Fig.1.

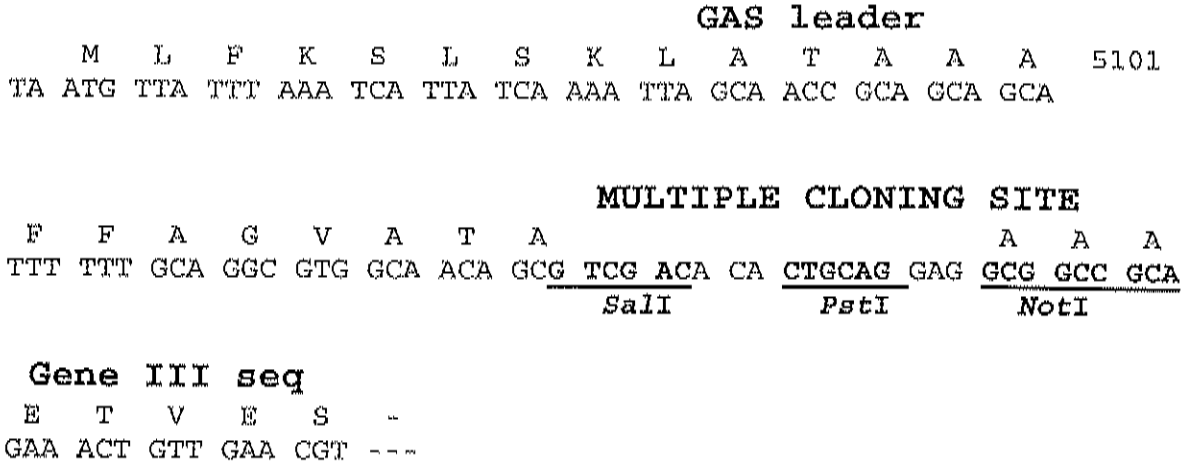
GAS leader
M L F K S L S K L A T A A A 5101
TA ATG TTA TTT AAA TCA TTA TCA AAA TTA GCA ACC GCA GCA GCA
MULTIPLE CLONING SITE
F F A G V A T A A A A
TTT TTT GCA GGC GTG GCA ACA GCG TCG ACA CA CTGCAG GAG GCG GCC GCA
SalI
PstI
NotI
Gene III seq
E T V E S -
GAA ACT GTT GAA CGT ---

Fig.2.

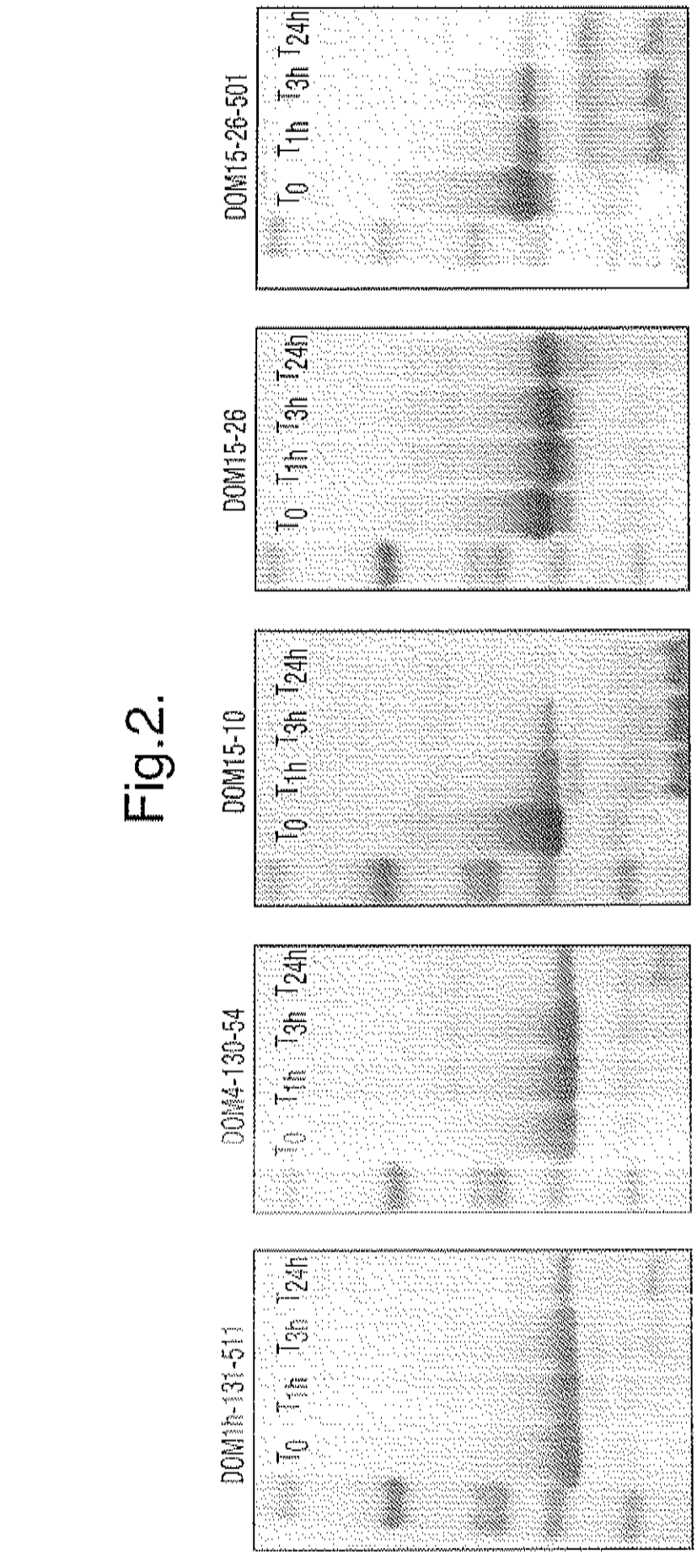
DOM15-26-501
T0 T1h T3h T24h
DOM15-26
T0 T1h T3h T24h
DOM15-10
T0 T1h T3h T24h
DOM4-130-54
T0 T1h T3h T24h
DOM15-131-511
T0 T1h T3h T24h

Fig.3.

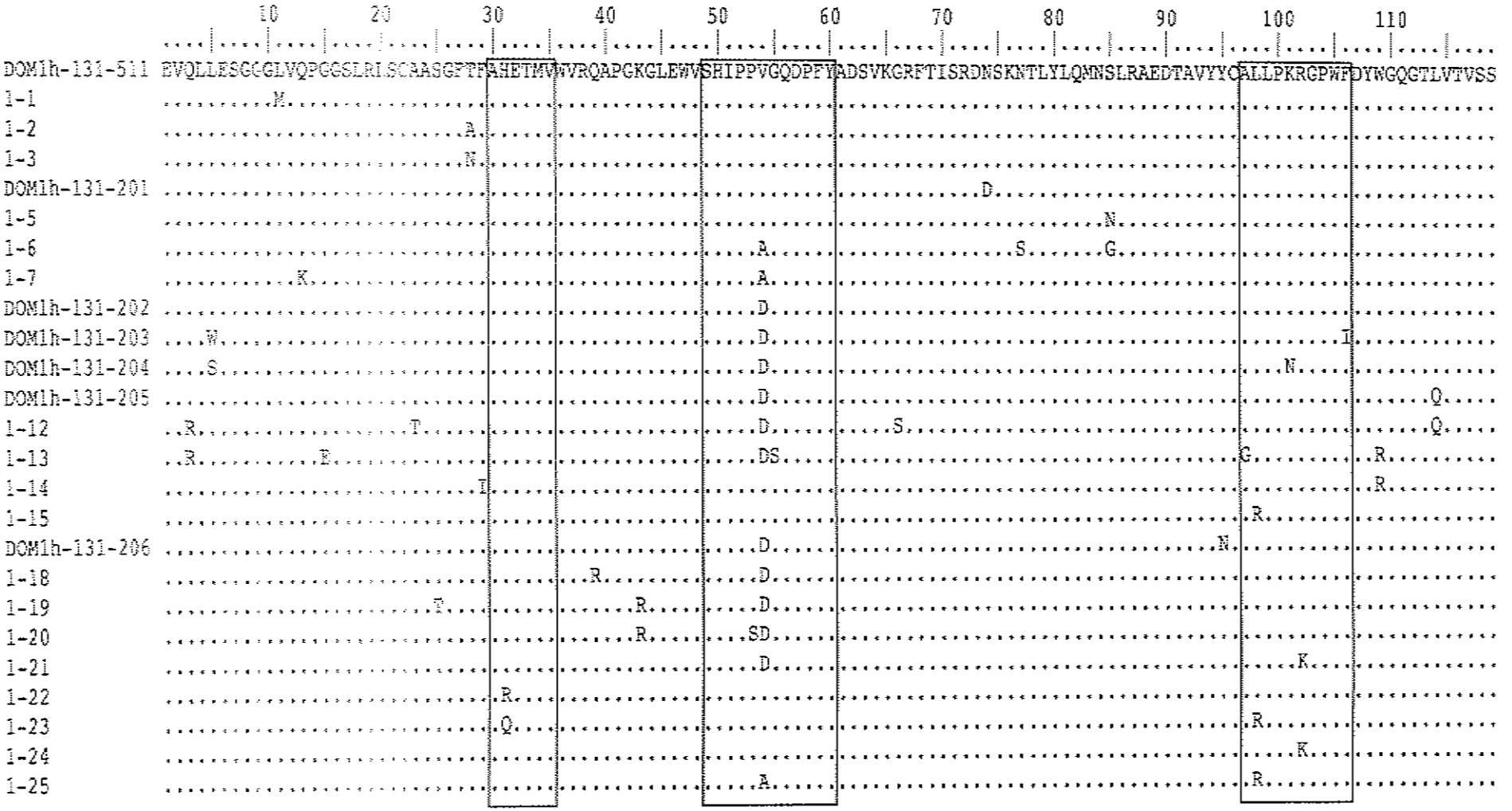
10 20 30 40 50 60 70 80 90 100 110
DOM1h-131-511 EVQLLESGGGLVQPGGSLRLSCAASGFTFAHETMWVRQAPGKGLEWVSHIPPVGQDPFYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCALLPKRGPWFDYWGQGTLVTVSS
1-1 M
1-2 A
1-3 N
DOM1h-131-201 D
1-5 N
1-6 A S G
1-7 K A
DOM1h-131-202 D
DOM1h-131-203 W D I
DOM1h-131-204 S D N
DOM1h-131-205 D Q
1-12 R T D S Q
1-13 R E DS G R
1-14 I R
1-15 R
DOM1h-131-206 D N
1-18 R D
1-19 T R D
1-20 R SD
1-21 D K
1-22 R
1-23 Q R
1-24 K
1-25 A R

Fig.4.

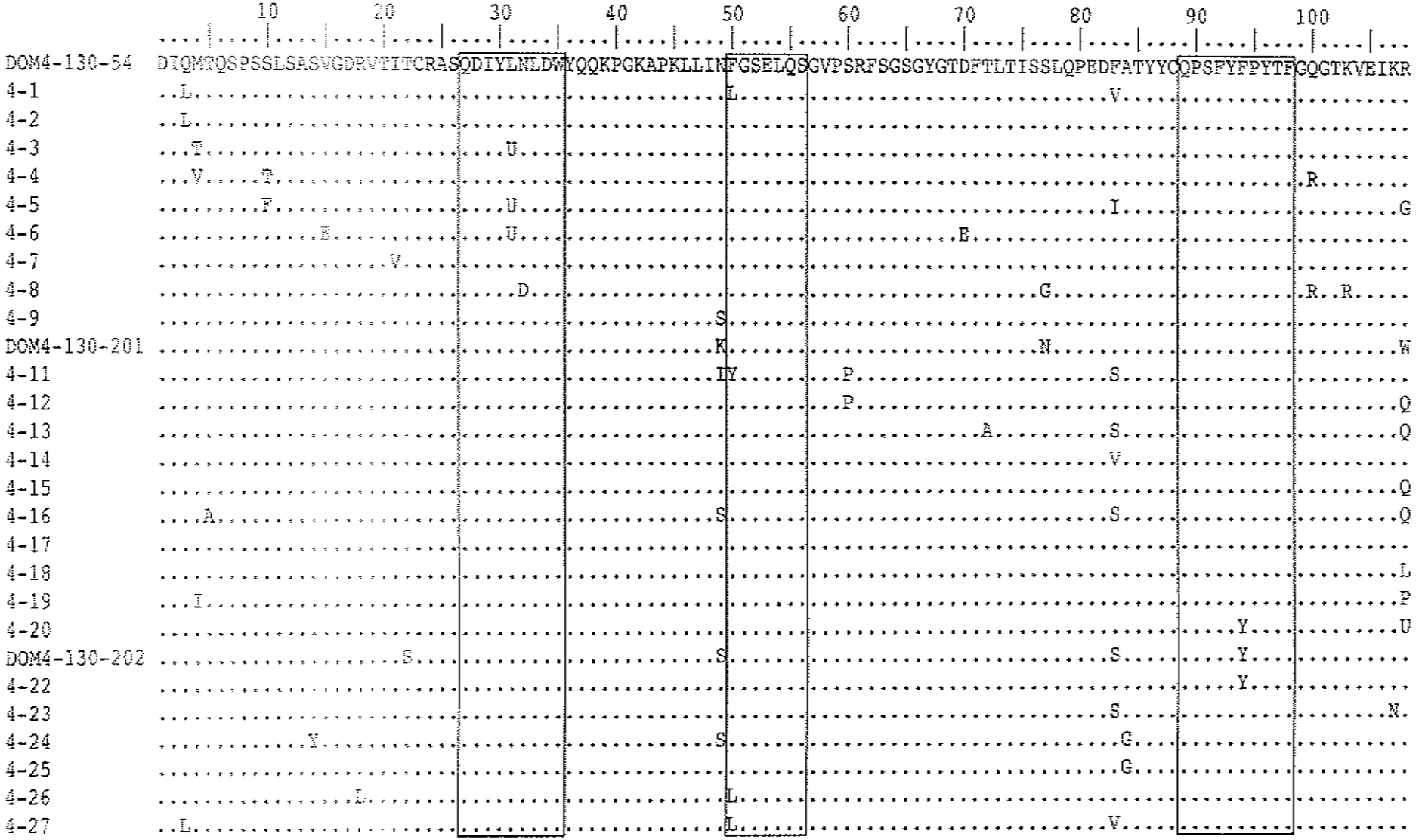
10 20 30 40 50 60 70 80 90 100
DOM4-130-54 DIQMTQSPSSLSASVGDRVTITCRASQDIYLNLDWYQQKPGKAPKLLIYFGSELQSGVPSRFSGSGYGTDFTLTISSLQPEDFATYYCQQPSFYFPYTFGQGTKVEIKR
4-1 ..L.....L.....V.....
4-2 ..L.....
4-3 ...T.....U.....
4-4 ...V.....T.....R.....
4-5 .....F.....U.....I.....G
4-6 .....E.....U.....E.....
4-7 .....V.....
4-8 .....D.....G.....R..R.....
4-9 .....S.....
DOM4-130-201 .....K.....N.....W
4-11 .....IY.....P.....S.....
4-12 .....P.....Q
4-13 .....A.....S.....Q
4-14 .....V.....
4-15 .....Q
4-16 ....A.....S.....S.....Q
4-17 .....
4-18 L
4-19 ...I.....P
4-20 .....Y.....U
DOM4-130-202 .....S.....S.....S.....Y.....
4-22 .....Y.....
4-23 .....S.....N.
4-24 .....Y.....S.....G.....
4-25 .....G.....
4-26 .....L.....L.....
4-27 ..L.....L.....V.....

Fig.5.

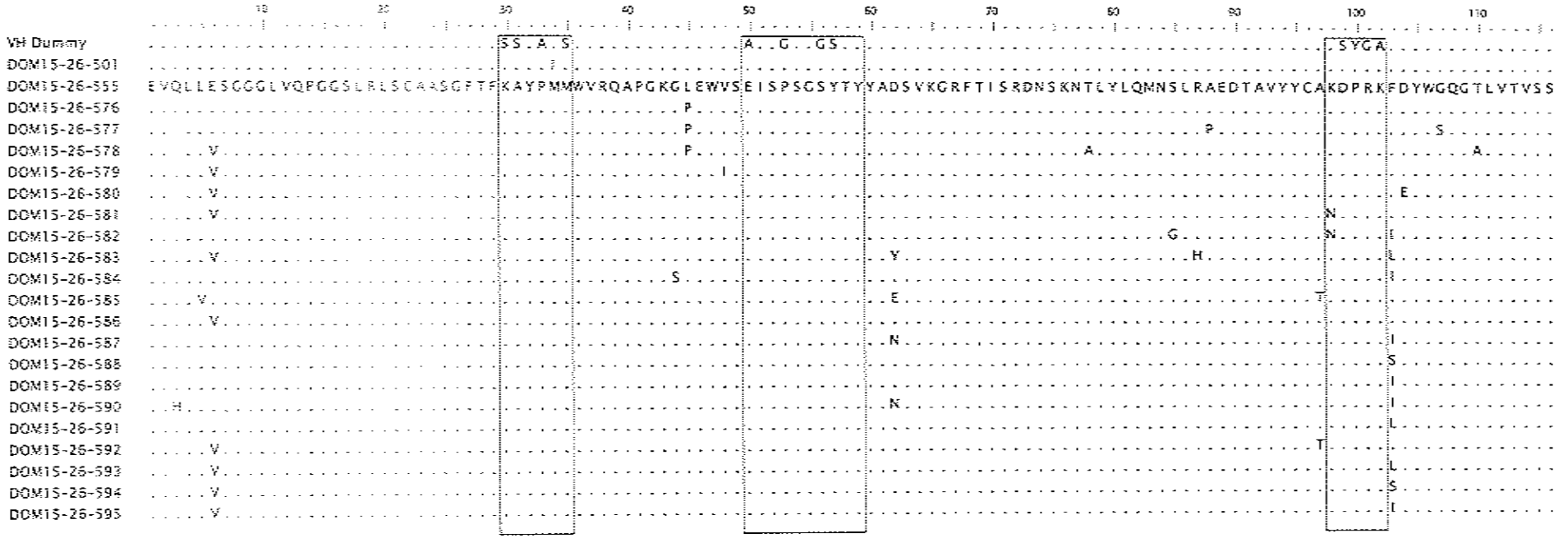
VH Dummy
DOM15-26-501
DOM15-26-555
DOM15-26-576
DOM15-26-577
DOM15-26-578
DOM15-26-579
DOM15-26-580
DOM15-26-581
DOM15-26-582
DOM15-26-583
DOM15-26-584
DOM15-26-585
DOM15-26-586
DOM15-26-587
DOM15-26-588
DOM15-26-589
DOM15-26-590
DOM15-26-591
DOM15-26-592
DOM15-26-593
DOM15-26-594
DOM15-26-595

Fig.6.

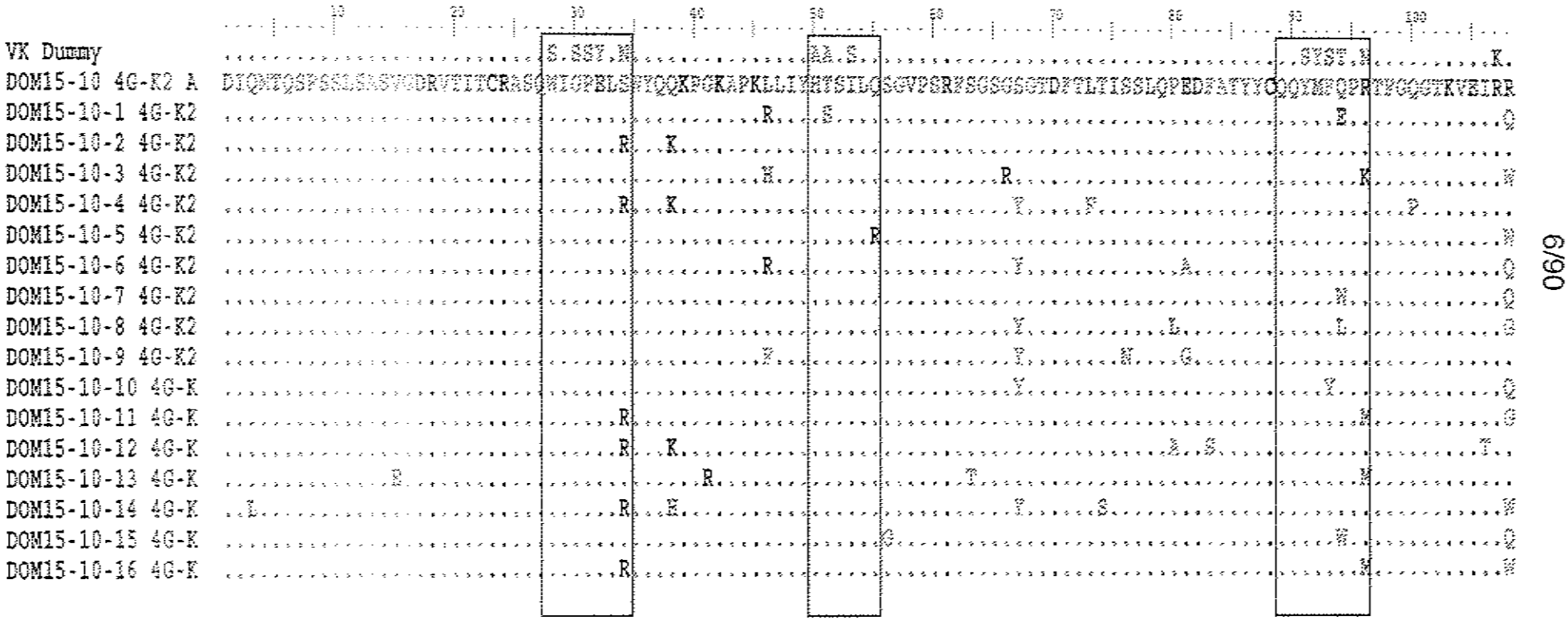
VK Dummy
DOM15-10 4G-K2 A
DOM15-10-1 4G-K2
DOM15-10-2 4G-K2
DOM15-10-3 4G-K2
DOM15-10-4 4G-K2
DOM15-10-5 4G-K2
DOM15-10-6 4G-K2
DOM15-10-7 4G-K2
DOM15-10-8 4G-K2
DOM15-10-9 4G-K2
DOM15-10-10 4G-K
DOM15-10-11 4G-K
DOM15-10-12 4G-K
DOM15-10-13 4G-K
DOM15-10-14 4G-K
DOM15-10-15 4G-K
DOM15-10-16 4G-K

Fig.7A.

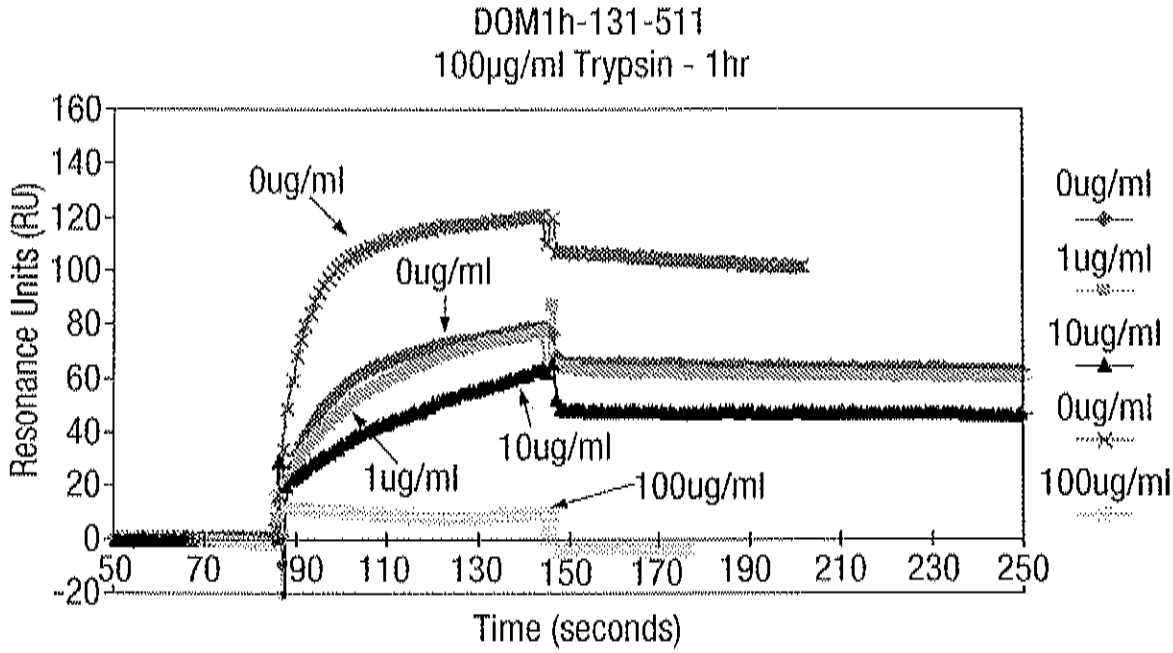
DOM1h-131-511
100µg/ml Trypsin - 1hr
Resonance Units (RU)
Time (seconds)
0ug/ml
0ug/ml
1ug/ml
10ug/ml
100ug/ml
0ug/ml
1ug/ml
10ug/ml
0ug/ml
100ug/ml

Fig.7B.

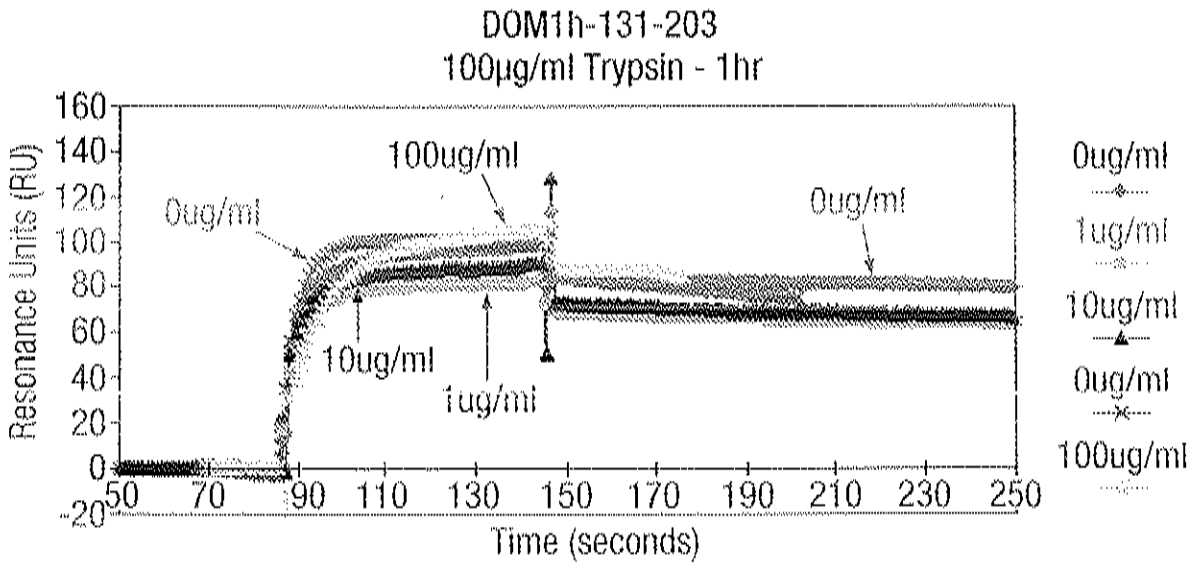
DOM1h-131-203
100µg/ml Trypsin - 1hr
Resonance Units (RU)
Time (seconds)
100ug/ml
0ug/ml
0ug/ml
10ug/ml
1ug/ml
0ug/ml
1ug/ml
10ug/ml
0ug/ml
100ug/ml

Fig.7C.

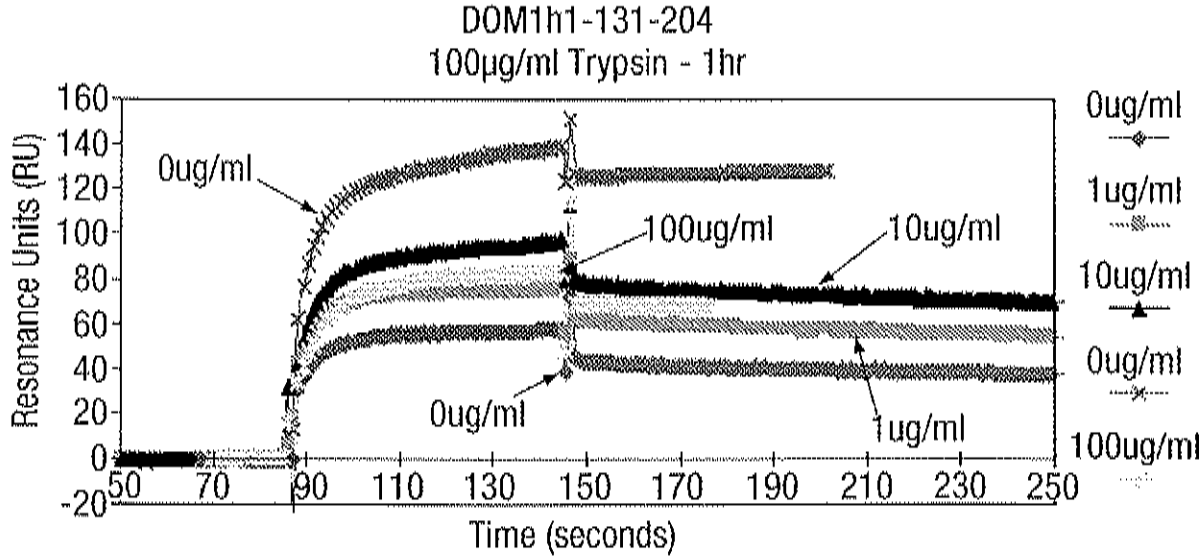
DOM1h1-131-204
100µg/ml Trypsin - 1hr
Resonance Units (RU)
160
140
120
100
80
60
40
20
0
-20
50
70
90
110
130
150
170
190
210
230
250
Time (seconds)
0ug/ml
100ug/ml
10ug/ml
0ug/ml
1ug/ml
0ug/ml
1ug/ml
10ug/ml
0ug/ml
100ug/ml

Fig.7D.

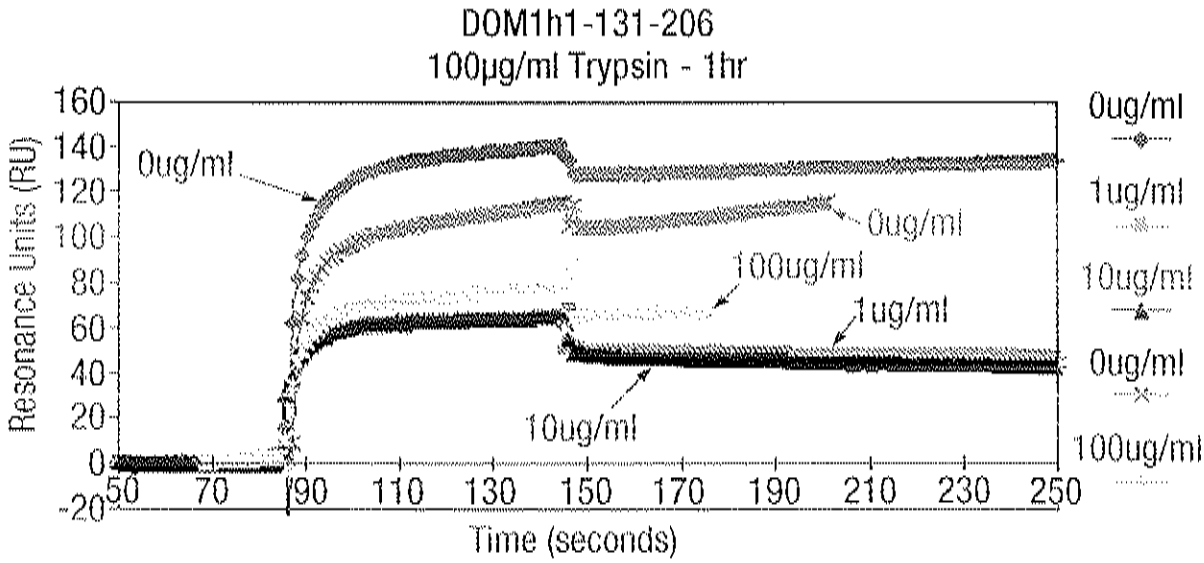
DOM1h1-131-206
100µg/ml Trypsin - 1hr
Resonance Units (RU)
160
140
120
100
80
60
40
20
0
-20
50
70
90
110
130
150
170
190
210
230
250
Time (seconds)
0ug/ml
0ug/ml
100ug/ml
1ug/ml
10ug/ml
0ug/ml
1ug/ml
10ug/ml
0ug/ml
100ug/ml

Fig.8A.

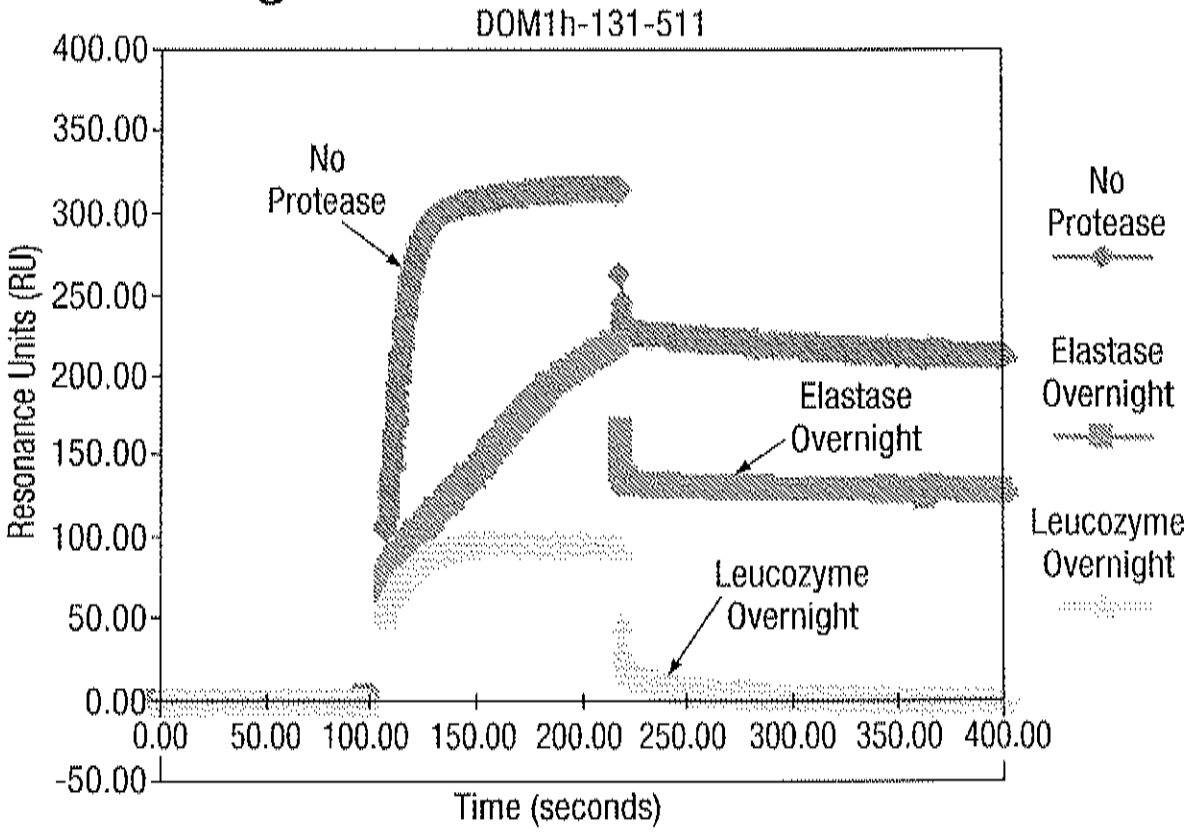
DOM1h-131-511
400.00
350.00
300.00
250.00
200.00
150.00
100.00
50.00
0.00
-50.00
Resonance Units (RU)
0.00
50.00
100.00
150.00
200.00
250.00
300.00
350.00
400.00
Time (seconds)
No Protease
Elastase Overnight
Leucozyme Overnight
No Protease
Elastase Overnight
Leucozyme Overnight

Fig.8B.

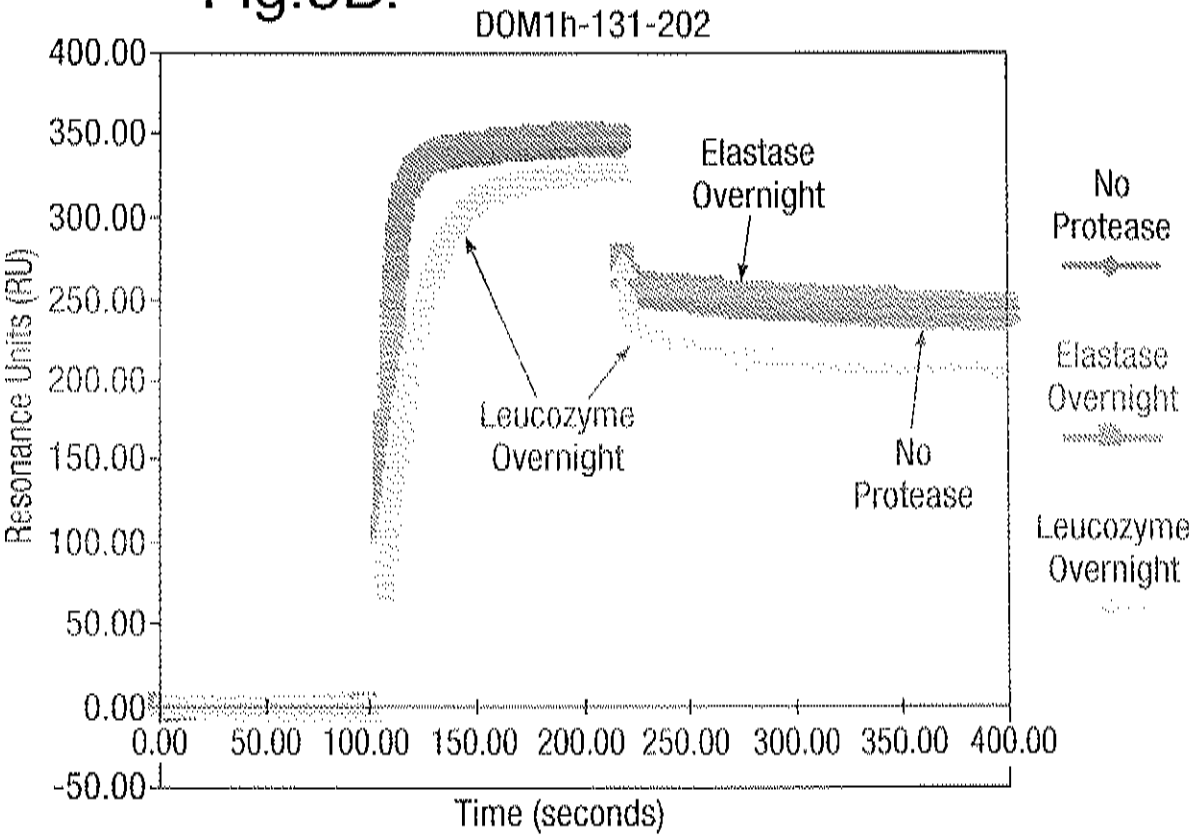
DOM1h-131-202
400.00
350.00
300.00
250.00
200.00
150.00
100.00
50.00
0.00
-50.00
Resonance Units (RU)
0.00
50.00
100.00
150.00
200.00
250.00
300.00
350.00
400.00
Time (seconds)
Elastase Overnight
Leucozyme Overnight
No Protease
No Protease
Elastase Overnight
Leucozyme Overnight

Fig.8C.

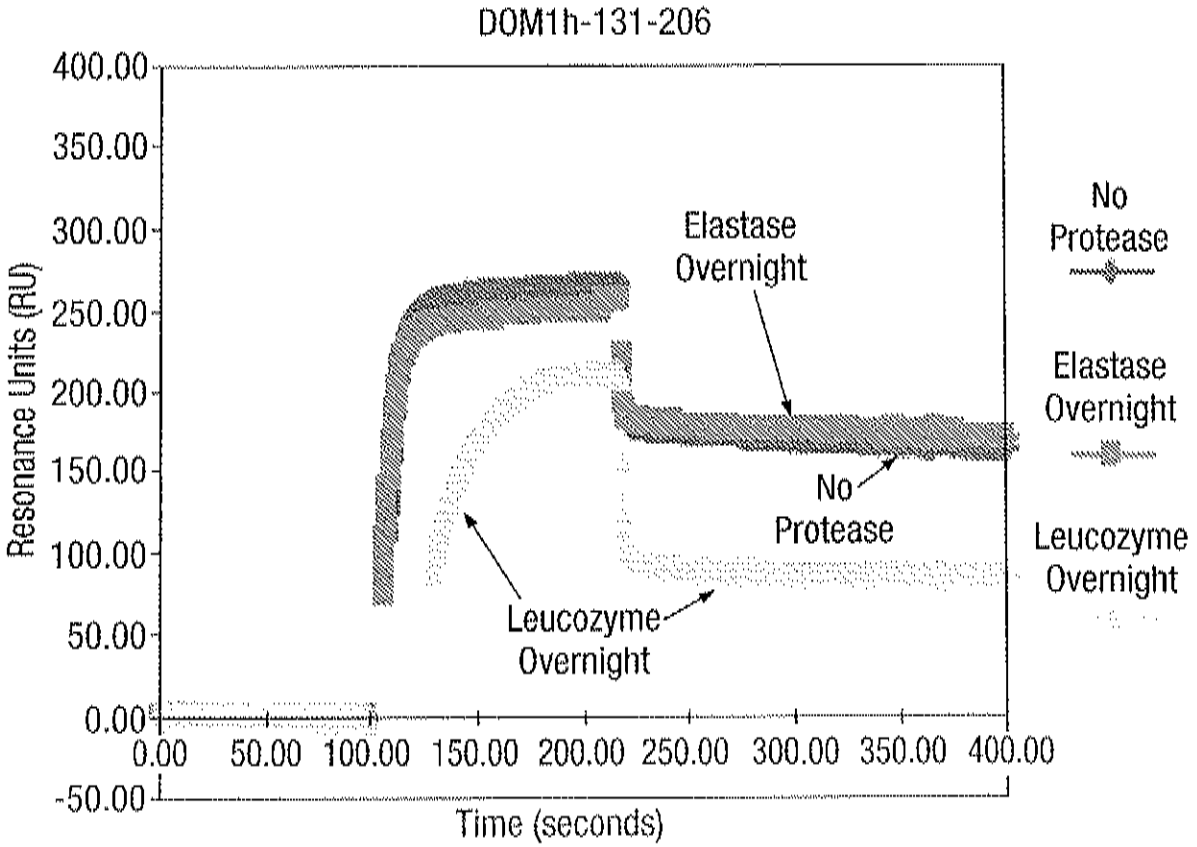
DOM1h-131-206
400.00
350.00
300.00
250.00
200.00
150.00
100.00
50.00
0.00
-50.00
Resonance Units (RU)
0.00
50.00
100.00
150.00
200.00
250.00
300.00
350.00
400.00
Time (seconds)
Elastase Overnight
No Protease
Leucozyme Overnight
No Protease
Elastase Overnight
Leucozyme Overnight

Fig.9.

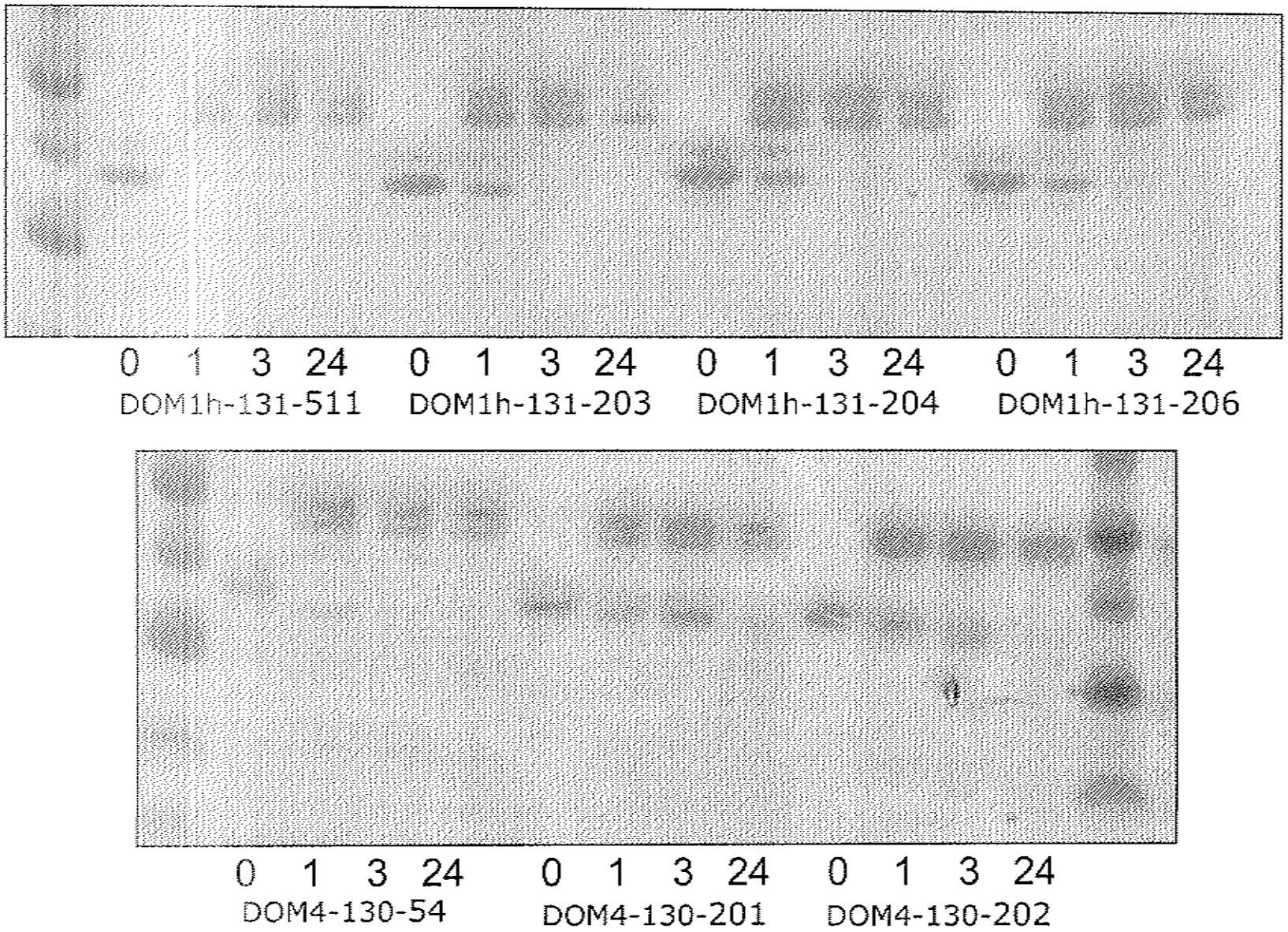
0 1 3 24 0 1 3 24 0 1 3 24 0 1 3 24
DOM1h-131-511 DOM1h-131-203 DOM1h-131-204 DOM1h-131-206
0 1 3 24 0 1 3 24 0 1 3 24
DOM4-130-54 DOM4-130-201 DOM4-130-202

Fig.10A.

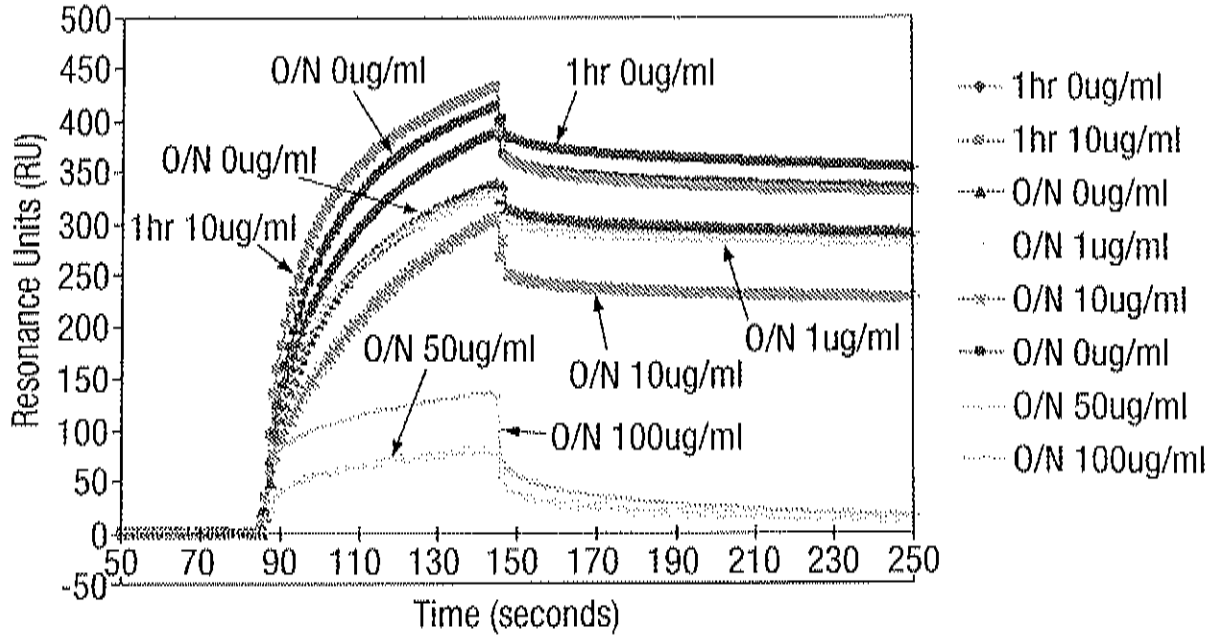

Fig.10B.

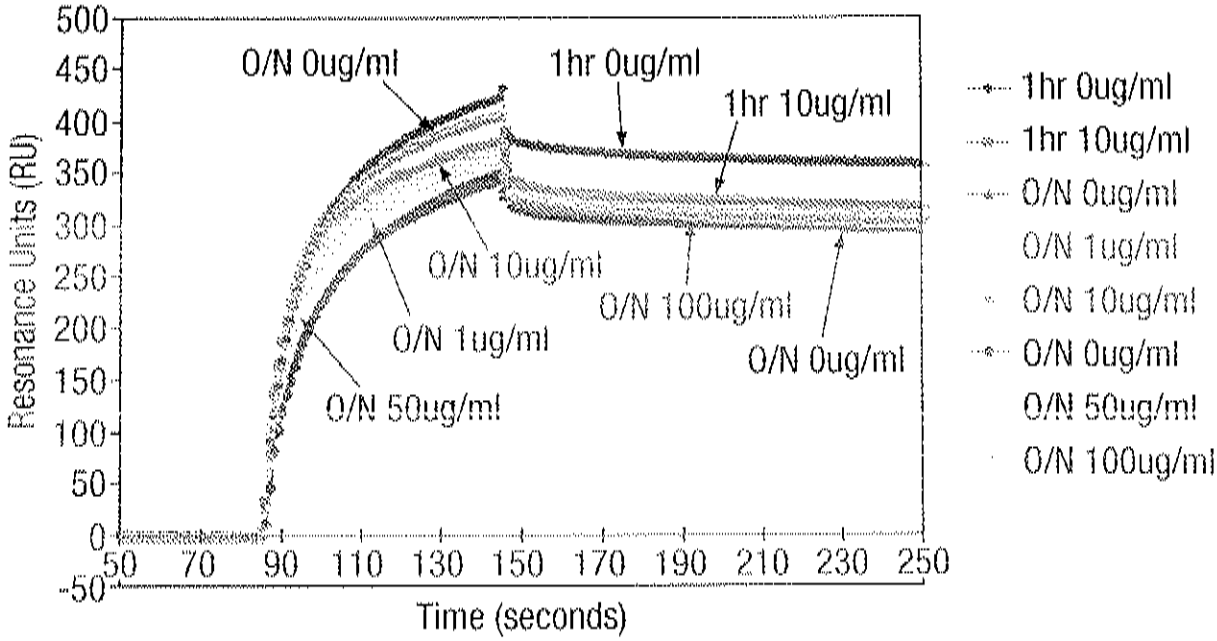

Fig.10C.

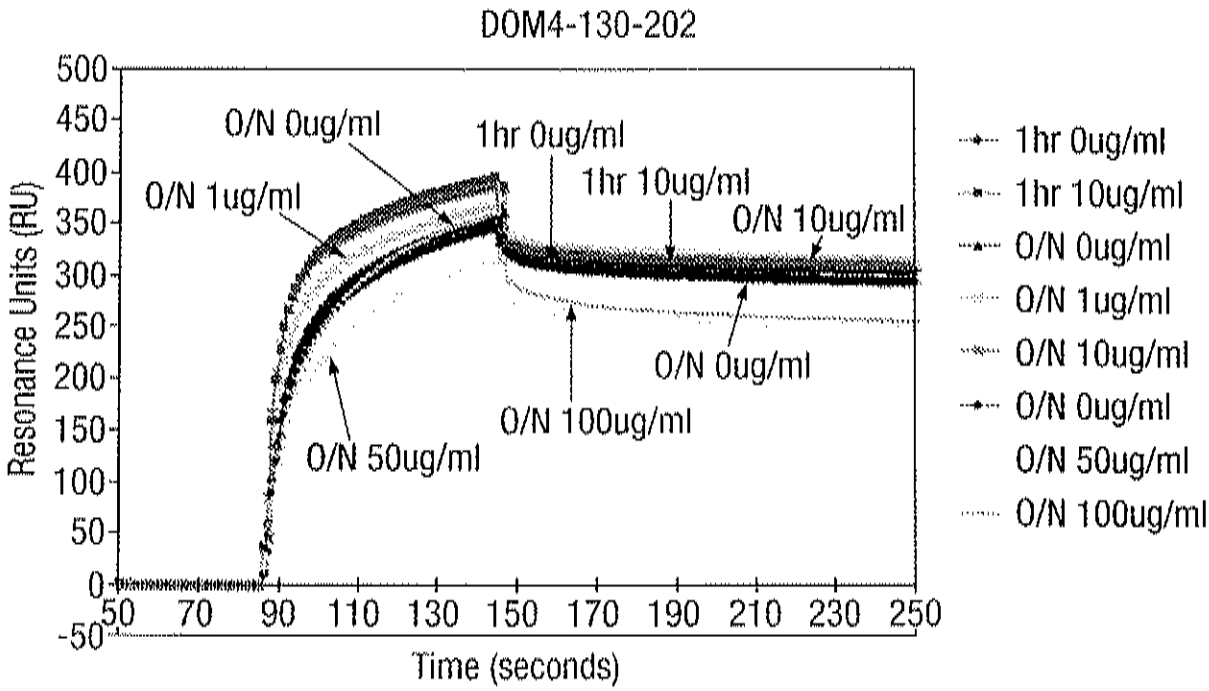
DOM4-130-202
Resonance Units (RU)
500
450
400
350
300
250
200
150
100
50
0
-50
50
70
90
110
130
150
170
190
210
230
250
Time (seconds)
O/N 0ug/ml
1hr 0ug/ml
O/N 1ug/ml
1hr 10ug/ml
O/N 10ug/ml
O/N 0ug/ml
O/N 100ug/ml
O/N 50ug/ml
1hr 0ug/ml
1hr 10ug/ml
O/N 0ug/ml
O/N 1ug/ml
O/N 10ug/ml
O/N 0ug/ml
O/N 50ug/ml
O/N 100ug/ml

Fig.11A.

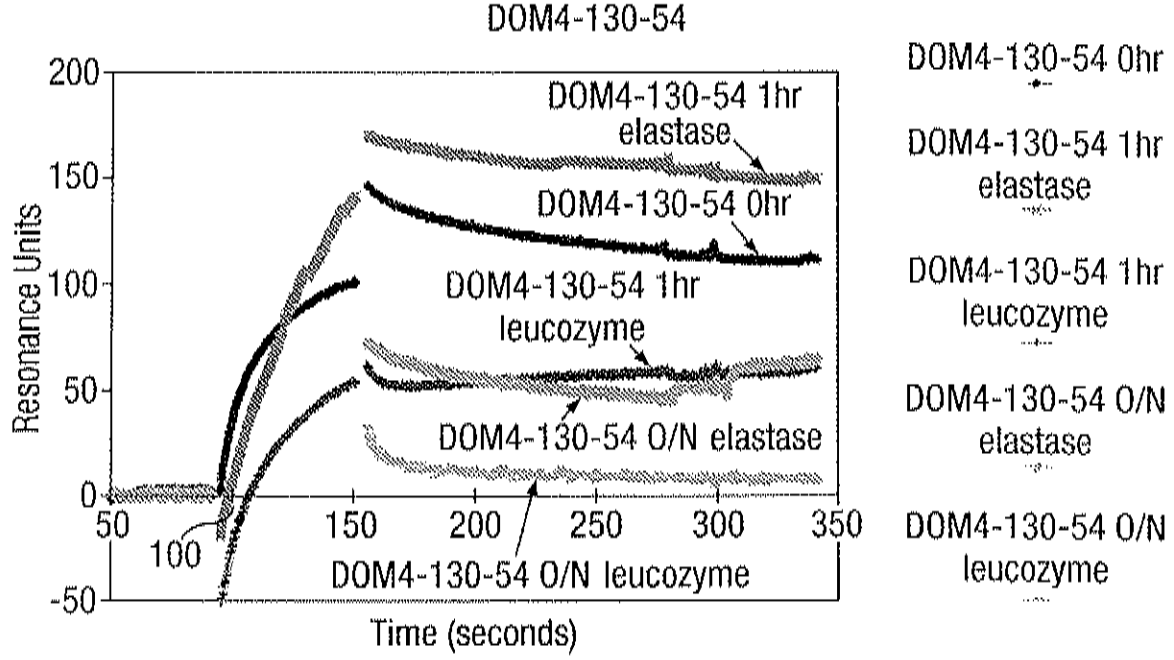

Fig.11B.

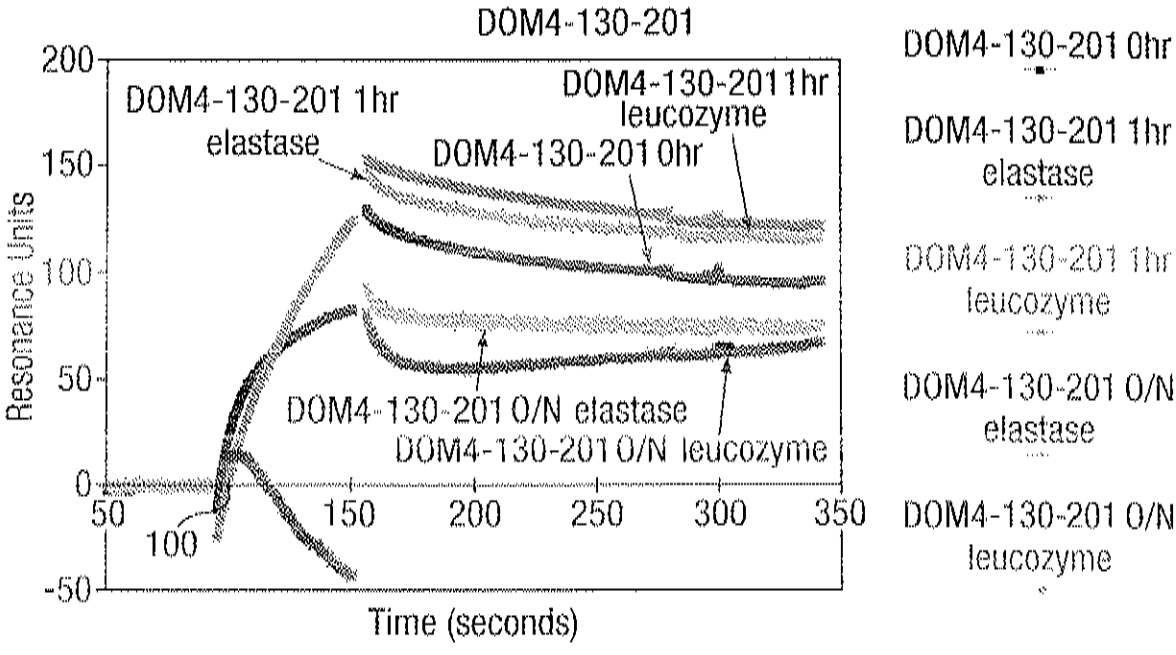

Fig.11C.

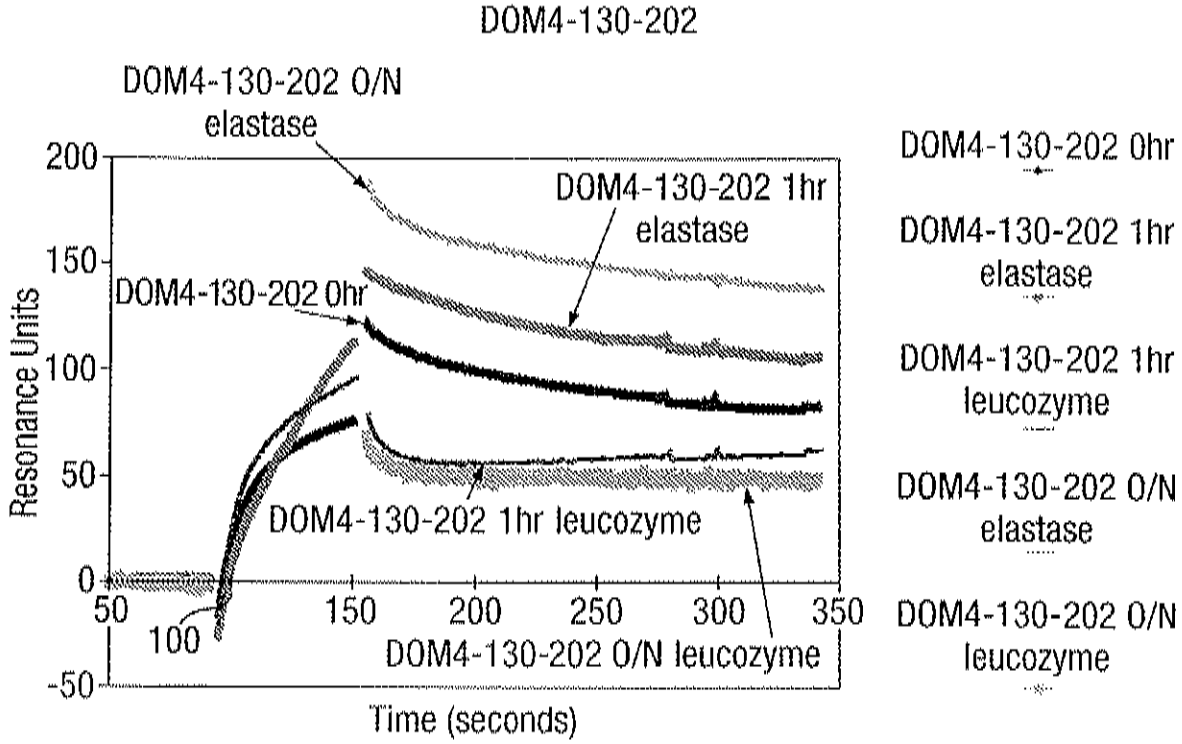
DOM4-130-202
DOM4-130-202 O/N elastase
DOM4-130-202 1hr elastase
DOM4-130-202 0hr
DOM4-130-202 1hr leucozyme
DOM4-130-202 O/N leucozyme
Resonance Units
Time (seconds)
200
150
100
50
0
-50
50
100
150
200
250
300
350
DOM4-130-202 0hr
DOM4-130-202 1hr elastase
DOM4-130-202 1hr leucozyme
DOM4-130-202 O/N elastase
DOM4-130-202 O/N leucozyme

Fig.12.

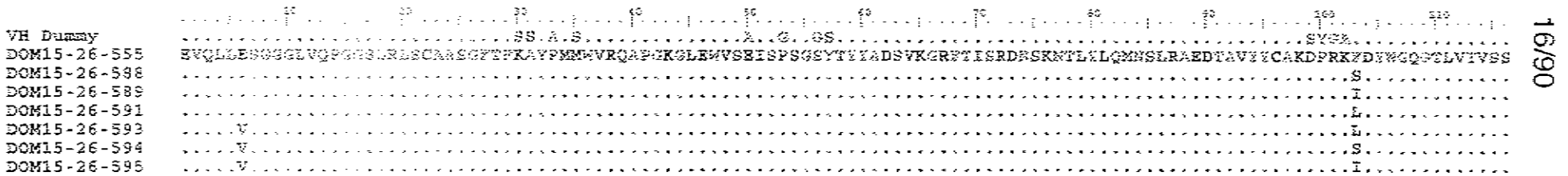
VH Dummy
DOM15-26-555
DOM15-26-588
DOM15-26-589
DOM15-26-591
DOM15-26-593
DOM15-26-594
DOM15-26-595

Fig.13A.

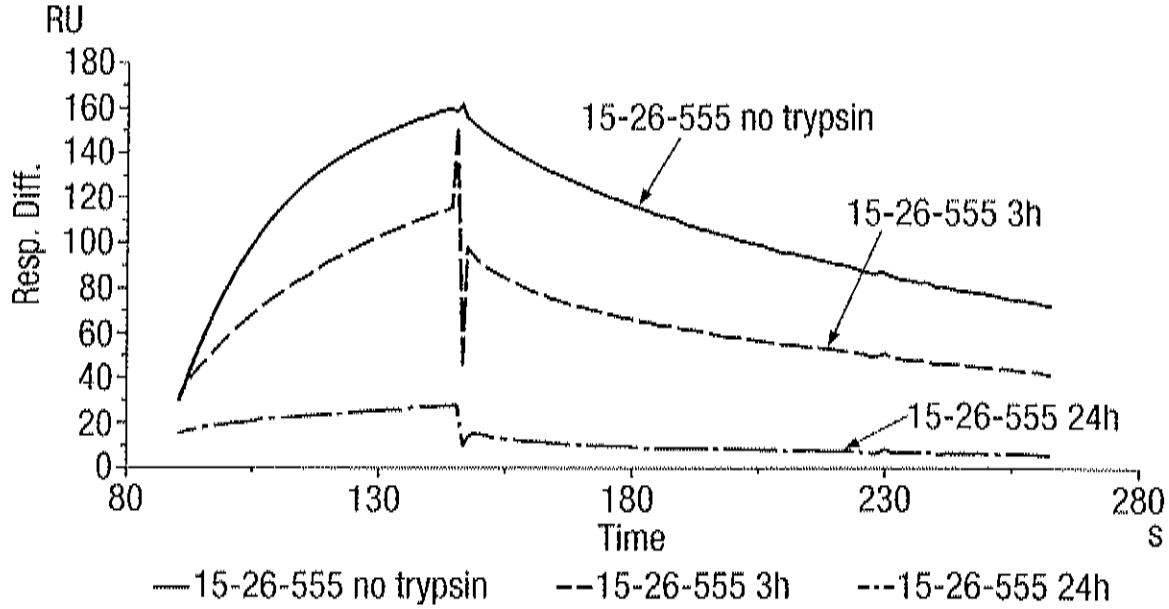

Fig.13B.

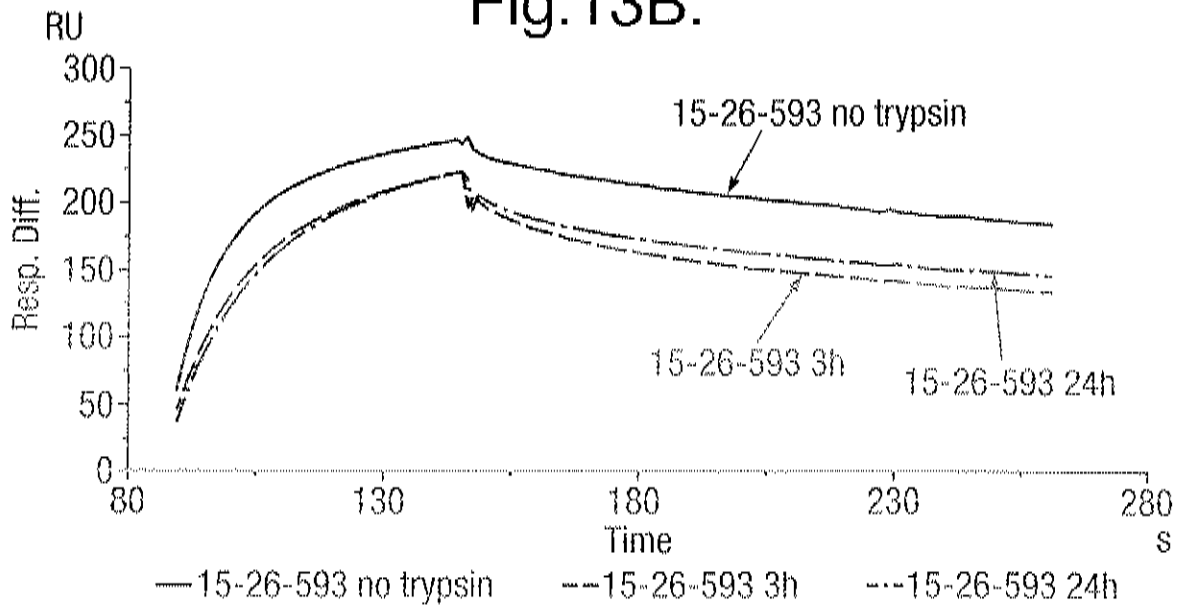

Fig.14.

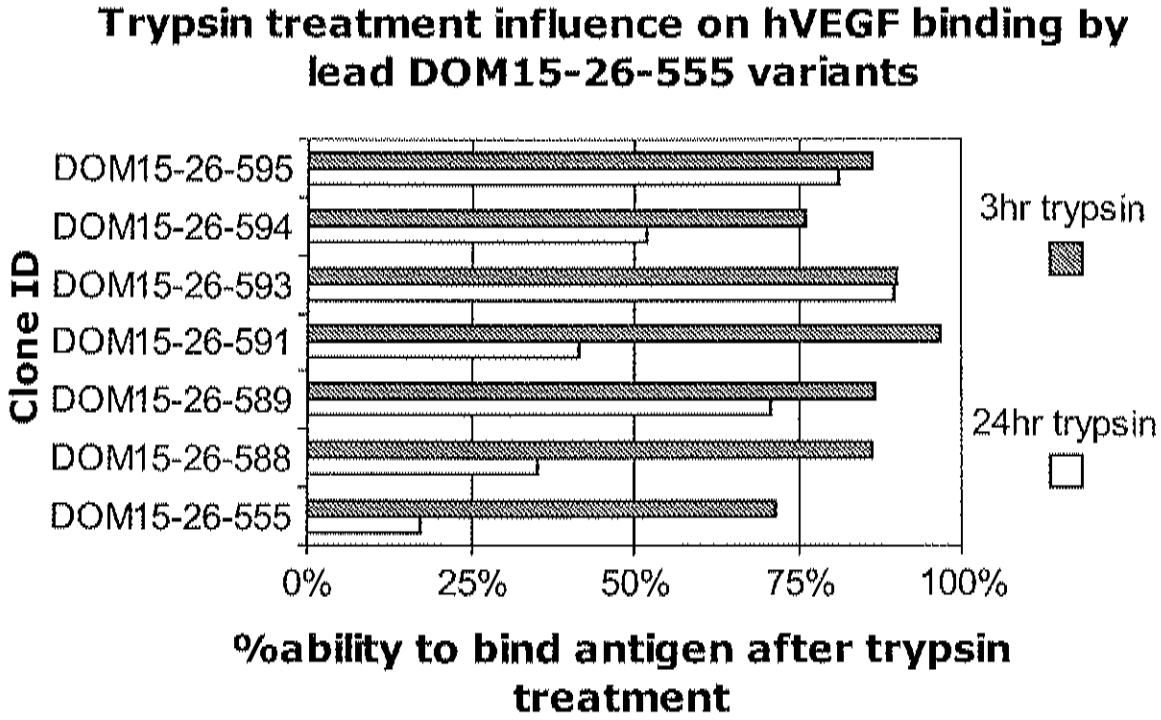
Trypsin treatment influence on hVEGF binding by lead DOM15-26-555 variants
DOM15-26-595
DOM15-26-594
DOM15-26-593
DOM15-26-591
DOM15-26-589
DOM15-26-588
DOM15-26-555
Clone ID
3hr trypsin
24hr trypsin
0%
25%
50%
75%
100%
%ability to bind antigen after trypsin treatment

Fig.15.

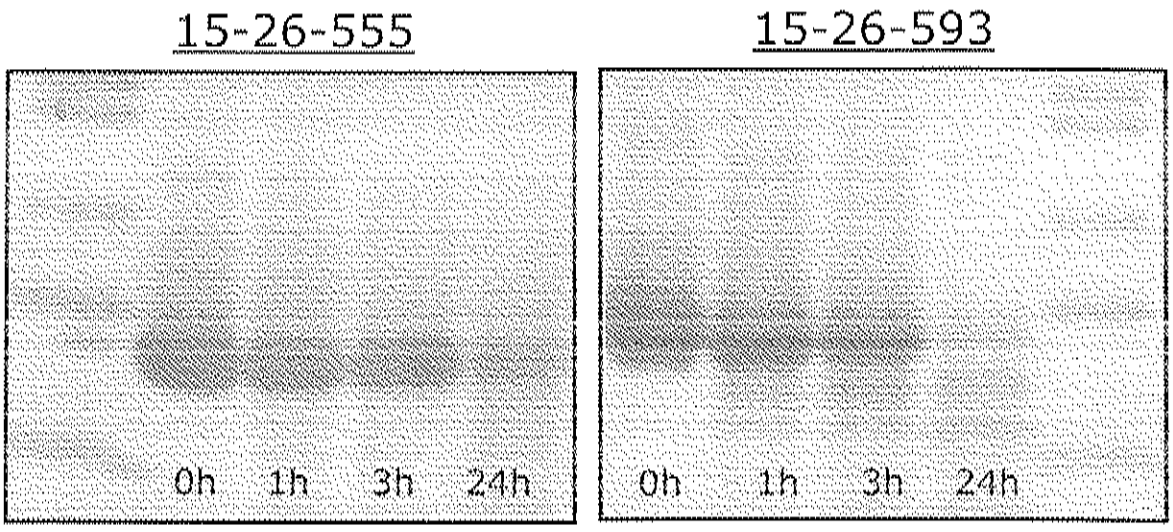
15-26-555
15-26-593
0h
1h
3h
24h
0h
1h
3h
24h

Fig.16.

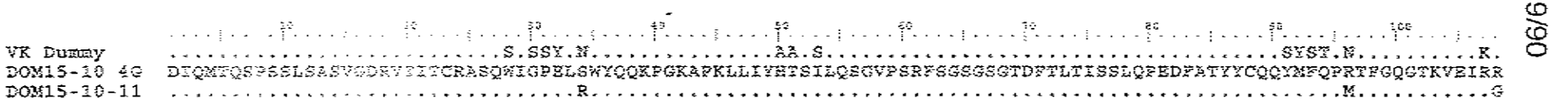
VK Dummy .....S.SSY.M.....AA.S.....SYST.M.....K.
DOM15-10 4G DIQMTQSPSSLSASVGDRVTITCRASQWIGPELSWYQQKPGKAPKLLIYWTSILQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYMFQPRTFGQGTKVEIKR
DOM15-10-11 .....R.....M.....G

Fig.17A.

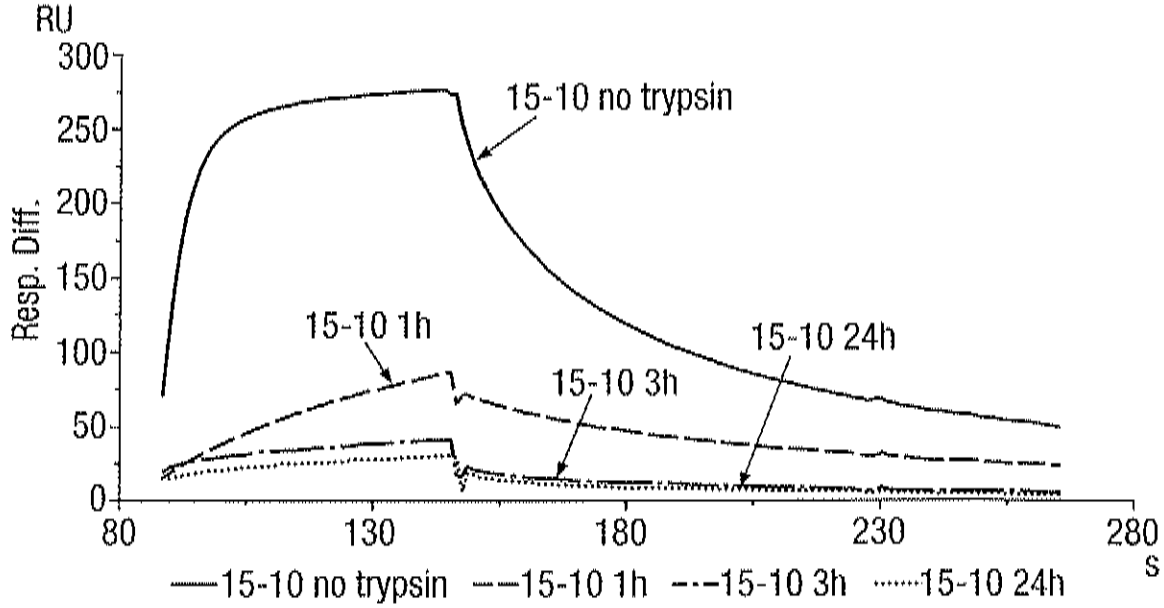

Fig.17B.

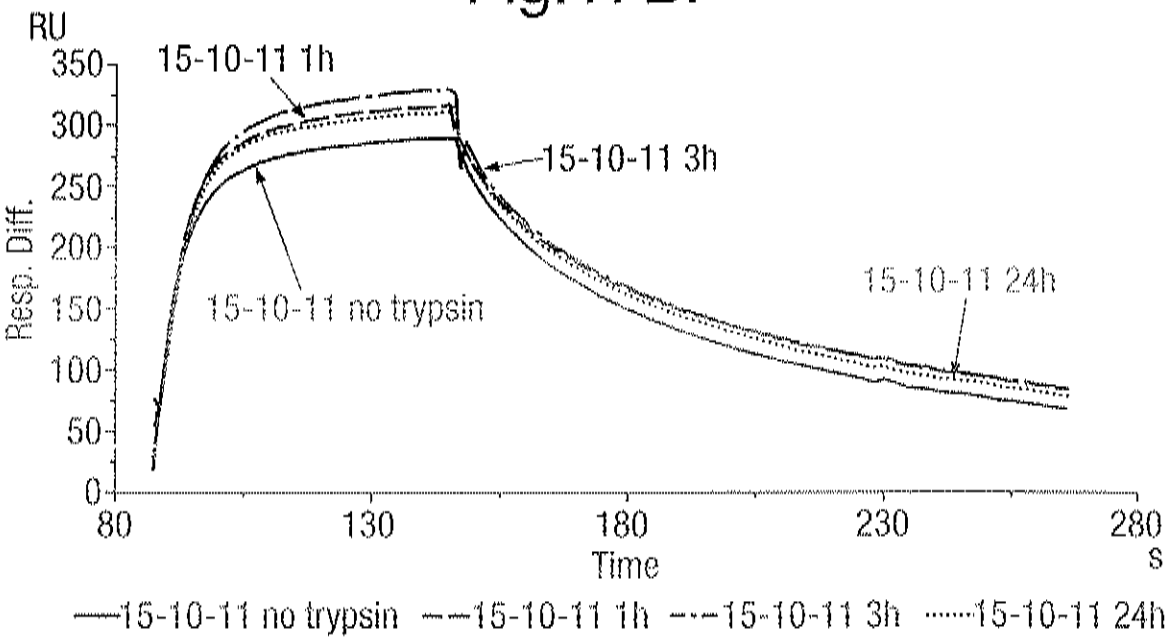

Fig.18.

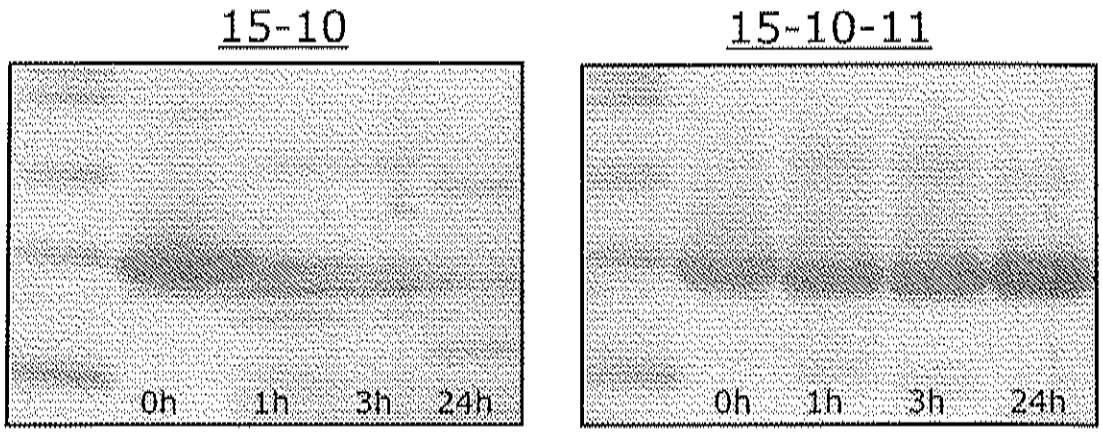

Fig.19A.

DOM1h-131-511 derived sequences

>1-1

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCATGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

>1-2

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCGCCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGG
AAGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGAGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

>1-3

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCAACTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

>DOM1h-131-201

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

Fig.19B.

>1-5

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTATGCAGACTCCGTG
AAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAACCT
GCGCGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTGAC
TACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

>1-6

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCCCCAGGG
AAGGGTCTAGAGTGGGTCTCACATATTCCCCCGGCTGGTCAGGATCCCTTCTACGCAGACTCCG
TGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAGCACGCTATATCTGCAAATGAACGG
CCTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTT
GACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

>1-7

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCTGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGCTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCCCCAGGG
AAGGGTCTAGAGTGGGTCTCACATATTCCCCCGGACGGTCAAGATCCCTTCTACGCAGACTCCG
TGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

Fig.19C.

>DOM1h-131-203

GAGGTGCAGCTGTGGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGATGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGATTG
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GAGGTGCAGCTGTCGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCAGATGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAATAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGATGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAGCG

>1-12

GAGGTGCGGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTACAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGATGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGAGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAGATGAACAGC
CTGCGTGCCGAGGACACAGCGGTGTATTACTGTGCGCTGCTTCCTAAGAGAGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAGCG

Fig.19D.

>1-13

GAGGTGCGGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGAGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGATAGCCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGGGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
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>1-14

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCATTGCGCATGAAACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
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ACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCG

>1-15

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCTCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGTG
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GCGTGCCGAGGACACAGCGGTATATTACTGTGCGCGGCTTCCTAAGAGGGGGCCTTGGTTTGAC
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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCACCAGGG
AAGGGTCTAGAGTGGGTCTCACATATTCCCCCGGATGGTCAGGATCCCTTCTACGCAGACTCCG
TGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATCACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

Fig.19E.

>1-18

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCGGGCTCCAGGG
AAGGGTCTAGAGTGGGTCTCACATATTCCCCCGGATGGTCAGGATCCCTTCTACGCAGACTCCG
TGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
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>1-19

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
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AGGGGTCTAGAGTGGGTCTCACATATTCCCCCGGATGGTCAGGATCCCTTCTACGCAGACTCCG
TGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
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>1-20

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
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GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTCG
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>1-21

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AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGATGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAAGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

Fig.19F.

>1-22

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCGTGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGG
AAGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

>1-23

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
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AAGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
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ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

>1-24

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCTTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGTTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCTGCTTCCTAAGAAGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

>1-25

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
TGTGCAGCCTCCGGATTCACCTTTGCGCATGAGACGATGGTGTGGGTCCGCCAGGCTCCAGGGA
AGGGTCTAGAGTGGGTCTCACATATTCCCCCGGCTGGTCAGGATCCCTTCTACGCAGACTCCGT
GAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGCAAATGAACAGC
CTGCGTGCCGAGGACACAGCGGTATATTACTGTGCGCGGCTTCCTAAGAGGGGGCCTTGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

Fig.19G.

DOM4-130-54 derived sequences

>4-1

GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACTT
GCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAGGCCCCT
AAGCTCCTGATCAATCTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGGA
TATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATGTCGCTACGTACTACTGT
CAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGGG

>4-2

GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACTT
GCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCCT
AAGCTCCTGATCAATTTTGGCTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGCGGA
TATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACTACTGT
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>4-3

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TAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCTCGTTTCAGTGGCAGTGG
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GGGACCAAGGTGGAAATCAAACGGG

>4-4

GACATCCAGGTGACCCAGTCTCCATCCACCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACT
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ATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACTACTG
TCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCGAGGGACCAAGGTGGAAATCAAACGGG

>4-5

GACATCCAGATGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACTT
GCCGGGCAAGTCAGGATATTTACCAGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCCT
AAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGGA
TACGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATATCGCTACGTACTACTGT
CAACCGTCTTTTTACTTCCCTTATACGTTTGGCCAAGGGACCAAGGTGGAAATCAAAGGGG

Fig.19H.

>4-6

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCGGCATCTGAAGGAGACCGTGTCACCATCACT
TGCCGGGCAAGTCAGGATATTTACCAGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCC
TAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGG
ATATGGGACAGAATTCACTCTCACCATCAGCAGTCTGCAACCTGAAGACTTCGCTACGTACTACTG
TCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGGG

>4-7

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCGTCACT
TGCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCC
TAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGG
ATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGATTTCGCTACGTACTACTG
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>4-8

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TGCCGGGCAAGTCAGGATATTTACCTGGATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCC
TAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGG
ATATGGGACAGATTTCACTCTCACCATCAGCGGTCTGCAACCTGAAGATTTCGCTACGTACTACTG
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>4-9

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TGCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCC
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GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACT
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TAAGCTCCTGATCAAATTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGG
ATATGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCTGAAGATTTCGCTACGTACTACTG
TCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAATGGG

Fig.19l.

>4-11

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACT
TGCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCC
TAAGCTCCTGATCATTTATGGTTCCGAGTTGCAAAGTGGTGTCCCACCACGTTTCAGTGGCAGTGG
ATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTCCGCTACGTACTACTG
TCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGGG

>4-12

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACT
TGCCGGGCAAGTCAGGATATATACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCC
TAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCACCACGTTTCAGTGGCAGTGG
ATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACTACTG
TCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACAGG

>4-13

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACT
TGCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCC
TAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGG
ATATGGGACAGATTTCGCTCTCACCATCAGCAGTCTGCAACCTGAAGATTCCGCTACGTACTACTG
TCAACCGTCTTTTTACTTCCCATATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACAGG

>4-14

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AAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGGA
TATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATGTCGCTACGTACTACTGT
CAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGGG

>4-15

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACT
TGCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCCCC
TAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAGTGG
ATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGACTTCGCTACGTACTACTG
TCAACCGTCTTTTTACTTCCCATATACGTTTGGCCAAGGGACCAAGGTGGAAATCAAACAGG

Fig.19J.

>4-16

GACATCCAAATGGCCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCAC
TTGCCGGGCAAGTCAGGATATTTACCTGAATTTGGACTGGTATCAGCAGAAACCAGGGAAAGCC
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TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTCCGCTACGTACT
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>4-17

GACATCCAGATGACCCAGTCACCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCAC
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TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACT
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>4-18

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TGGATATGGGACAGATTTCACACTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACT
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>4-19

GACATCCAGATAACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCAC
TTGCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCC
CCTAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAG
TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACT
ACTGTCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACCG

>4-20

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCAC
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TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACT
ACTGTCAACCGTCTTTTTACTACCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACAG

Fig.19K.

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GACATCCAGATGACACAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCTC
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CCTAAGCTCCTGATCAGTTTTGGTTCCGAGTTGCAAAGTGGTGTTCCTTCACGTTTCAGTGGCAG
TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGATTCCGCTACGTACT
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>4-22

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCAC
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CCTAAGCTCCTGATCAATTTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAG
TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACT
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>4-23

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCAC
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TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTCCGCTACGTACT
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>4-24

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATATGTAGGAGACCGTGTCACCATCAC
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TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGGTACGTACT
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>4-25

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCAC
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TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGGTACGTACT
ACTGTCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGG

Fig.19L.

>4-26

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TTGCCGGGCAAGTCAGGATATTTACCTGAATTTAGACTGGTATCAGCAGAAACCAGGGAAAGCC
CCTAAGCTCCTGATCAATTTAGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAG
TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTCGCTACGTACT
ACTGTCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGT

>4-27

GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCAC
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CCTAAGCTCCTGATCAATCTTGGTTCCGAGTTGCAAAGTGGTGTCCCATCACGTTTCAGTGGCAG
TGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATGTCGCTACGTACT
ACTGTCAACCGTCTTTTTACTTCCCTTATACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGG

Fig.20A.

>DOM15-26-555
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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
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CGGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
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>DOM15-26-578
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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACGCGCTGTAT
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>DOM15-26-579
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CCAGGGAAGGGTCTAGAGTGGATCTCAGAGATTTCGCCTTCGGGTTCTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
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>DOM15-26-580
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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
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>DOM15-26-581
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CGGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
>DOM15-26-582
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CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTTCGCCTTCGGGTTCTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACGGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAACGATCCT
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Fig.20B.

>DOM15-26-583
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>DOM15-26-584
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CCAGGGAAGAGTCTAGAGTGGGTCTCAGAGATTTCGCCTTCGGGTTCTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACAATCTCCCGCGACAATTCCAAGAACACGCTGTAT
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CGGAAGATTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
>DOM15-26-585
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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
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CGGAAGTCTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
>DOM15-26-589
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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCCT
CGGAAGATTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

Fig.20C.

>DOM15-26-590
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GCAAACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
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CGGAAGATTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
>DOM15-26-591
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CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTTCGCCTTCGGGTTCTTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
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CGGAAGTTAGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
>DOM15-26-592
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>DOM15-10
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>DOM15-10-2
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GGGACCAAGGTGGAAATCAGACGG

Fig.20D.

>DOM15-10-3
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>DOM15-10-4
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>DOM15-10-6
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GGGACCAAGGTGGAAATCAGACGG

Fig.20E.

>DOM15-10-10
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CGTTTCAGTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
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GGGACCAAGGTGGAAATCAGACAG
>DOM15-10-11
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>DOM15-10-12
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>DOM15-10-13
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GGGACCAAGGTGGAAATCAGACGG
>DOM15-10-14
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CGTTTCAGTGGCAGTGGATATGGGACAGATTTCACTCTCTCCATCAGCAGTCTGCAACCT
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GGGACCAAGGTGGAAATCAGATGG
>DOM15-10-15
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CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
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>DOM15-10-16
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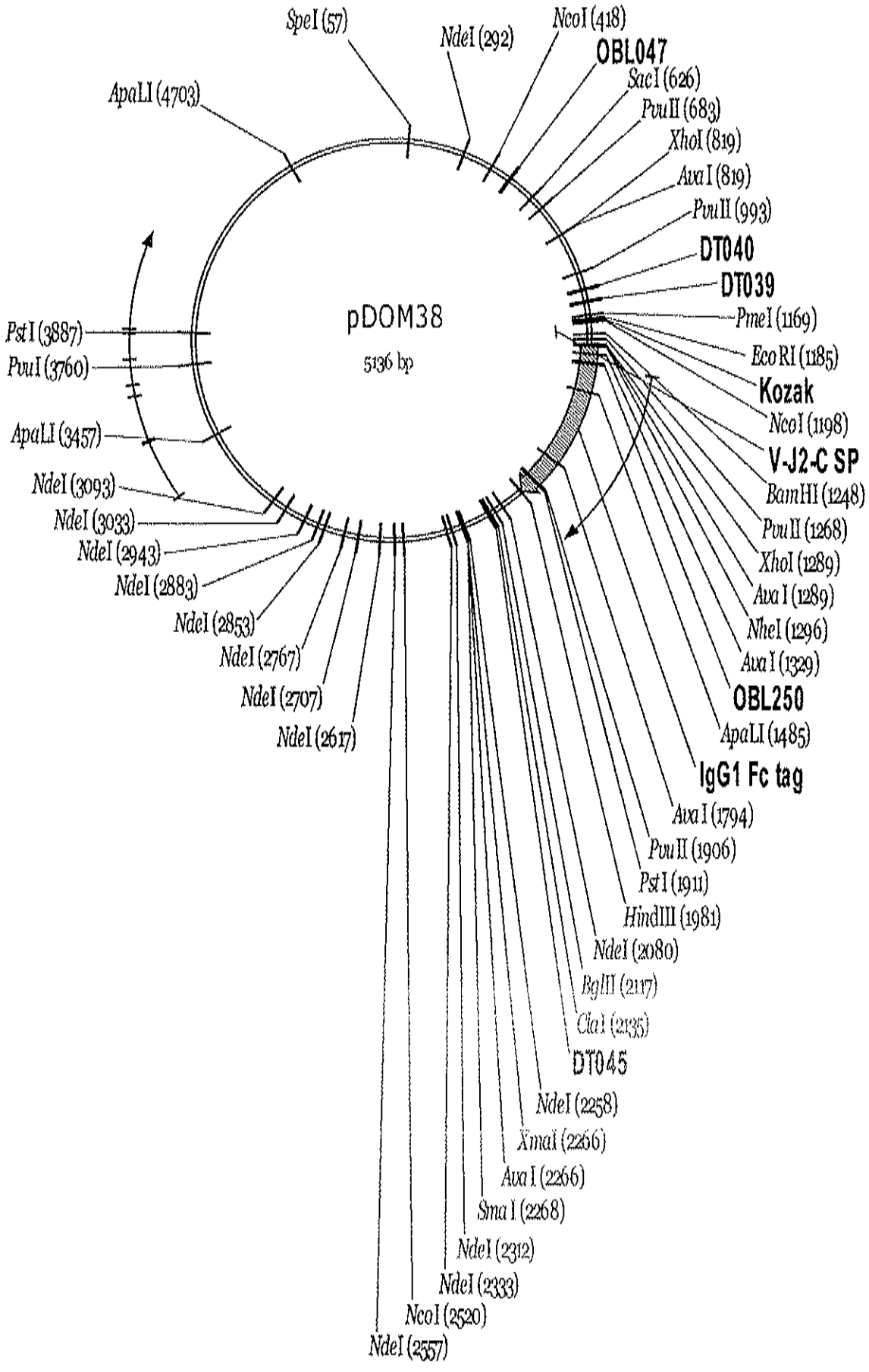
Fig.21.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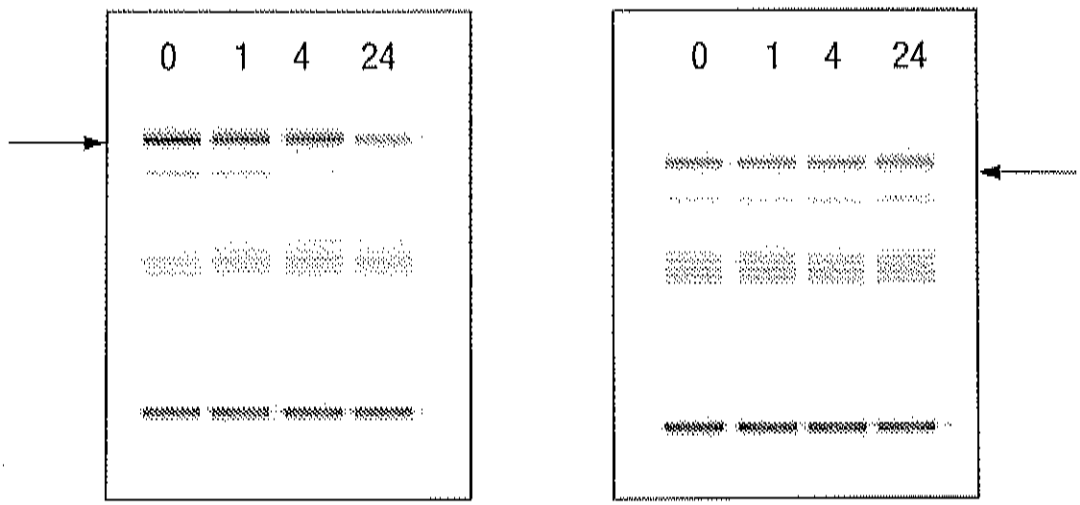
5136 bp
SpeI (57)
NdeI (292)
NcoI (418)
OBL047
SacI (626)
PvuII (683)
XhoI (819)
AvaI (819)
PvuII (993)
DT040
DT039
PmeI (1169)
EcoRI (1185)
Kozak
NcoI (1198)
V-J2-C SP
BamHI (1248)
PvuII (1268)
XhoI (1289)
AvaI (1289)
NheI (1296)
AvaI (1329)
OBL250
ApaLI (1485)
IgG1 Fc tag
AvaI (1794)
PvuII (1906)
PstI (1911)
HindIII (1981)
NdeI (2080)
BglII (2117)
ClaI (2135)
DT045
NdeI (2258)
XmaI (2266)
AvaI (2266)
SmaI (2268)
NdeI (2312)
NdeI (2333)
NcoI (2520)
NdeI (2557)
NdeI (2617)
NdeI (2707)
NdeI (2767)
NdeI (2853)
NdeI (2883)
NdeI (2943)
NdeI (3033)
NdeI (3093)
ApaLI (3457)
PstI (3887)
PvuI (3760)
ApaLI (4703)

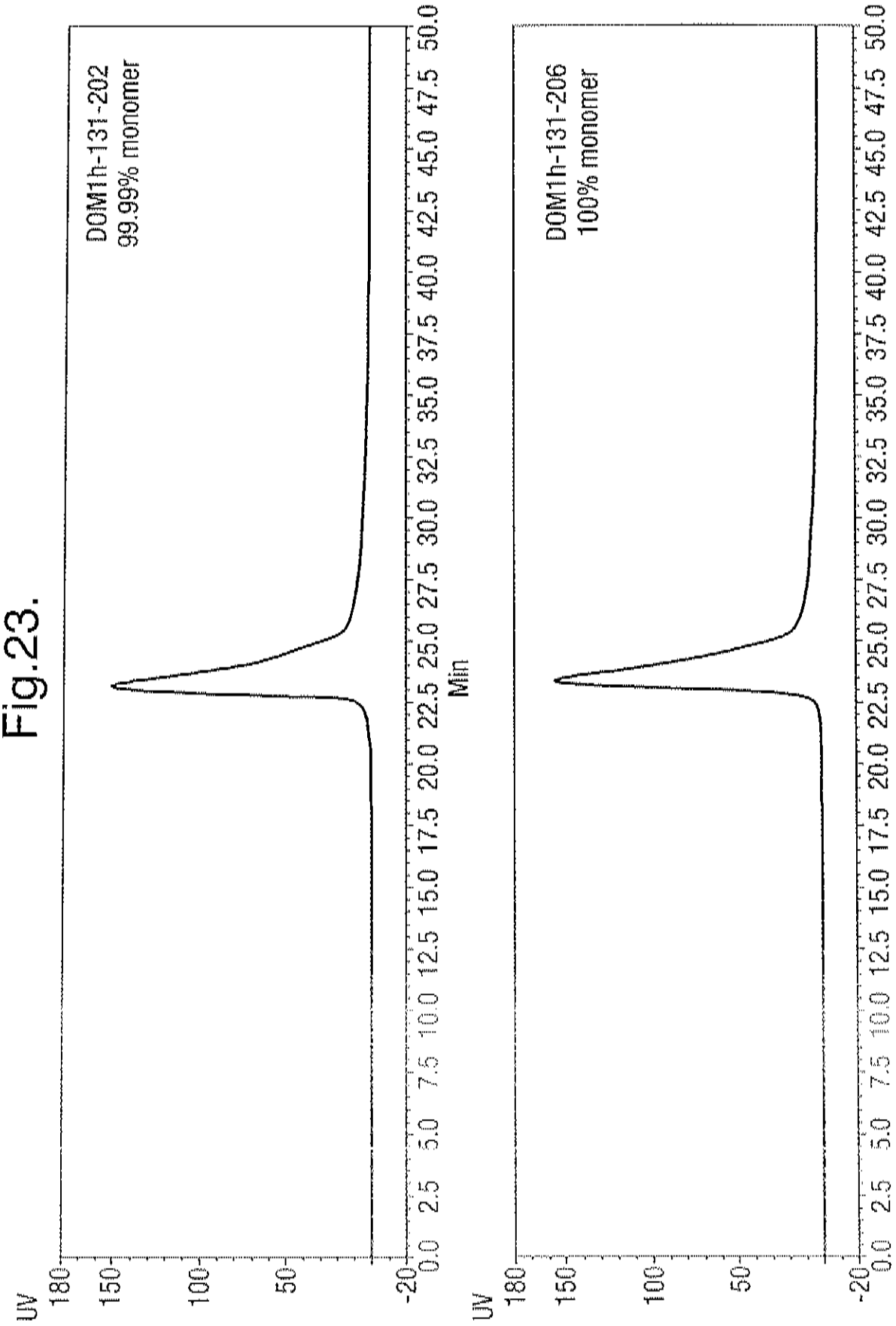
Fig.22.



10-53-474

15-26-593
Control

Fig.23.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99.99% monomer
UV
180
150
100
50
-20
0.0 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0 22.5 25.0 27.5 30.0 32.5 35.0 37.5 40.0 42.5 45.0 47.5 50.0
Min
DOM1h-131-206
100% monomer
UV
180
150
100
50
-20
0.0 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0 22.5 25.0 27.5 30.0 32.5 35.0 37.5 40.0 42.5 45.0 47.5 50.0
Min

Fig.23 (Cont).

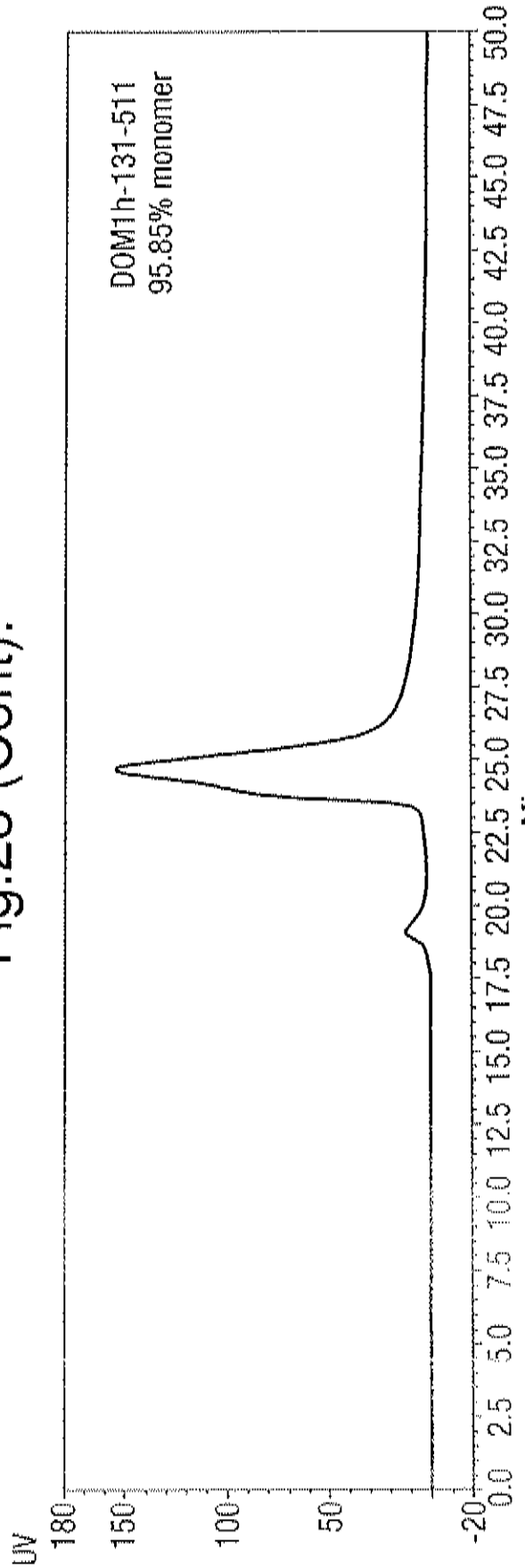

DOM1h-131-511
95.85% monomer
UV
180
150
100
50
-20
0.0 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0 22.5 25.0 27.5 30.0 32.5 35.0 37.5 40.0 42.5 45.0 47.5 50.0
Min

Fig.24.

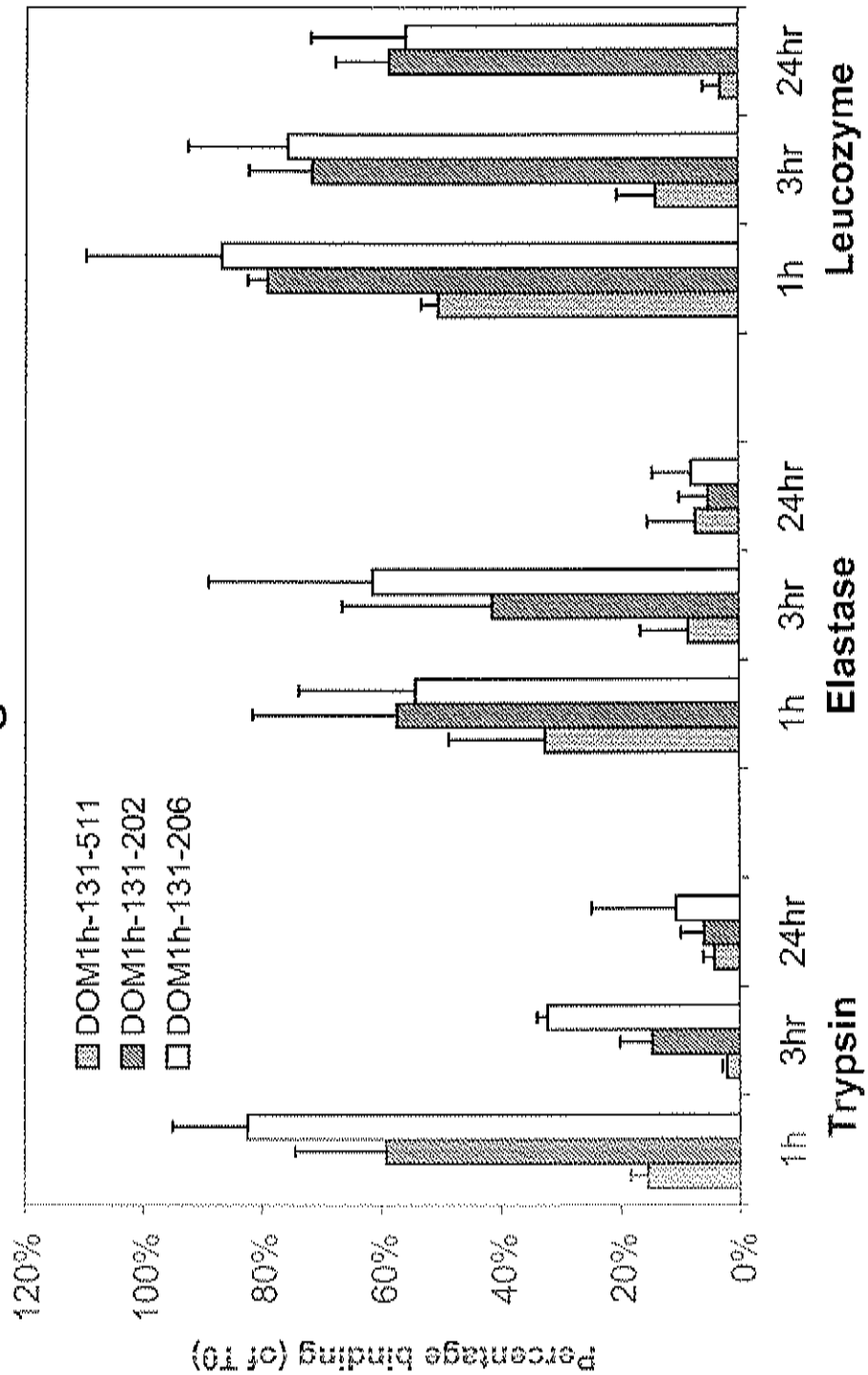

DOM1h-131-511
DOM1h-131-202
DOM1h-131-206
Percentage binding (of T0)
120%
100%
80%
60%
40%
20%
0%
1h
3hr
24hr
Trypsin
Elastase
Leucozyme

Fig.25.

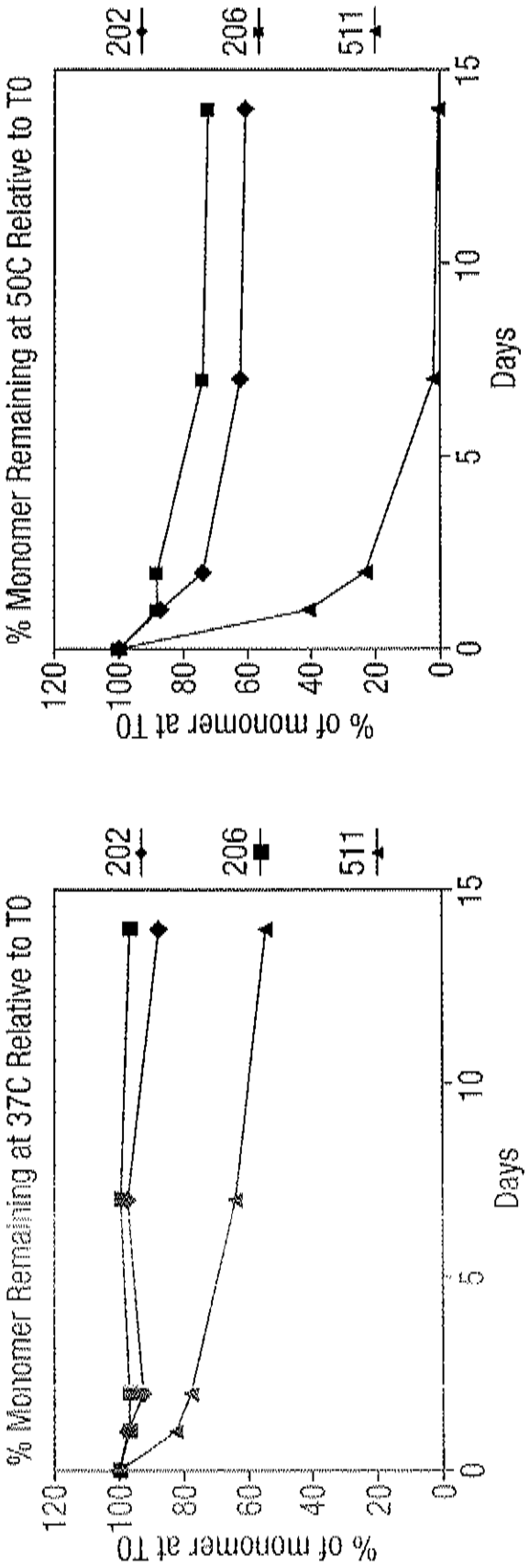

% Monomer Remaining at 37C Relative to T0
% of monomer at T0
Days
202
206
511
% Monomer Remaining at 50C Relative to T0
% of monomer at T0
Days
202
206
511

Fig.26.

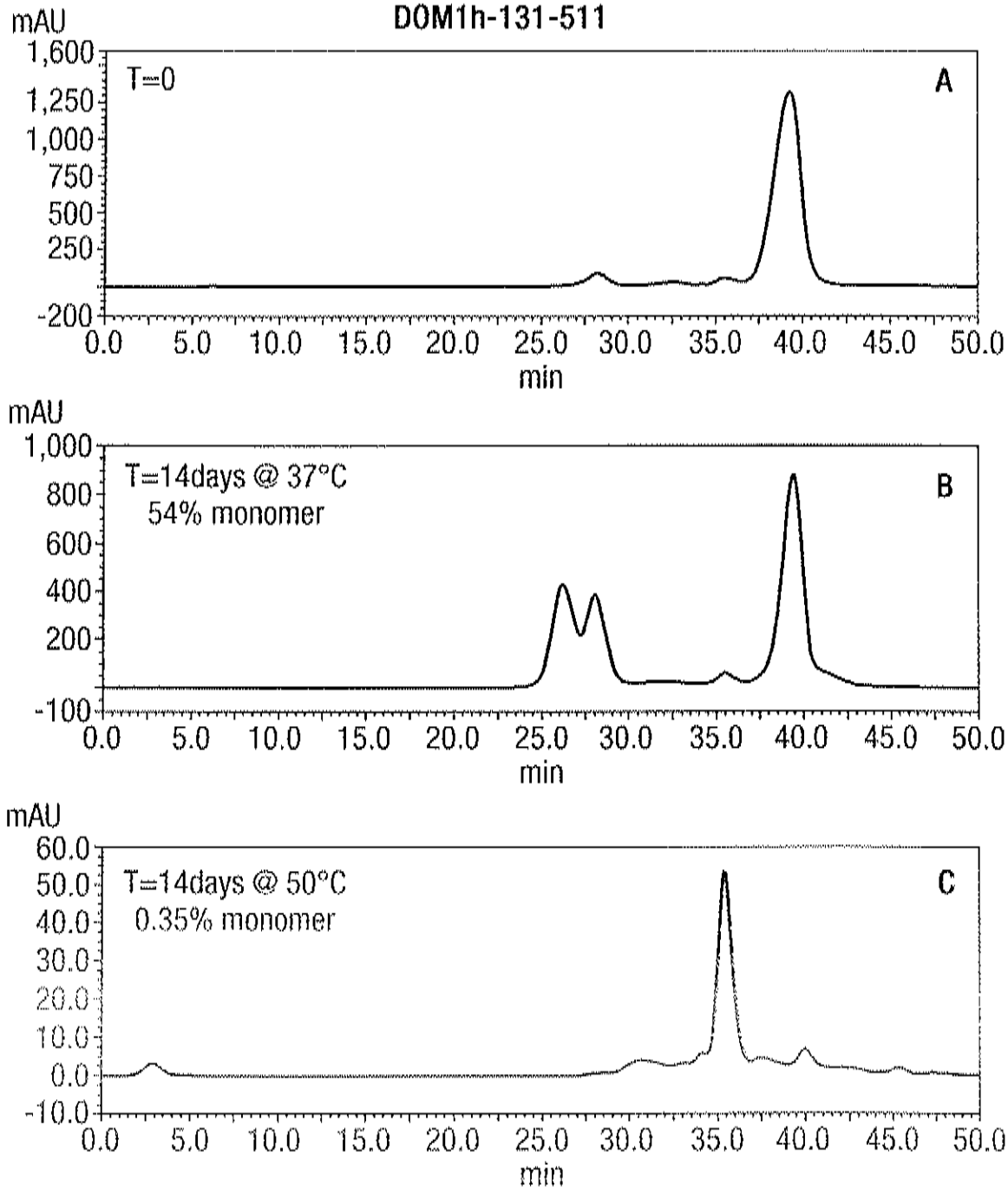

DOM1h-131-511
mAU
1,600
1,250
1,000
750
500
250
-200
T=0
A
0.0 5.0 10.0 15.0 20.0 25.0 30.0 35.0 40.0 45.0 50.0
min
mAU
1,000
800
600
400
200
-100
T=14days @ 37°C
54% monomer
B
0.0 5.0 10.0 15.0 20.0 25.0 30.0 35.0 40.0 45.0 50.0
min
mAU
60.0
50.0
40.0
30.0
20.0
10.0
0.0
-10.0
T=14days @ 50°C
0.35% monomer
C
0.0 5.0 10.0 15.0 20.0 25.0 30.0 35.0 40.0 45.0 50.0
min

Fig.26 (Cont I).

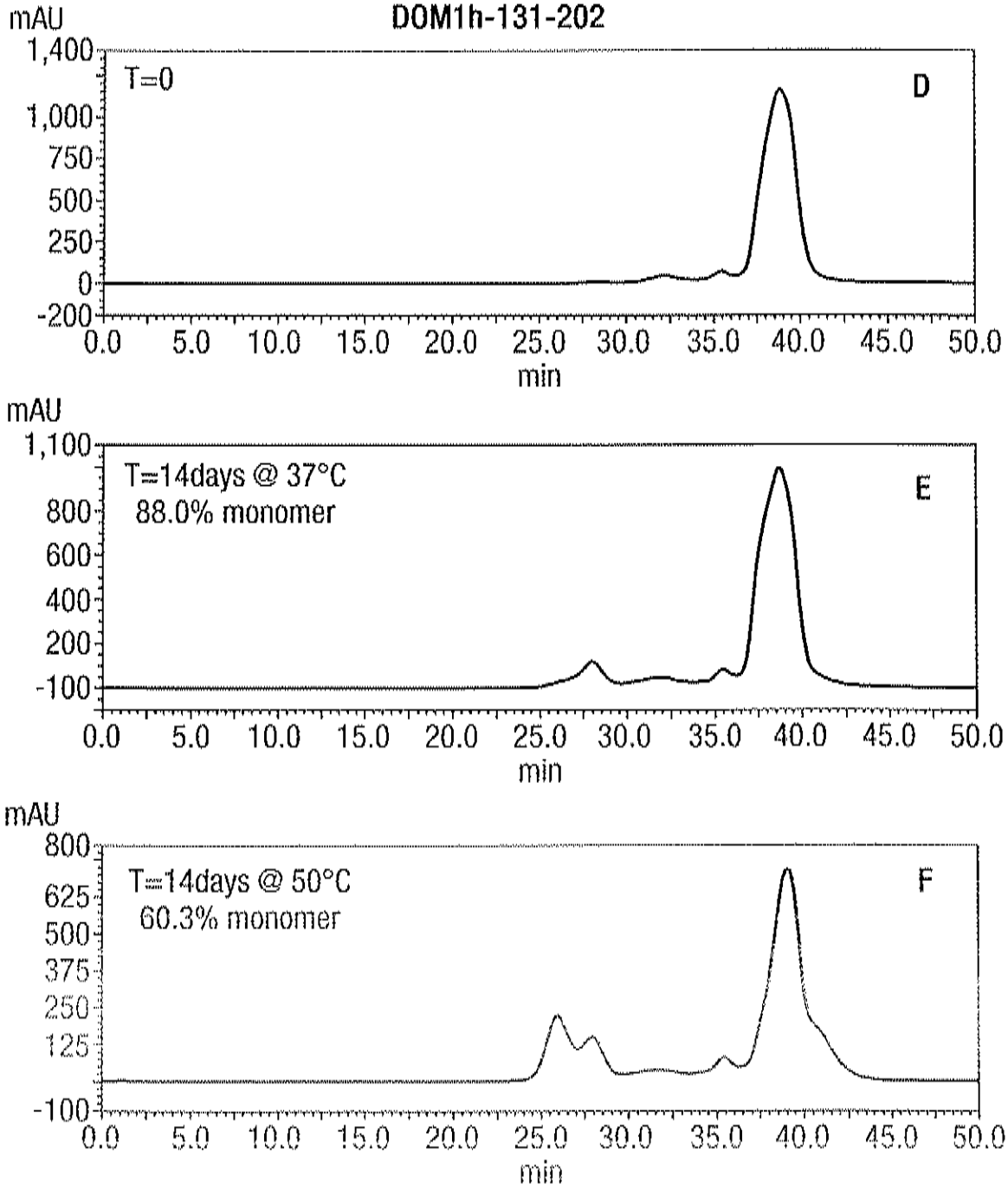

mAU
DOM1h-131-202
1,400
1,000
750
500
250
0
-200
T=0
D
0.0
5.0
10.0
15.0
20.0
25.0
30.0
35.0
40.0
45.0
50.0
min
mAU
1,100
800
600
400
200
-100
T=14days @ 37°C
88.0% monomer
E
0.0
5.0
10.0
15.0
20.0
25.0
30.0
35.0
40.0
45.0
50.0
min
mAU
800
625
500
375
250
125
-100
T=14days @ 50°C
60.3% monomer
F
0.0
5.0
10.0
15.0
20.0
25.0
30.0
35.0
40.0
45.0
50.0
min

Fig.26 (Cont II).

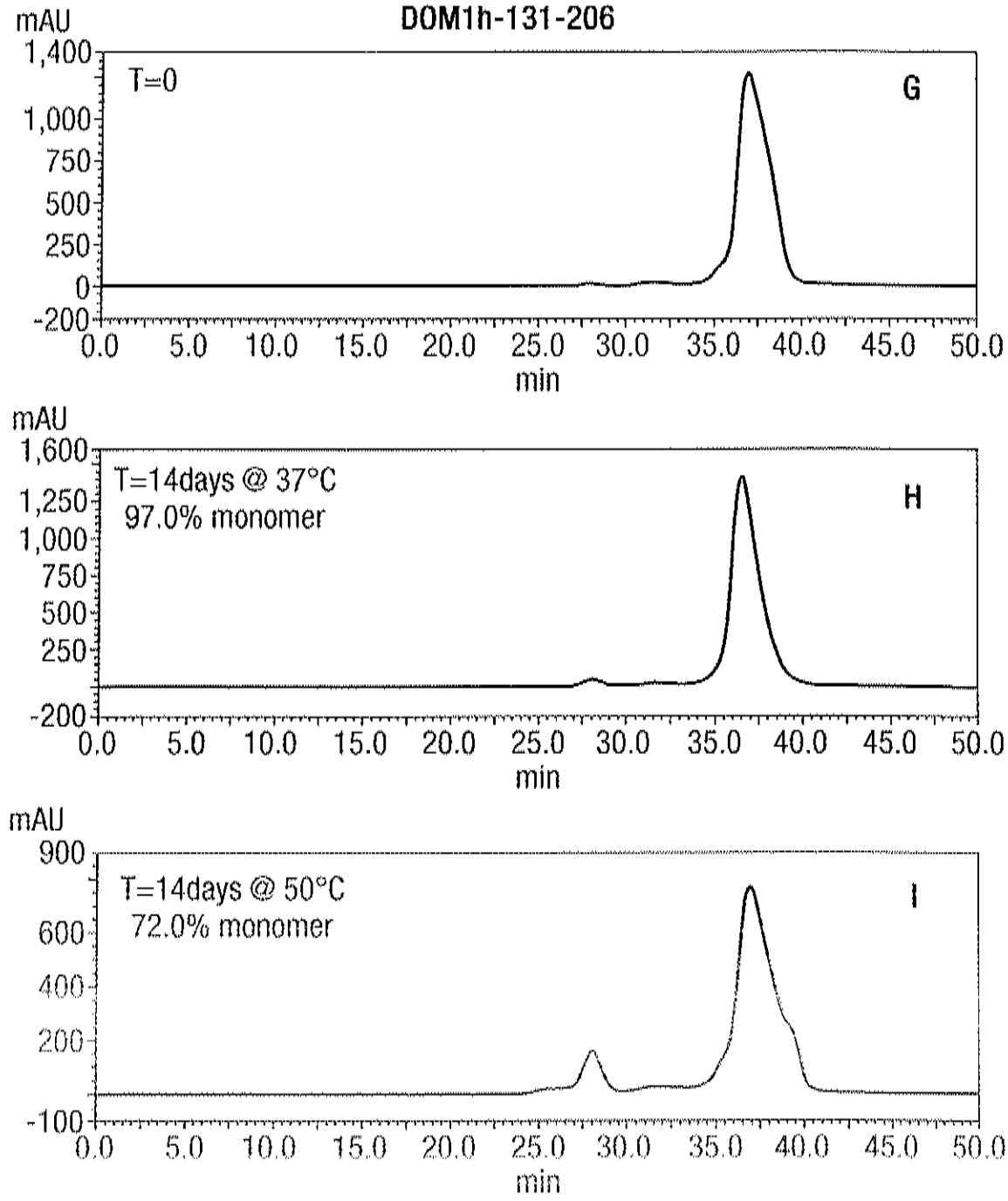


Fig.27.

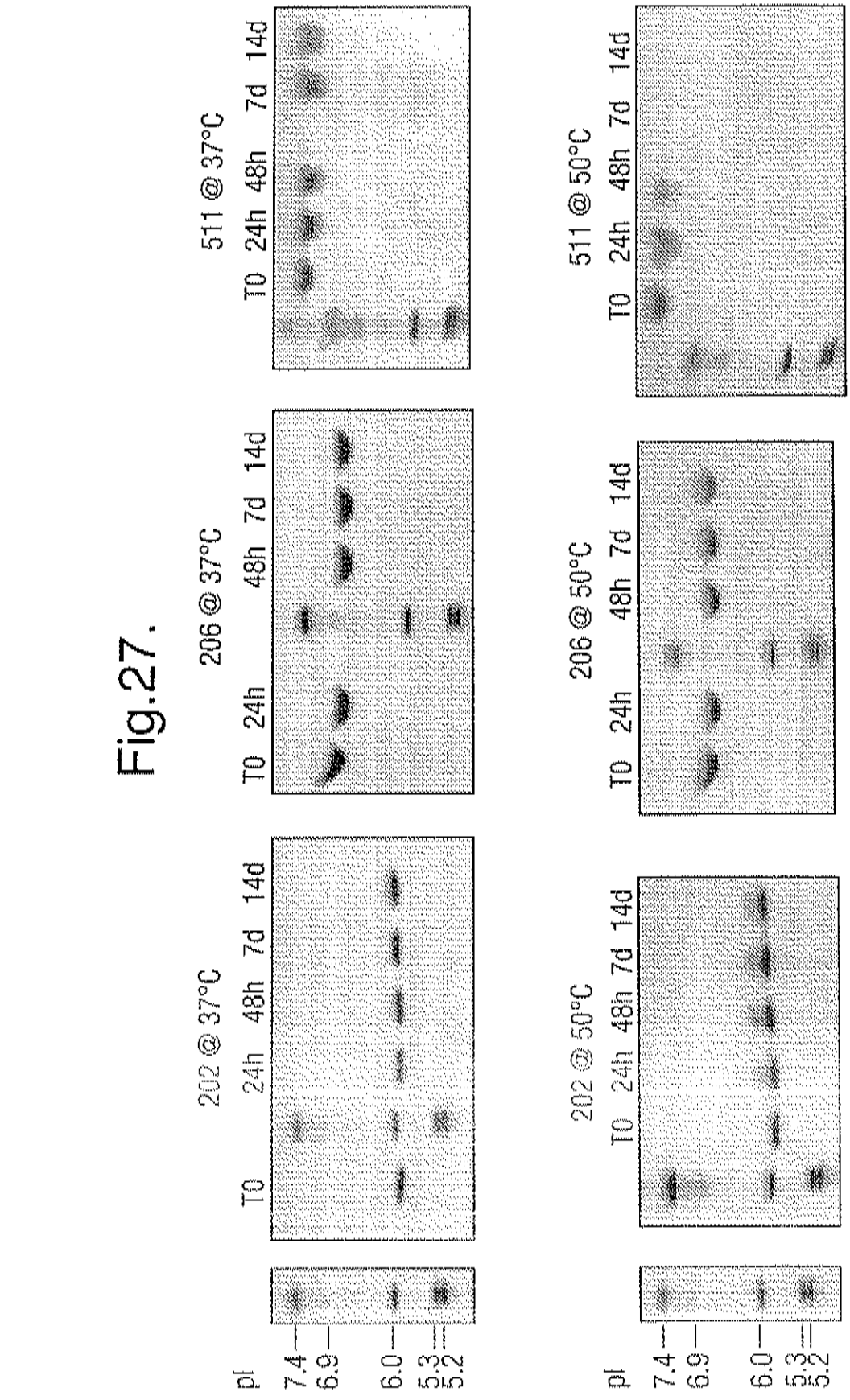

202 @ 37°C
206 @ 37°C
511 @ 37°C
202 @ 50°C
206 @ 50°C
511 @ 50°C
T0 24h 48h 7d 14d
pI
7.4
6.9
6.0
5.3
5.2

Fig.28.

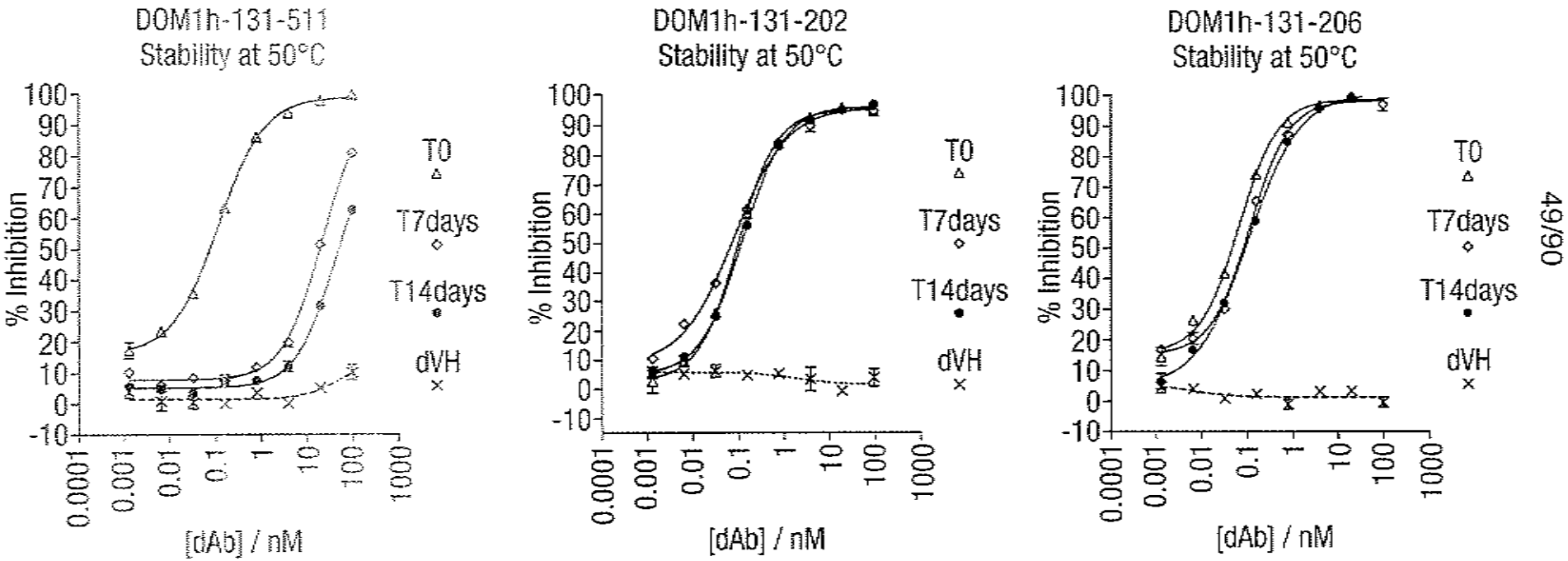

DOM1h-131-511
Stability at 50°C
% Inhibition
[dAb] / nM
T0
T7days
T14days
dVH
DOM1h-131-202
Stability at 50°C
% Inhibition
[dAb] / nM
T0
T7days
T14days
dVH
DOM1h-131-206
Stability at 50°C
% Inhibition
[dAb] / nM
T0
T7days
T14days
dVH

Fig.29.

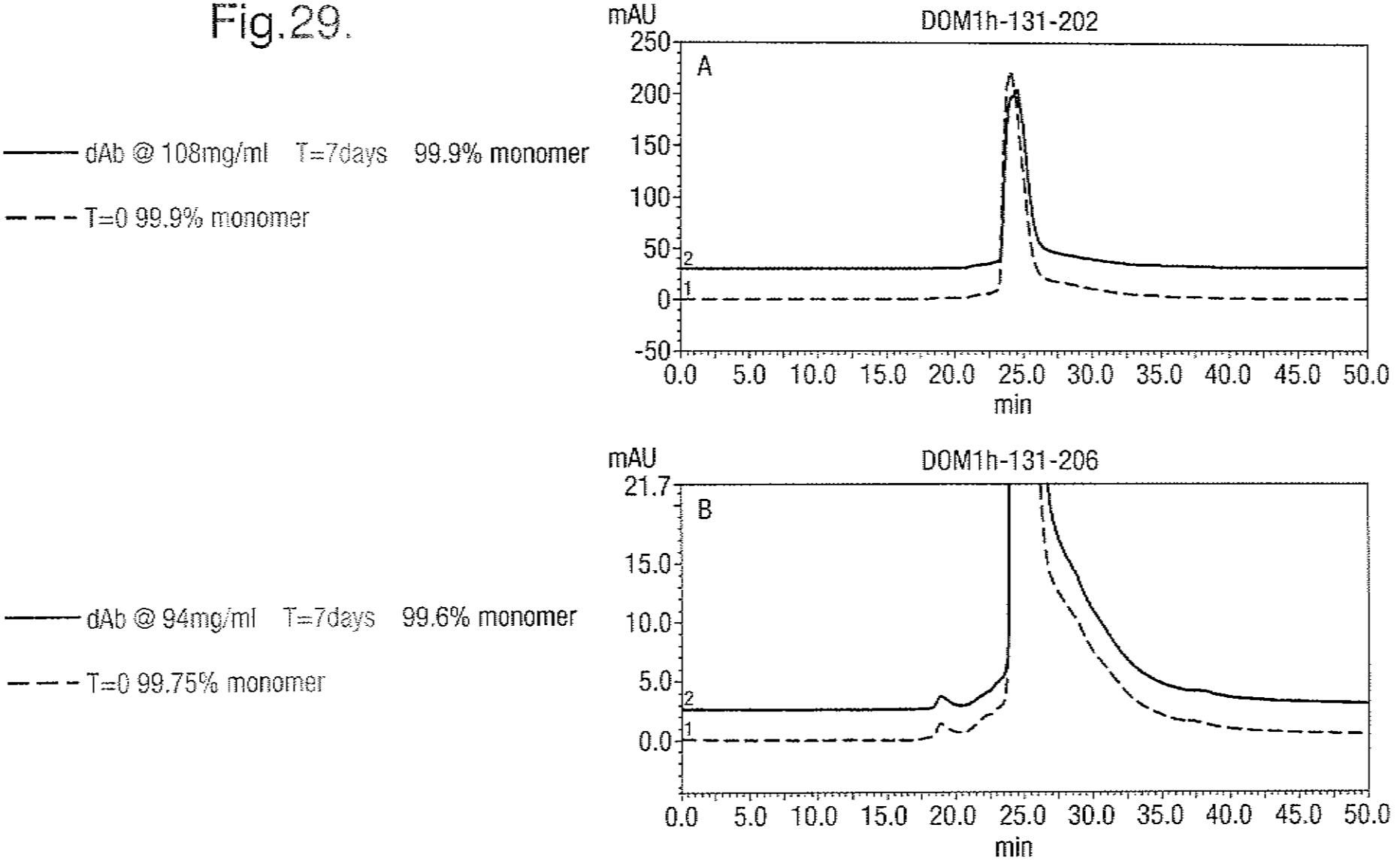

dAb @ 108mg/ml T=7days 99.9% monomer
T=0 99.9% monomer
mAU
DOM1h-131-202
A
250
200
150
100
50
0
-50
2
1
0.0 5.0 10.0 15.0 20.0 25.0 30.0 35.0 40.0 45.0 50.0
min
dAb @ 94mg/ml T=7days 99.6% monomer
T=0 99.75% monomer
mAU
DOM1h-131-206
B
21.7
15.0
10.0
5.0
0.0
2
1
0.0 5.0 10.0 15.0 20.0 25.0 30.0 35.0 40.0 45.0 50.0
min

Fig.29 (Cont).

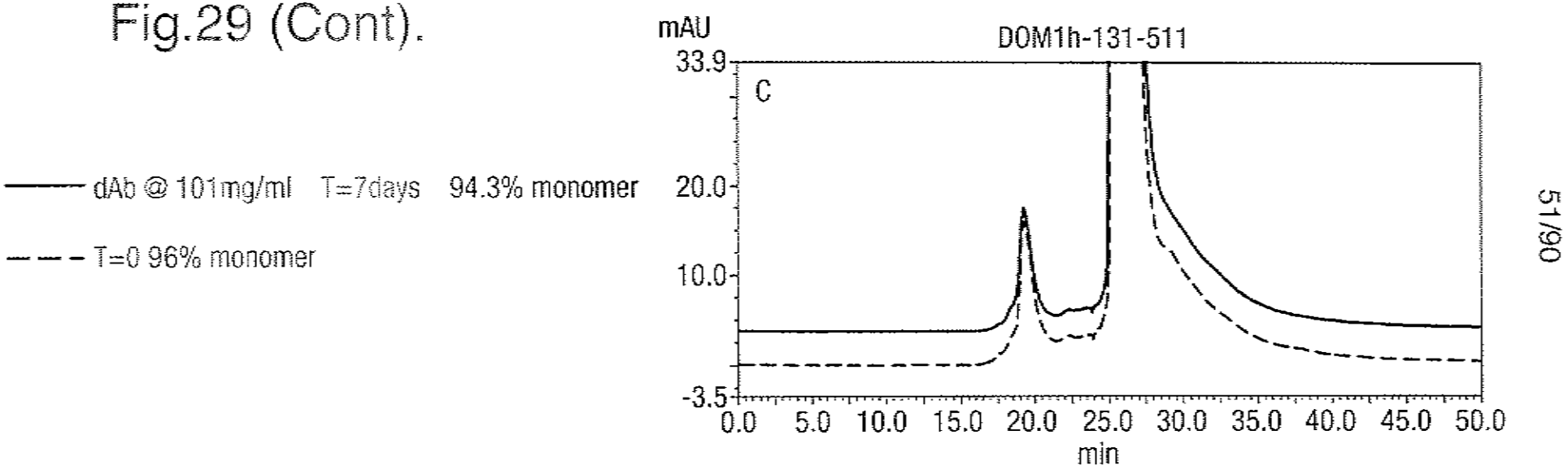

dAb @ 101mg/ml T=7days 94.3% monomer
T=0 96% monomer
mAU
DOM1h-131-511
C
33.9
20.0
10.0
-3.5
0.0
5.0
10.0
15.0
20.0
25.0
30.0
35.0
40.0
45.0
50.0
min

Fig.30.

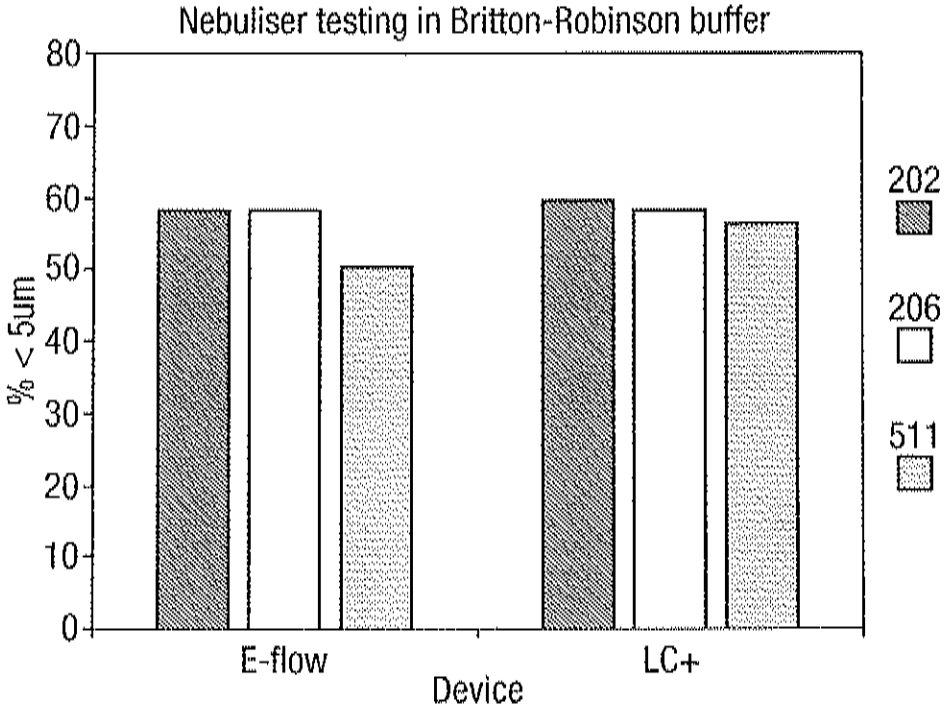

Nebuliser testing in Britton-Robinson buffer
% < 5um
80
70
60
50
40
30
20
10
0
E-flow
LC+
Device
202
206
511

Fig.31.

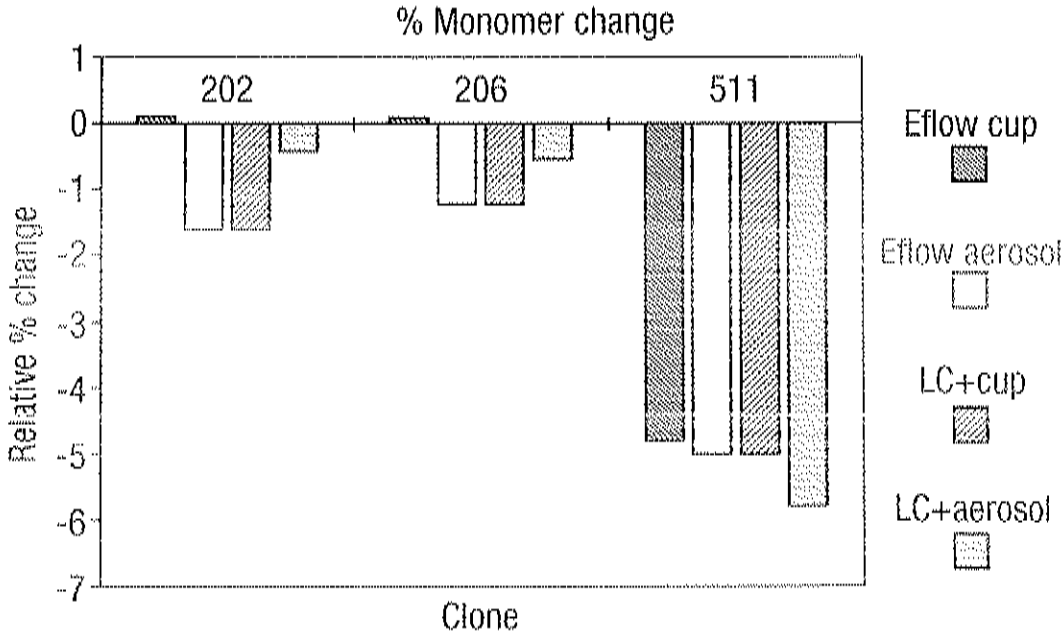
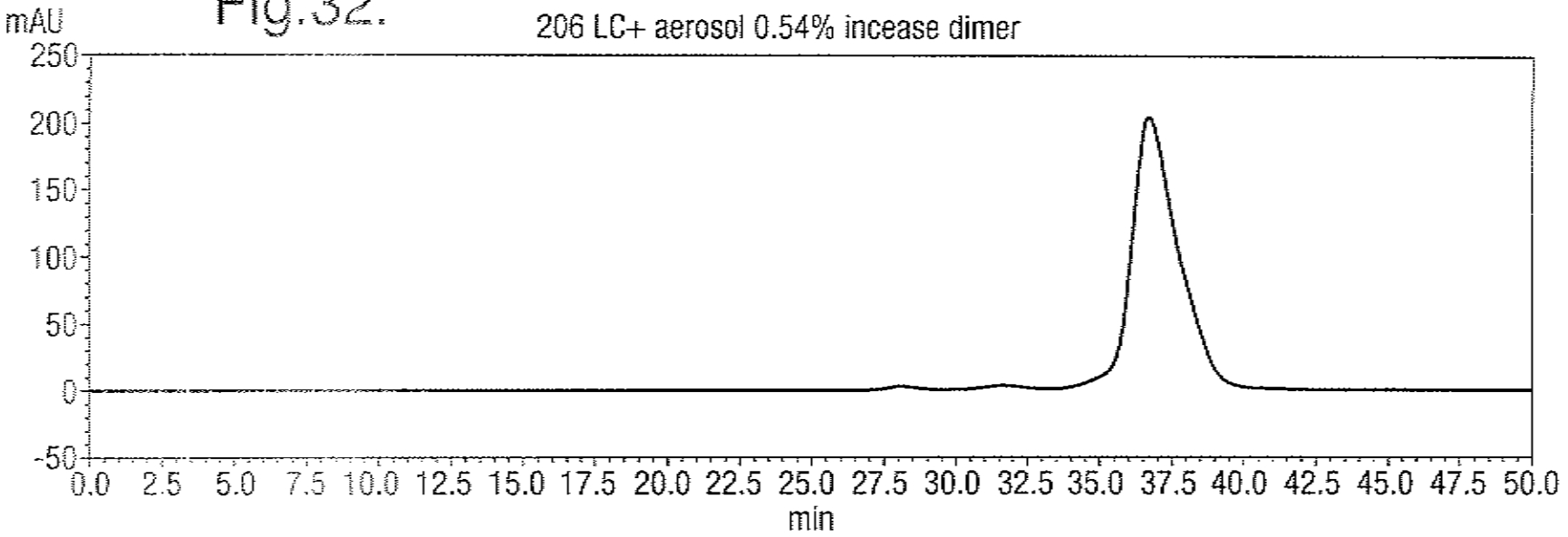

% Monomer change
Relative % change
1
0
-1
-2
-3
-4
-5
-6
-7
202
206
511
Clone
Eflow cup
Eflow aerosol
LC+cup
LC+aerosol

Fig.32.


206 LC+ aerosol 0.54% incease dimer
mAU
250
200
150
100
50
0
-50
0.0 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0 22.5 25.0 27.5 30.0 32.5 35.0 37.5 40.0 42.5 45.0 47.5 50.0
min

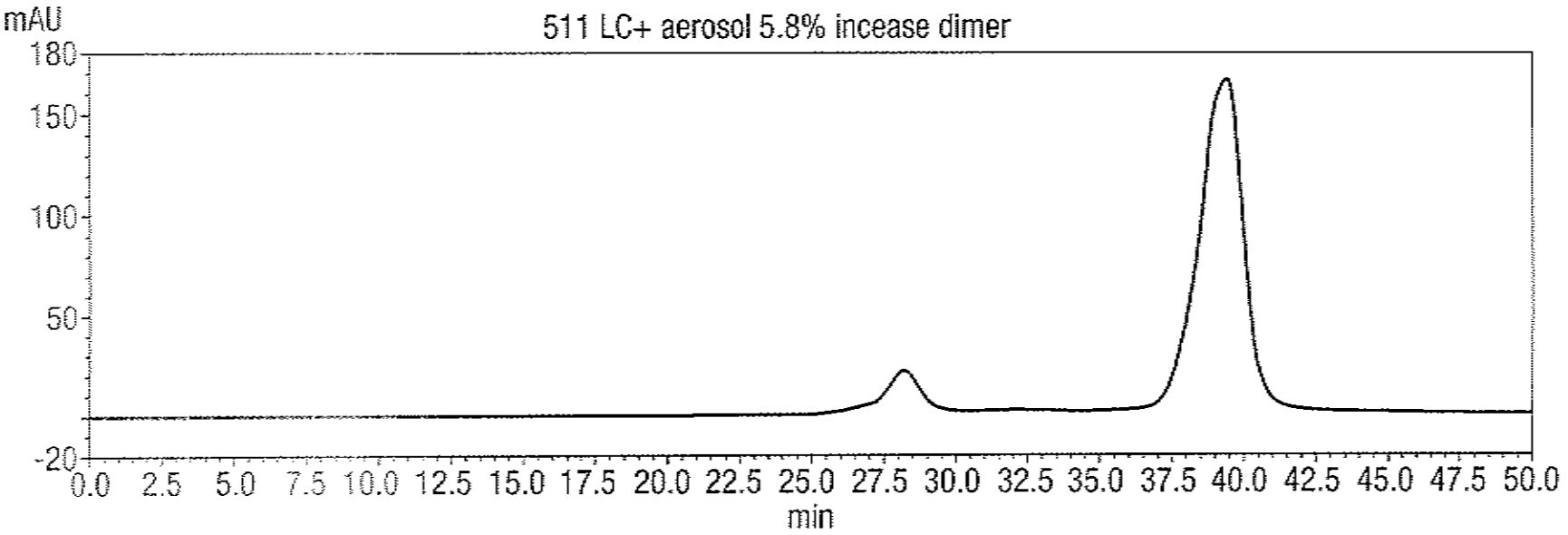

511 LC+ aerosol 5.8% incease dimer
mAU
180
150
100
50
-20
0.0 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0 22.5 25.0 27.5 30.0 32.5 35.0 37.5 40.0 42.5 45.0 47.5 50.0
min

Fig.33.

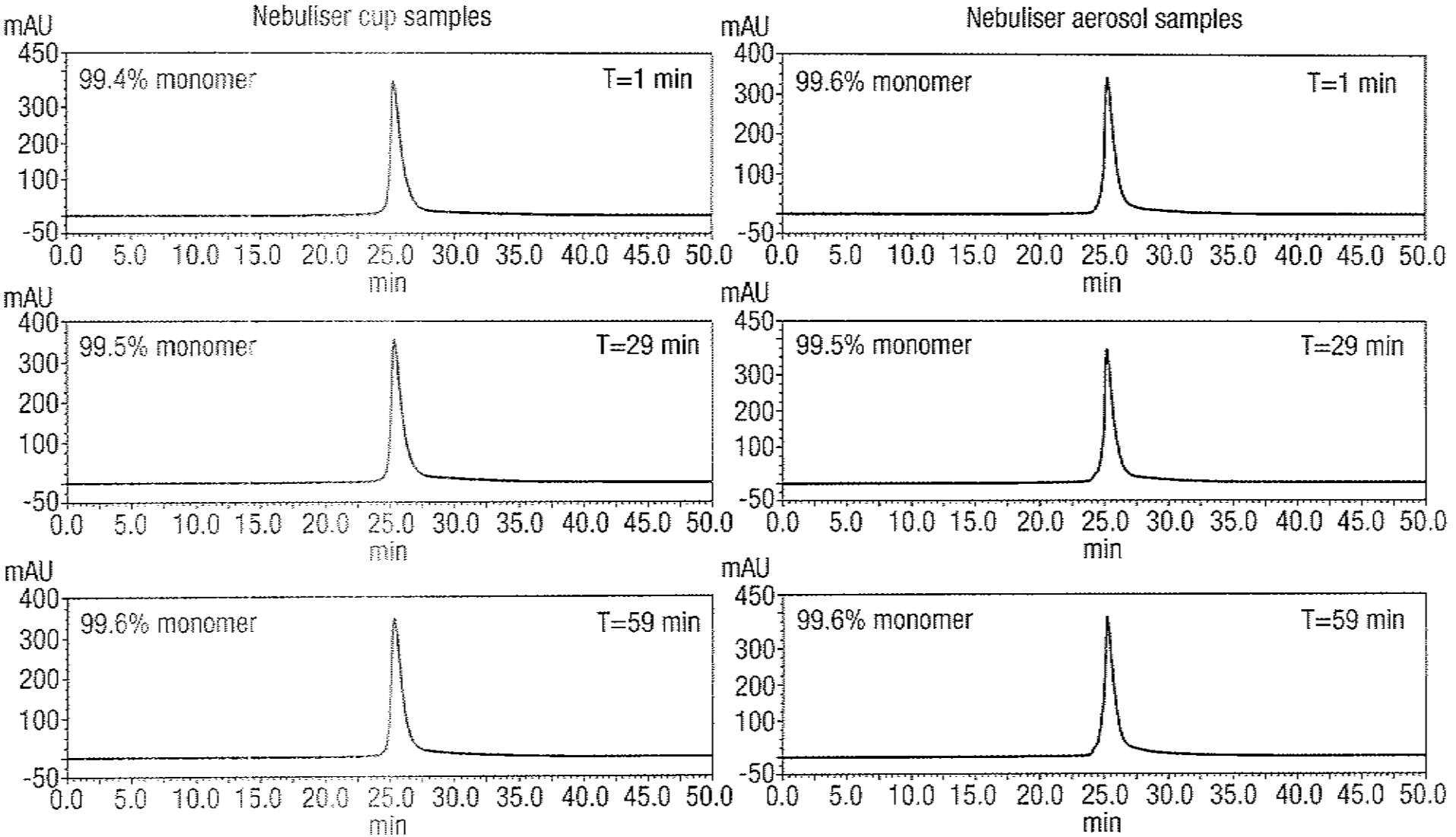

Nebuliser cup samples
Nebuliser aerosol samples
mAU
99.4% monomer
T=1 min
99.6% monomer
T=1 min
99.5% monomer
T=29 min
99.5% monomer
T=29 min
99.6% monomer
T=59 min
99.6% monomer
T=59 min
min

Fig.34.

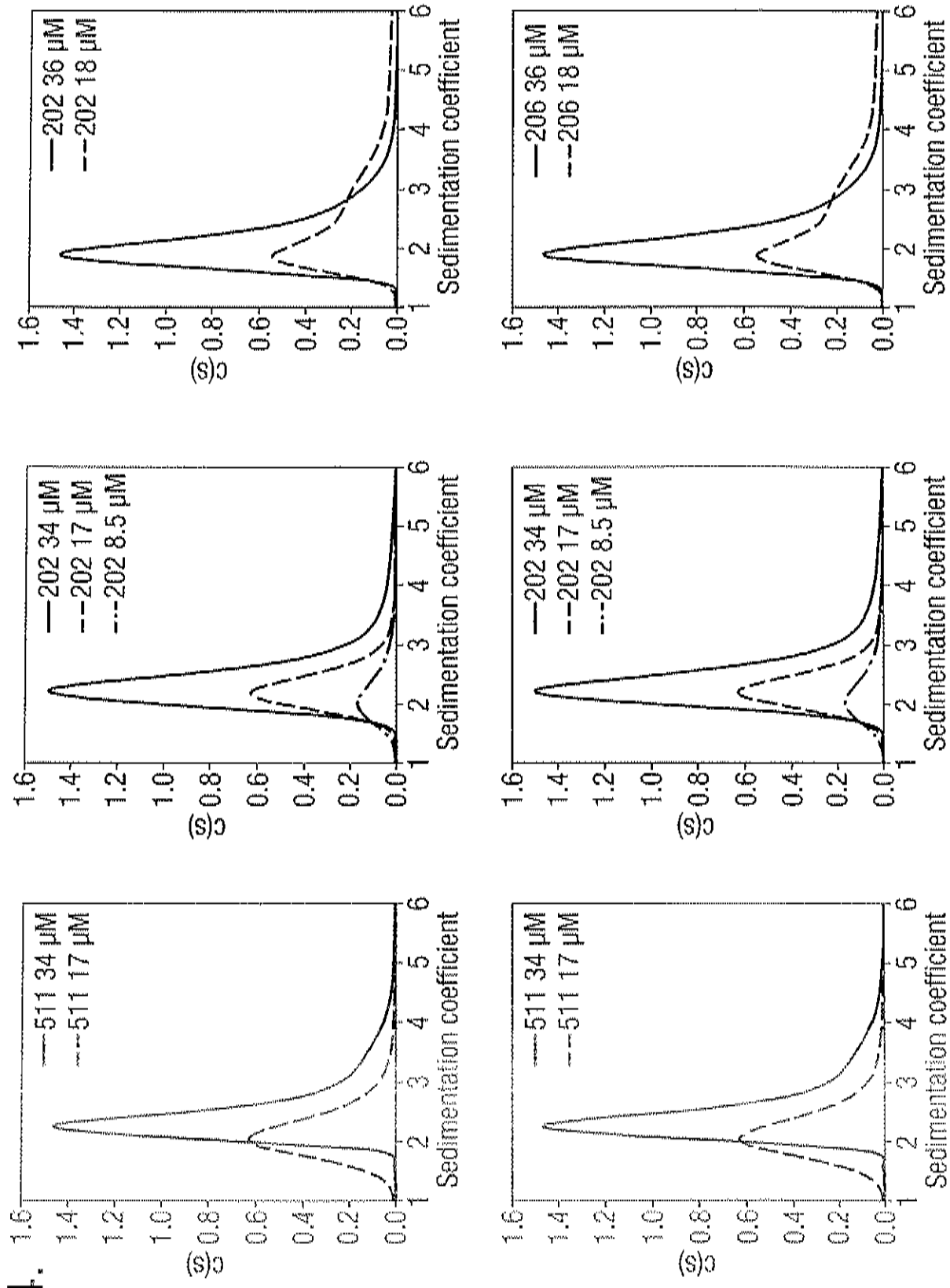

511 34 µM
511 17 µM
202 34 µM
202 17 µM
202 8.5 µM
202 36 µM
202 18 µM
206 36 µM
206 18 µM
c(s)
Sedimentation coefficient

Fig.35.

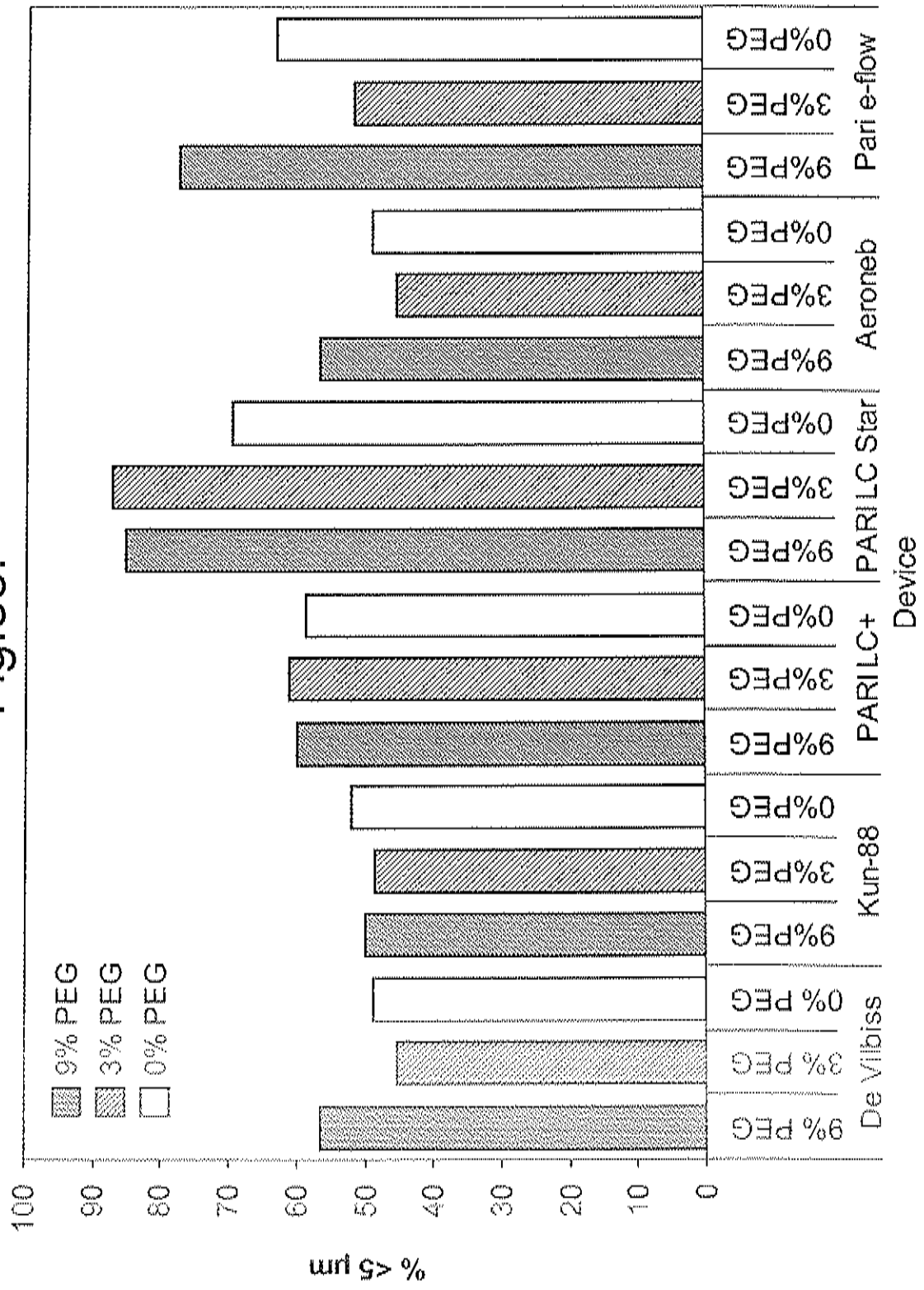
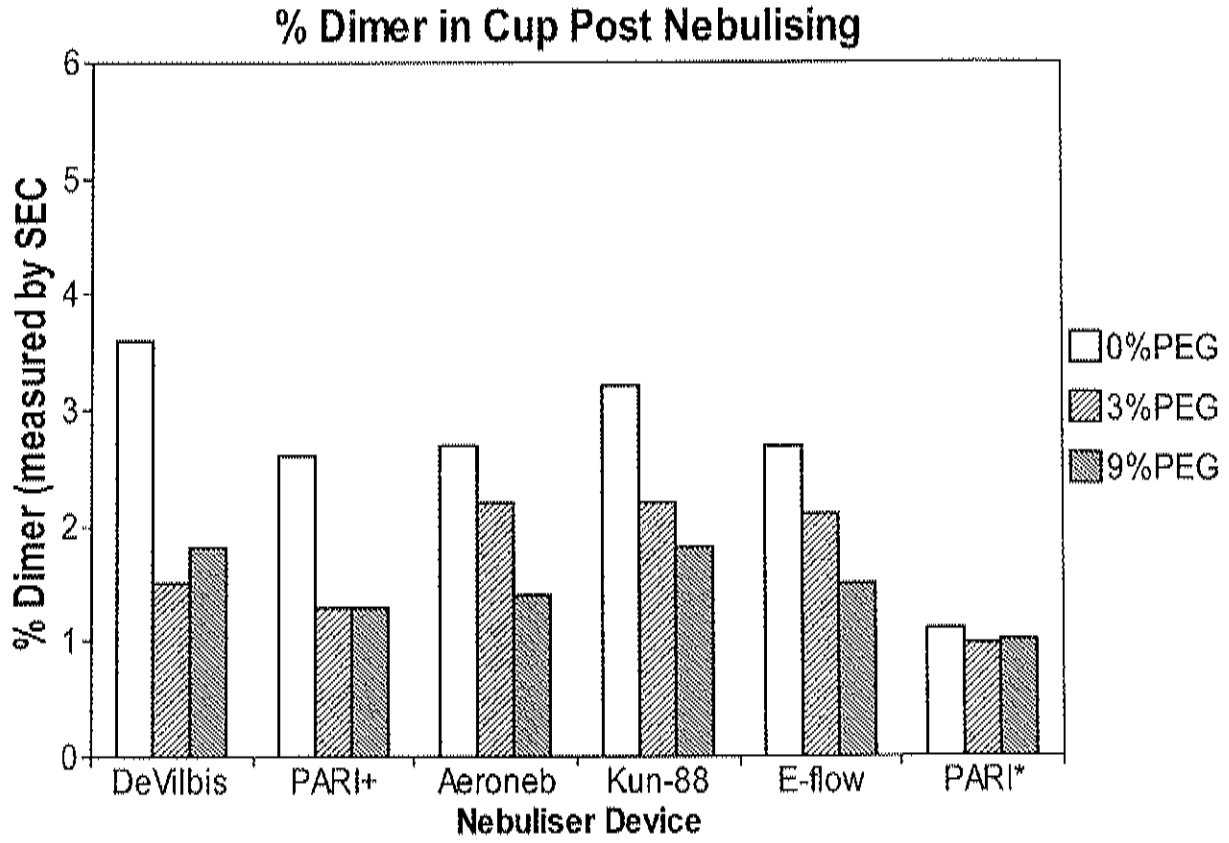

9% PEG
3% PEG
0% PEG
% <5 µm
100
90
80
70
60
50
40
30
20
10
0
9% PEG
3% PEG
0% PEG
De Vilbiss
9%PEG
3%PEG
0%PEG
Kun-88
9%PEG
3%PEG
0%PEG
PARI LC+
9%PEG
3%PEG
0%PEG
PARI LC Star
9%PEG
3%PEG
0%PEG
Aeroneb
9%PEG
3%PEG
0%PEG
Pari e-flow
Device

Fig.36.


% Dimer in Cup Post Nebulising
% Dimer (measured by SEC
0
1
2
3
4
5
6
DeVilbis
PARI+
Aeroneb
Kun-88
E-flow
PARI*
Nebuliser Device
0%PEG
3%PEG
9%PEG

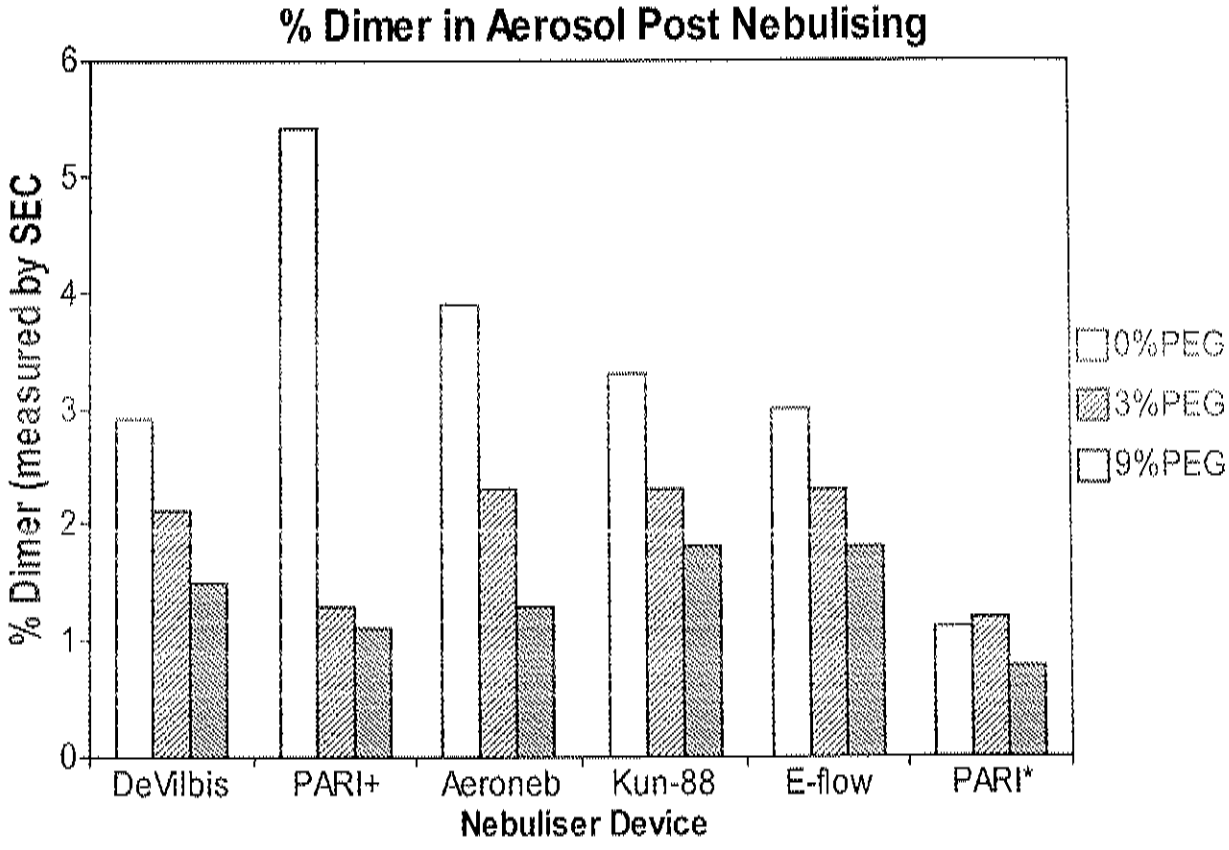

% Dimer in Aerosol Post Nebulising
% Dimer (measured by SEC
0
1
2
3
4
5
6
DeVilbis
PARI+
Aeroneb
Kun-88
E-flow
PARI*
Nebuliser Device
0%PEG
3%PEG
9%PEG

Fig.37.

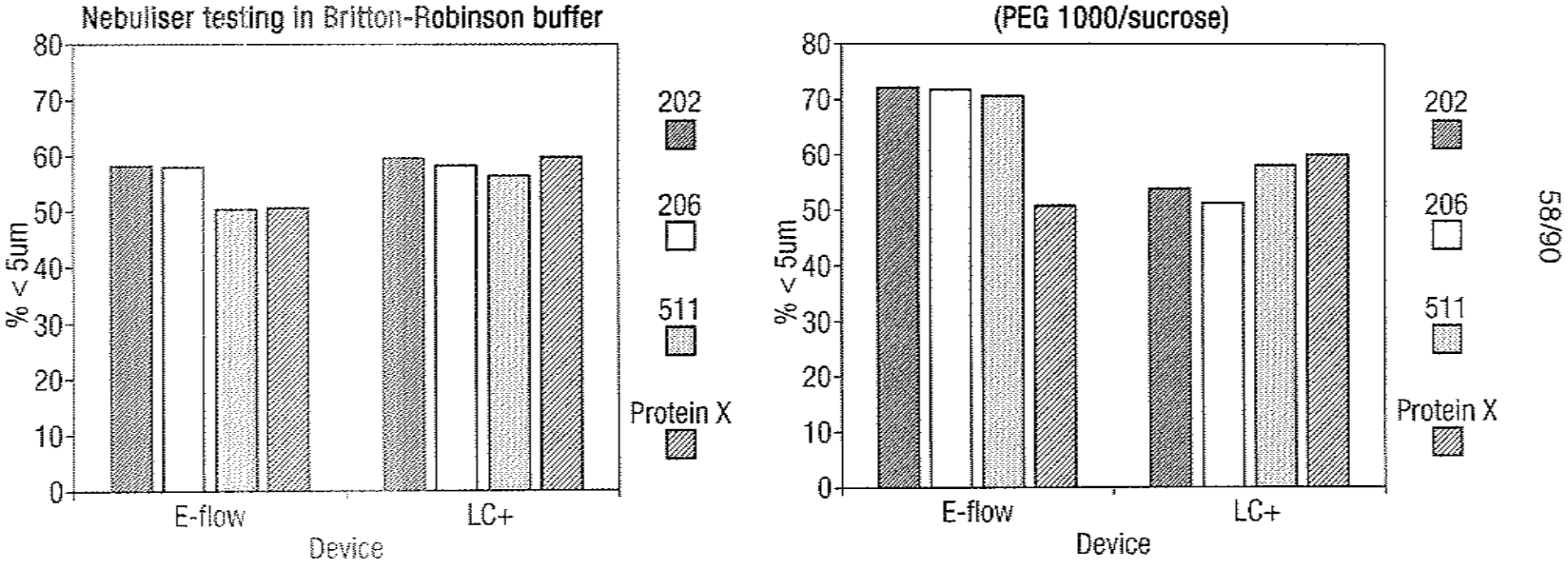

Nebuliser testing in Britton-Robinson buffer
% < 5um
80
70
60
50
40
30
20
10
0
E-flow
LC+
Device
202
206
511
Protein X
Nebuliser testing in formulation buffer
(PEG 1000/sucrose)
% < 5um
80
70
60
50
40
30
20
10
0
E-flow
LC+
Device
202
206
511
Protein X

Fig.38.

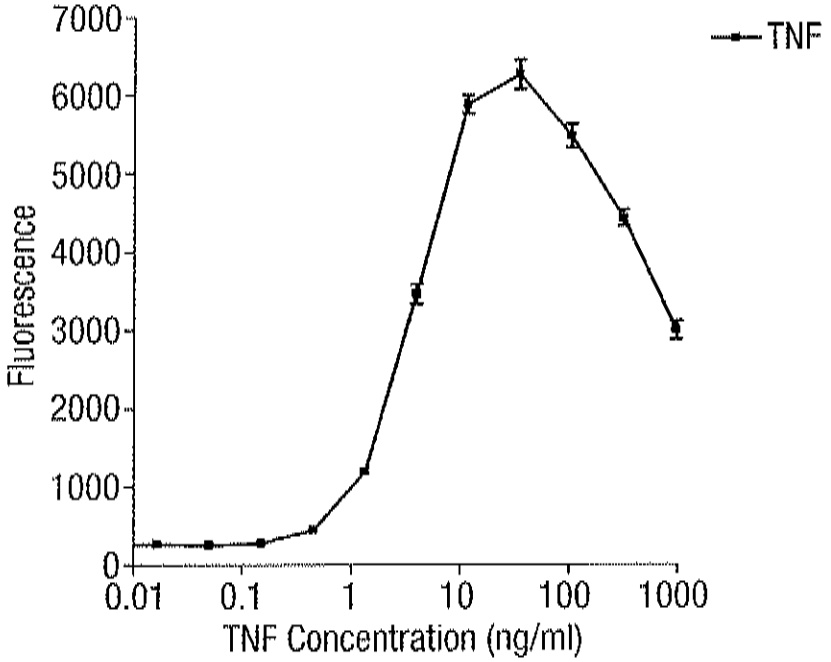

TNF
Fluorescence
7000
6000
5000
4000
3000
2000
1000
0
0.01
0.1
1
10
100
1000
TNF Concentration (ng/ml)

Fig.39.

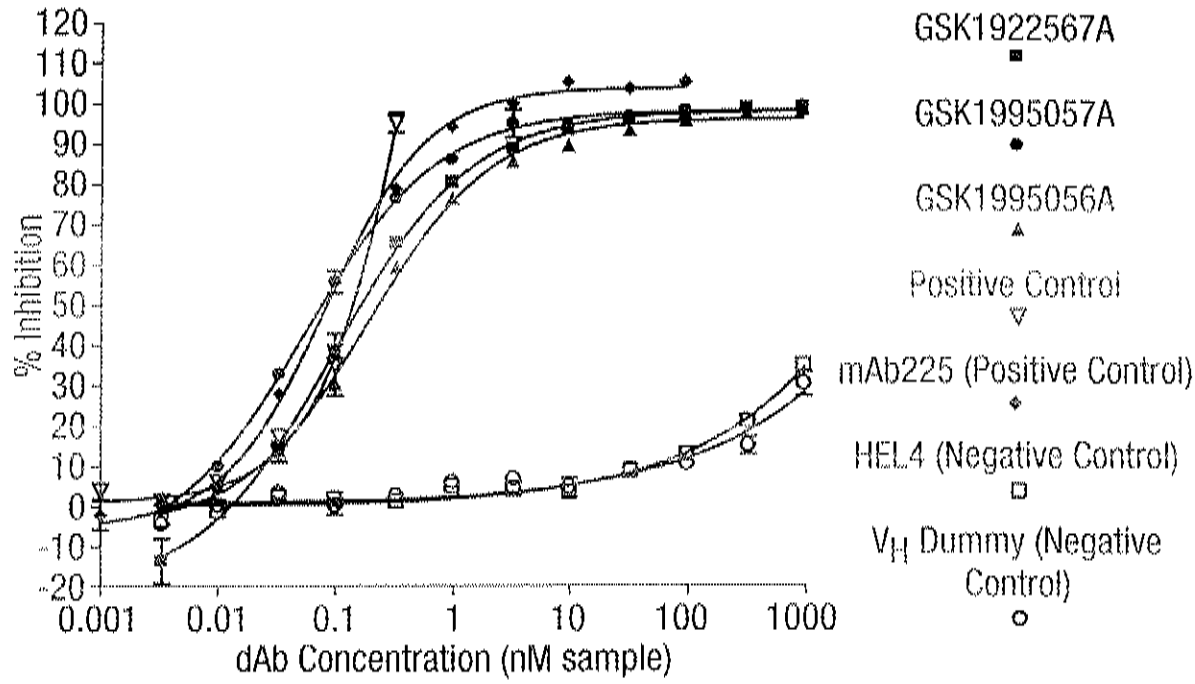
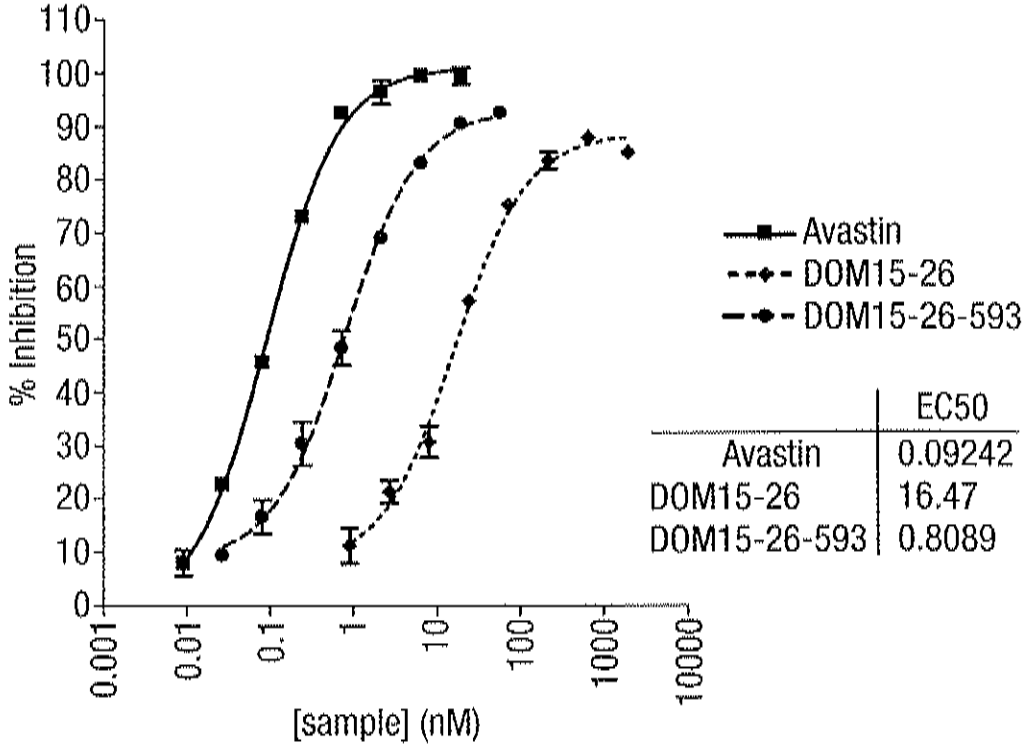

% Inhibition
120
110
100
90
80
70
60
50
40
30
20
10
0
-10
-20
0.001
0.01
0.1
1
10
100
1000
dAb Concentration (nM sample)
GSK1922567A
GSK1995057A
GSK1995056A
Positive Control
mAb225 (Positive Control)
HEL4 (Negative Control)
V_H Dummy (Negative Control)

Fig.40.



	EC50
Avastin	0.09242
DOM15-26	16.47
DOM15-26-593	0.8089

Fig.41.

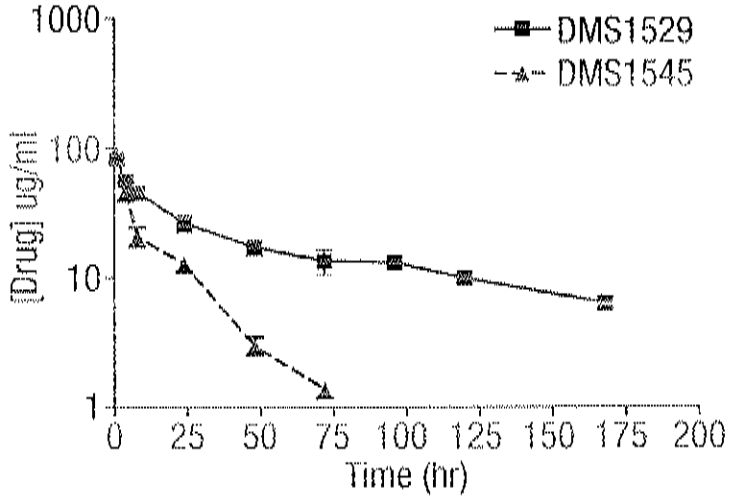


Fig.42a.

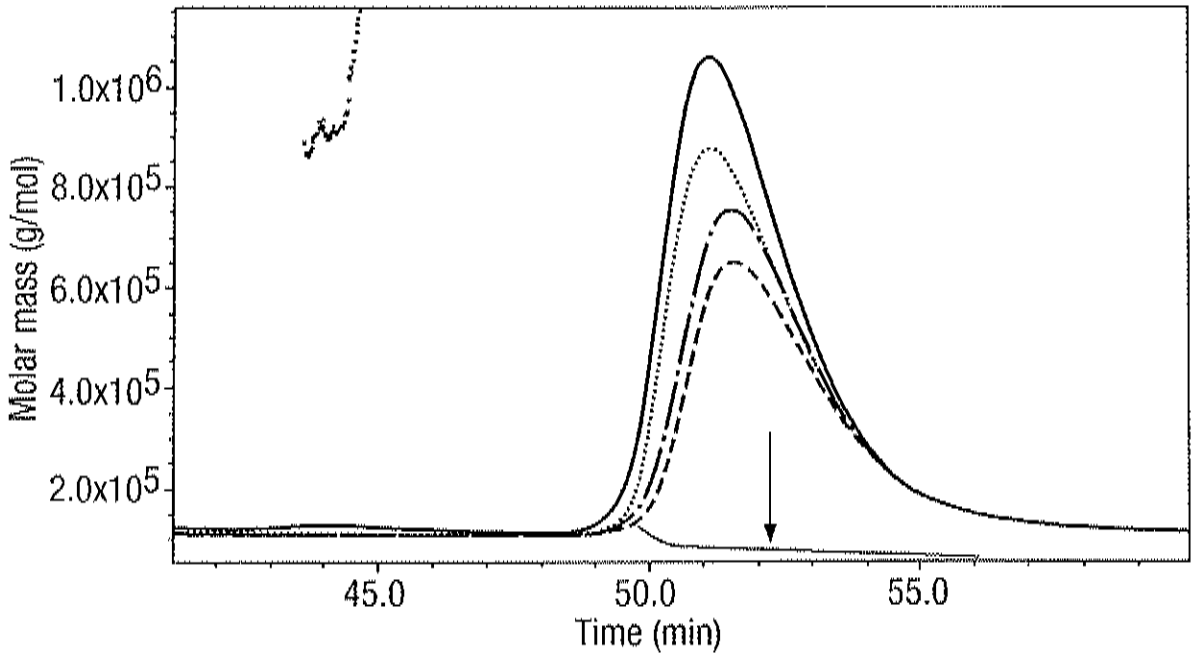


Fig.42b.

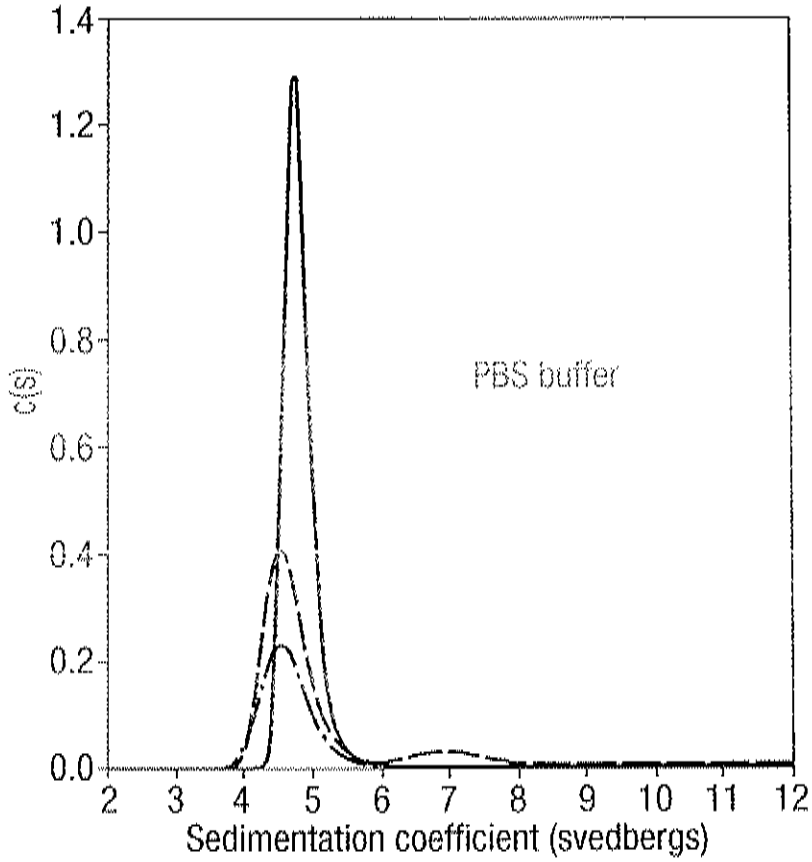


Fig.43.

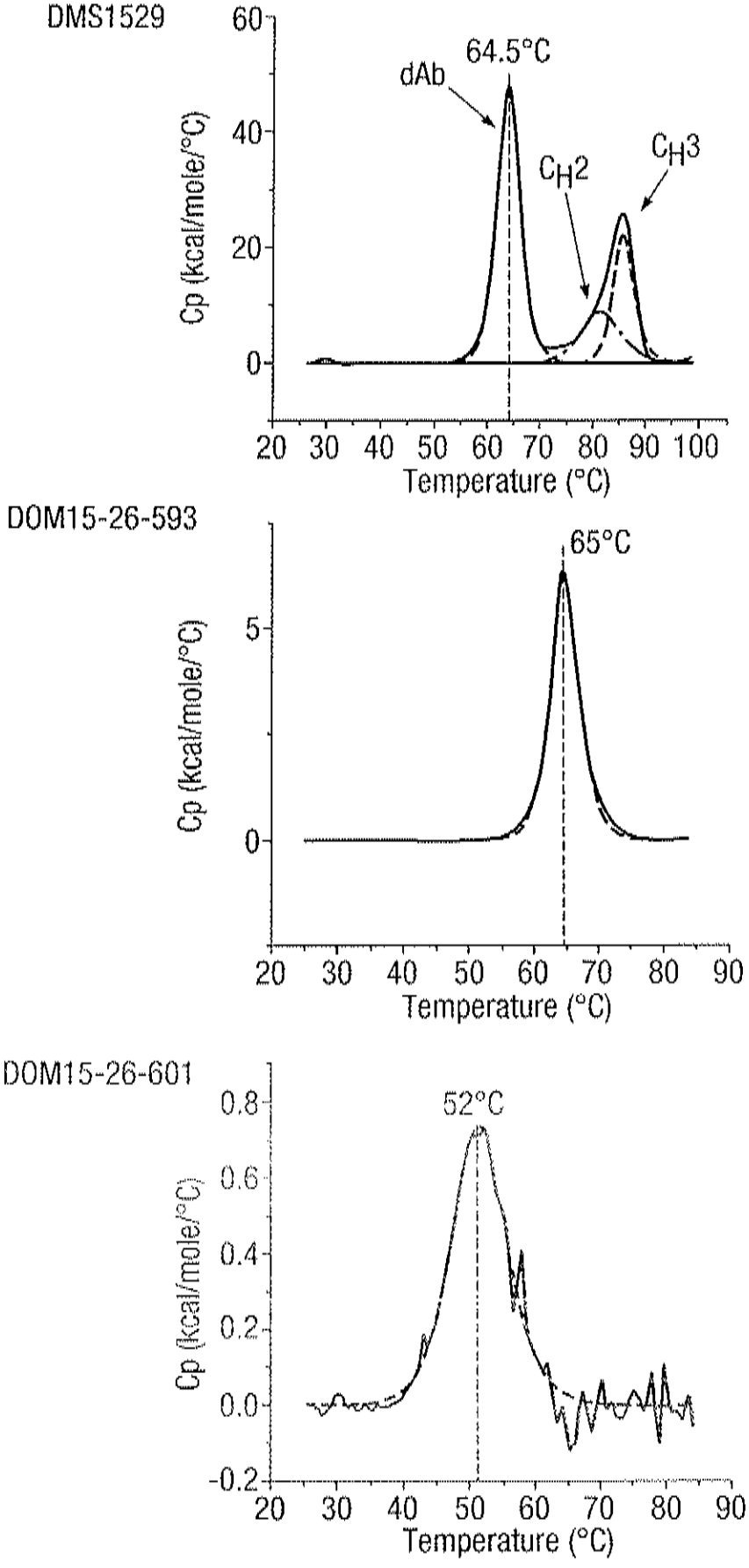
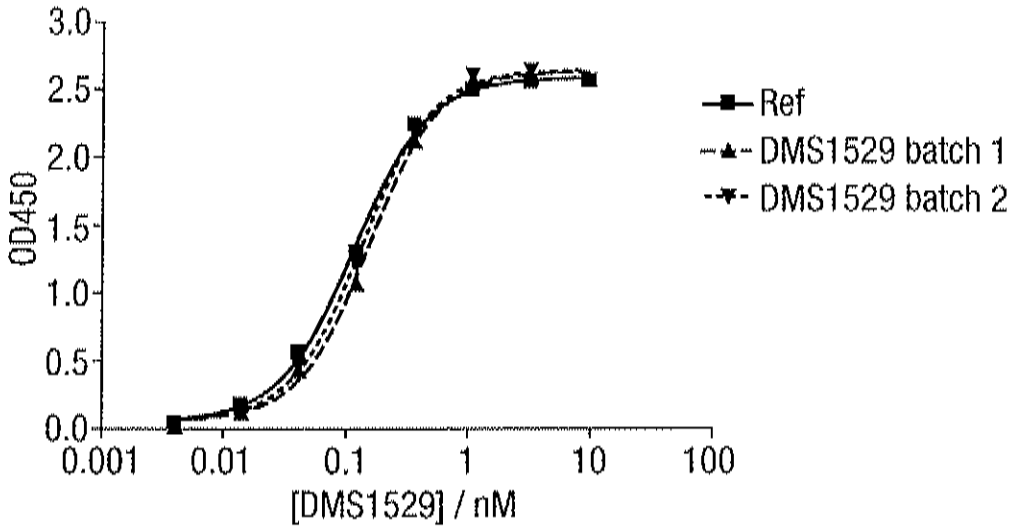

DMS1529
60
40
20
0
Cp (kcal/mole/°C)
64.5°C
dAb
CH2
CH3
20 30 40 50 60 70 80 90 100
Temperature (°C)
DOM15-26-593
5
0
Cp (kcal/mole/°C)
65°C
20 30 40 50 60 70 80 90
Temperature (°C)
DOM15-26-601
0.8
0.6
0.4
0.2
0.0
-0.2
Cp (kcal/mole/°C)
52°C
20 30 40 50 60 70 80 90
Temperature (°C)

Fig.44.



	Ref	DMS1529 batch 1	DMS1529 batch 2
EC50	0.1167	0.1539	0.1358

Fig.45.

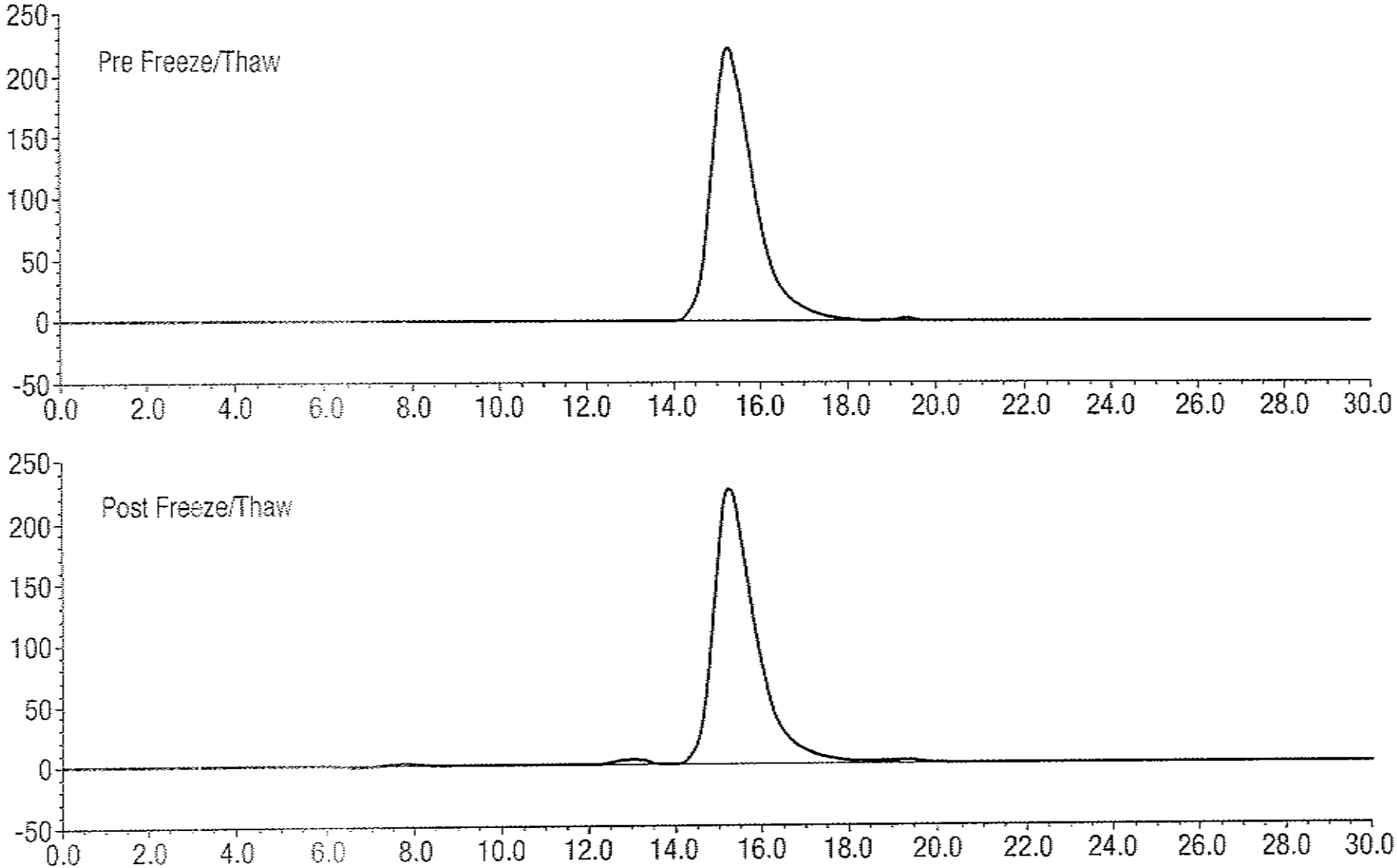
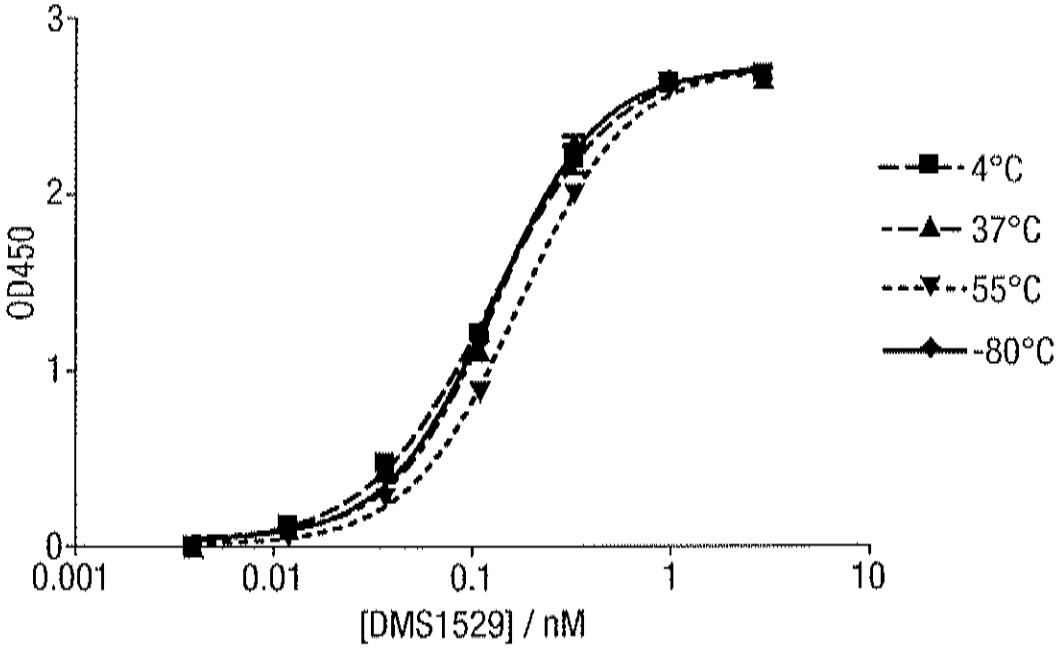
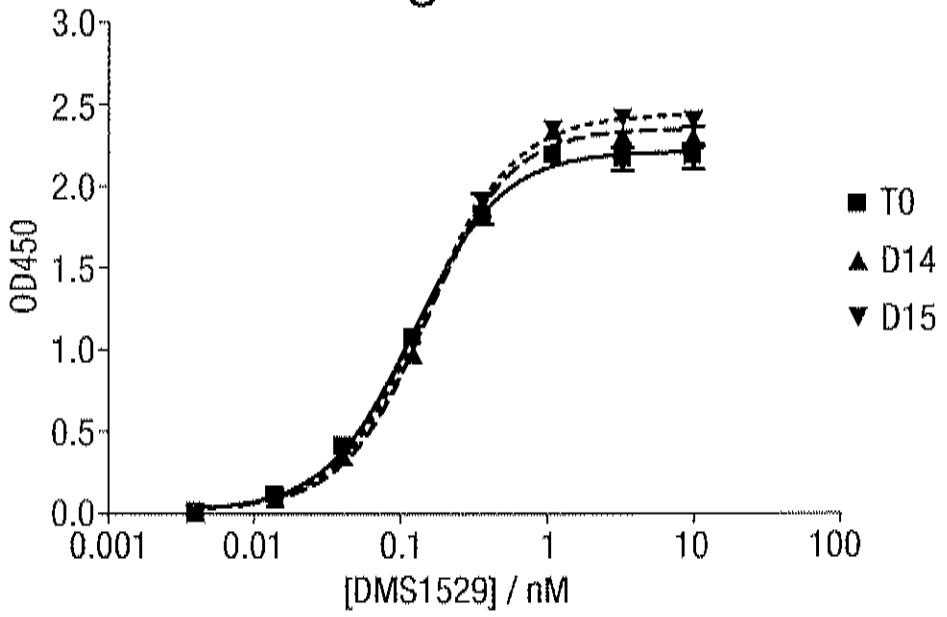

Pre Freeze/Thaw
250
200
150
100
50
0
-50
0.0
2.0
4.0
6.0
8.0
10.0
12.0
14.0
16.0
18.0
20.0
22.0
24.0
26.0
28.0
30.0
Post Freeze/Thaw
250
200
150
100
50
0
-50
0.0
2.0
4.0
6.0
8.0
10.0
12.0
14.0
16.0
18.0
20.0
22.0
24.0
26.0
28.0
30.0

Fig.46.



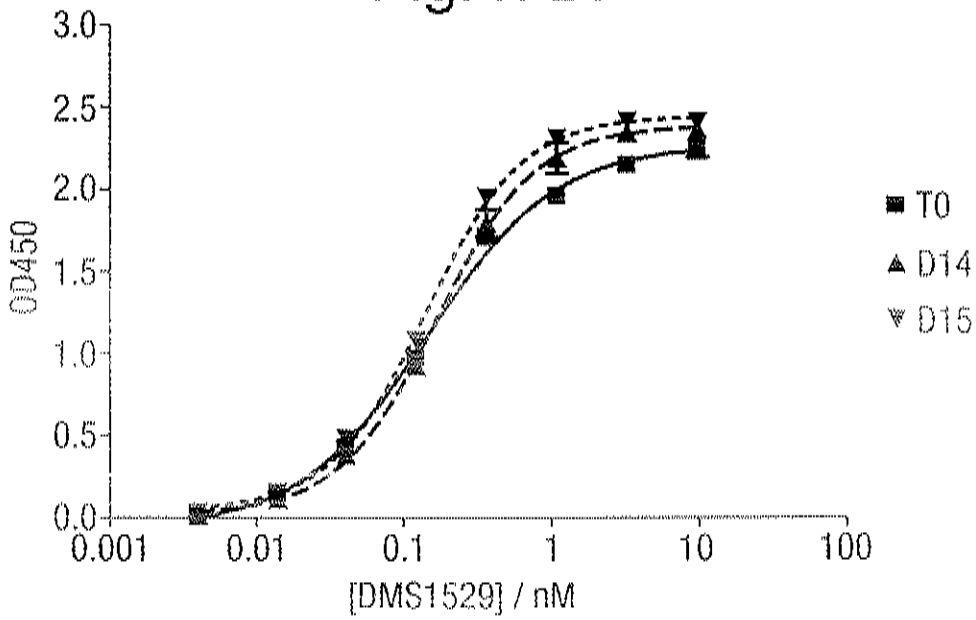
	4°C	37°C	55°C	-80°C
EC50	0.1269	0.1334	0.1748	0.1288

Fig.47A.



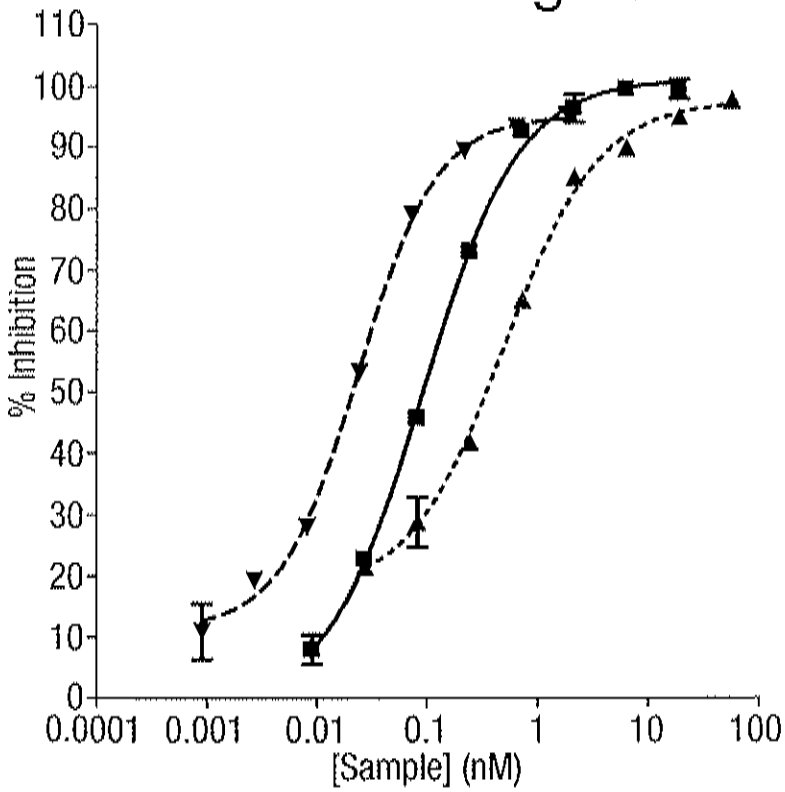
	T0	D14	D15
EC50	0.1253	0.1520	0.1495

Fig.47B.



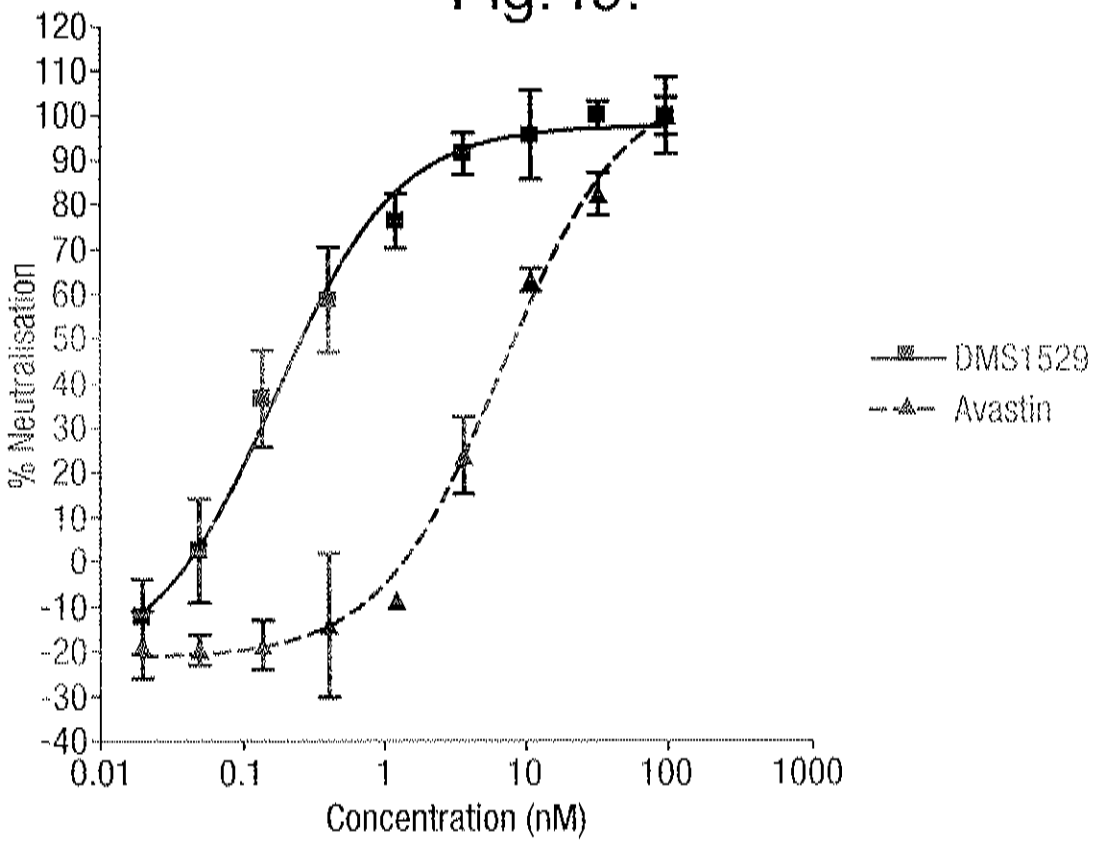
	T0	D14	D15
EC50	0.1453	0.1681	0.1422

Fig.48.



	EC50
Avastin	0.09242
DMS1564/1	0.5056
DMS1529/8	0.2417

Fig.49.



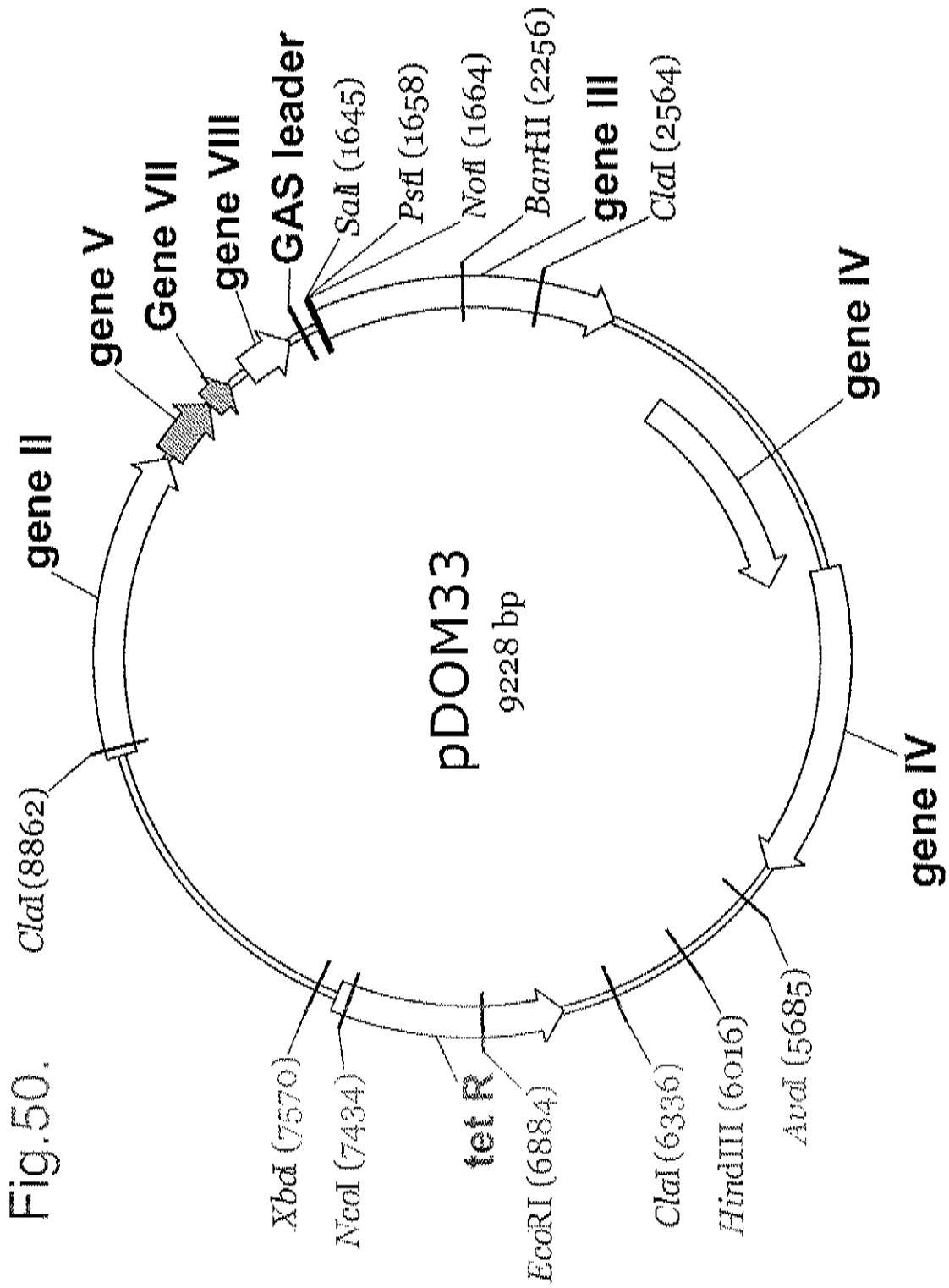

pDOM33
9228 bp
gene II
gene V
Gene VII
gene VIII
GAS leader
SalI (1645)
PstI (1658)
NotI (1664)
BamHI (2256)
gene III
ClaI (2564)
gene IV
gene IV
AvaI (5685)
HindIII (6016)
ClaI (6336)
EcoRI (6884)
tet R
NcoI (7434)
XbaI (7570)
ClaI (8862)

Fig.50.

Fig.51a.

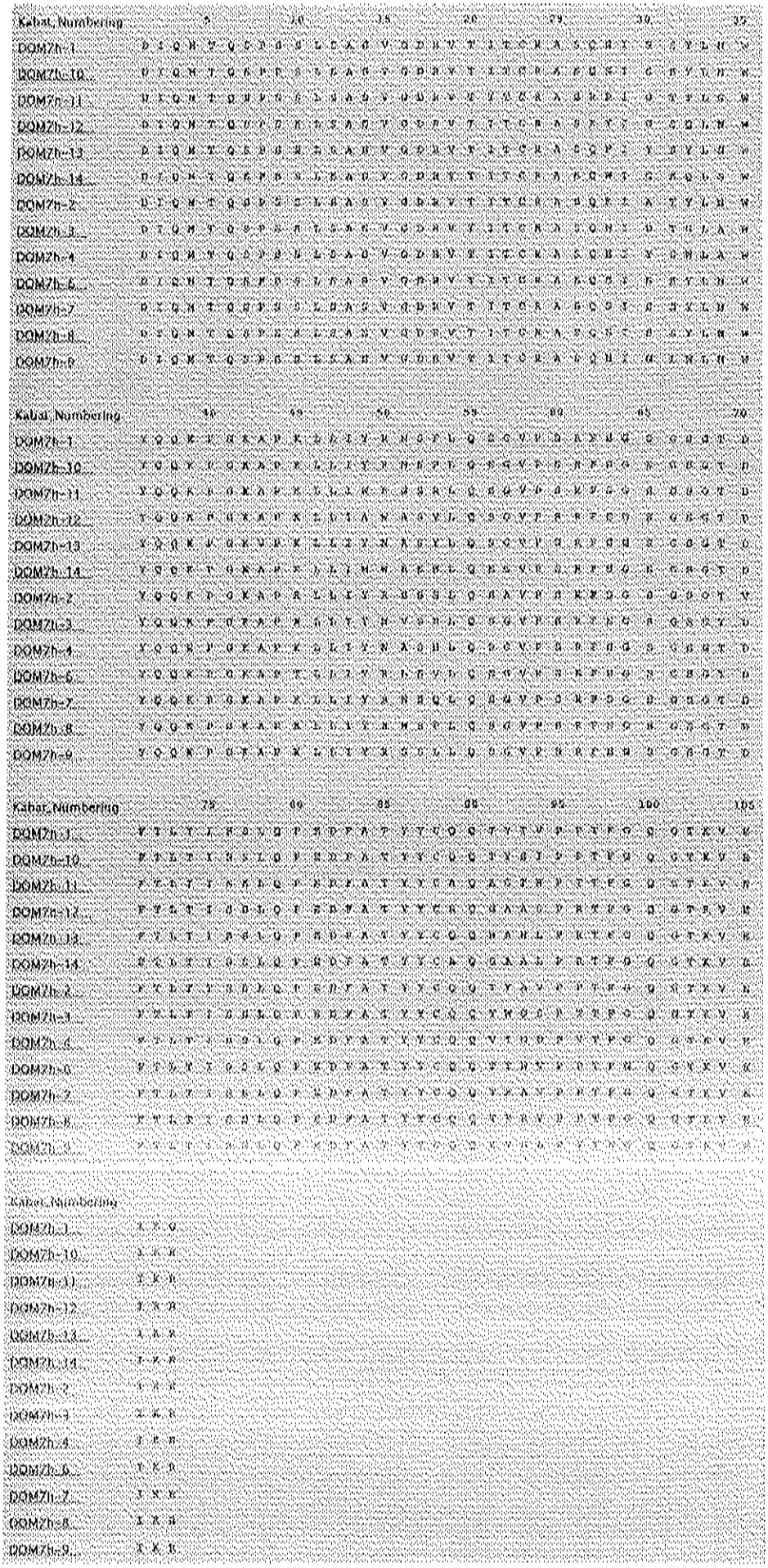

Kabat Numbering
DOM7h-1
DOM7h-10
DOM7h-11
DOM7h-12
DOM7h-13
DOM7h-14
DOM7h-2
DOM7h-3
DOM7h-4
DOM7h-5
DOM7h-7
DOM7h-8
DOM7h-9

Fig.51a (Cont I).

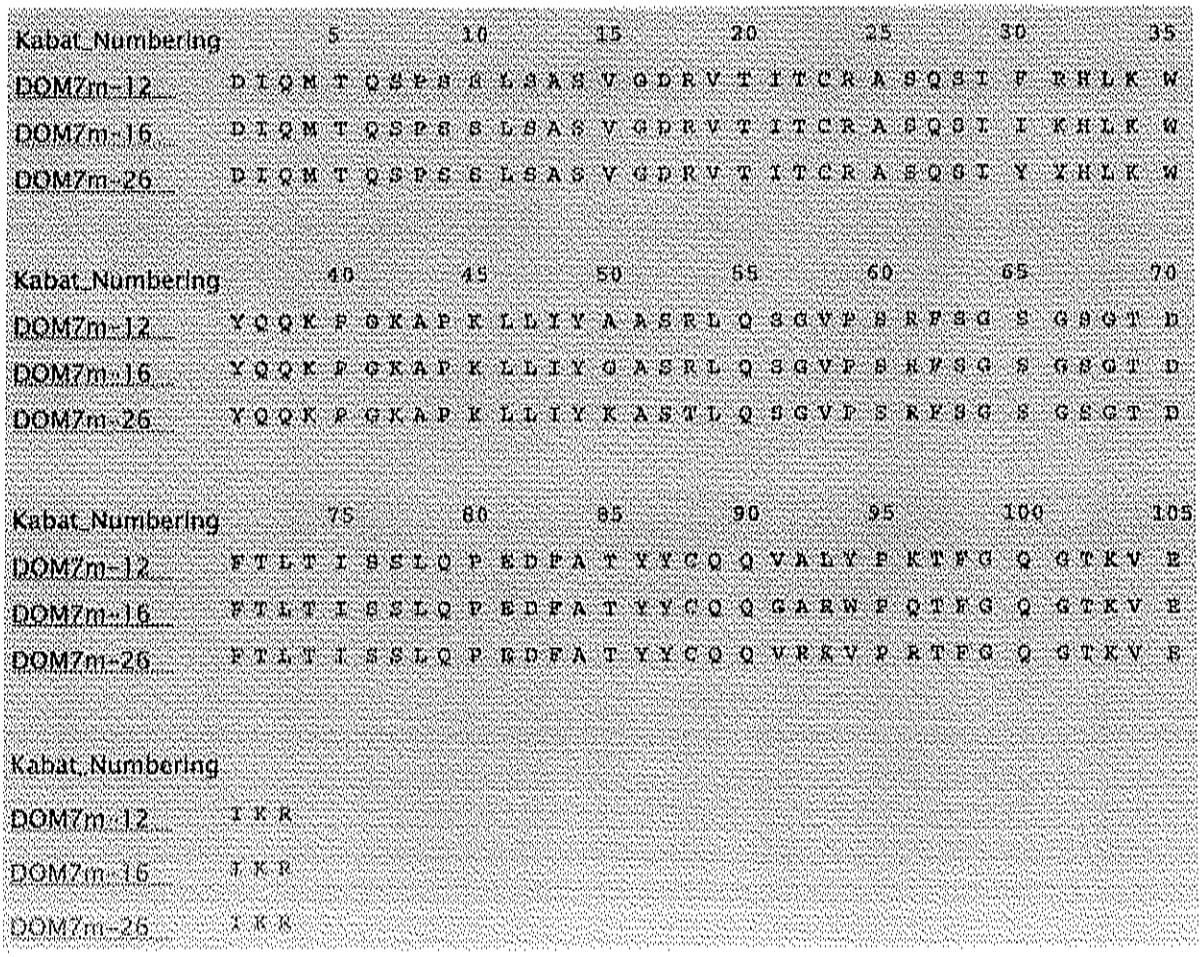


Fig.51a (Cont II).

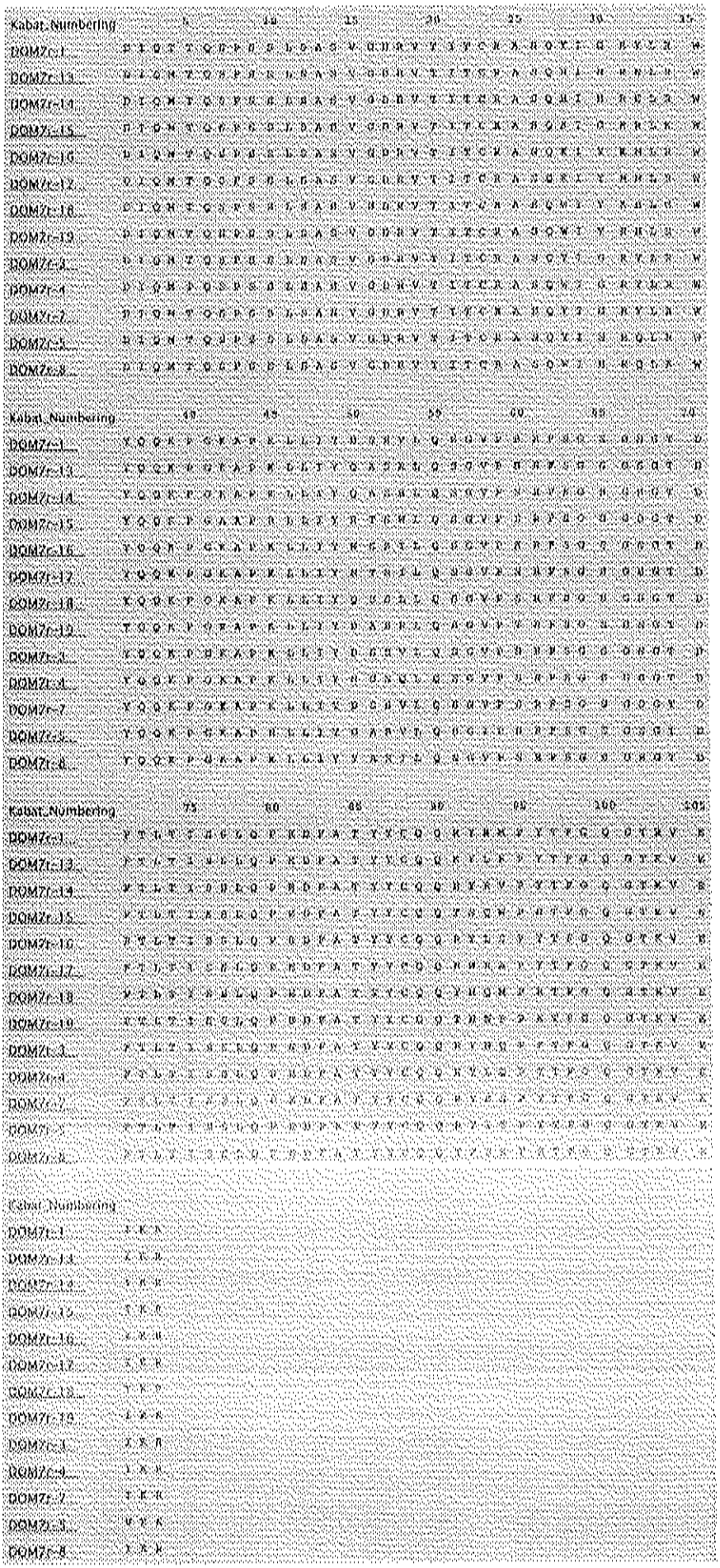
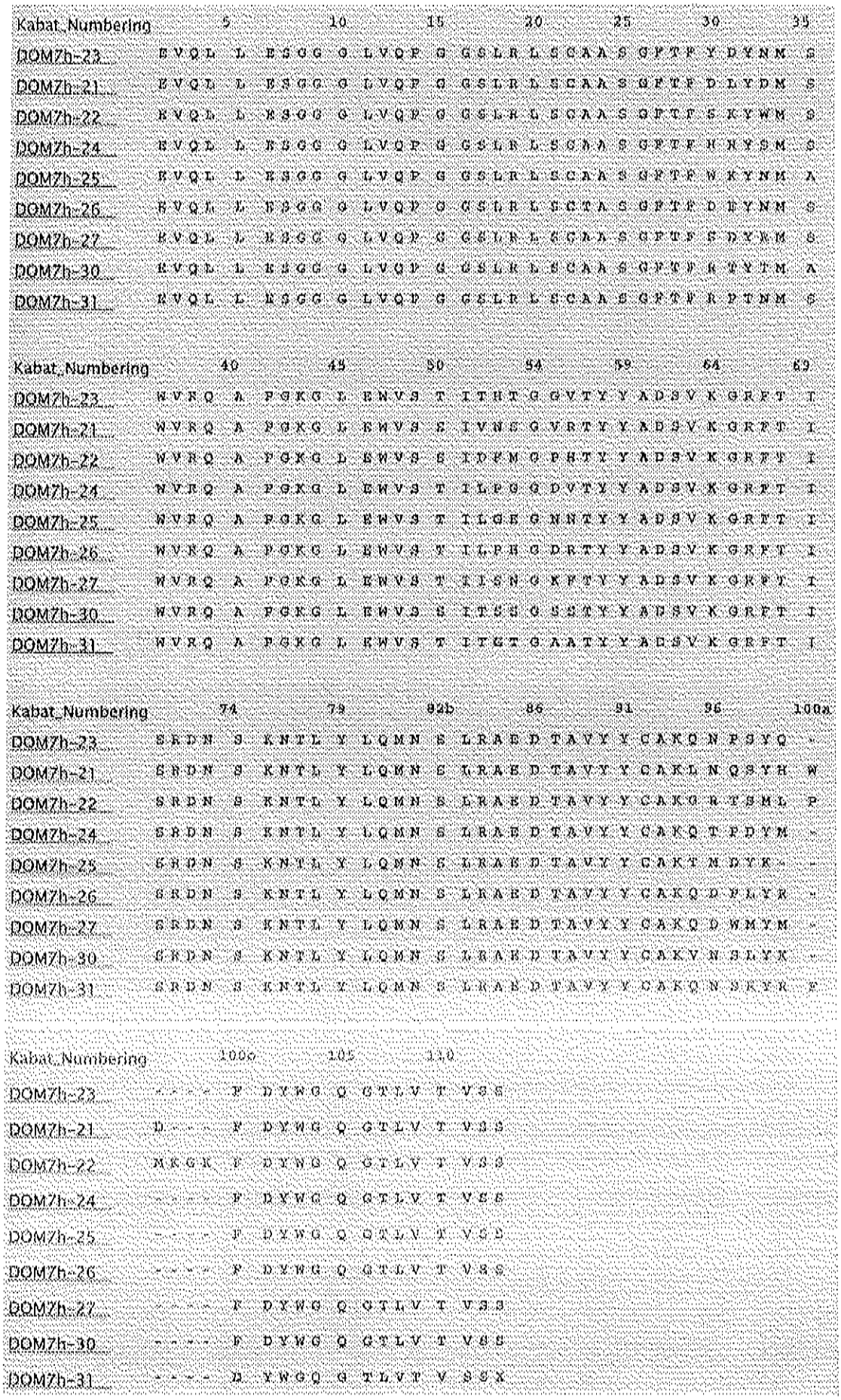


Fig.51a (Cont III).



Kabat_Numbering	5	10	15	20	25	30	35
DOMZh-23	EVQL	LESGG	GLVQP	GGSLR	LSCAA	SGFTF	YDYNM	S
DOMZh-21	EVQL	LESGG	GLVQP	GGSLR	LSCAA	SGFTF	DLYDM	S
DOMZh-22	EVQL	LESGG	GLVQP	GGSLR	LSCAA	SGFTF	SKYWM	S
DOMZh-24	EVQL	LESGG	GLVQP	GGSLR	LSCAA	SGFTF	HNYSM	S
DOMZh-25	EVQL	LESGG	GLVQP	GGSLR	LSCAA	SGFTF	WKYNM	A
DOMZh-26	EVQL	LESGG	GLVQP	GGSLR	LSCTA	SGFTF	DEYNM	S
DOMZh-27	EVQL	LESGG	GLVQP	GGSLR	LSCAA	SGFTF	SDYAM	S
DOMZh-30	EVQL	LESGG	GLVQP	GGSLR	LSCAA	SGFTF	RTYTM	A
DOMZh-31	EVQL	LESGG	GLVQP	GGSLR	LSCAA	SGFTF	RPTNM	S

Kabat_Numbering	40	45	50	54	59	64	69
DOMZh-23	WVRQ	APGKG	LEWVS	TITHT	GGVTY	YADSV	KGRFT	I
DOMZh-21	WVRQ	APGKG	LEWVS	SIVNS	GVRTY	YADSV	KGRFT	I
DOMZh-22	WVRQ	APGKG	LEWVS	SIDFM	GPRTY	YADSV	KGRFT	I
DOMZh-24	WVRQ	APGKG	LEWVS	TILPG	GDVTY	YADSV	KGRFT	I
DOMZh-25	WVRQ	APGKG	LEWVS	TILGE	GNNTY	YADSV	KGRTT	I
DOMZh-26	WVRQ	APGKG	LEWVS	TILPH	GDRTY	YADSV	KGRFT	I
DOMZh-27	WVRQ	APGKG	LEWVS	TIIGN	GKFTY	YADSV	KGKFT	I
DOMZh-30	WVRQ	APGKG	LEWVS	SITSS	GSSTY	YADSV	KGRFT	I
DOMZh-31	WVRQ	APGKG	LKWVS	TITGT	GAATY	YADSV	KGRFT	I

Kabat_Numbering	74	79	82b	86	91	96	100a
DOMZh-23	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKQ	NPSYQ	-
DOMZh-21	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKL	NQSYH	W
DOMZh-22	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKQ	RTSML	P
DOMZh-24	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKQ	TPDYM	-
DOMZh-25	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKT	NDYK	-
DOMZh-26	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKQ	DPLYR	-
DOMZh-27	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKQ	DWMYM	-
DOMZh-30	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKV	NSLYK	-
DOMZh-31	SRDN	SKNTL	YLQMN	SLRAE	DTAVY	YCAKQ	NSRYR	F

Kabat_Numbering	100c	105	110
DOMZh-23	- - - -	FDYWG	QGTLV	TVSS
DOMZh-21	D - - -	FDYWG	QGTLV	TVSS
DOMZh-22	MKGK	FDYWG	QGTLV	TVSS
DOMZh-24	- - - -	FDYWG	QGTLV	TVSS
DOMZh-25	- - - -	FDYWG	QGTLV	TVSS
DOMZh-26	- - - -	FDYWG	QGTLV	TVSS
DOMZh-27	- - - -	FDYWG	QGTLV	TVSS
DOMZh-30	- - - -	FDYWG	QGTLV	TVSS
DOMZh-31	- - - -	DYWGQ	GTLVT	VSSX

Fig.51a (Cont IV).

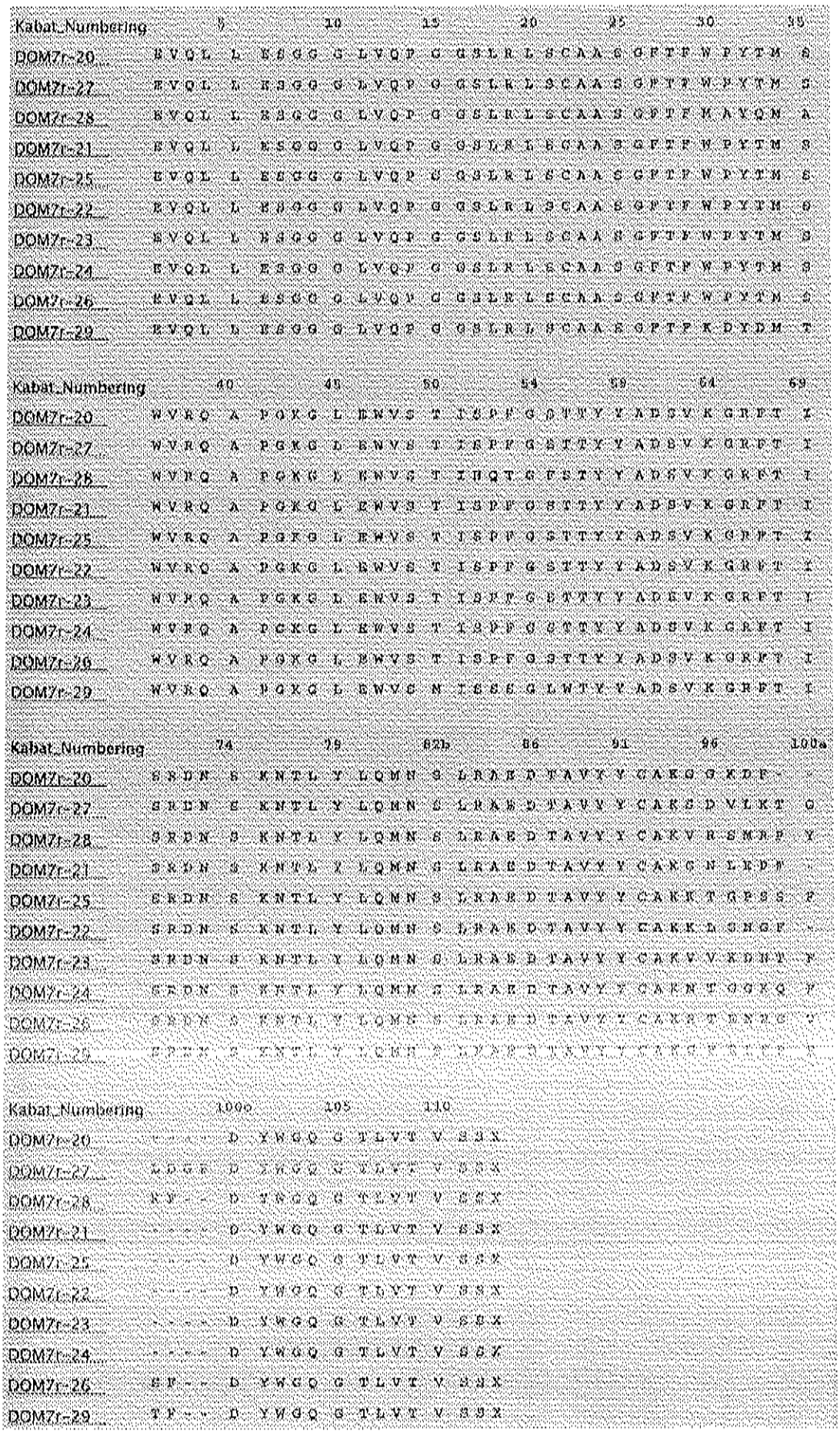


Fig.51a (Cont V).

dAb 2, 4, 7, 41
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASPLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSVPPTFGQGTKVEIKR

dAb 38, 54
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYRASPLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYRIPPTFGQGTKVEIKR

dAb 46, 47, 52, 56
DIQMTQSPSSLSASVGDRVTITCRASQSIFKSLKWYQQKPGKAPKLLIYNASYLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVVYWPVTFGQGTKVEIKR

dAb 13, 15
DIQMTQSPSSLSASVGDRVTITCRASQSIYYHLKWYQQKPGKAPKLLIYKSTLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVRKVPRTFGQGTKVEIKR

dAb 30, 35
DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLKWYQQKPGKAPKLLIYQASVLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQGLYPPITFGQGTKVEIKR

dAb 19,
DIQMTQSPSSLSASVGDRVTITCRASQSIYNWLKWYQQKPGKAPKLLIYRASSLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQNVVIPRTFGQGTKVEIKR

dAb22
DIQMTQSPSSLSASVGDRVTITCRASQSILWHLRWYQQKPGKAPKLLIYHASLLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQSAVYPKTFGQGTKVEIKR

dAb23
DIQMTQSPSSLSASVGDRVTITCRASQSIFRYLAWYQQKPGKAPKLLIYHASHLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQRLLYPKTFGQGTKVEIKR

dAb24
DIQMTQSPSSLSASVGDRVTITCRASQSIFYHLAWYQQKPGKAPKLLIYPASKLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQRARWPRTFGQGTKVEIKR

dAb31
DIQMTQSPSSLSASVGDRVTITCRASQSIIWHLNWYQQKPGKAPKLLIYRASRLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVARVPRTFGQGTKVEIKR

dAb33
DIQMTQSPSSLSASVGDRVTITCRASQSIYRYLRWYQQKPGKAPKLLIYKASSLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQYVGYPRTFGQGTKVEIKR

dAb34
DIQMTQSPSSLSASVGDRVTITCRASQSILKYLKWYQQKPGKAPKLLIYNASHLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQTTYYPITFGQGTKVEIKR

dAb53
DIQMTQSPSSLSASVGDRVTITCRASQSILRYLRWYQQKPGKAPKLLIYKASWLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVLYYPQTFGQGTKVEIKR

dAb11
DIQMTQSPSSLSASVGDRVTITCRASQSILRSLKWYQQKPGKAPKLLIYAASRLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVVYWPATFGQGTKVEIKR

Fig.51a (Cont VI).

dAb12
DIQMTQSPSSLSASVGDRVTITCRASQSIFRHLKWYQQKPGKAPKLLIYAASRLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVALYPKTFGQGTKVEIKR

dAb17
DIQMTQSPSSLSASVGDRVTITCRASQSIRKYLRWYQQKPGKAPKLLIYTASSLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQNLFWPRTFGQGTKVEIKR

dAb18
DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLNWYQQKPGKAPKLLIYAASSLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQMLFYPKTFGQGTKVEIKR

dAb16, 21
DIQMTQSPSSLSASVGDRVTITCRASQSIIKHLKWYQQKPGKAPKLLIYGASRLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQGARWPQTFGQGTKVEIKR

dAb25, 26
DIQMTQSPSSLSASVGDRVTITCRASQSIYYHLKWYQQKPGKAPKLLIYKASTLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVRKVPRTFGQGTKVEIKR

dAb27
DIQMTQSPSSLSASVGDRVTITCRASQSIYKHLKWYQQKPGKAPKLLIYNASHLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVGRYPKTFGQGTKVEIKR

dAb55
DIQMTQSPSSLSASVGDRVTITCRASQSIFKSLKWYQQKPGKAPKLLIYNASYLQSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCQQVVYWPVTFGQGTKVEIKR

dAb 8, 10
EVQLLESGGGLVQPGGSLRLSCAASGFTFWVYQMDWVRQAPGKGLEWVSSISAFGAKTL
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLSGKFDYWGQGTLVTVSS

dAb 36
EVQLLESGGGLVQPGGSLRLSCAASGFTFWSYQMTWVRQAPGKGLEWVSSISSFGSSTL
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGRDHNYSLFDYWGQGTLVTVSS

Fig.51b.

>DOM7h-1

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGCATTAGC AGCTATTTAA ATTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATCGG AATTCCTTTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCC
GAAGATTTTG CTACGTACTA CTGTCAACAG ACGTATACTG TTCCTCCTAC GTTTGGCCAA
GGGACCAAGG TGGAAATCAA ACAG

>DOM7h-10

GACATCCAGA TGACCCAGTC TCCACCCTCC CTGTCCGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGCATTAGC AGCTATTTAA ATTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATCGG AATTCCCCTT TGCAAAGTGG GGTCCCATCA
CGGTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG ACTTATTCGA TTCCTCCTAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7h-11

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCG TCCGATTGGG ACGACGTTAA GTTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTGGTTT GGTTCCCGGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTGCGCAG GCTGGGACGC ATCCTACGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7h-12

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTAA GTATATTGGT TCGCAGTTAA ATTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCGCTTGG GCGTCCGTTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCGTCAG GGTGCTGCGT CGCCTCGGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7h-13

GACATTCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTTTATTTAT CGGTATTTAT CGTGGTATCA GCAGAAACCA
GGGAAAGTCC CTAAGCTCCT GATCTATAAT GCGTCCTATT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG CATGCTCATT TGCCTCGTAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

Fig.51b (Cont I).

>DOM7h-14

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTGGATTGGG TCTCAGTTAT CTTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCATGTGG CGTTCCTCGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT

GAAGATTTTG CTACGTACTA CTGTGCTCAG GGTGCGGCGT TGCCTAGGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

Fig.51b (Cont II).

>DOM7h-2

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAAGATTGCT ACTTATTTAA ATTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATAGG TCTTCCTCTT TGCAAAGCGC GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGTT TTCACACTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG ACGTATGCTG TTCCTCCTAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7h-3

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTGGATTGAT ACTGGGTTAG CGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAGGCTCCT GATCTATAAT GTGTCCAGGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG TATTGGGGTA GTCCTACGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7h-4

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GGAGATTTAT TCGTGGTTAG CGTGGTACCA GCAGAGACCA
GGGAAAGCCC CTAAGCTCCT GATCTATAAT GCTTCCCATT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG GTGATTGGTG ATCCTGTTAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7h-6

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGCATTAGC AGCTATTTAA ATTGGTACCA GCAGAAACCA
GGGAAAGCCC CTACGCTCCT GATCTATCGG TTGTCCGTGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG ACTTATAATG TTCCTCCTAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7h-7

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGCATTAGC AGCTATCTAA ATTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATAGG AATTCCCAGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG ACTTTTGCGG TTCCTCCTAC GTTCGGCCAA
GGGACCAAGG TGGAGATCAA ACGG

Fig.51b (Cont III).

>DOM7h-8

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGCATTAGC AGCTATTTAA ATTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATCGG AATTCCCCTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG ACGTATAGGG TGCCTCCTAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

Fig.51b (Cont IV).

>DOM7h-9

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GCATATTGGG TTGTGGTTAC ATTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATAGG TCTTCCTTGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG AAGTATAATT TGCCTTATAC GTCCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7m-12

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGCATTTTT CGGCATTTAA AGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATGCG GCATCCCGTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG GTTGCGCTGT ATCCTAAGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7m-16

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGCATTATT AAGCATTTAA AGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATGGT GCATCCCGGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG GGGGCTCGGT GGCCTCAGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7m-26

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGCATTTAT TATCATTTAA AGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATAAG GCATCCACGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG GTTCGGAAGG TGCCTCGGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7r-1

GACATCCAGA CGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTATATTGGT AGGTATTTAC GTTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATGAT TCTTCCGTGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG CGTTATCGTA TGCCTTATAC GTTCGGCCAA
GGGACCAGGG TAGAAATCAA ACGG

Fig.51b (Cont V).

>DOM7r-13

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GCATATTCAT AGGGAGTTAA GGTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATCAG GCGTCCCGTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG AAGTATCTGC CTCCTTATAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

Fig.51b (Cont VI).

>DOM7r-14

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GCATATTCAT AGGGAGTTAA GGTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATCAG GCGTCCCGTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG CGTTATAGGG TGCCTTATAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7r-15

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAGTATTGGG CGGAGGTTAA AGTGGTACCA GCAGAAACCA
GGGGCAGCCC CTAGGCTCCT GATCTATCGT ACGTCCTGGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG ACGTCGCAGT GGCCTCATAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7r-16

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAAGATTTAT AAGAATTTAC GTTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATAAT TCTTCCATTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG AGGTATCTGT CGCCTTATAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7r-17

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GAAGATTTAT AATAATTTAA GGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATAAT ACTTCCATTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG CGATGGCGTG CGCCTTATAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7r-18

GACATTCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTGGATTTAT AAGTCGTTAG GGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATCAG TCTTCTTTGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG TATCATCAGA TGCCTCGGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

Fig.51b (Cont VII).

>DOM7r-19

GACATCCAGA TGACCCAGTC TCCATCCTCC CTATCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTGGATTTAT AGGCATTTAA GGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATGAT GCGTCCAGGT TGCAAAGTGG GGTCCCAACA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG ACTCATAATC CTCCTAAGAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

Fig.51b (Cont VIII).

>DOM7r-3

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTATATTGGT AGGTATTTAC GTTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATGAT TCTTCCGTGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG AGGTATATGC AGCCTTTTAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7r-4

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCCGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTGGATTGGT CGGTATTTAC GGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATAAT GGGTCCCAGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG CGGTATCTTC AGCCTTATAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

>DOM7r-7

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTATATTGGT AGGTATTTAC GTTGGTATCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATGAT TCTTCCGTGT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG CGTTATTCTT CGCCTTATAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA GCGG

>DOM7r-5

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTATATTTCG CGTCAGTTAA GGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAGGCTCCT GATCTATGGG GCGTCCGTTT TGCAAAGCGG GATCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG AGGTATATTA CTCCTTATAC GTTCGGCCAA
GGGACCAAGG TGGAAGTCAA ACGG

>DOM7r-8

GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CCGTGTCACC
ATCACTTGCC GGGCAAGTCA GTGGATTCAT AGGCAGTTAA AGTGGTACCA GCAGAAACCA
GGGAAAGCCC CTAAGCTCCT GATCTATTAT GCTTCCATTT TGCAAAGTGG GGTCCCATCA
CGTTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
GAAGATTTTG CTACGTACTA CTGTCAACAG ACGTTTTCTA AGCCTTCTAC GTTCGGCCAA
GGGACCAAGG TGGAAATCAA ACGG

Fig.51b (Cont IX).

>DOM7h-23

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTAT GATTATAATA TGTCTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACT ATTACGCATA CGGGTGGGGT TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAT ACCGCGGTAT ATTACTGTGC GAAACAGAAT
CCTTCTTATC AGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGC

Fig.51b (Cont X).

>DOM7h-21

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTGAT CTTTATGATA TGTCGTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCATCG ATTGTTAATT CGGGTGTTAG GACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAACTTAAT
CAGAGTTATC ATTGGGATTT TGACTACTGG GGTCAGGGAA CCCTGGTCAC CGTCTCGAGC

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GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTCG AAGTATTGGA TGTCGTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCATCT ATTGATTTTA TGGGTCCGCA TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAT ACCGCGGTAT ATTACTGTGC GAAAGGGAGG
ACGTCGATGT TGCCGATGAA GGGGAAGTTT GACTACTGGG GTCAGGGAAC CCTGGTCACC
GTCTCGAGC

>DOM7h-24

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTCAT CGTTATTCGA TGTCTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTTGCCTG GTGGTGATGT TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAT ACCGCGGTAT ATTACTGTGC GAAACAGACG
CCTGATTATA TGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGC

>DOM7h-25

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG AAGTATAATA TGGCGTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACT ATTCTTGGTG AGGGTAATAA TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAT ACCGCGGTAT ATTACTGTGC GAAAACGATG
GATTATAAGT TTGACTACTG GGGTCAGGGA ACCCTGGTCA CCGTCTCGAG C

>DOM7h-26

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTACAG CCTCCGGATT CACCTTTGAT GAGTATAATA TGTCTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTCTGCCGC ATGGTGATCG GACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAT ACCGCGGTAT ATTACTGTGC GAAACAGGAT
CCTTTGTATA GGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGC

Fig.51b (Cont XI).

>DOM7h-27

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTCG GATTATCGGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTATTTCGA ATGGTAAGTT TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAACAGGAT
TGGATGTATA TGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGC

>DOM7h-30

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTCGG ACGTATACTA TGGCTTGGGT CCGCCAGGCC
CCAGGGAAGG GTCTAGAGTG GGTCTCATCG ATTACTAGTA GTGGTTCTTC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAT ACCGCGGTAT ATTACTGTGC GAAAGTGAAT
TCTTTGTATA AGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGC

>DOM7h-31

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTCGG CCGACTAATA TGTCGTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACT ATTACTGGTA CTGGTGCTGC GACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAACAGAAT
TCTCGTTATA GGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGCG

>DOM7r-20

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG CCGTATACGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTCGCCGT TTGGTTCGAC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAAGGGGGG
AAGGATTTTG ACTACTGGGG TCAGGGAACC CTGGTCACCG TCTCGAGCG

>DOM7r-27

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG CCGTATACGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTCGCCGT TTGGTTCGAC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAAAGTGAT
GTTCTTAAGA CGGGTCTGGA TGGTTTTGAC TACTGGGGTC AGGGAACCCT GGTCACCGTC
TCGAGCG

Fig.51b (Cont XII).

>DOM7r-28

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTATG GCGTATCAGA TGGCTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACT ATTCATCAGA CGGGTTTTTC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAT ACCGCGGTAT ATTACTGTGC GAAAGTGCGT
TCTATGCGTC CTTATAAGTT TGACTACTGG GGTCAGGGAA CCCTGGTCAC CGTCTCGAGC
G

>DOM7r-21

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG CCGTATACGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTCGCCGT TTGGTTCGAC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAAGGTAAT
CTTGAGCCGT TTGACTACTG GGGTCAGGGA ACCCTGGTCA CCGTCTCGAG CG

Fig.51b (Cont XIII).

>DOM7r-25

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG CCGTATACGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTCGCCGT TTGGTTCGAC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAAAAGACG
GGTCCGTCGT CGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGCG

>DOM7r-22

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGT TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG CCGTATACGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTCGCCGT TTGGTTCGAC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAT ACCGCGGTAT ATTACTGTGC GAAAAAGCTT
AGTAATGGTT TTGACTACTG GGGTCAGGGA ACCCTGGTCA CCGTCTCGAG CG

>DOM7r-23

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG CCGTATACGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTCGCCGT TTGGTTCGAC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAAGTGGTT
AAGGATAATA CGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGCG

>DOM7r-24

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG CCGTATACGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTCGCCGT TTGGTTCGAC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATT TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAAAATACT
GGGGGTAAGC AGTTTGACTA CTGGGGTCAG GGAACCCTGG TCACCGTCTC GAGCG

>DOM7r-26

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTTGG CCGTATACGA TGAGTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAACG ATTTCGCCGT TTGGTTCGAC TACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAAAGGACT
GAGAATAGGG GGGTTTCTTT TGACTACTGG GGTCAGGGAA CCCTGGTCAC CGTCTCGAGC
G

Fig.51b (Cont XIV).

>DOM7r-29

GAGGTGCAGC TGTTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGGGGTC CCTGCGTCTC
TCCTGTGCAG CCTCCGGATT CACCTTTAAG GATTATGATA TGACTTGGGT CCGCCAGGCT
CCAGGGAAGG GTCTAGAGTG GGTCTCAATG ATTTCTTCGT CGGGTCTTTG GACATACTAC
GCAGACTCCG TGAAGGGCCG GTTCACCATC TCCCGCGACA ATTCCAAGAA CACGCTGTAT
CTGCAAATGA ACAGCCTGCG TGCCGAGGAC ACCGCGGTAT ATTACTGTGC GAAAGGTTTT
AGGCTGTTTC CTCGGACTTT TGACTACTGG GGTCAGGGAA CCCTGGTCAC CGTCTCGAGC
G