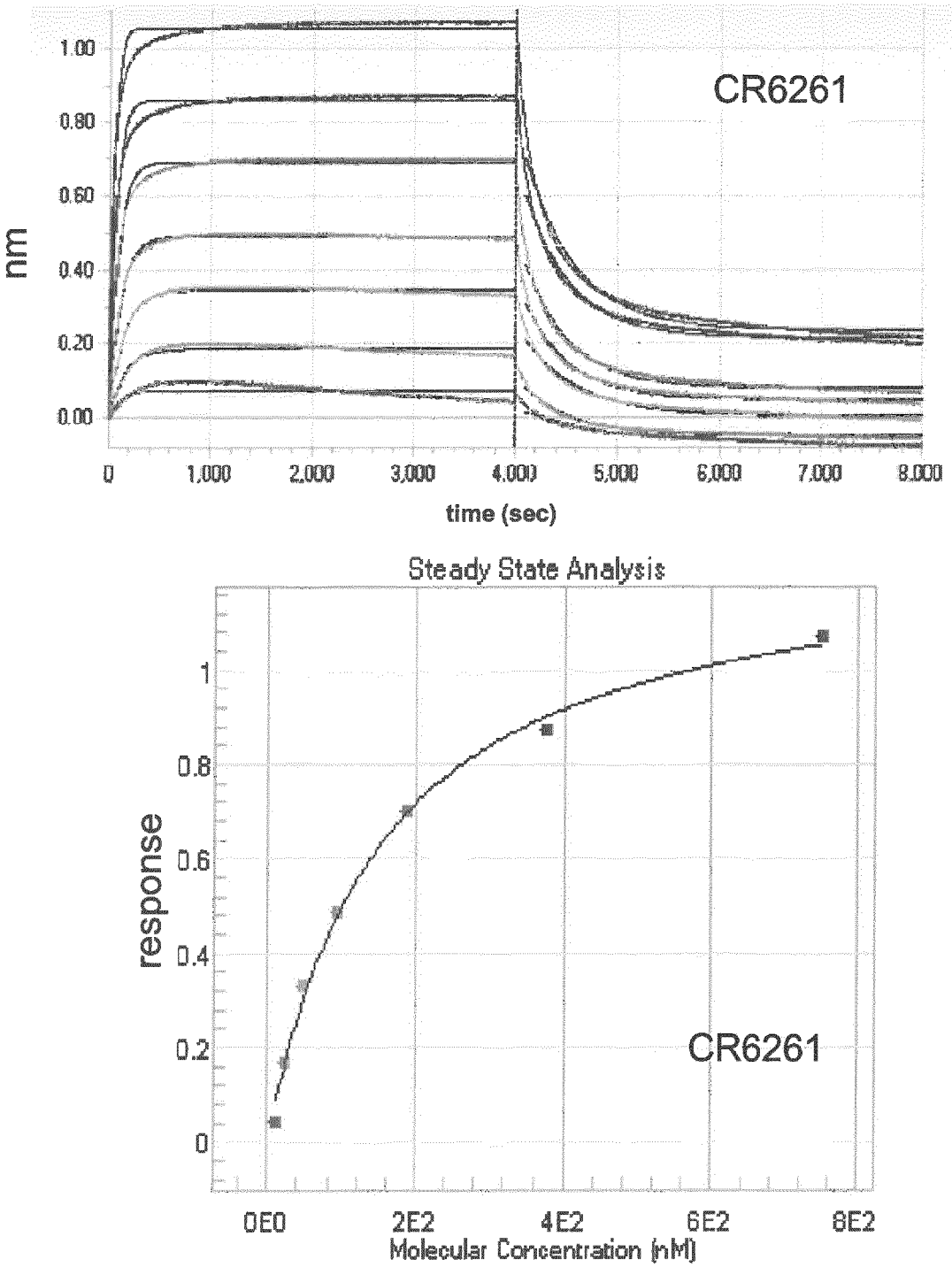


Fig. 2B s86B4 SEQ ID NO: 67

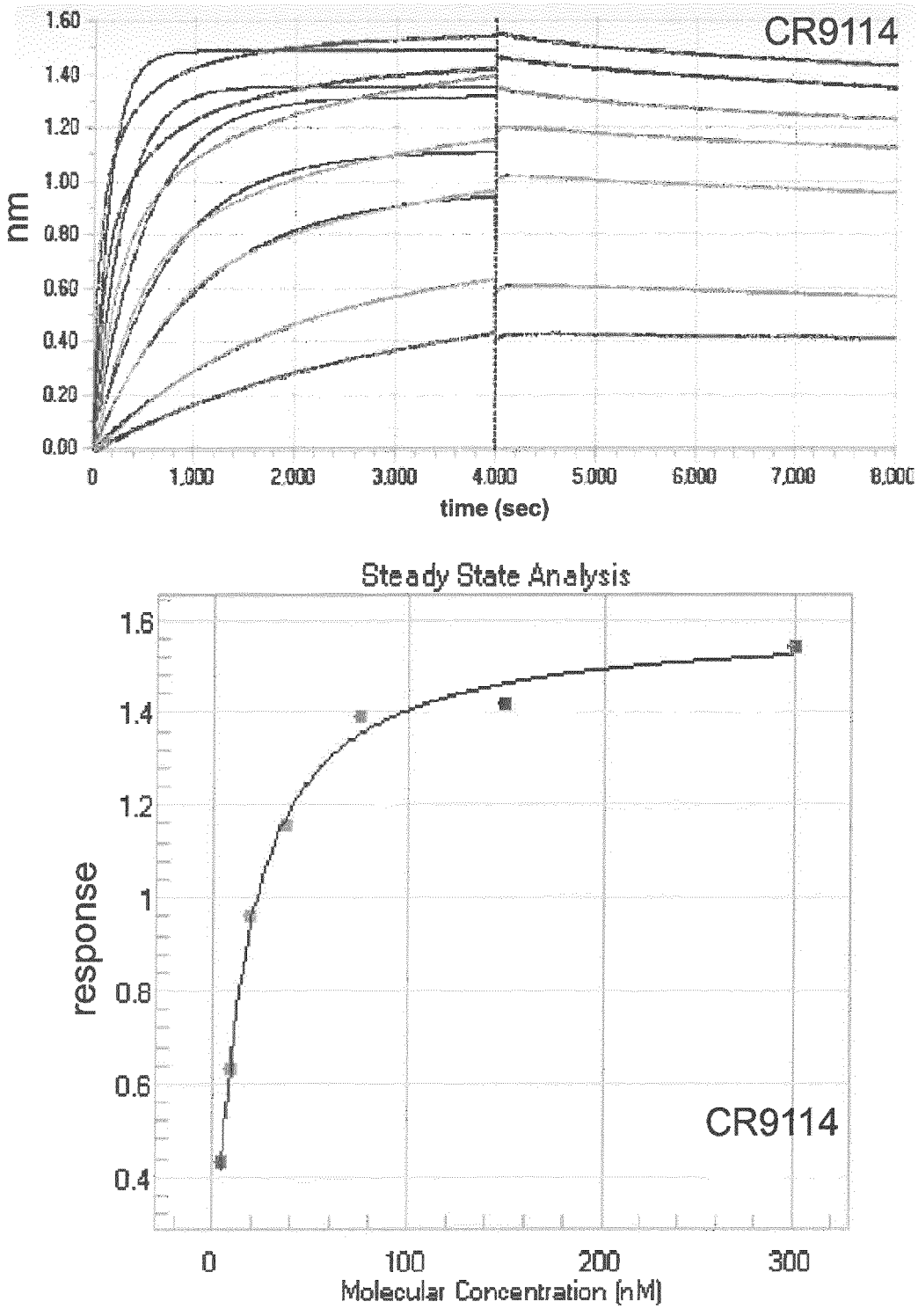


Fig. 2B – continued s86B4 SEQ ID NO: 67

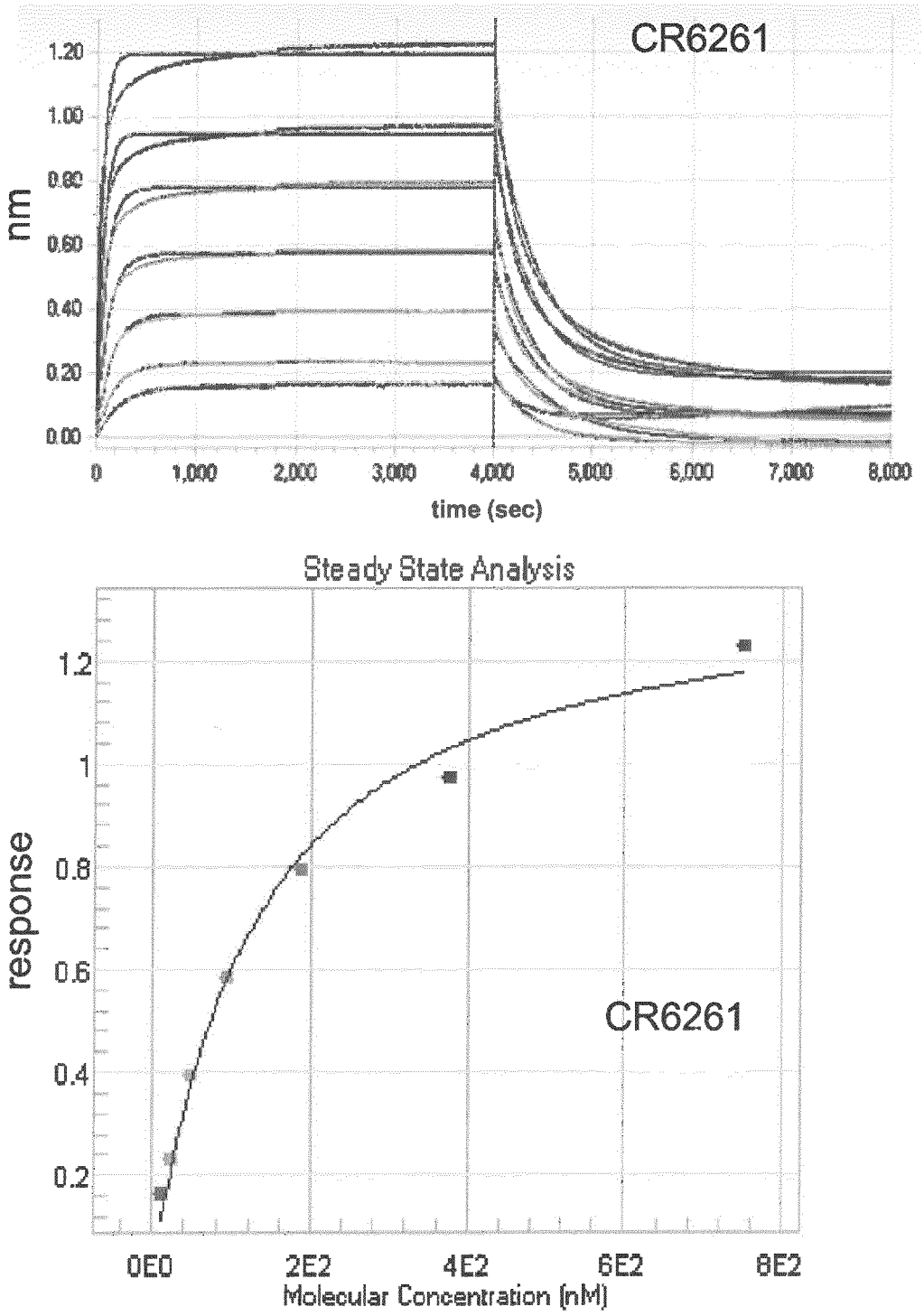


Fig. 2C s74H9 SEQ ID NO: 65

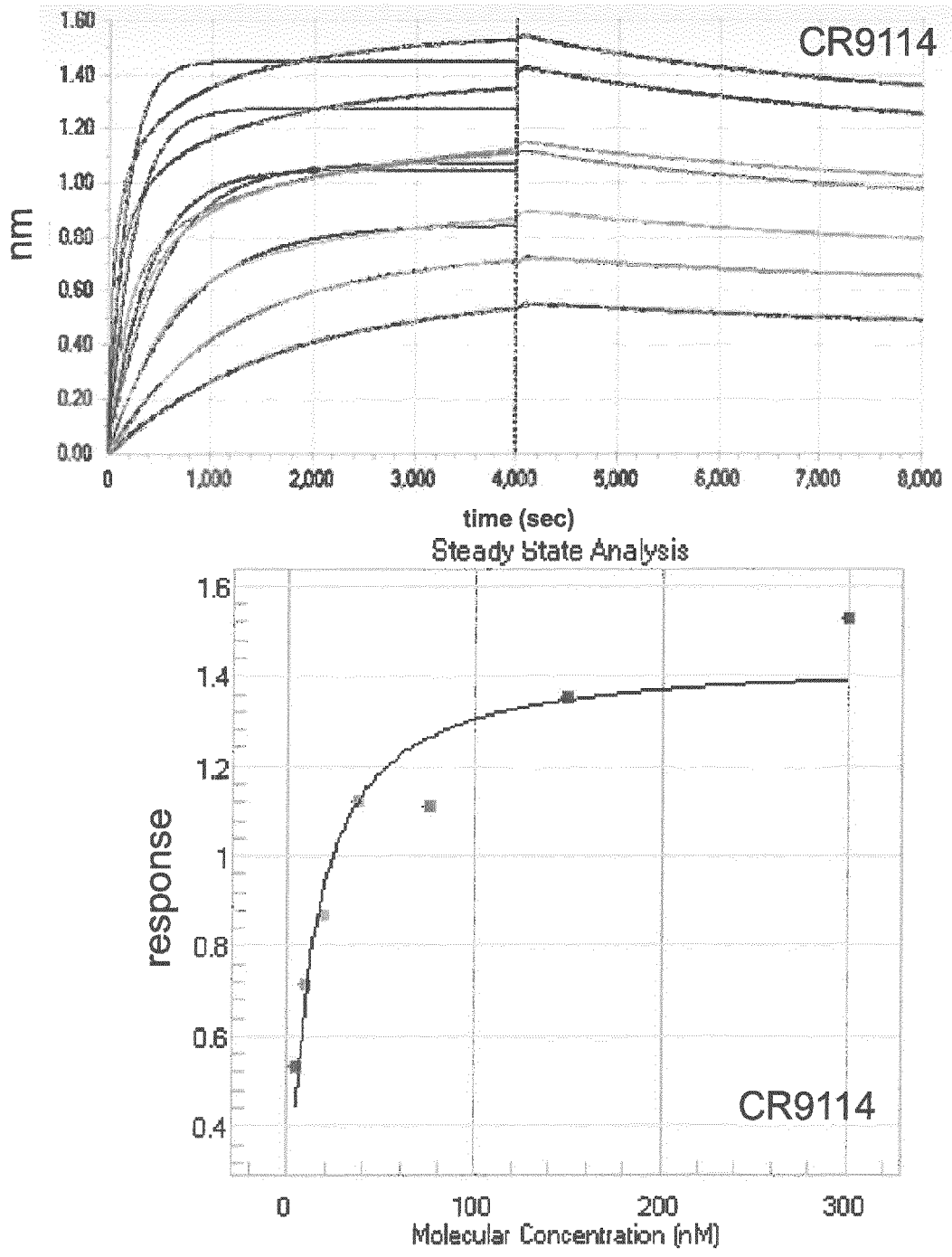


Fig. 2C - continued s74H9 SEQ ID NO: 65

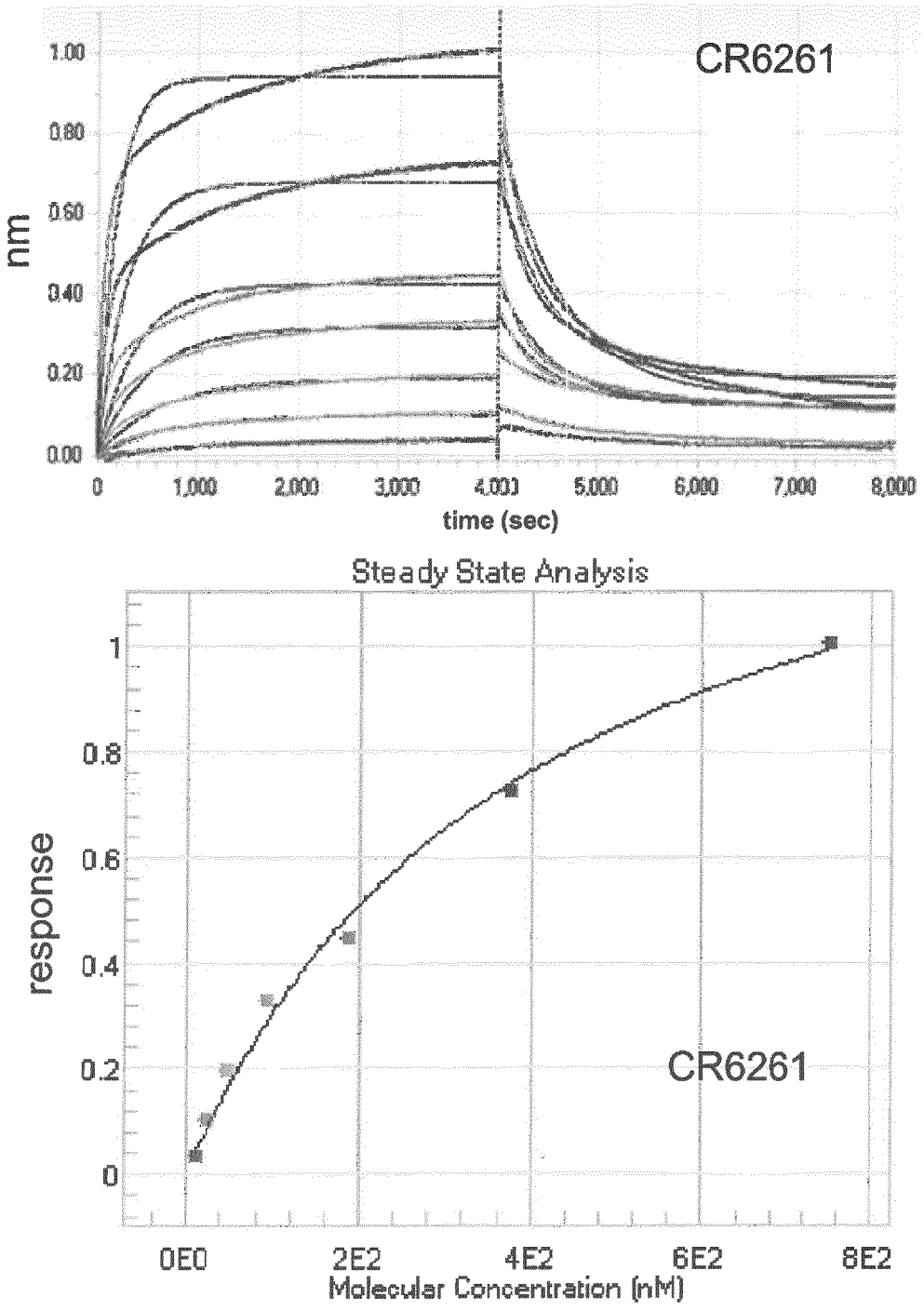
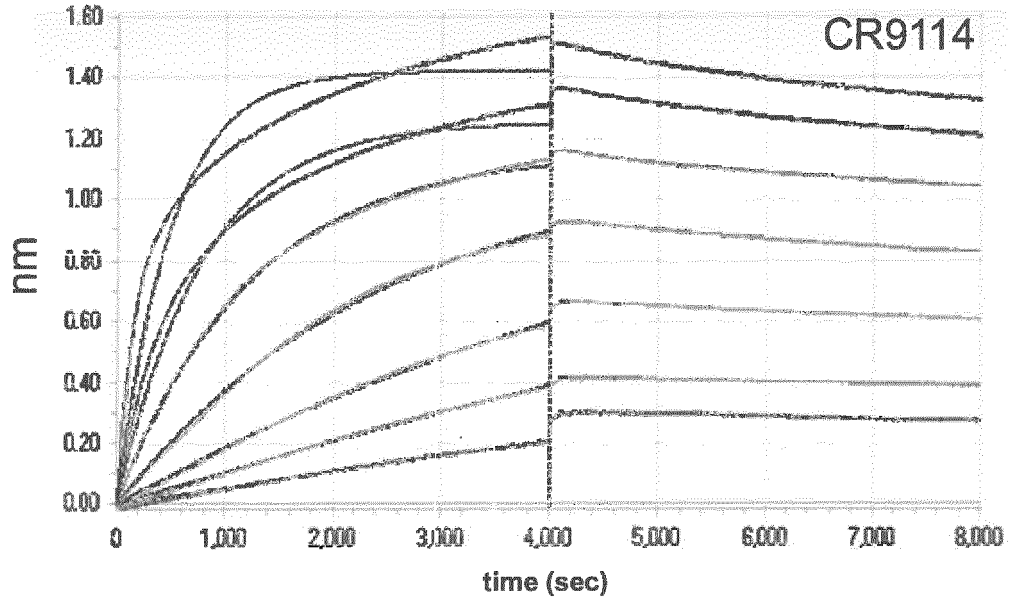


Fig. 2D s6E12 SEQ ID NO: 69



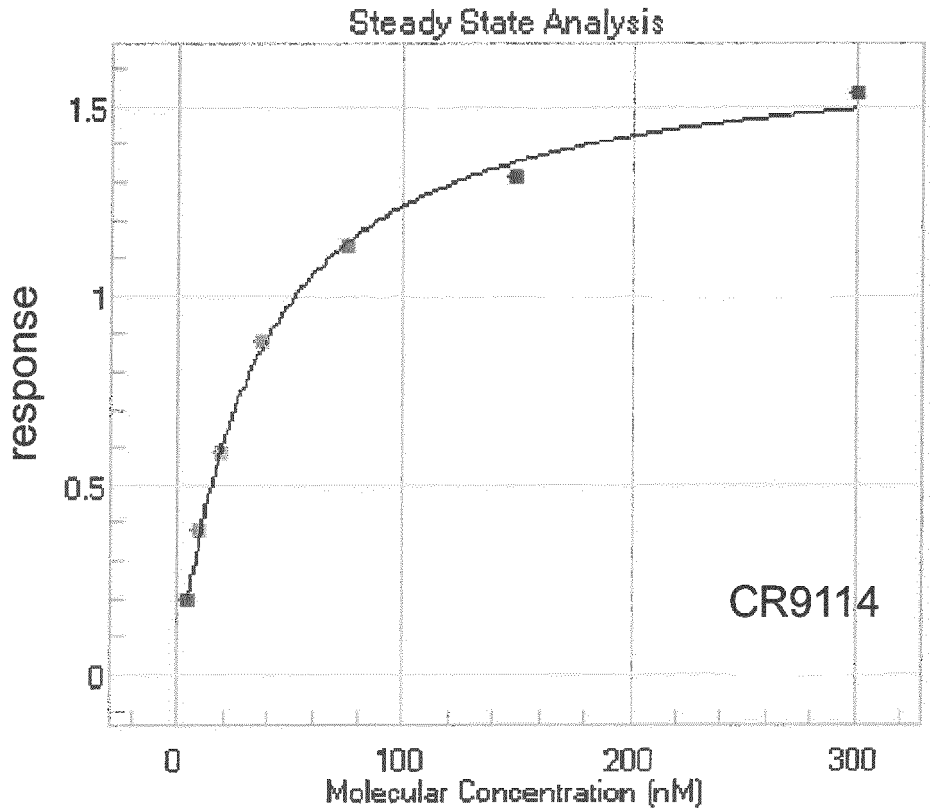
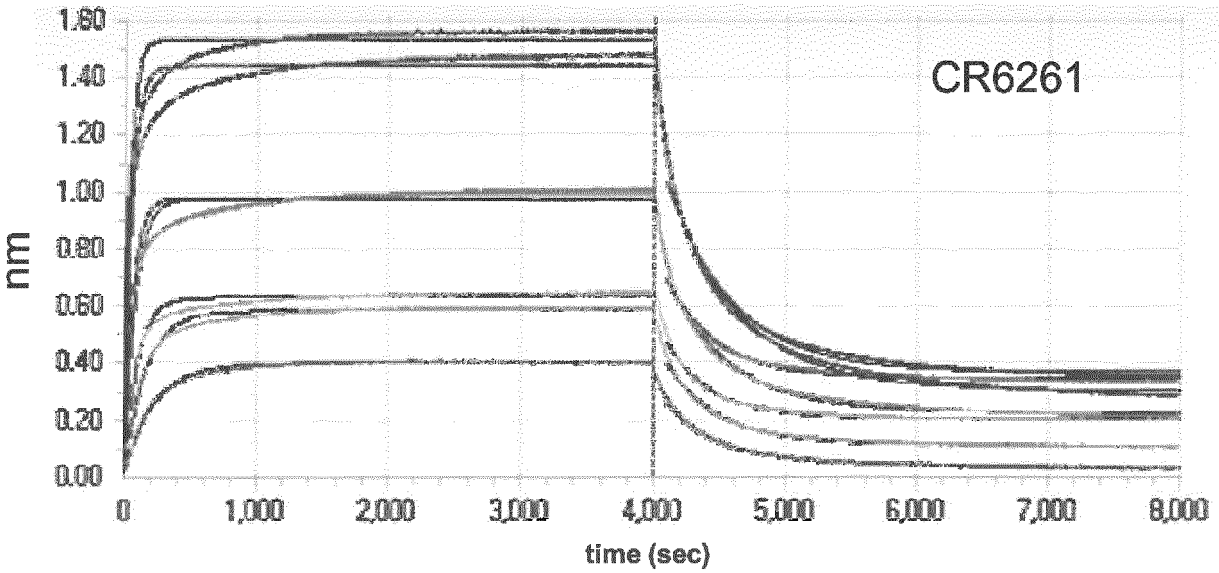


Fig. 2D - continued s6E12 SEQ ID NO: 69



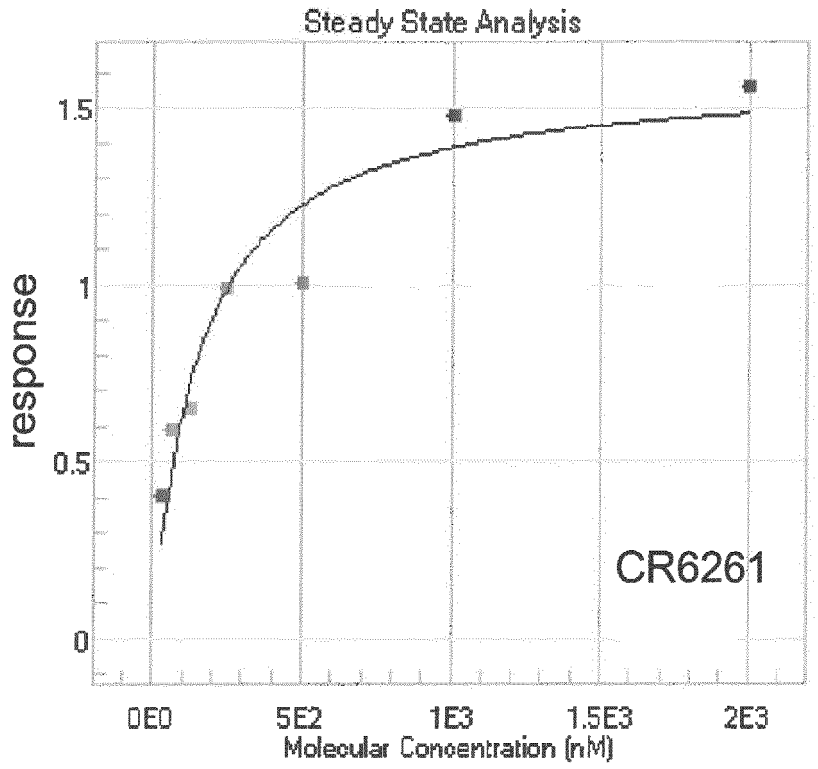
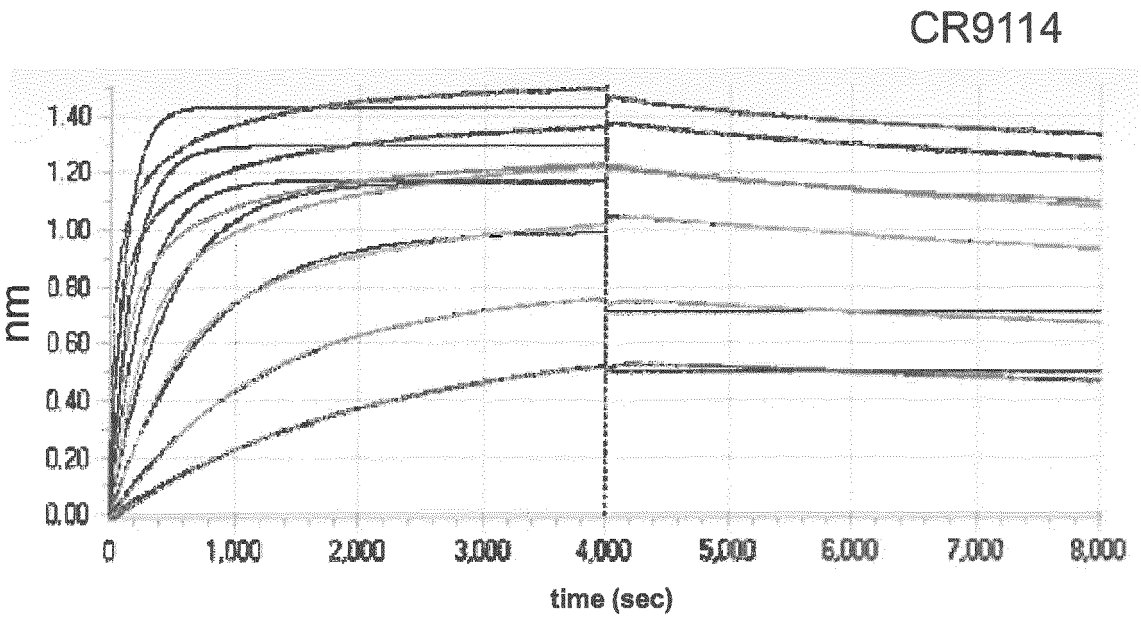


Fig. 2E s55G7 SEQ ID NO: 68



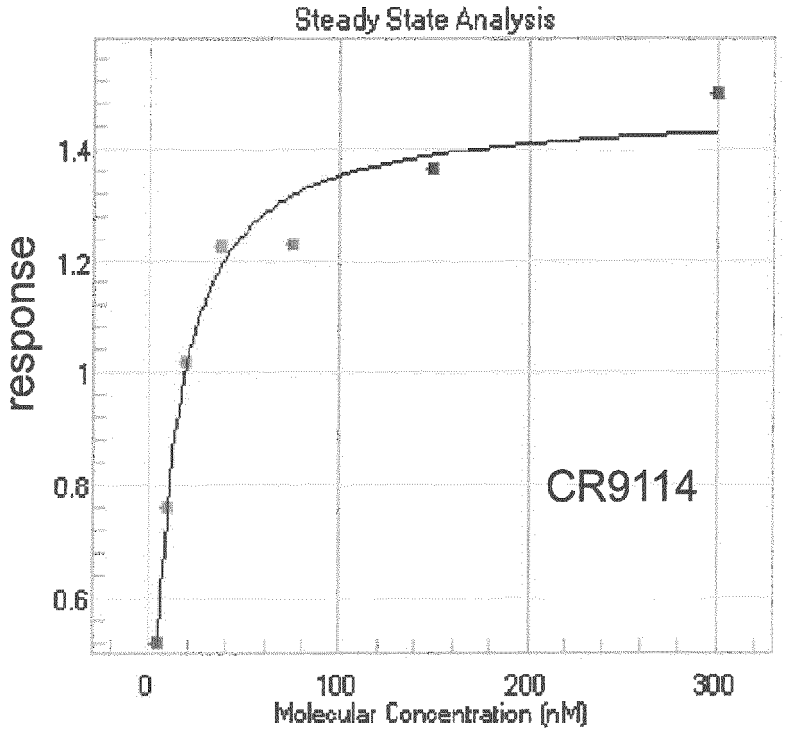
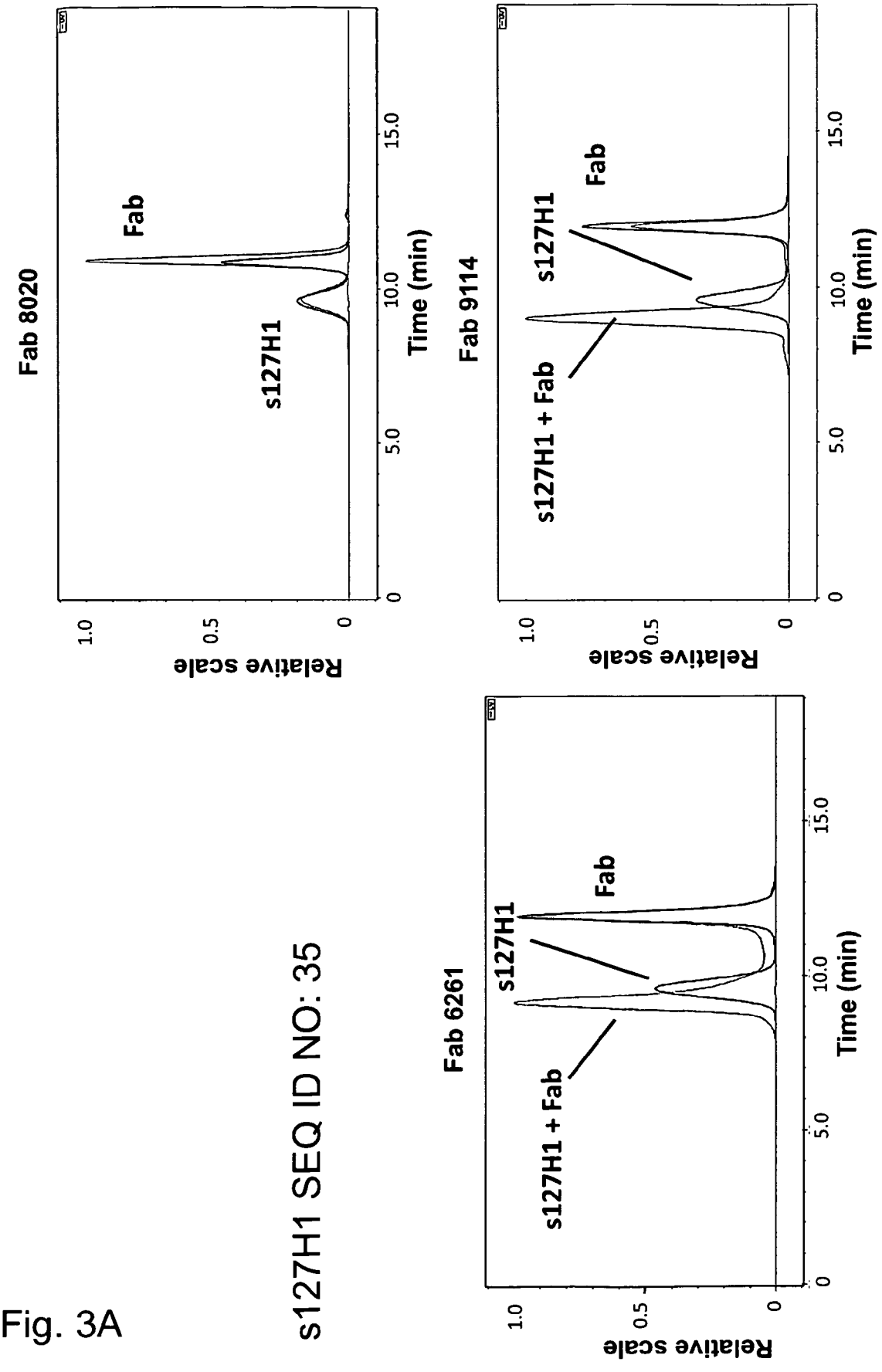
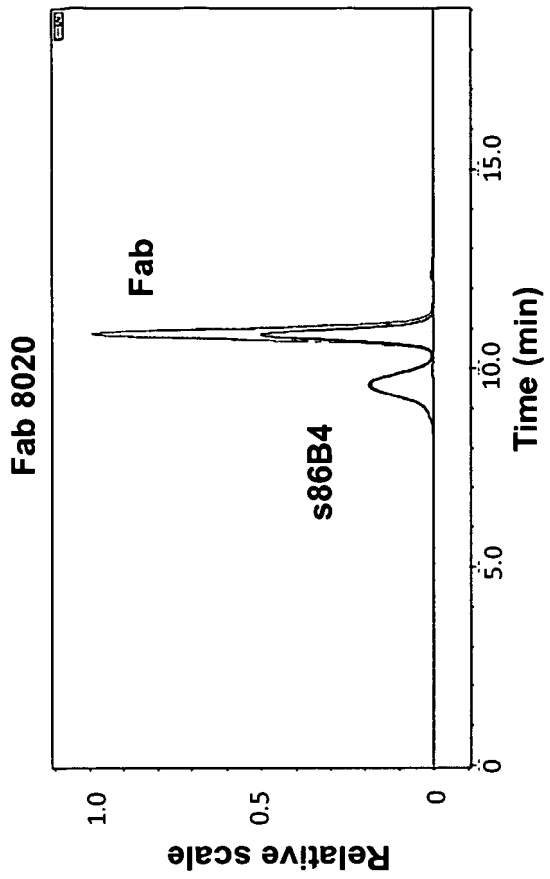


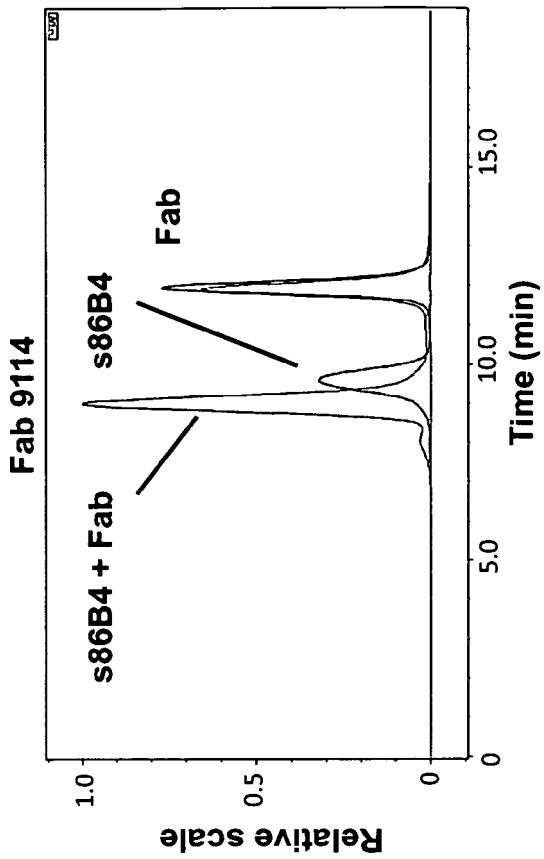
Fig. 2E - continued s55G7 SEQ ID NO: 68

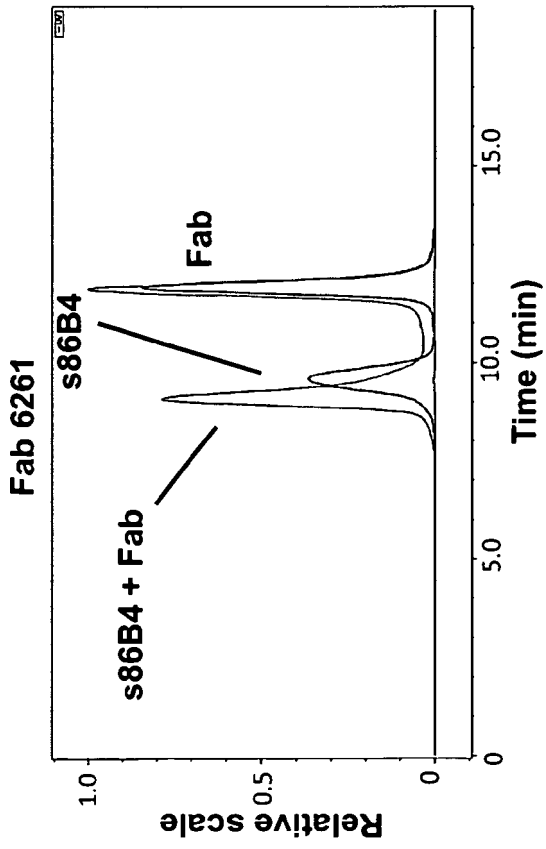


s127H1 SEQ ID NO: 35

Fig. 3A

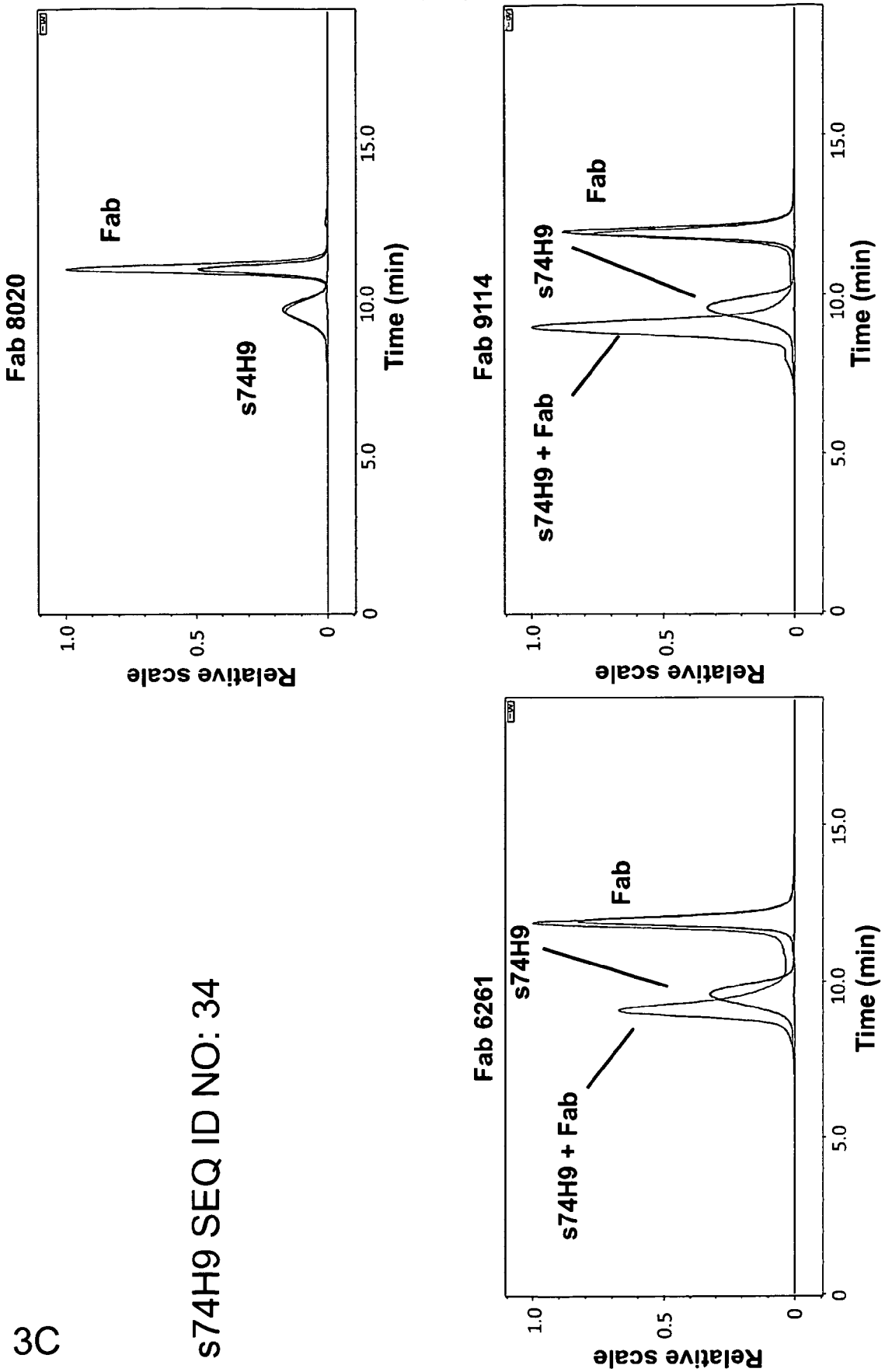






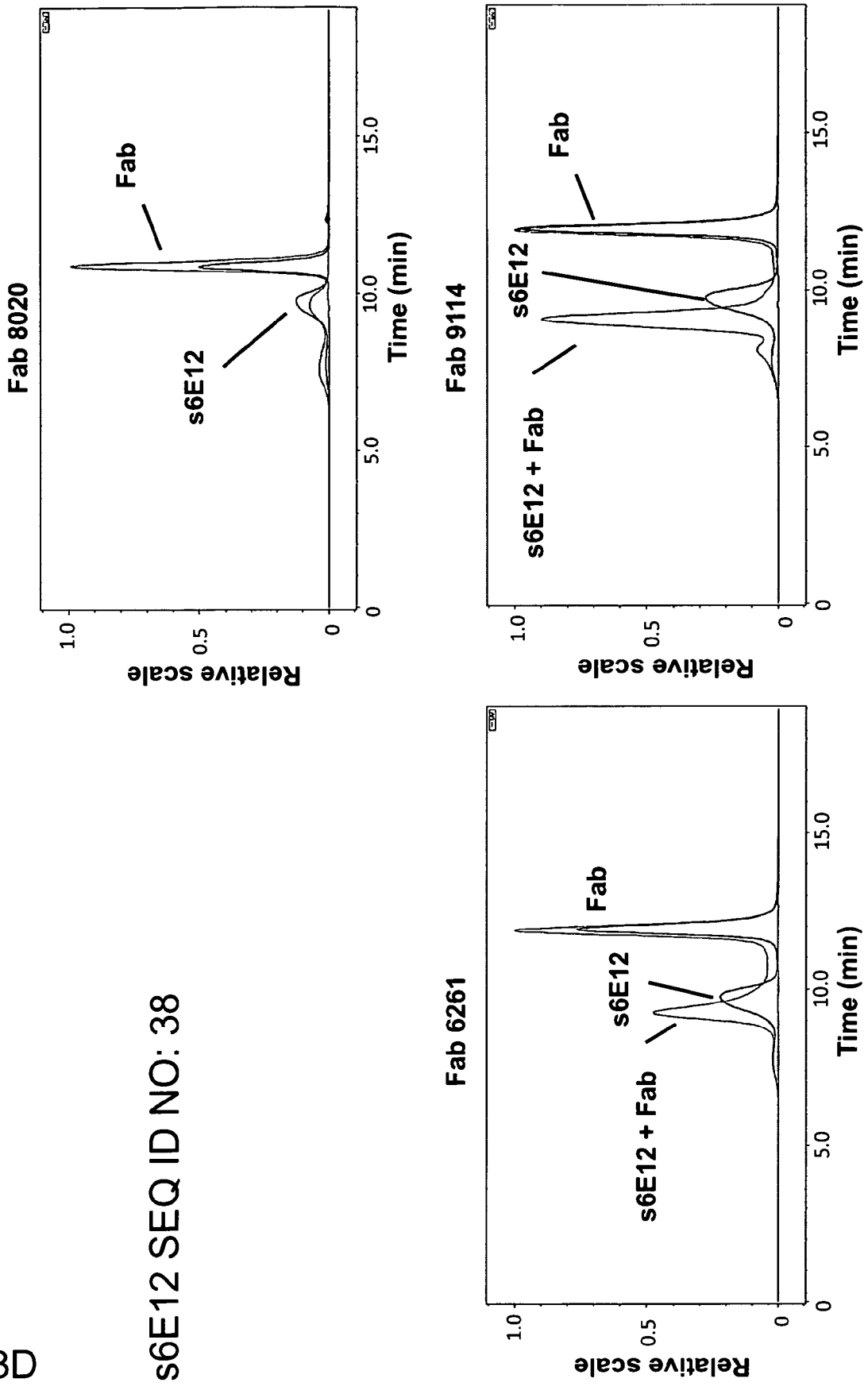
s86B4 SEQ ID NO: 36

Fig. 3B



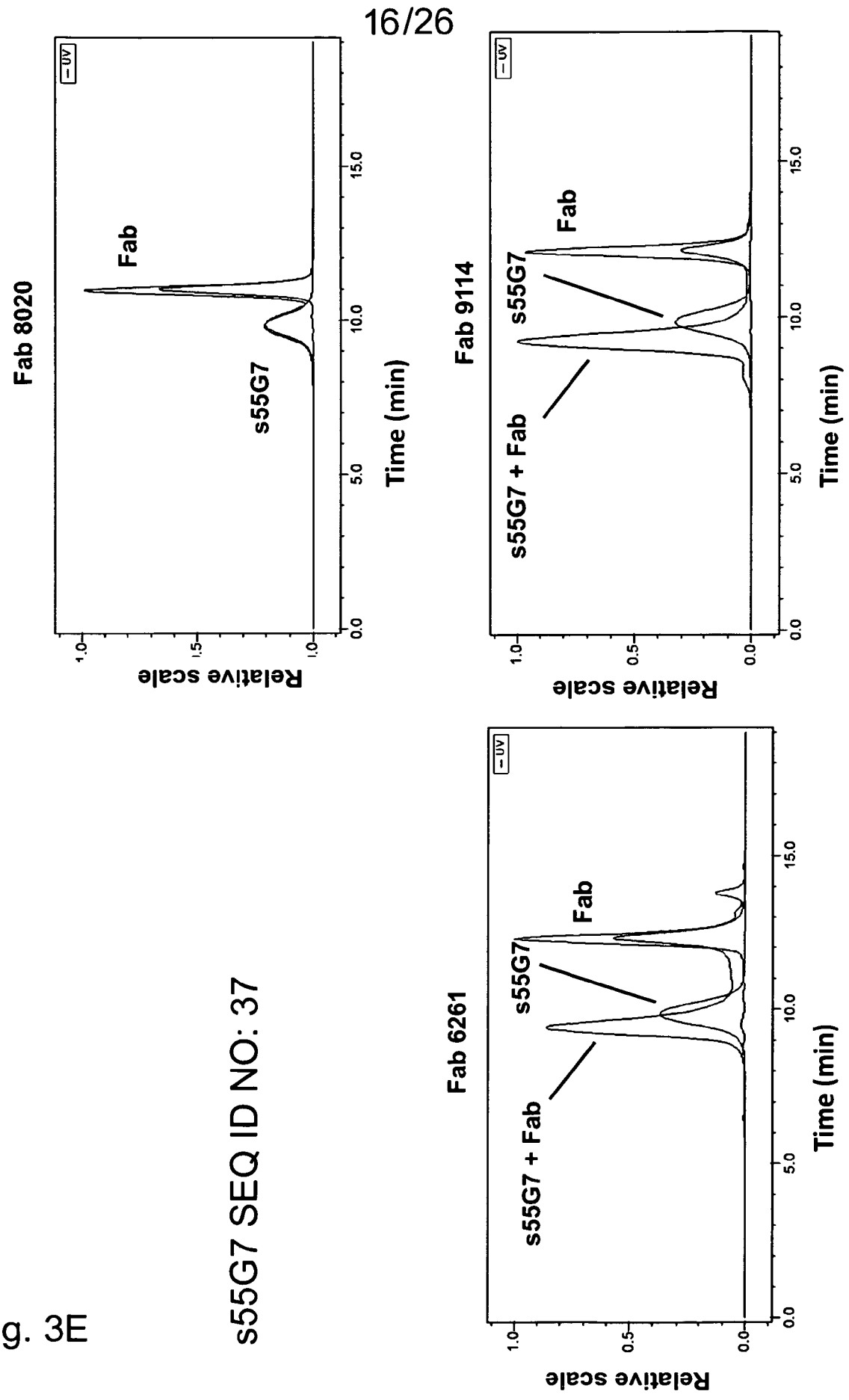
s74H9 SEQ ID NO: 34

Fig. 3C



s6E12 SEQ ID NO: 38

Fig. 3D



s55G7 SEQ ID NO: 37

Fig. 3E

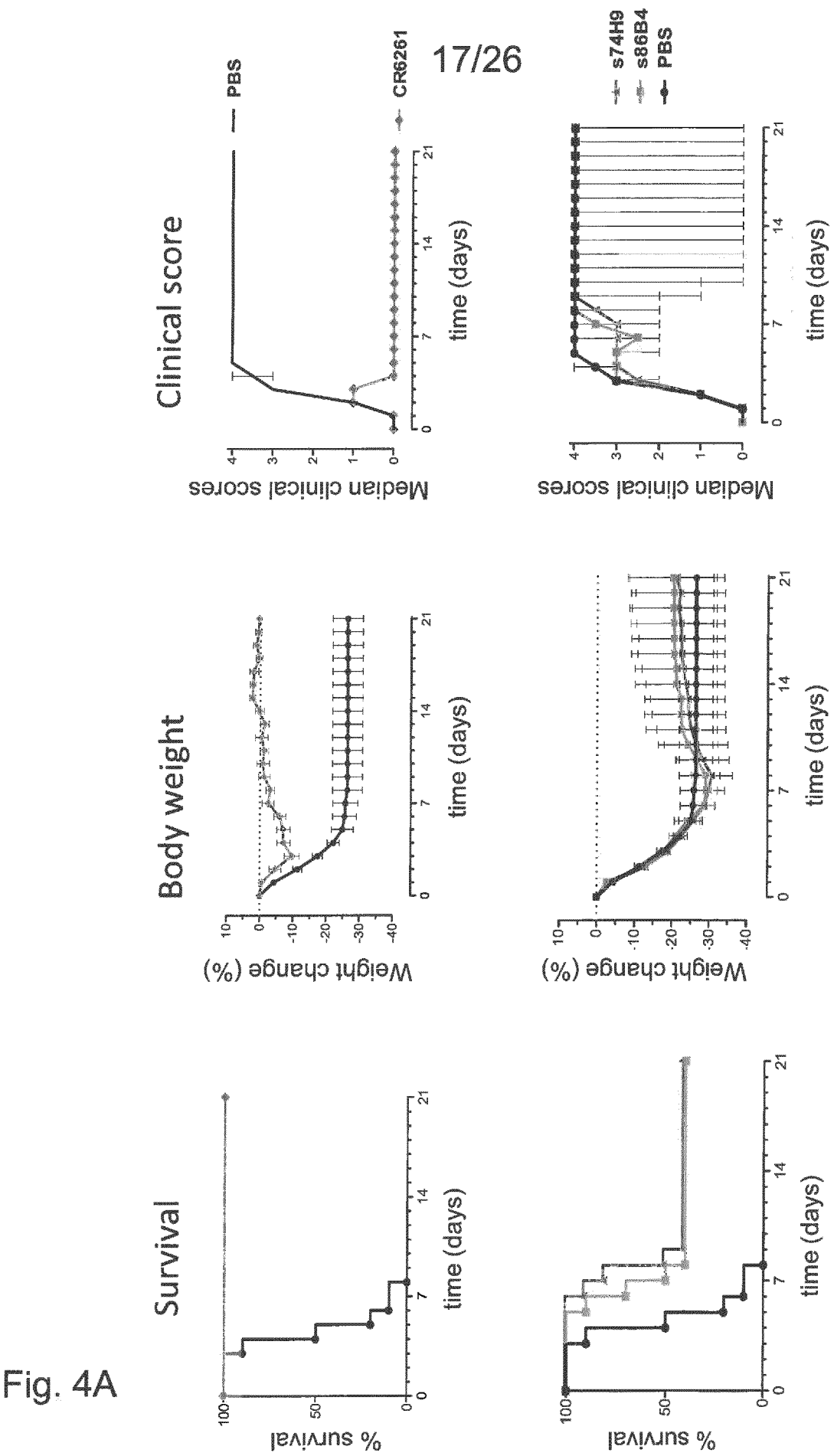

Clinical score
PBS
CR6261
Median clinical scores
time (days)
s74H9
s86B4
PBS
Median clinical scores
time (days)
Body weight
Weight change (%)
time (days)
Weight change (%)
time (days)
Survival
% survival
time (days)
% survival
time (days)

Fig. 4A

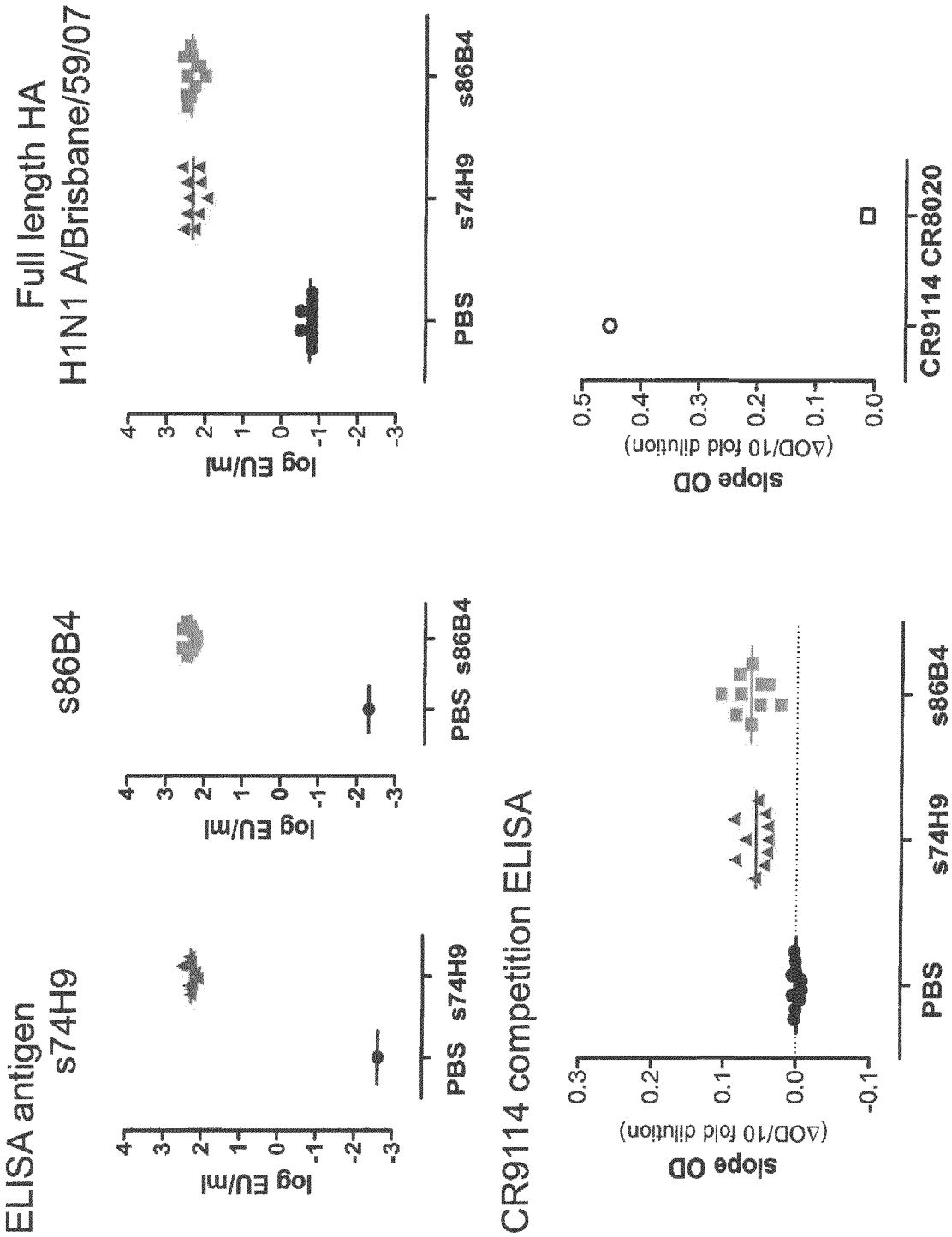

Full length HA
H1N1 A/Brisbane/59/07
log EU/ml
PBS
s74H9
s86B4
ELISA antigen
s74H9
s86B4
CR9114 competition ELISA
slope OD
(ΔOD/10 fold dilution)
CR9114
CR8020

Fig. 4B

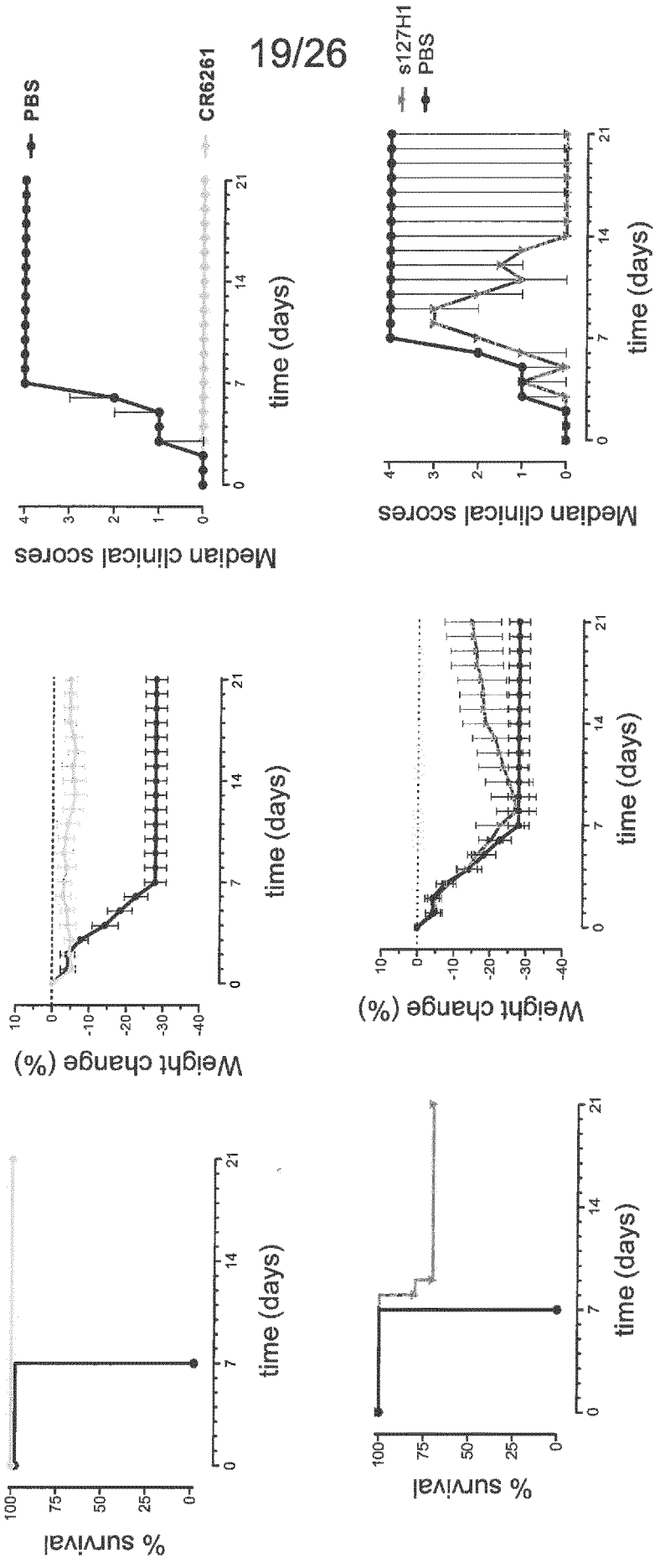

PBS
CR6261
s127H1
PBS
Median clinical scores
Weight change (%)
% survival
time (days)

Fig. 5A

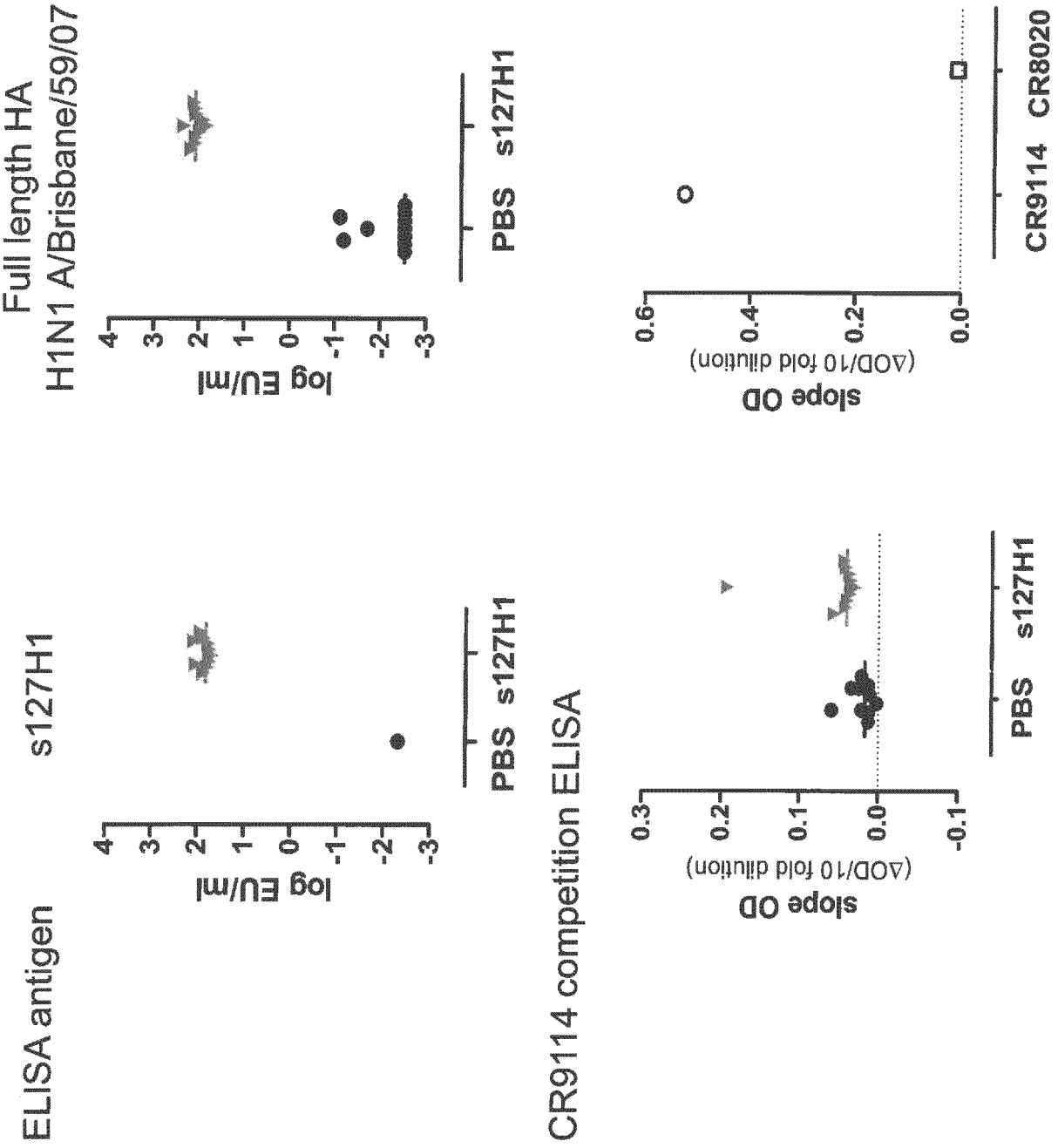

ELISA antigen
s127H1
log EU/ml
4
3
2
1
0
-1
-2
-3
PBS
s127H1
Full length HA
H1N1 A/Brisbane/59/07
log EU/ml
4
3
2
1
0
-1
-2
-3
PBS
s127H1
CR9114 competition ELISA
slope OD
(ΔOD/10 fold dilution)
0.3
0.2
0.1
0.0
-0.1
PBS
s127H1
slope OD
(ΔOD/10 fold dilution)
0.6
0.4
0.2
0.0
CR9114
CR8020

Fig. 5B

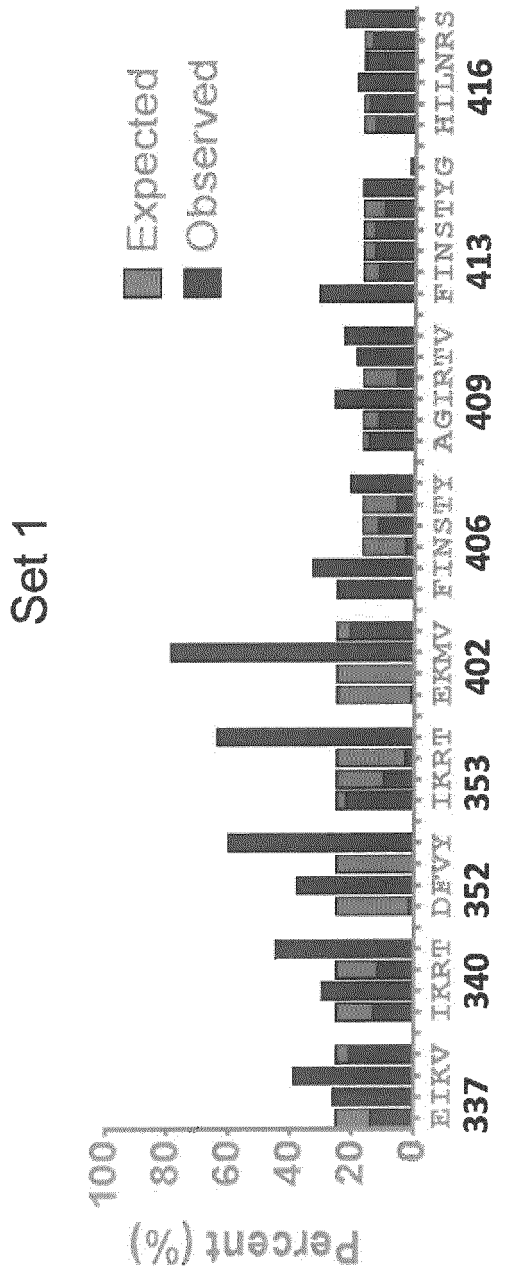

Set 1
Expected
Observed
Percent (%)
100
80
60
40
20
0
EIKV IKRT DFVY IKRT EKMV FINSTY AGIRMV FINSTYG HILNRS
337 340 352 353 402 406 409 413 416

Fig. 6

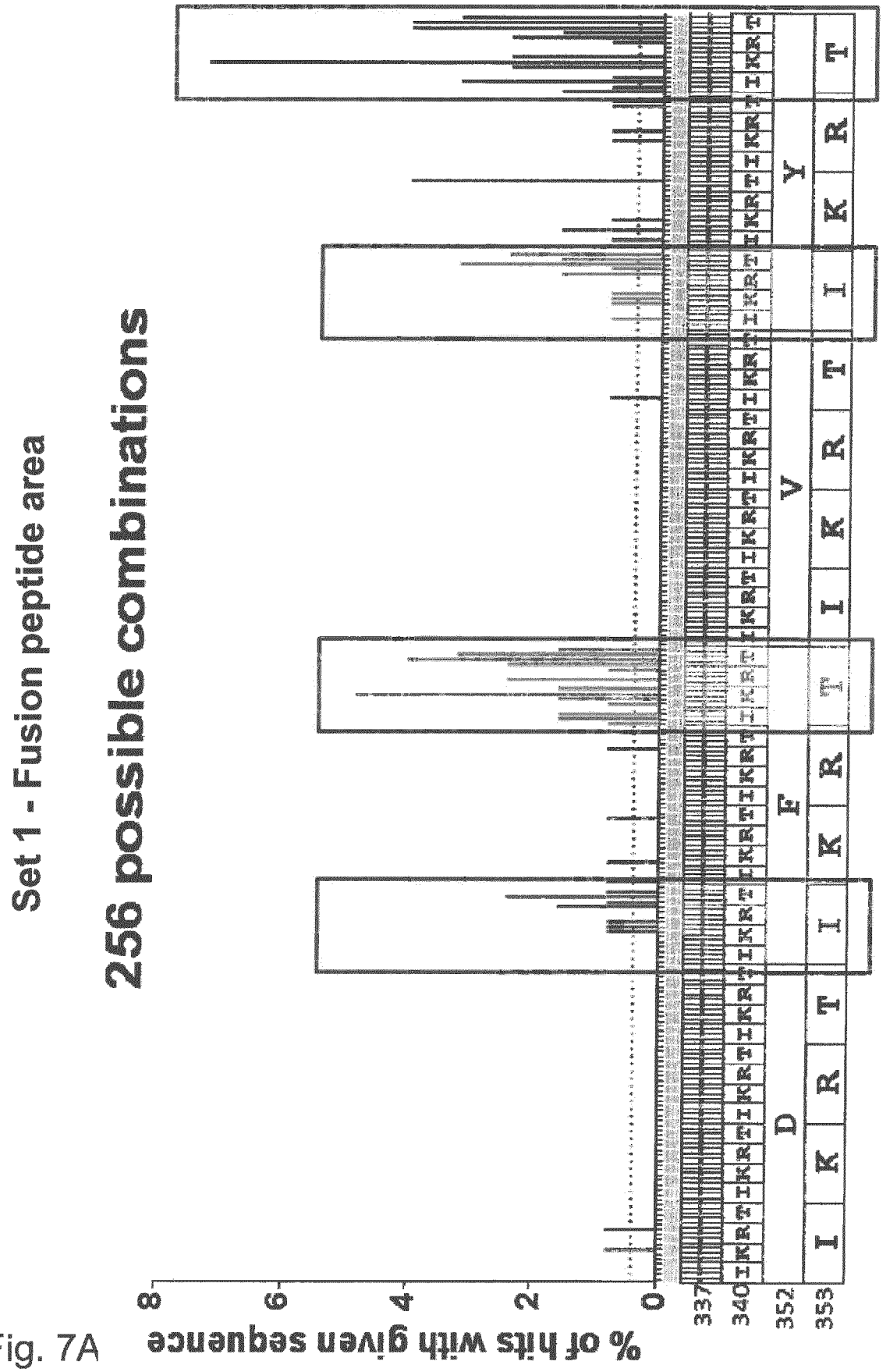
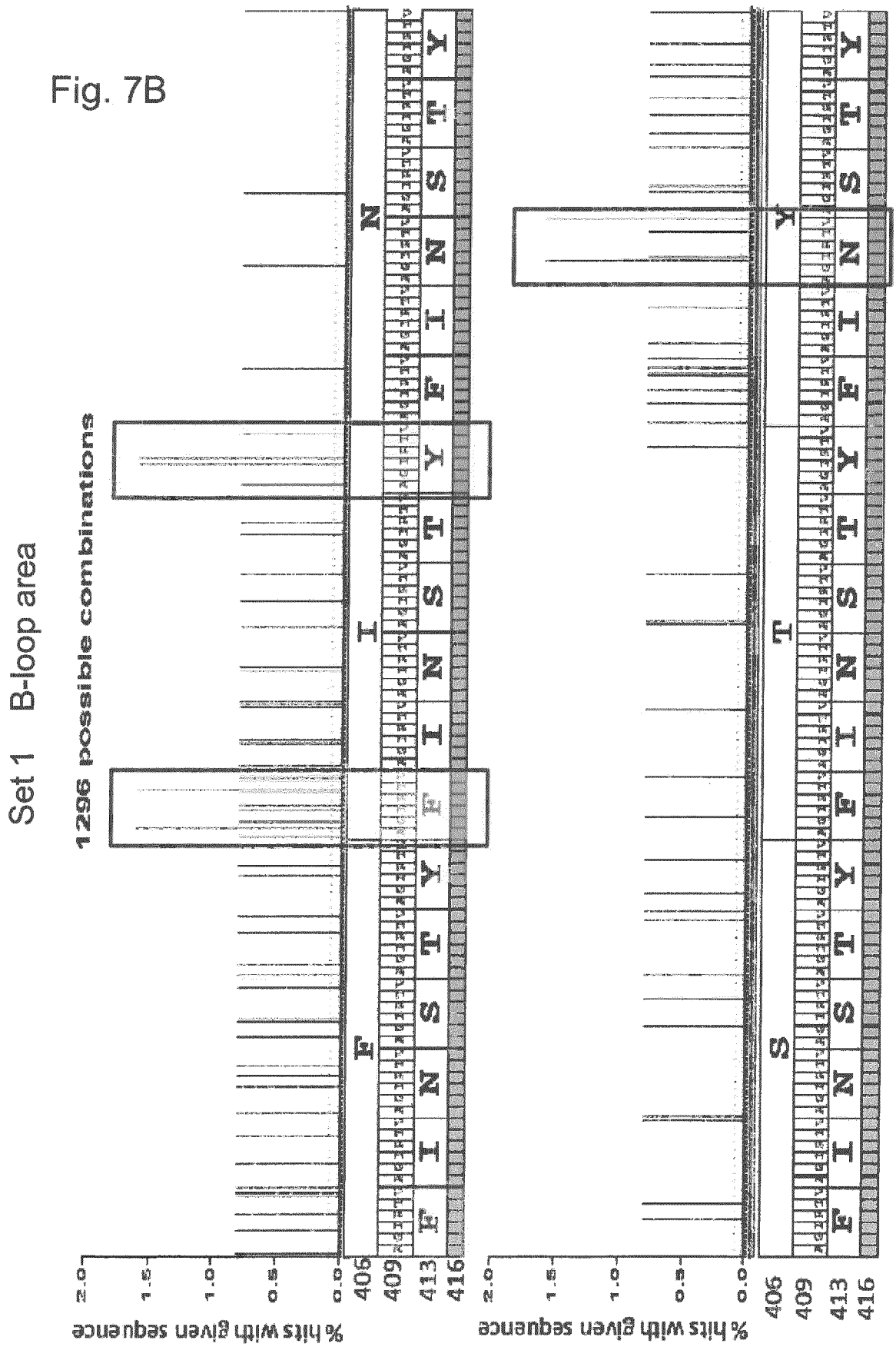

Set 1 - Fusion peptide area
256 possible combinations
% of hits with given sequence
0
2
4
6
8
337
340
352
353

Fig. 7A

Fig. 7B


Set 1 B-loop area
1296 possible combinations
% hits with given sequence
2.0
1.5
1.0
0.5
0.0
406
409
413
416
F I N S T Y
I N S T Y
N S T Y
S T Y
Y

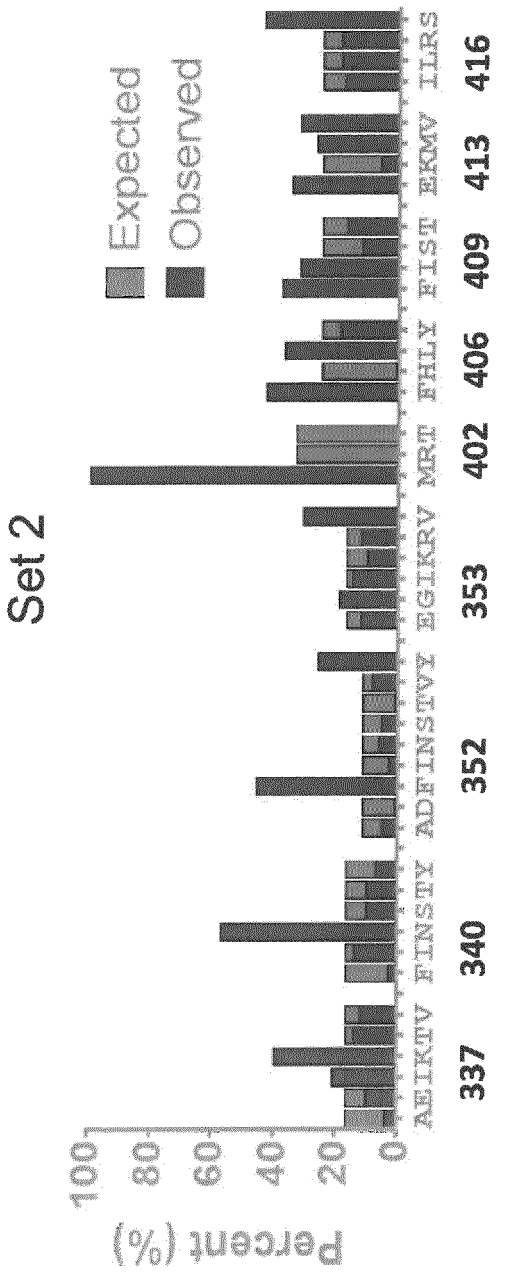

Set 2
Expected
Observed
Percent (%)
0
20
40
60
80
100
337
340
352
353
402
406
409
413
416
AEIKTV FINSTY ADFINSTVY EGIKRV MRT FHLY FIST EKMV ILRS

Fig. 8

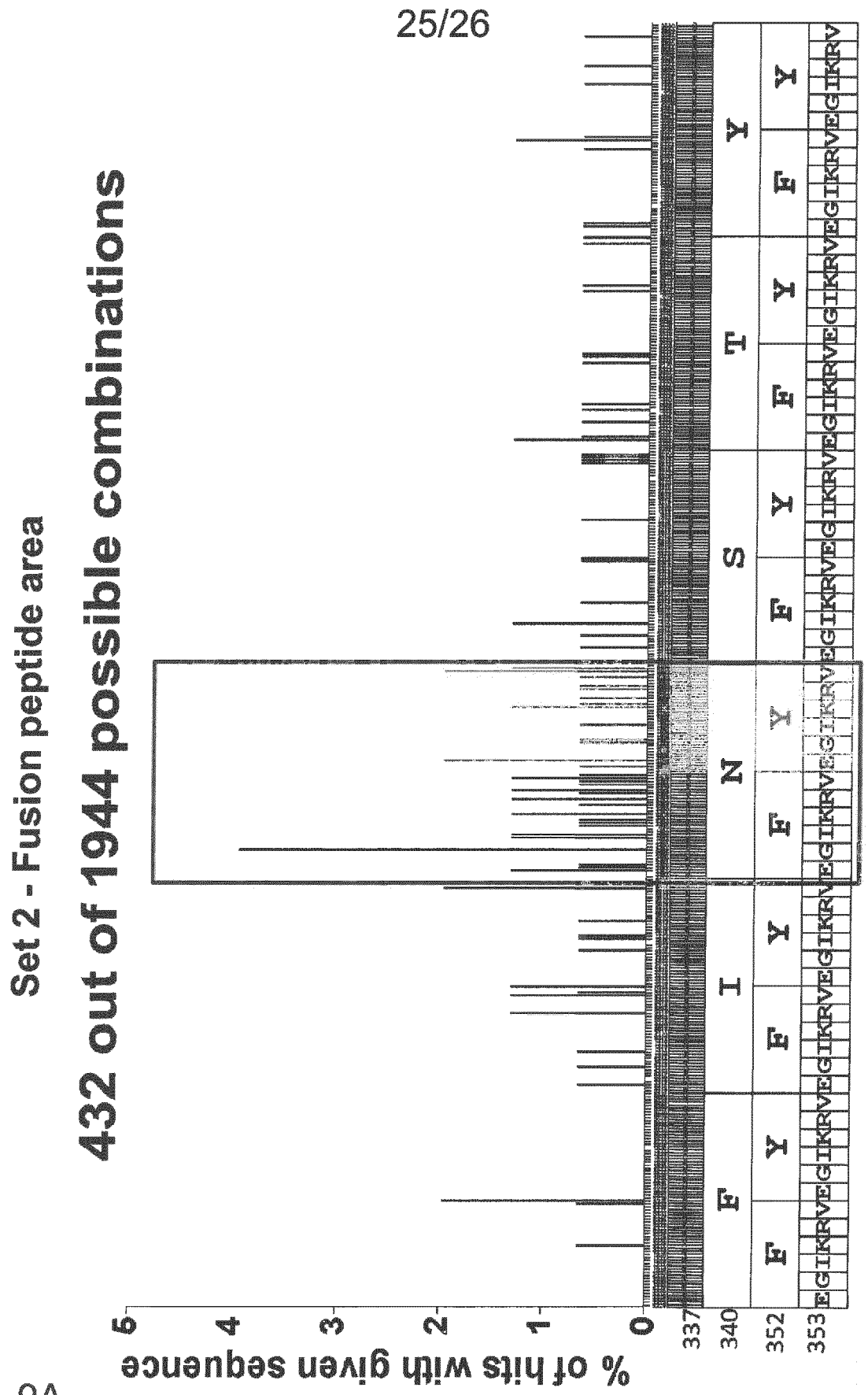

Set 2 - Fusion peptide area
432 out of 1944 possible combinations
% of hits with given sequence
0
1
2
3
4
5
337
340
352
353
F F I N S T Y
Y Y Y Y F F F
EGIIKRVEGIIKRVEGIIKRVEGIIKRV

Fig. 9A

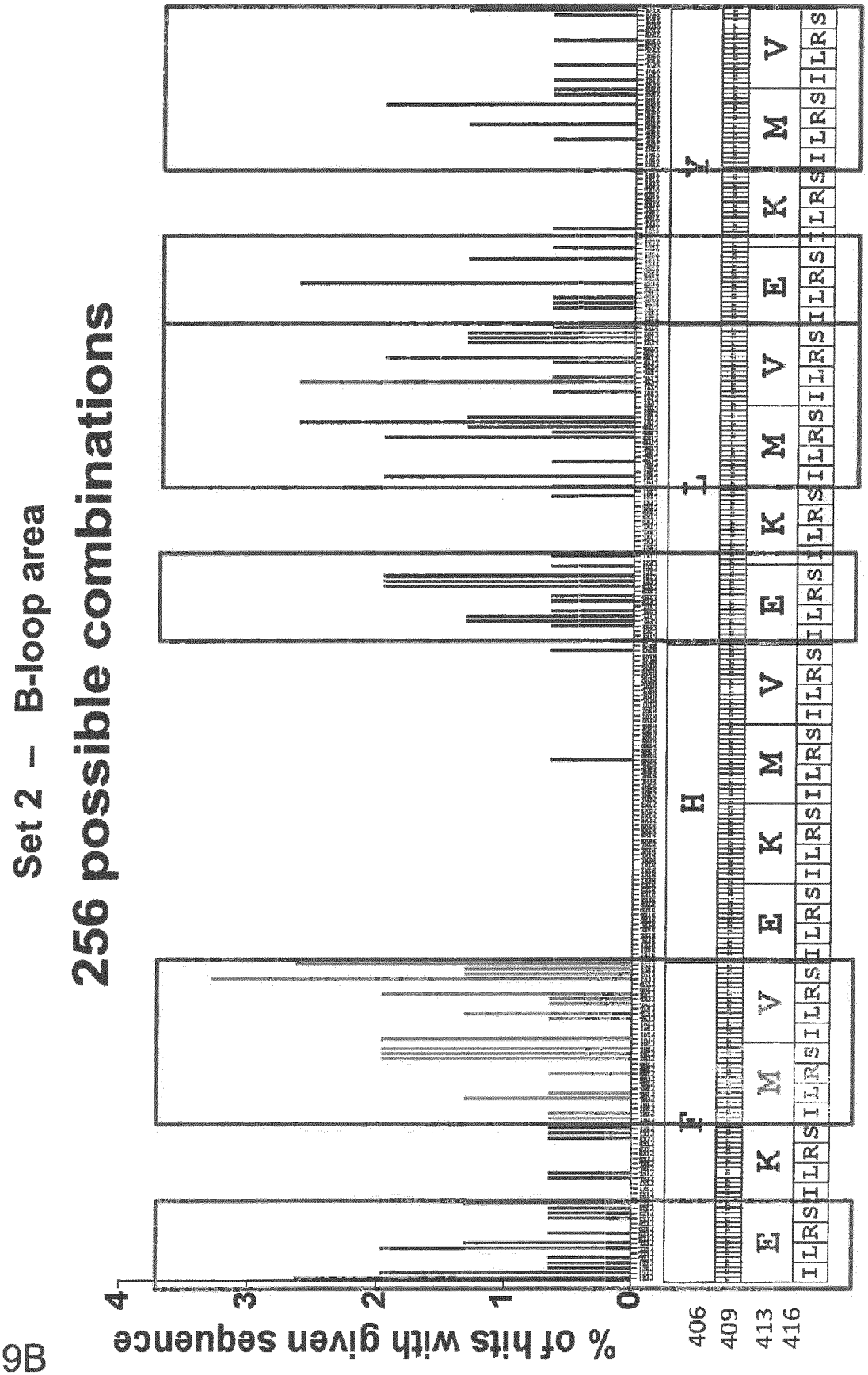

Set 2 – B-loop area
256 possible combinations
% of hits with given sequence
0
1
2
3
4
406
409
413
416
E K M V
F
H
T
Y
E K M V
I L R S I L R S I L R S I L R S

Fig. 9B