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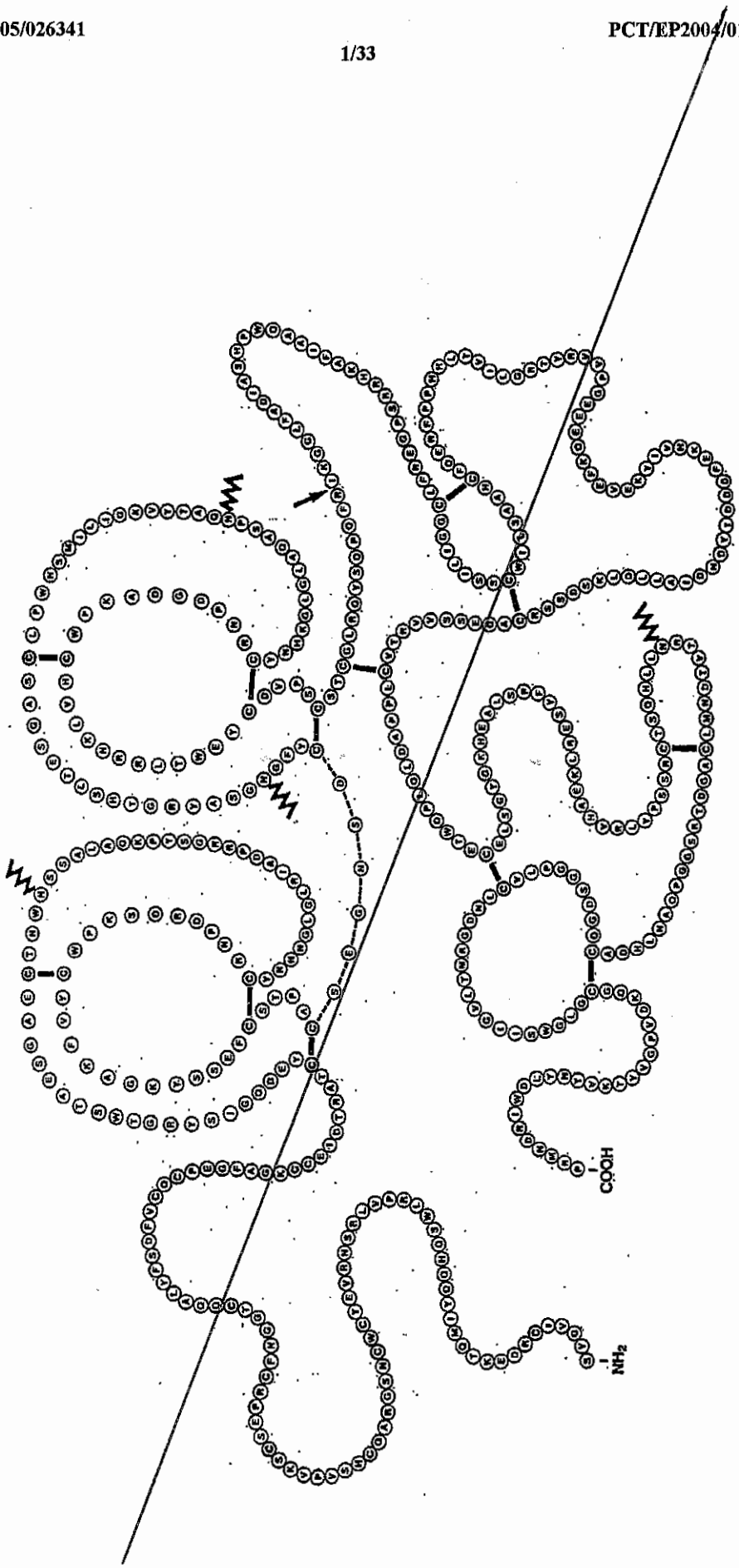
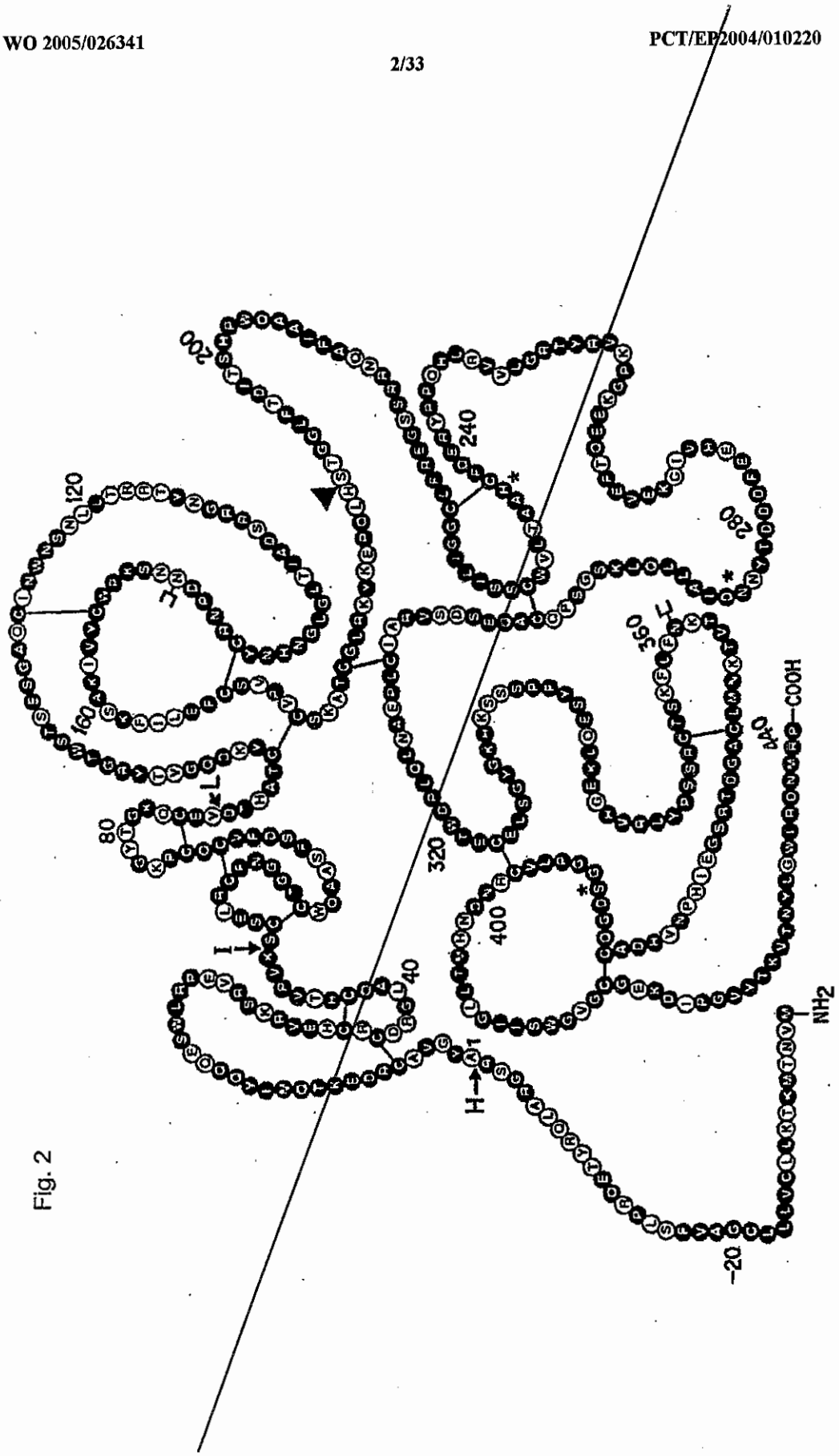


Fig. 1

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NH2
COOH
-20
1
40
80
120
160
200
240
280
320
360
400
440
H
I
L
L
L

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25 OCT 2006

Fig. 2b

[GENETYX-MAC: Multiple Alignment]
Date : 2003.08.23

tPA Isoform 1 vs DSPA alpha 1

```
tPA_AS      1 M-DAMKRGLCCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRP    59
DSPA_AS     1 MVNTMKTKLLCVLLLCGAVFSLPRQETYRQLARGSRAYGVACKDEITQMTYRRQESWLRP    60
              *   **  * **********  * **      ** * * * * ** *** *    *****

tPA_AS     60 VLRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCC   119
DSPA_AS    61 EVRSKRVEHCQCDRGQARCHTVPVNSCSEPRCFNGGTCWQAVYFSDFVCQCPAGYTGKRC   120
                ** *** * *  * * ** *** ************ ** ********** *  ** *

tPA_AS    120 EIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYC   179
DSPA_AS   121 EVDTRATCYEGQGVTYRGTWSTAESRVECINWNSSLLTRRTYNGRMPDAFNLGLGNHNYC   180
              * ******** **  **********  ** ***** *    * ** ***  *********

tPA_AS    180 RNPDRDSKPWCYVFKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPW   239
DSPA_AS   181 RNPNGAPKPWCYVIKAGKFTSESCSVPVCSK----------------------------   204
              ***    ****** ****

tPA_AS    240 NSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTC   299
DSPA_AS   205 ------------------------------------------------------------ATC   214
                                                                           **

tPA_AS    300 GLRQYSQPQF[redacted]KGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCF   359
DSPA_AS   215 GLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCF   274
              *** *  **    **** ** **********  *** *************** * *****

tPA_AS    360 QERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRC   419
DSPA_AS   275 QESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNDIALLQLKSDSPQC   334
              **   *  * * ******* ****** * * ************ ************  *

tPA_AS    420 AQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQ   479
DSPA_AS   335 AQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPK   394
              ****  **  *** * ****************   ****** *** **********

tPA_AS    480 HLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQ   539
DSPA_AS   395 FLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGE   454
               * * *** ***********    * ************** **  *** ****** ***

tPA_AS    540 KDVPGVYTKVTNYLDWIRDNMRP                                        562
DSPA_AS   455 KDVPGVYTKVTNYLGWIRDNMHL                                        477
              *************** ******
```

Kringel 2

[redacted]

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Fig. 3

Humanised DSPA

Sequence is based on tPA Isoform 1 with
a) Deletion of Kringel 2
b) tPA activation site mutated to corresponding DSPA sequence

```
   1 mdamkrglcc vlllcgavfv spsqeiharf rrgarsyqvi crdektqmiy qqhqswlrpv
  61 lrsnrveycw cnsgraqchs vpvkscsepr cfnggtcqqa lyfsdfvcqc pegfagkcce
 121 idtratcyed qgisyrgtws taesgaectn wnssalaqkp ysgrrpdair lglgnhnycr
 181 npdrdskpw cyvfkagky ssefcstpa csegnsdst cglrqysqp qf[redacted]kgglf
 241 adiashpwq aaifakhrr spgerflcg gilisscwi lsaahcfqe rfpphhltv
 301 ilgrtyrvv pgeeeqkfe vekyivhke fdddtydnd iallqlksd ssrcaqess
 361 vvrtvclpp adlqlpdwt ecelsgygk healspfys erlkeahvr lypssrcts
 421 qhllnrtvt dnmlcagdt rsggpqanl hdacqgdsg gplvclndg rmtlvgiis
 481 wglgcgqkd vpgvytkvt nyldwirdn mrp
```

Italics: Signal sequence

Kringel 2 Deletion: hsd-Kringel2-stc

[redacted]

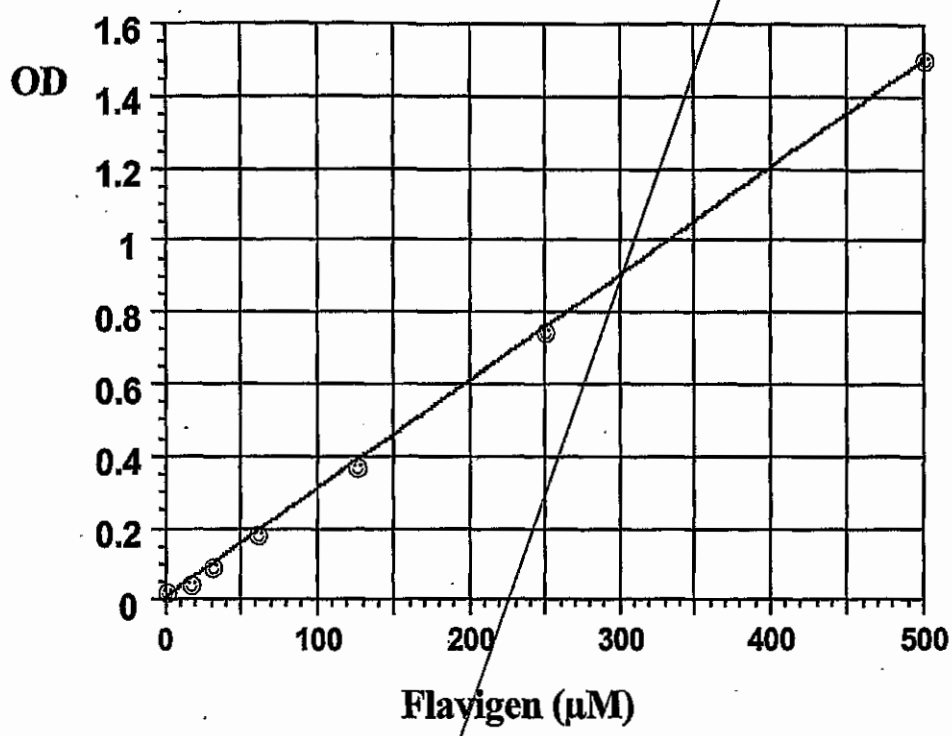
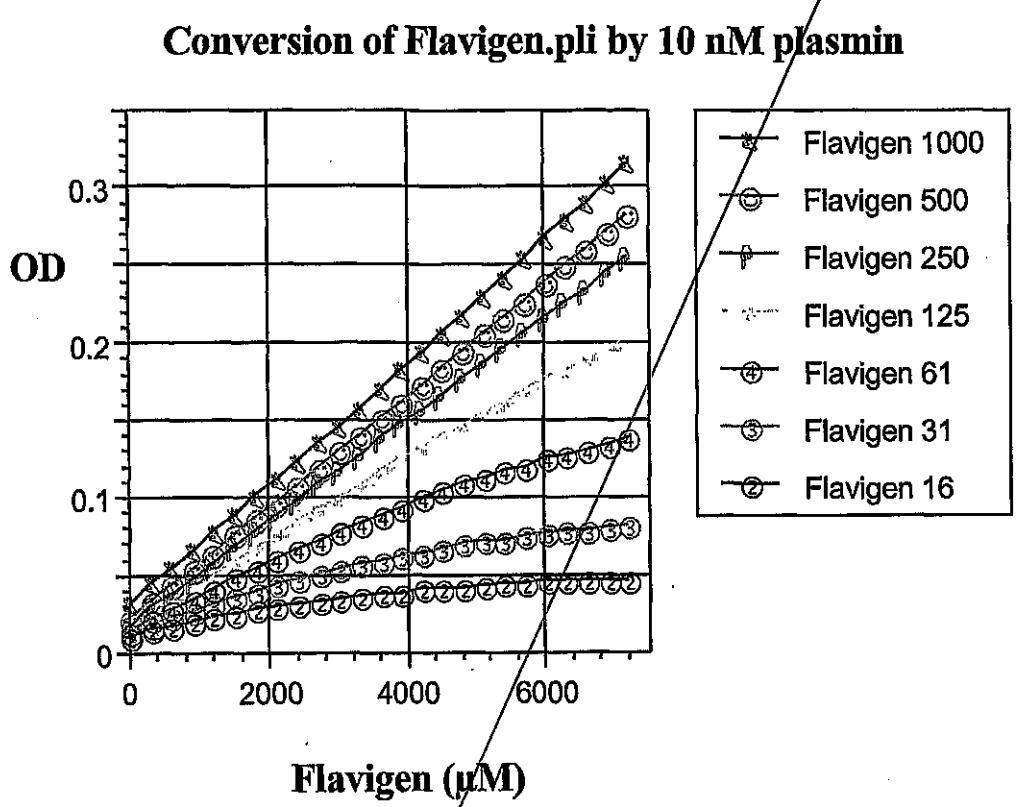

Conversion of OD405 into converted substrate
[Flavigen, µM] = (OD- 0.012)/0.00298
R^2 = 0.9996
OD
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
100
200
300
400
500
Flavigen (µM)

Figure 4a

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25 OCT 2006



~~Figure 4b~~

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Plot of pNA generation (nM/s) by 10 nM of plasmin as a function of Flavigen.pli concentration kcat = 1.36 s^{-1}; Km = 88.1 µM

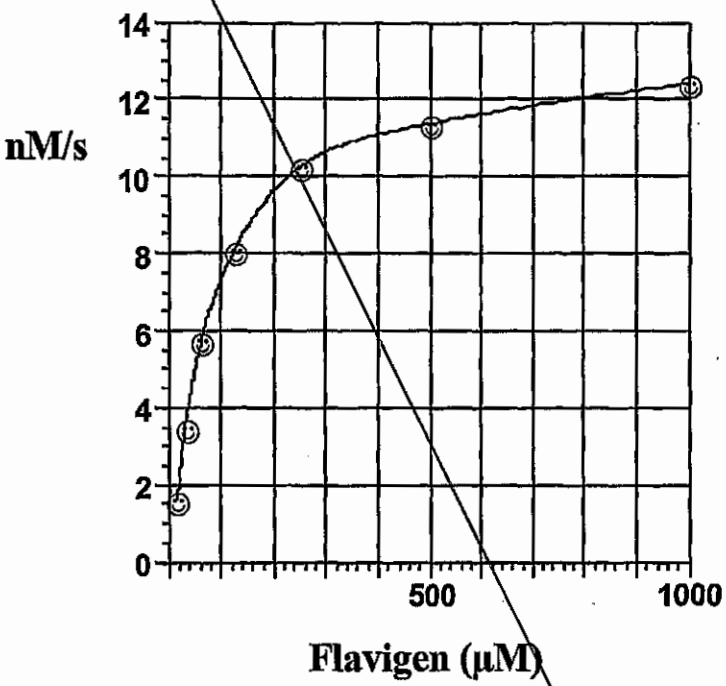


Figure 4c

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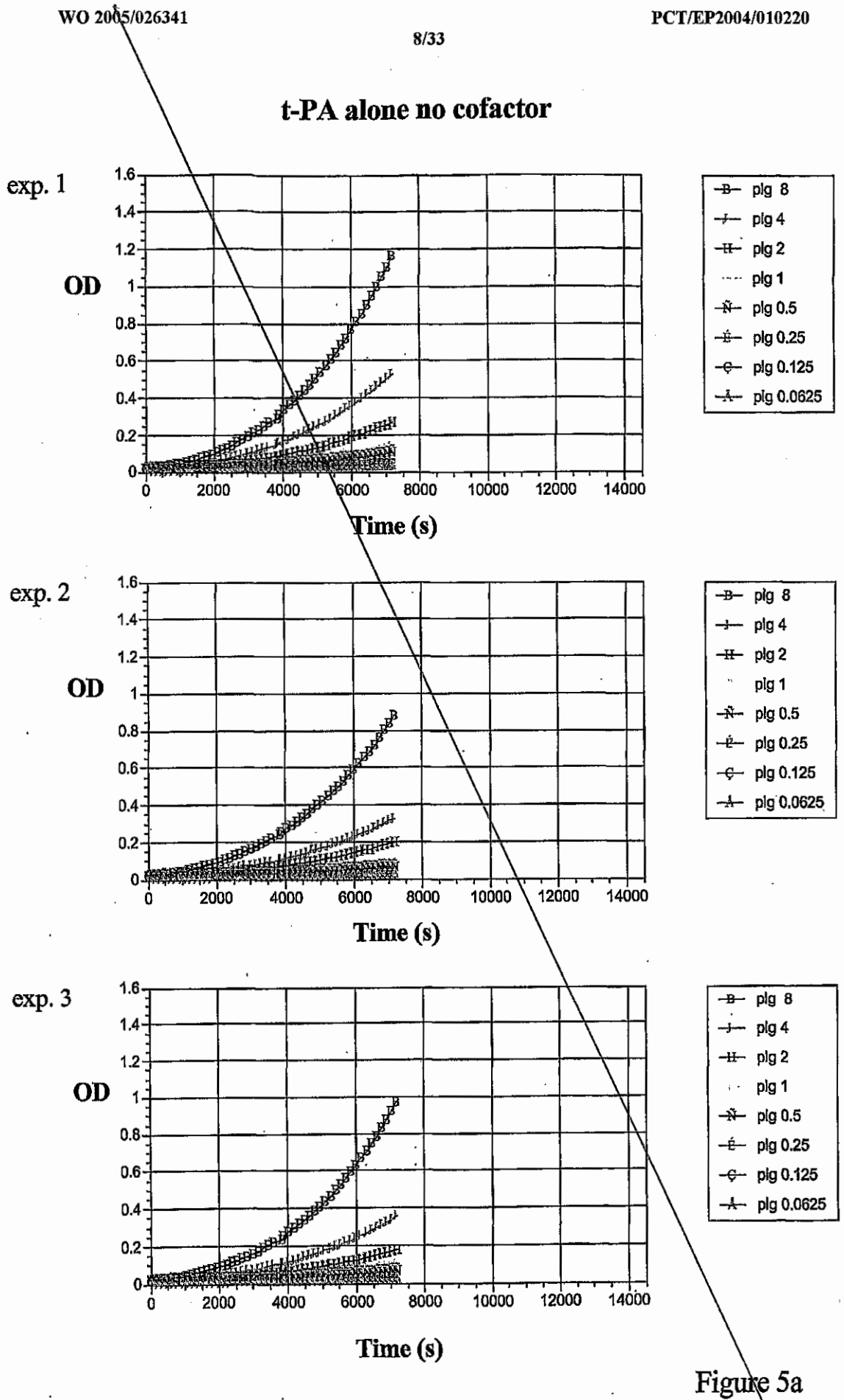


Figure 5a

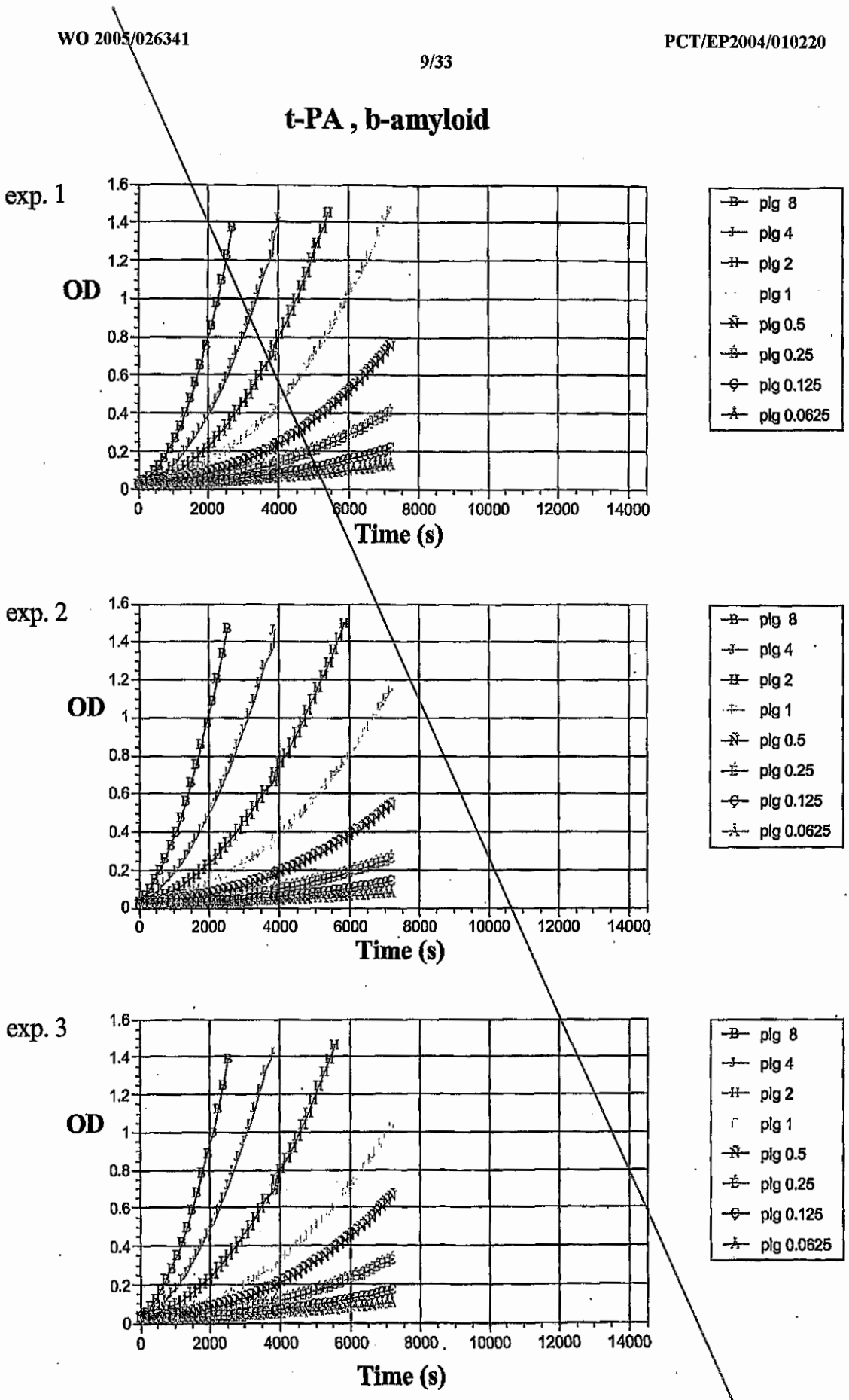

t-PA , b-amyloid
exp. 1
exp. 2
exp. 3
OD
Time (s)
plg 8
plg 4
plg 2
plg 1
plg 0.5
plg 0.25
plg 0.125
plg 0.0625

Figure 5b

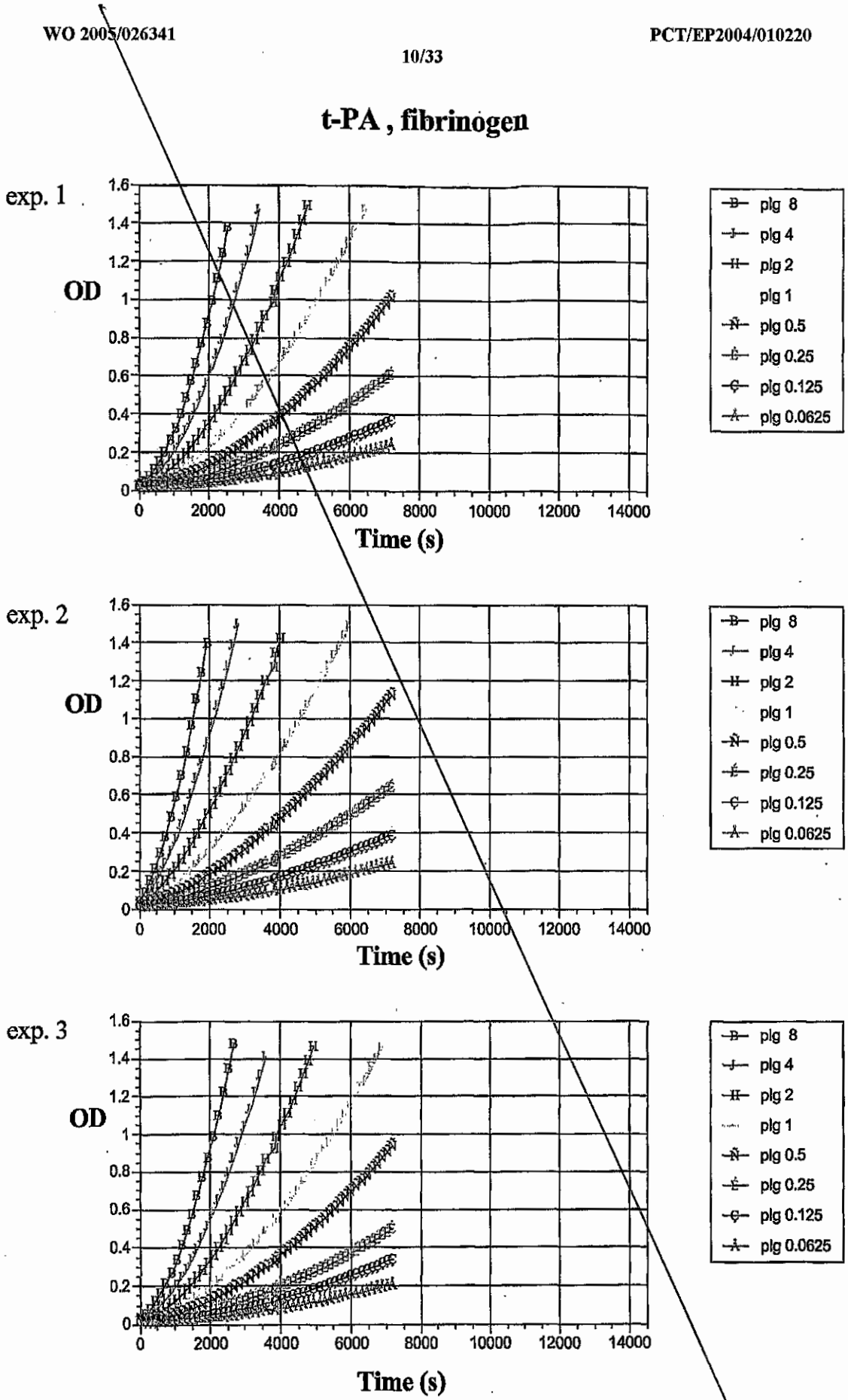

t-PA , fibrinogen
exp. 1
OD
Time (s)
plg 8
plg 4
plg 2
plg 1
plg 0.5
plg 0.25
plg 0.125
plg 0.0625
exp. 2
OD
Time (s)
plg 8
plg 4
plg 2
plg 1
plg 0.5
plg 0.25
plg 0.125
plg 0.0625
exp. 3
OD
Time (s)
plg 8
plg 4
plg 2
plg 1
plg 0.5
plg 0.25
plg 0.125
plg 0.0625

Figure 5c

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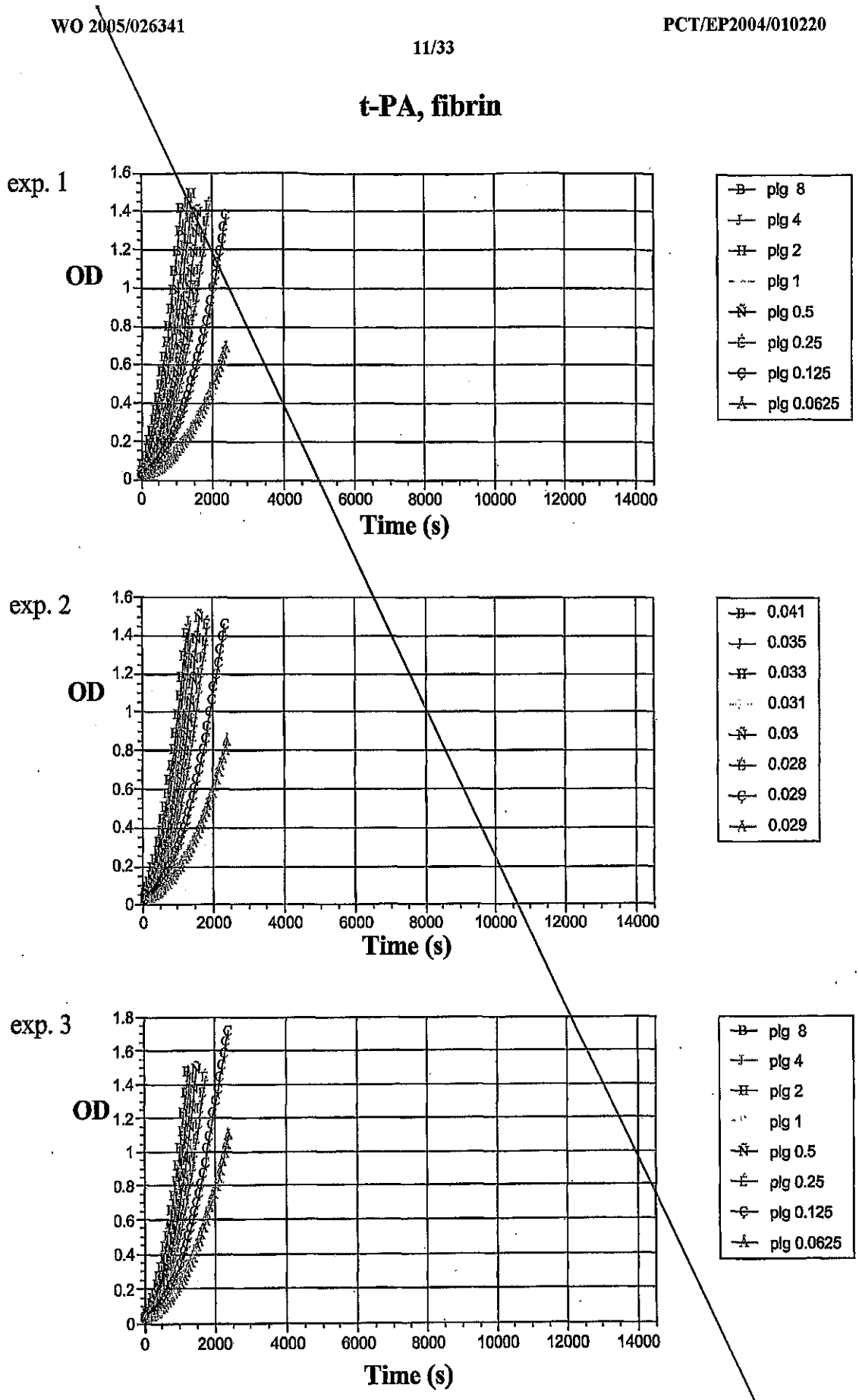


Figure 5d

REPLACEMENT SHEET
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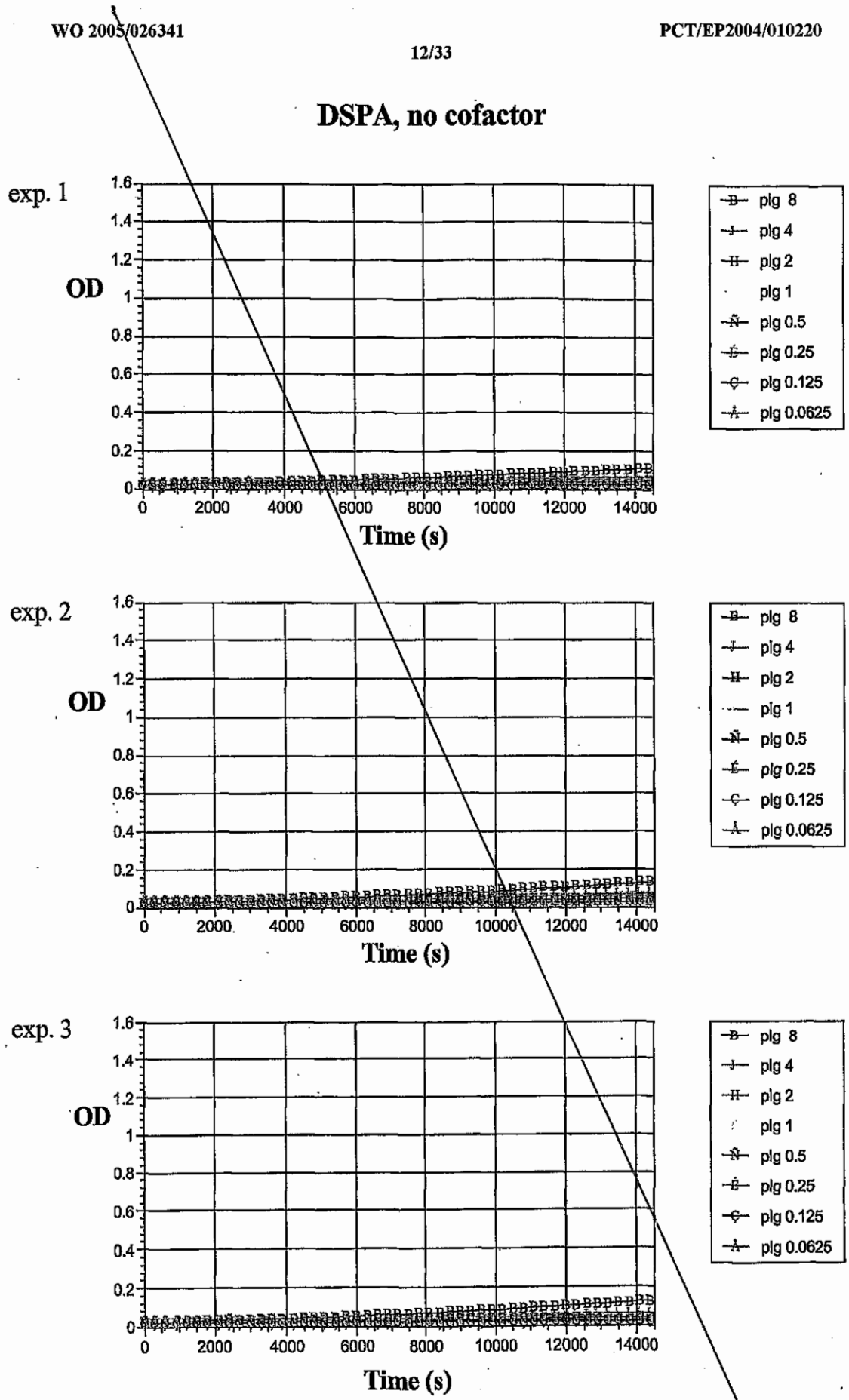


Figure 5e

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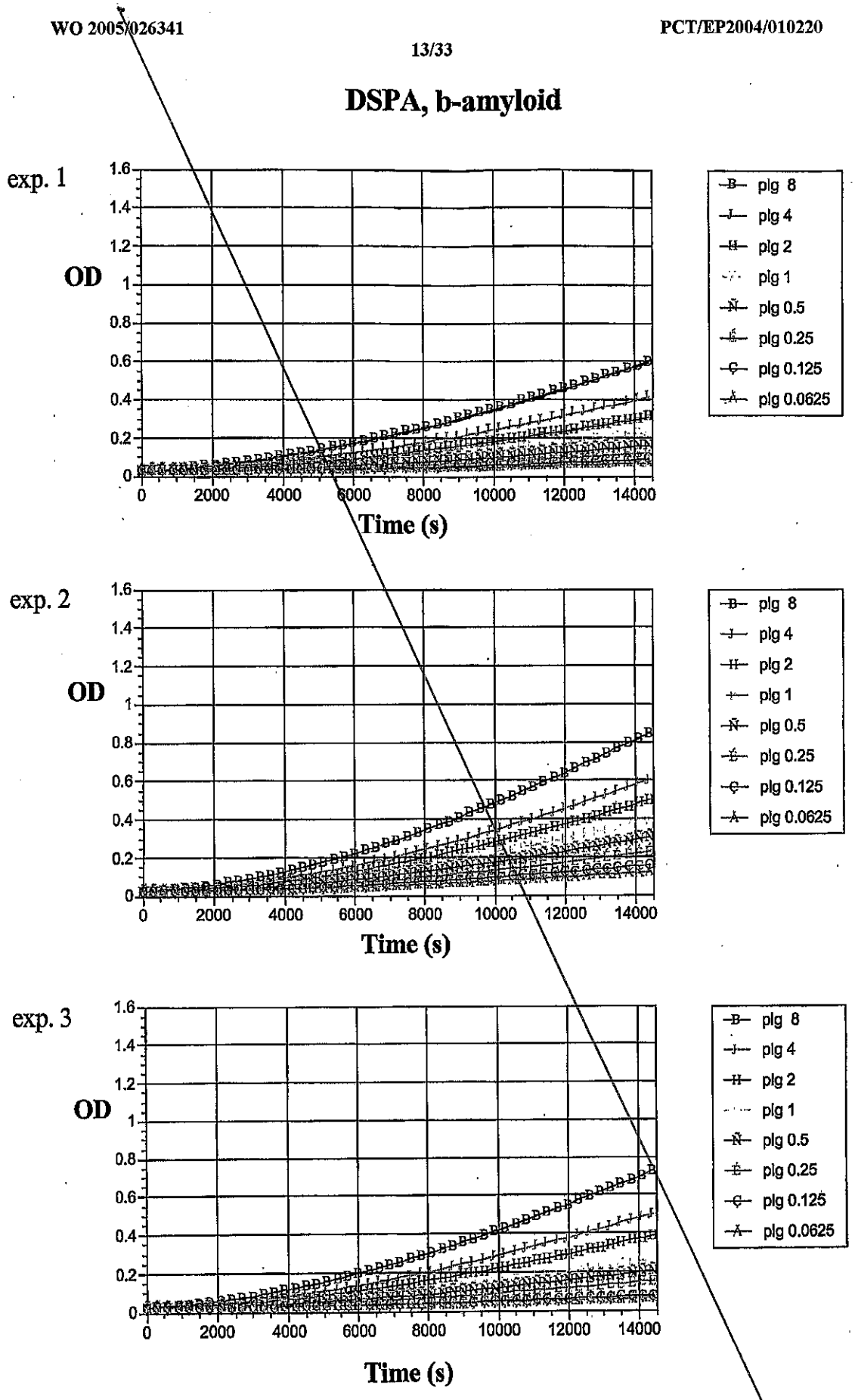
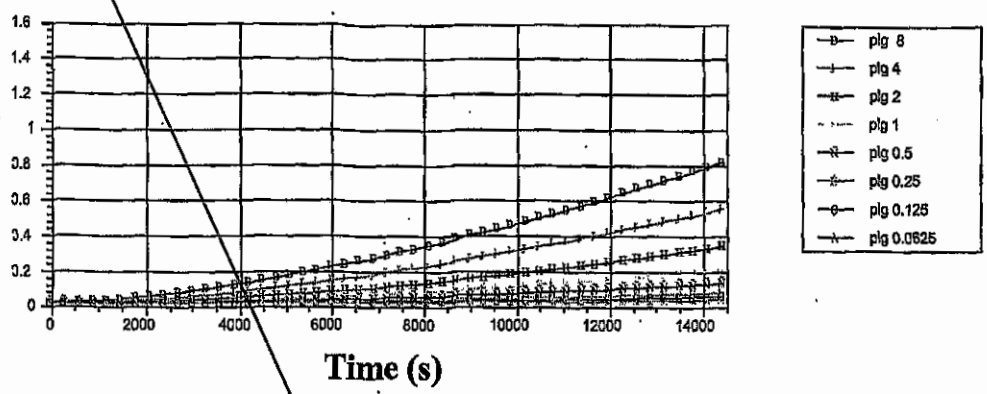


Figure 5f

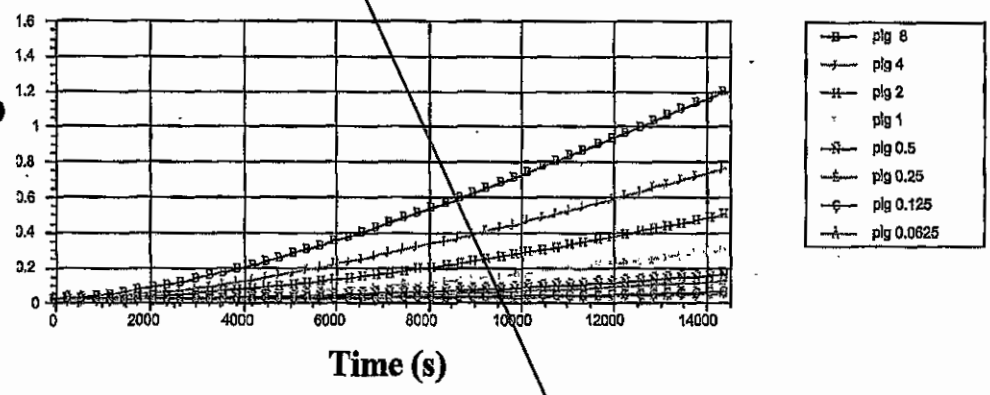
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DSPA, fibrinogen

exp. 1



exp. 2



exp. 3

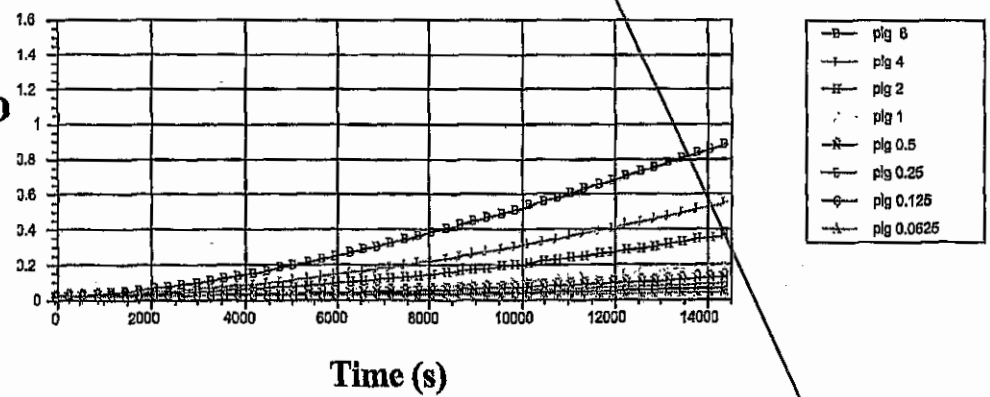


Figure 5g

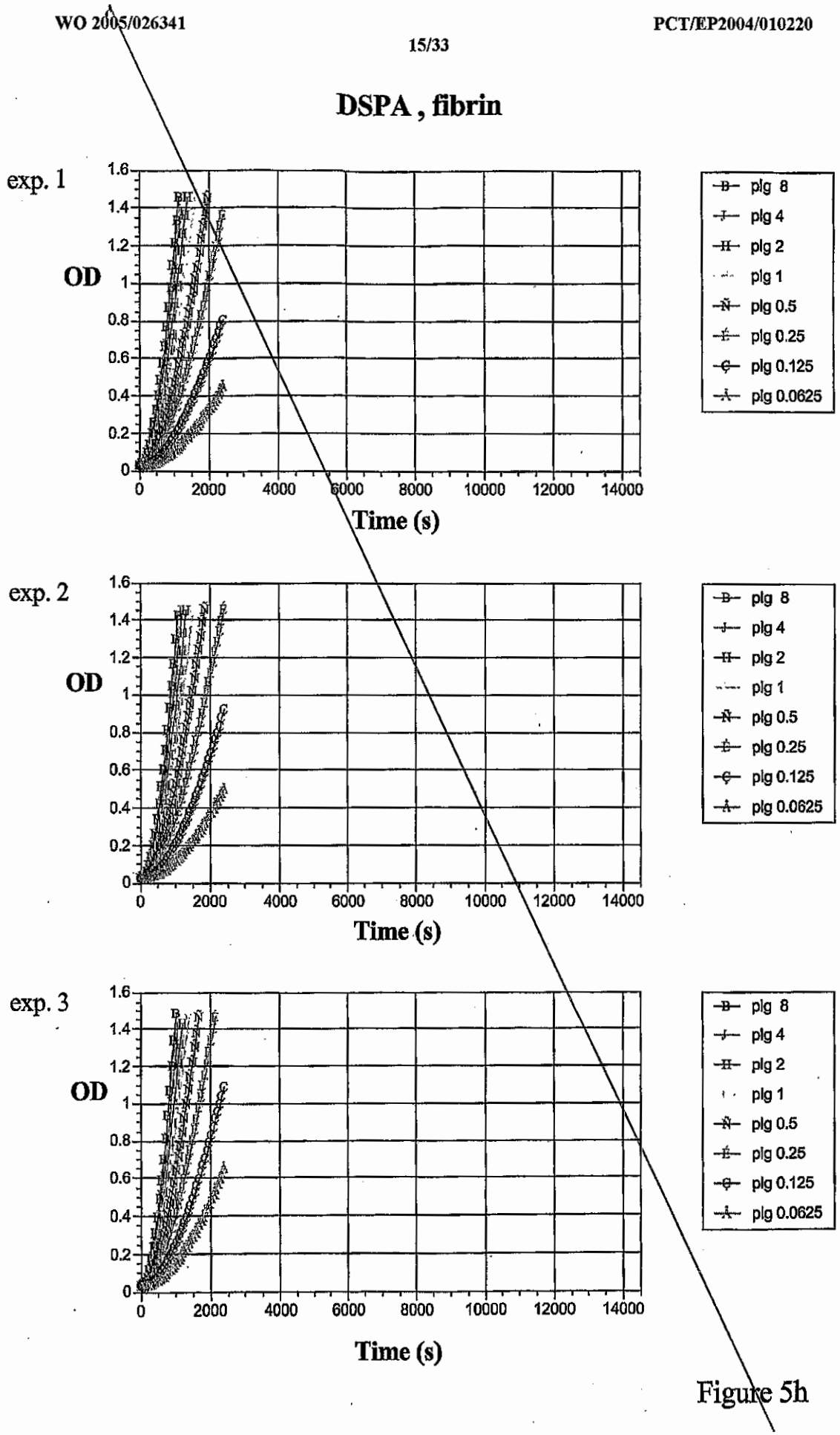

DSPA , fibrin
exp. 1
exp. 2
exp. 3
OD
Time (s)
plg 8
plg 4
plg 2
plg 1
plg 0.5
plg 0.25
plg 0.125
plg 0.0625

Figure 5h

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25 OCT 2006

Plots of **a** versus plasminogen concentration
a =ks.kcat.PA.E.P/(Km + P) The values were obtained by parabolic curve fitting to the equation OD (t) = a * t^2+ b * t + c

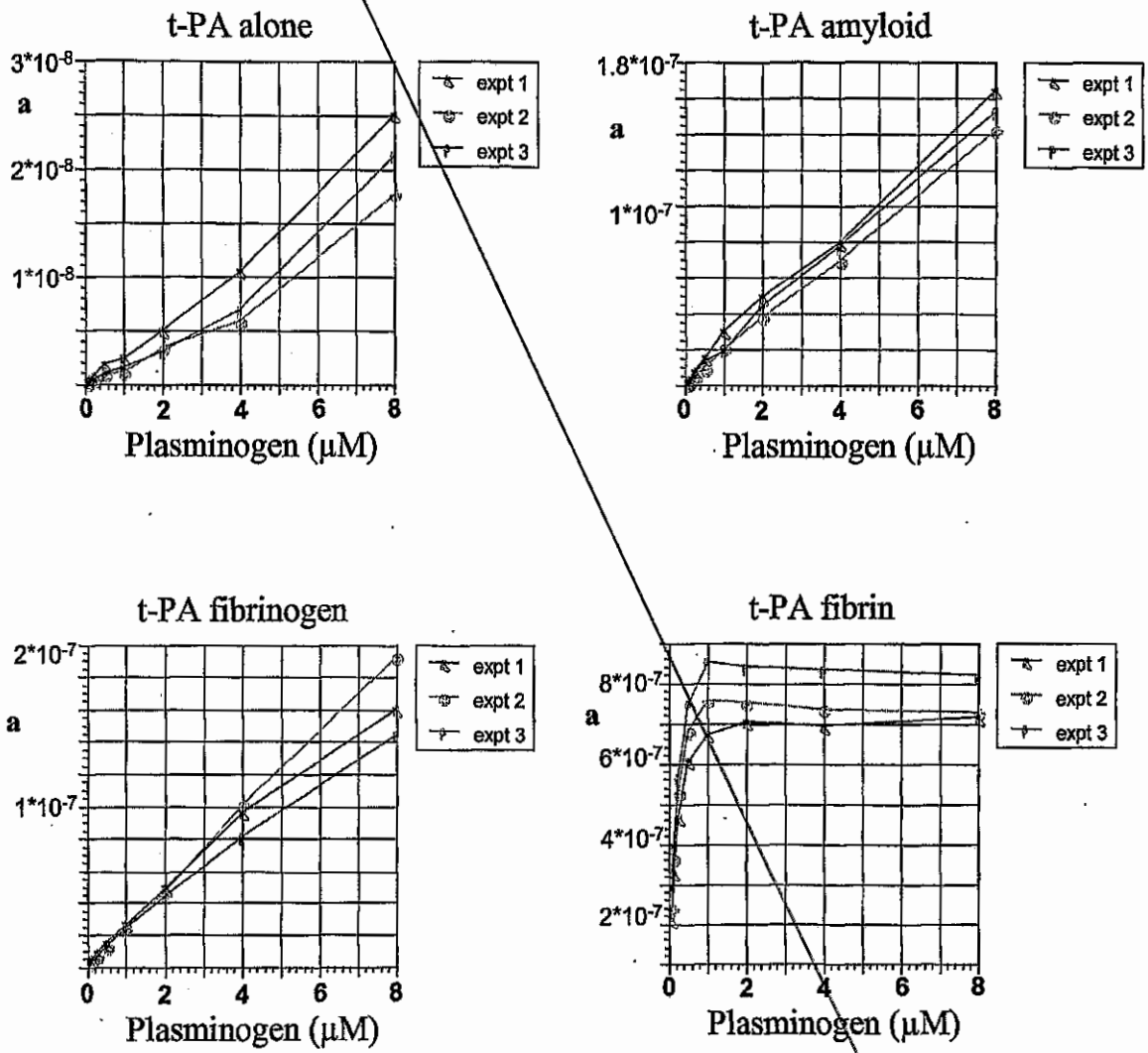


Figure 6a

REPLACEMENT SHEET
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Plots of a versus plasminogen concentration
a =ks.kcat.PA.E.P/(Km + P) The values were obtained by parabolic curve fitting to the equation OD (t) = a * t^2+ b * t + c

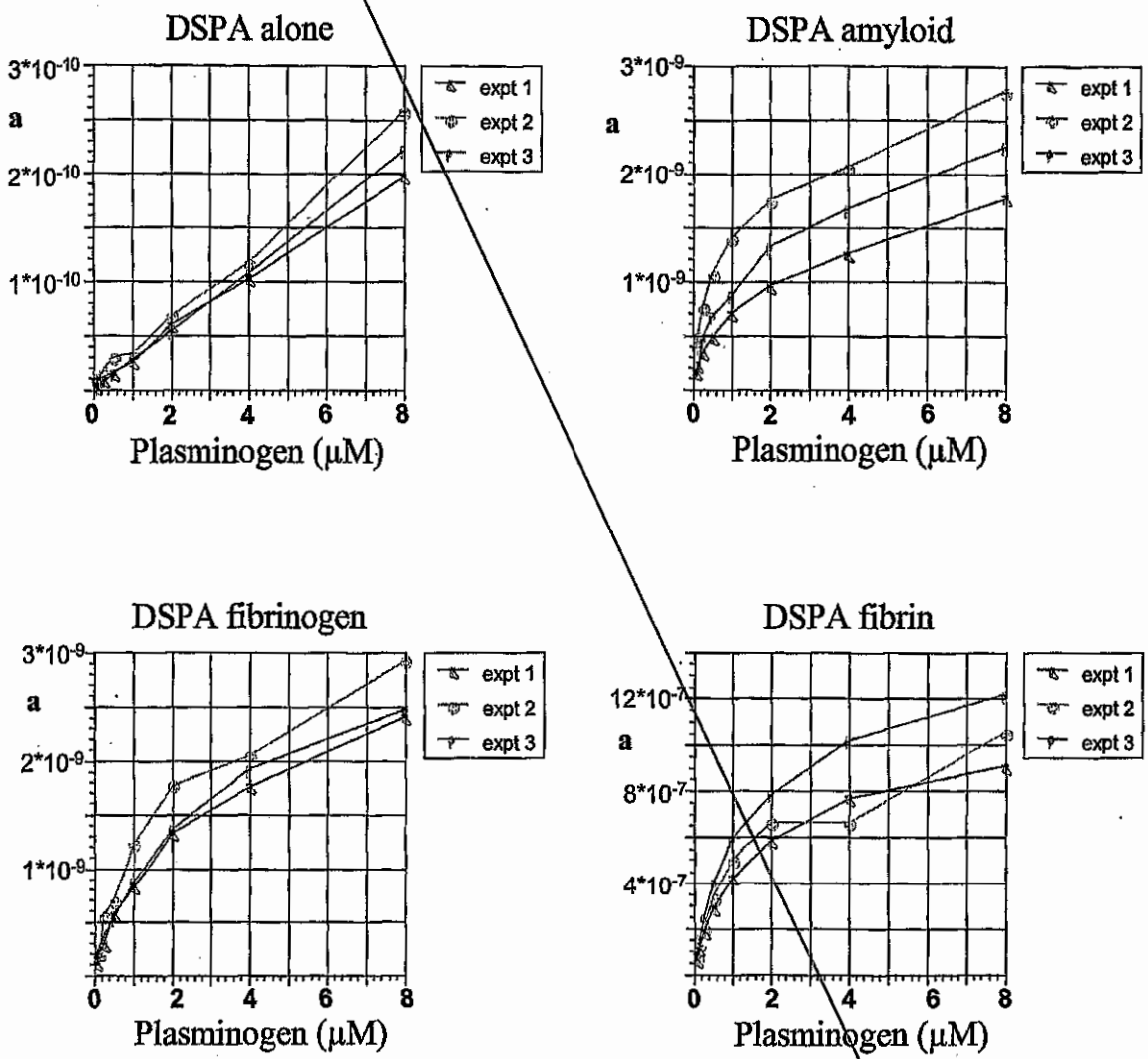


Figure 6b

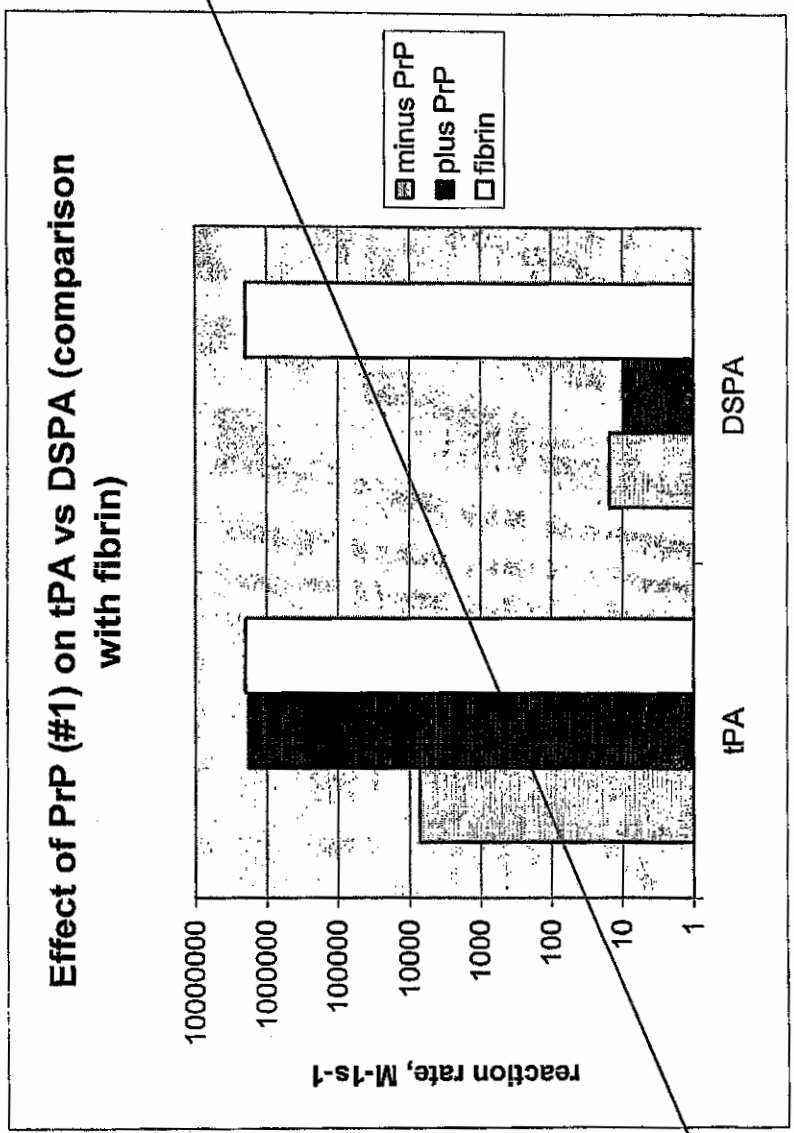

Effect of PrP (#1) on tPA vs DSPA (comparison with fibrin)
minus PrP
plus PrP
fibrin
reaction rate, M-1s-1
10000000
1000000
100000
10000
1000
100
10
1
tPA
DSPA

Fig. 7

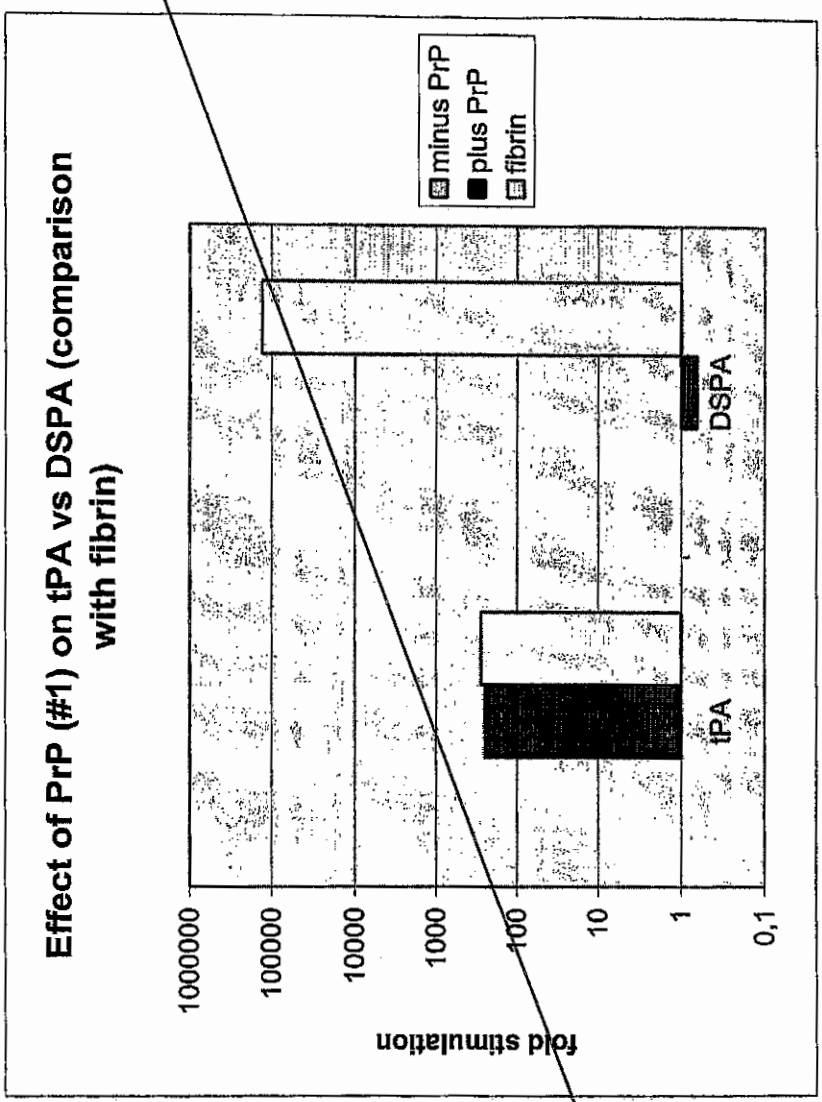

Effect of PrP (#1) on tPA vs DSPA (comparison with fibrin)
minus PrP
plus PrP
fibrin
fold stimulation
1000000
100000
10000
1000
100
10
1
0,1
tPA
DSPA

Fig. 8

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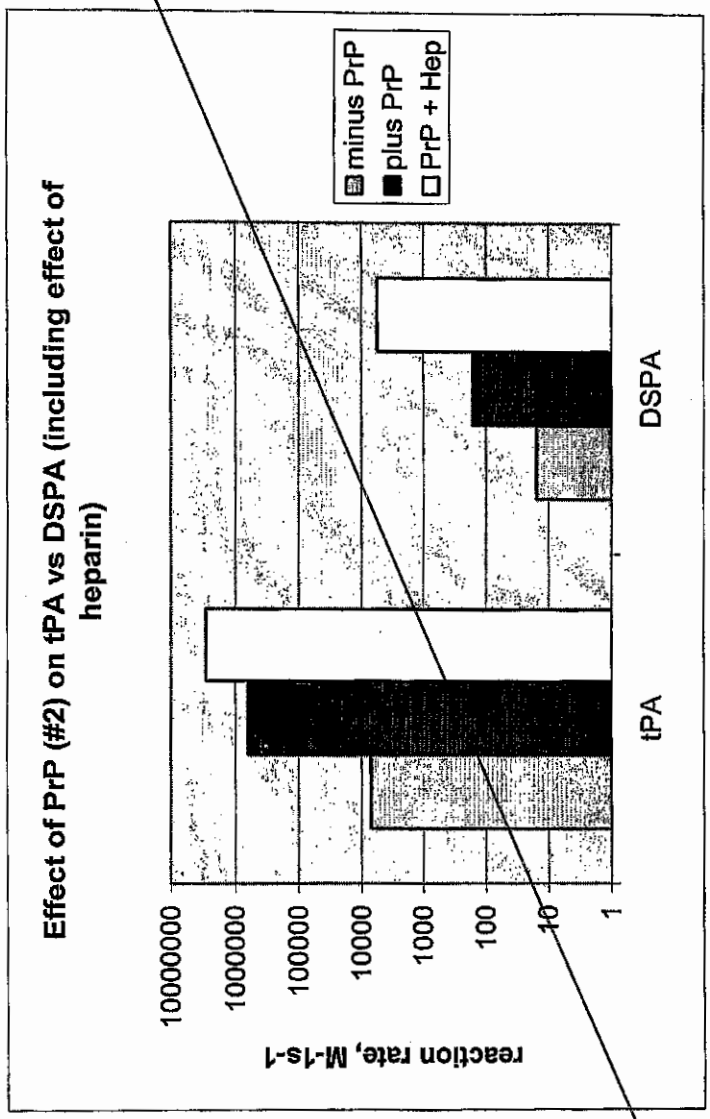


Fig. 9

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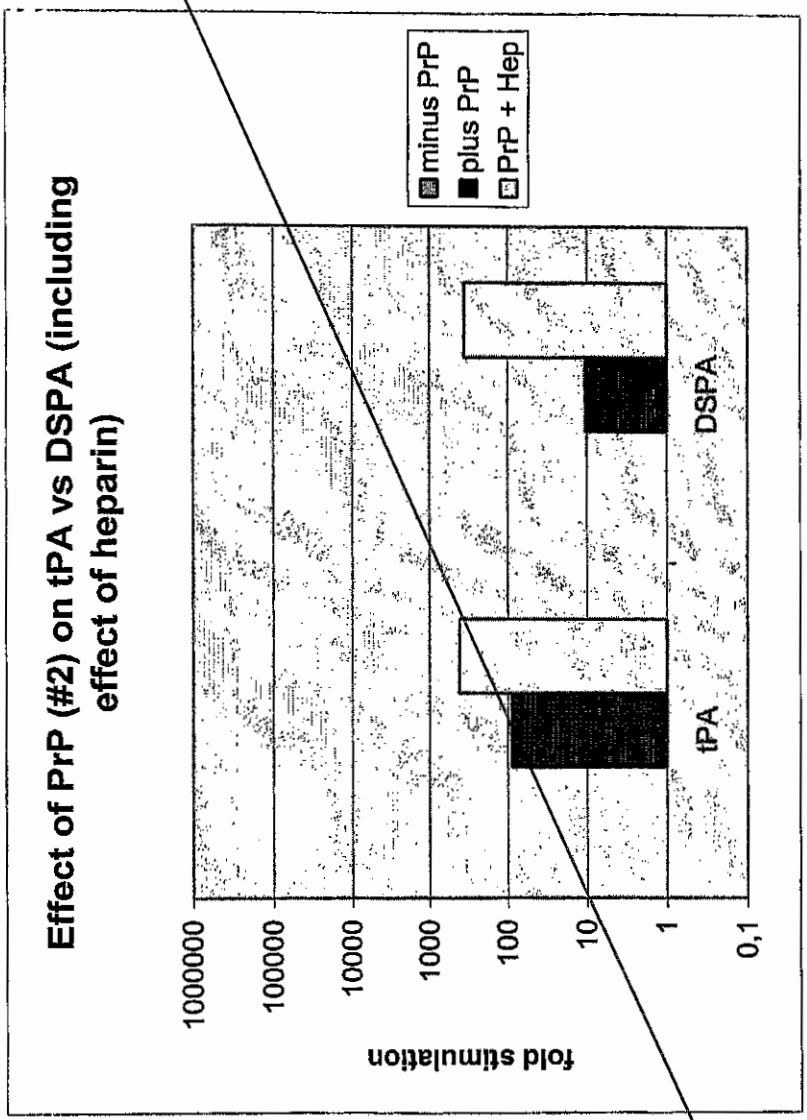


Fig. 10

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25 OCT 2006

Fig. 11

*MDAMKRGLCCVLLLCGAVFVSPS*QEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRPVLRSNRVEY
CWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCEIDTRATCYEDQGISYR
GTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYVFKAGKYSSEFCS
TPACSKATCGLRQYSQPQLHSTGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHC
FQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVV
RTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAG
DTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP

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25 OCT 2006

Fig. 12

```
tPA       M-DAMKRGLCCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRP 59
Fig. 3    M-DAMKRGLCCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRP 59
Fig. 11   M-DAMKRGLCCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRP 59
DSPA_a1   MVNTMKTKLLCVLLLCGAVFSLPRQETYRQLARGSRAYGVACKDEITQMTYRRQESWLRP 60
          : ::**  * **********  * ** : :: **:*:* * *:** *** *:.::*****

tPA       VLRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCC 119
Fig. 3    VLRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCC 119
Fig. 11   VLRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCC 119
DSPA_a1   EVRSKRVEHCQCDRGQARCHTVPVNSCSEPRCFNGGTCWQAVYFSDFVCQCPAGYTGKRC 120
           :**:***:* *: *:*:**:***:************* **:********** *::** *

tPA       EIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYC 179
Fig. 3    EIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYC 179
Fig. 11   EIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYC 179
DSPA_a1   EVDTRATCYEGQGVTYRGTWSTAESRVECINWNSSLLTRRTYNGRMPDAFNLGLGNHNYC 180
          *:********.**::********** .** ***** *::.:*.** ***:.*********

tPA       RNPDRDSKPWCYVFKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPW 239
Fig. 3    RNPDRDSKPWCYVFKAGKYSSEFCSTPACSEGNSD------------------------- 214
Fig. 11   RNPDRDSKPWCYVFKAGKYSSEFCSTPACSK---------------------------- 210
DSPA_a1   RNPNGAPKPWCYVIKAGKFTSESCSVPVCSK----------------------------- 211
          ***:  .******:****::** **.*.**:

tPA       NSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTC 299
Fig. 3    ----------------------------------------------------------STC 217
Fig. 11   ----------------------------------------------------------ATC 213
DSPA_a1   ----------------------------------------------------------ATC 214
                                                                      :**

tPA       GLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCF 359
Fig. 3    GLRQYSQPQFHSKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCF 277
Fig. 11   GLRQYSQPQLHSTGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCF 273
DSPA_a1   GLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCF 274
          ***:*.:**:: .****:**:**********::***.***************:*:*****

tPA       QERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRC 419
Fig. 3    QERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRC 337
Fig. 11   QERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRC 333
DSPA_a1   QESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNDIALLQLKSDSPQC 334
          ** : *.:*.*:******* ******.*:*:*************:************.:*

tPA       AQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQ 479
Fig. 3    AQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQ 397
Fig. 11   AQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQ 393
DSPA_a1   AQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPK 394
          ****.**:***** *:*****************:: ******:***.**********:.:

tPA       HLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQ 539
Fig. 3    HLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQ 457
Fig. 11   HLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQ 453
DSPA_a1   FLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGE 454
          .*:*:***:***********    .*:***************:**.:***:******:***:

tPA       KDVPGVYTKVTNYLDWIRDNMRP 562
Fig. 3    KDVPGVYTKVTNYLDWIRDNMRP 480
Fig. 11   KDVPGVYTKVTNYLDWIRDNMRP 476
DSPA_a1   KDVPGVYTKVTNYLGWIRDNMHL 477
```

REPLACEMENT SHEET
25 OCT 2006

Fig. 13

MDAMKRGLCCVLLLCGAVFSLPSQETHRQLARGSRAYQVACRDEITQMIYQQHQSWLRPVLRSKRVEH
CQCNRGQARCHSVPVKSCSEPRCFNGGTCWQALYFSDFVCQCPEGYTGKCCEIDTRATCYEGQGISYR
GTWSTAESRVECTNWNSSLLTRRTYNGRMPDAFNLGLGNHNYCRNPNGAPKPWCYVIKAGKFSSESCS
VPACSKATCGLRKYKEPQLHSTGGLFTDIASHPWQAAIFAQHRRSSGERFLCGGILISSCWILSAAHC
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RAICLPEANLQLPDWTECELSGYGKHESSSPFYSEQLKEGHVRLYPSSRCAPKFLFNRTVTNNMLCAG
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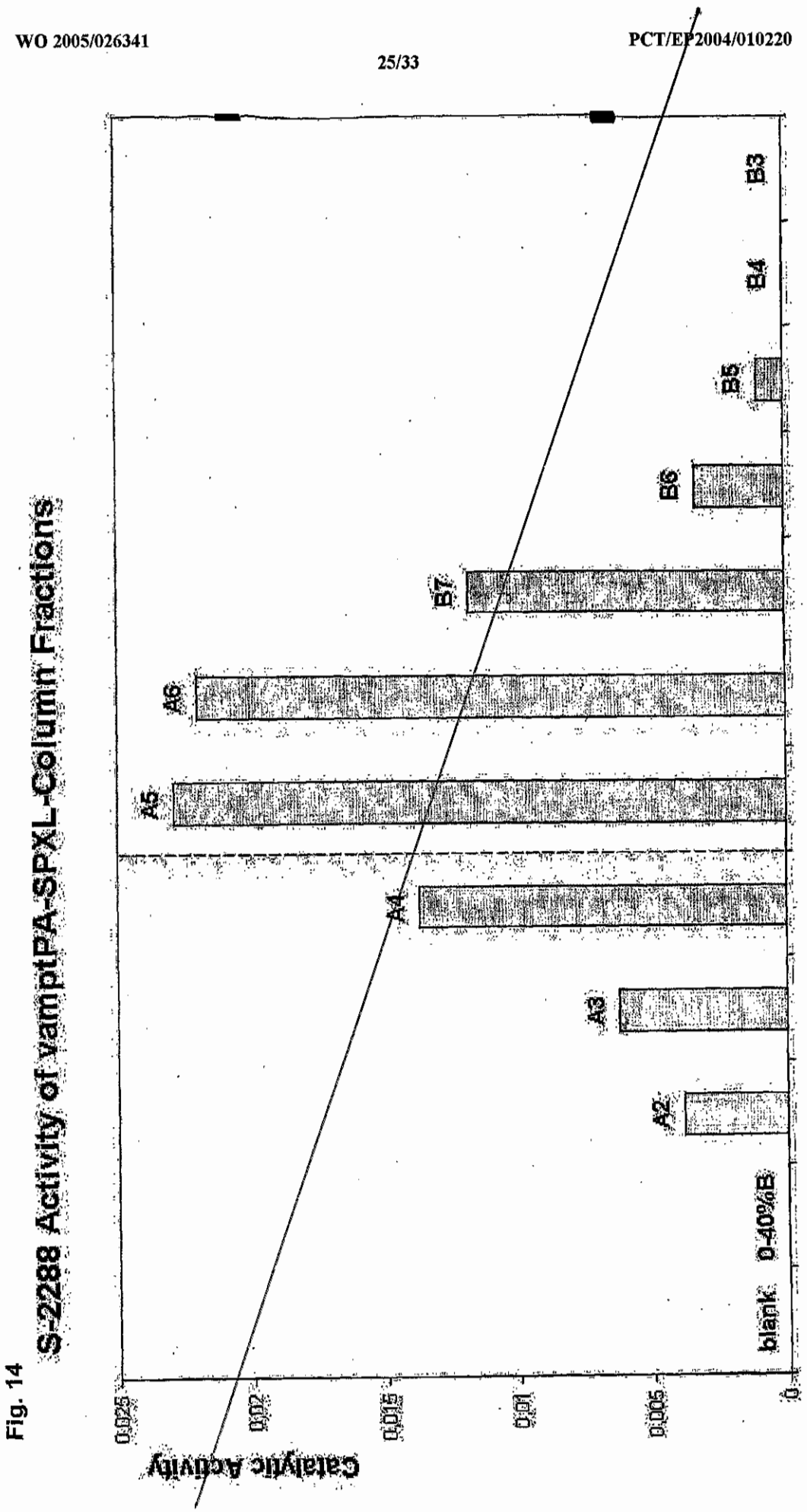

S-2288 Activity of vamptPA-SPXL-Column Fractions
Catalytic Activity
0.025
0.02
0.015
0.01
0.005
0
blank
0-40%B
A2
A3
A4
A5
A6
B7
B6
B5
B4
B3

Fig. 14

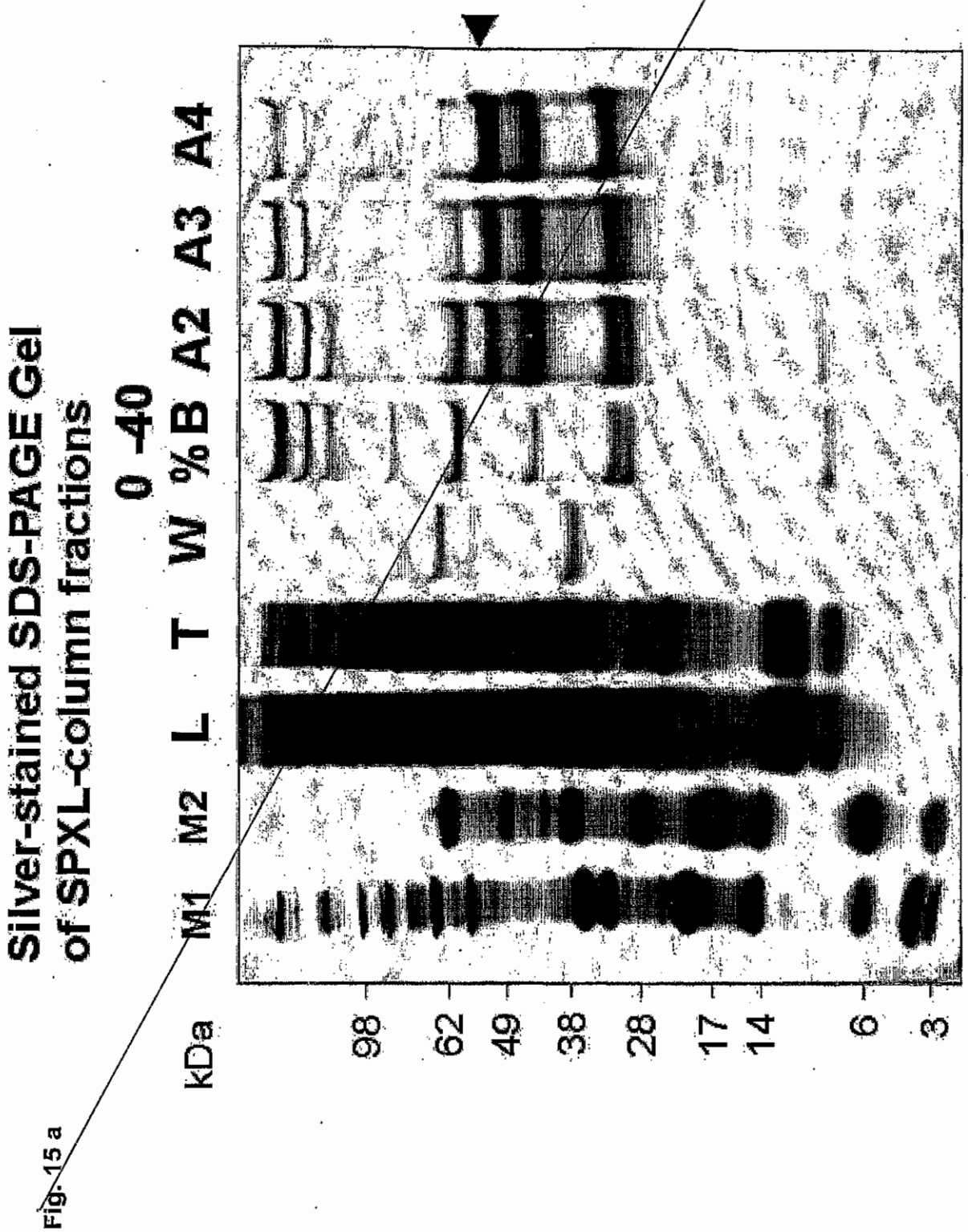
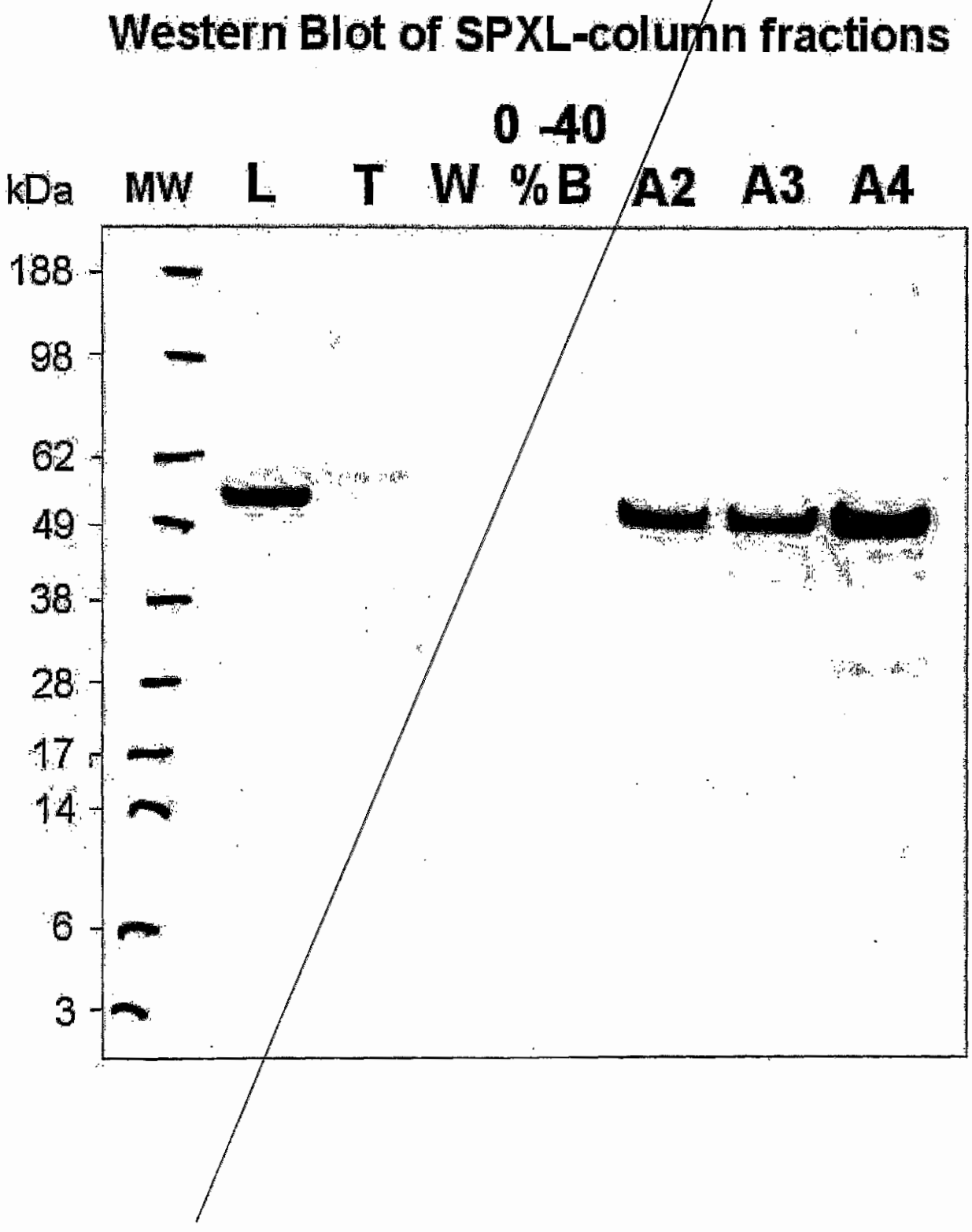

Silver-stained SDS-PAGE Gel
of SPXL-column fractions
0 -40
M1 M2 L T W %B A2 A3 A4
kDa
98
62
49
38
28
17
14
6
3

Fig. 15 a


Western Blot of SPXL-column fractions
0 -40
kDa
MW
L
T
W
%B
A2
A3
A4
188
98
62
49
38
28
17
14
6
3

REPLACEMENT SHEET
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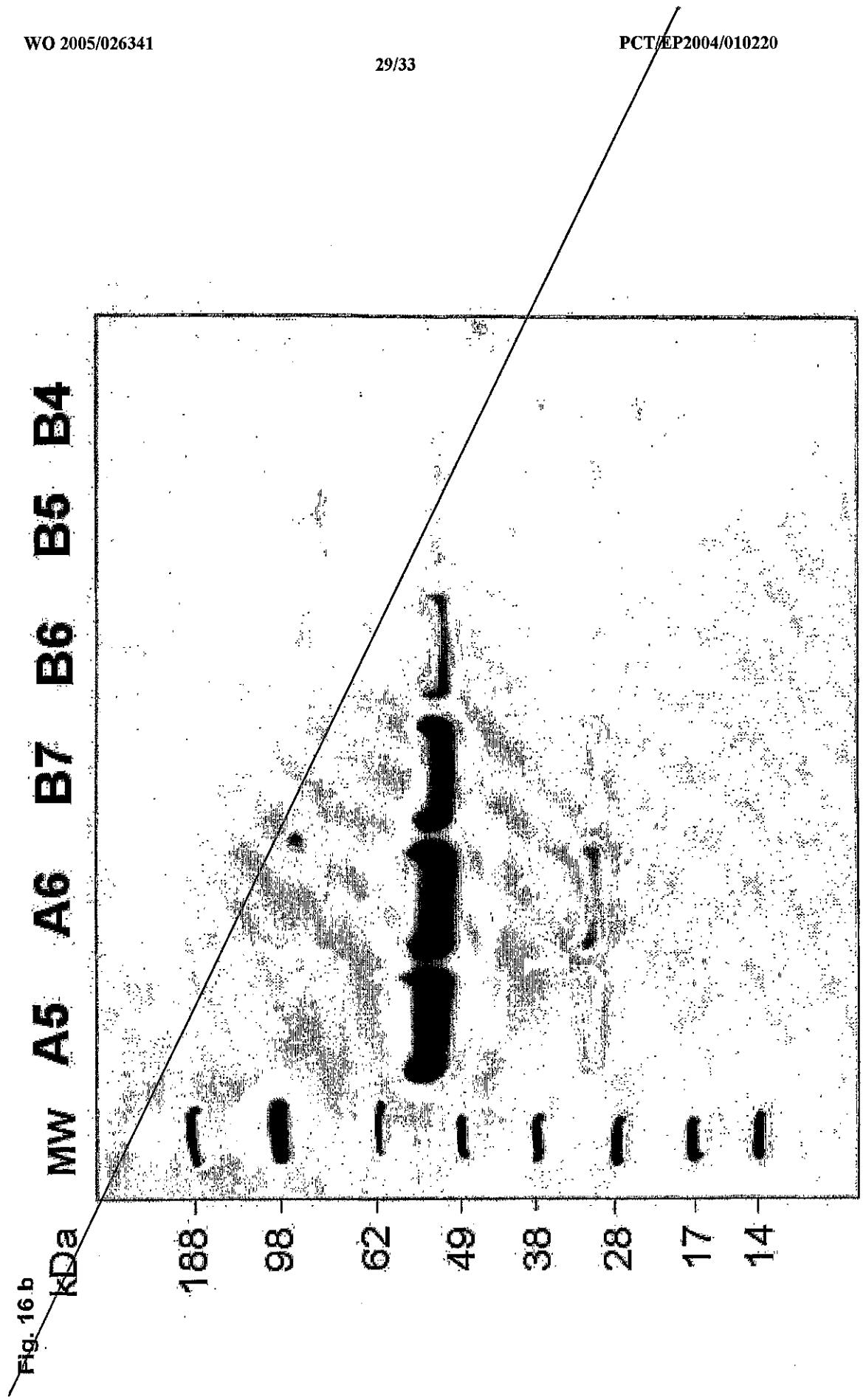


Fig. 16 b

REPLACEMENT SHEET
25 OCT 2006

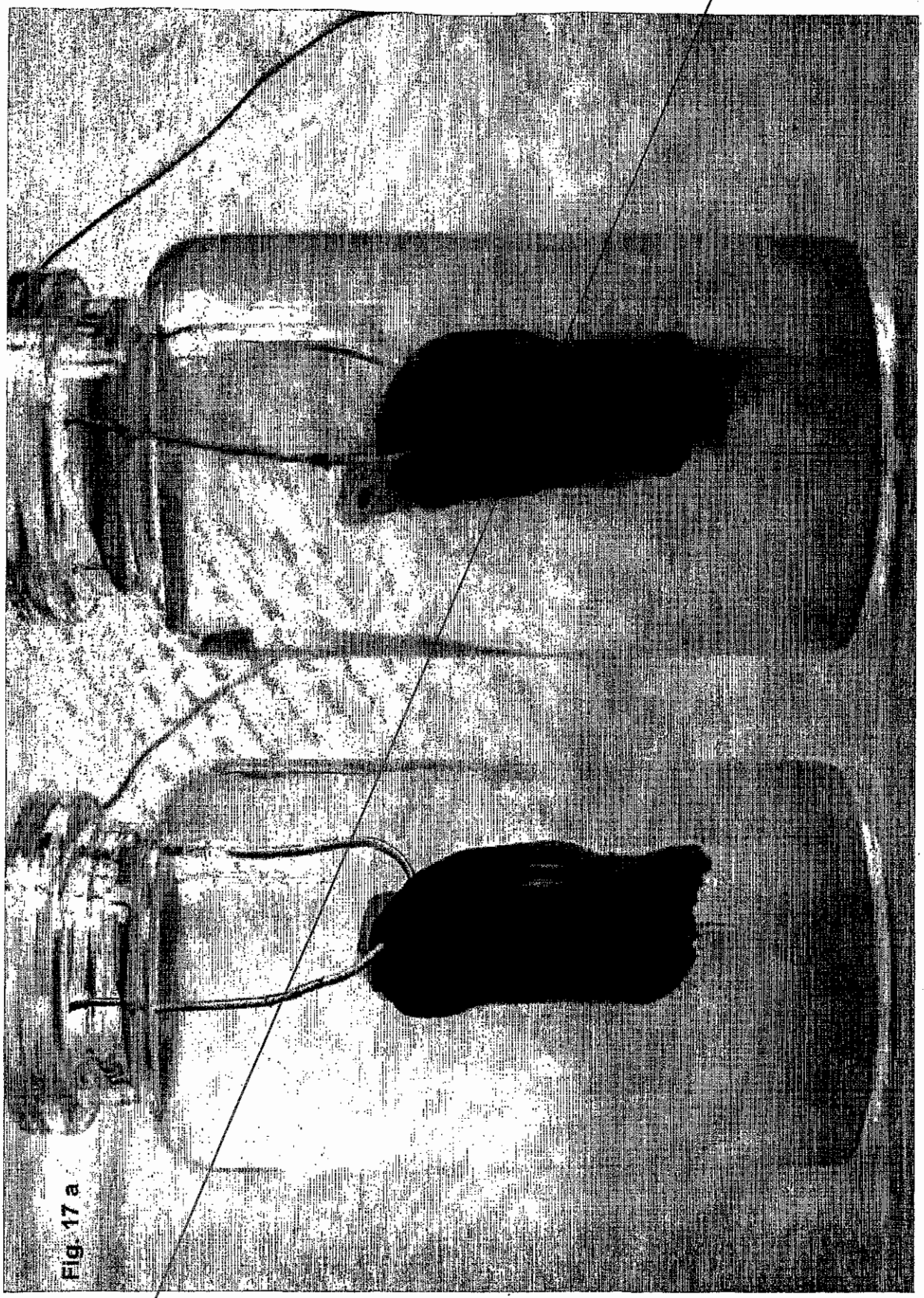


Fig. 17 a

REPLACEMENT SHEET
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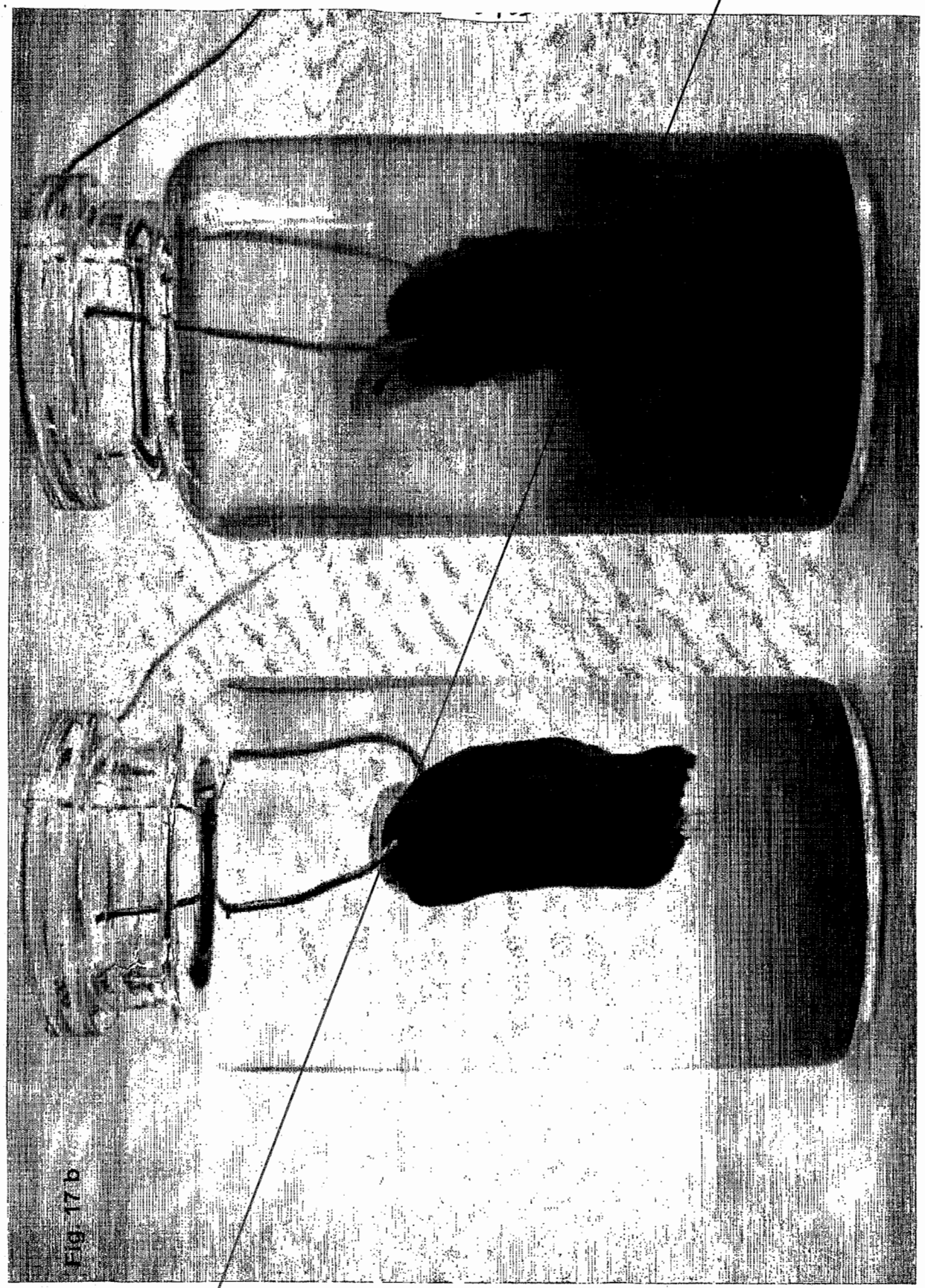


Fig 17b

REPLACEMENT SHEET
25 OCT 2006

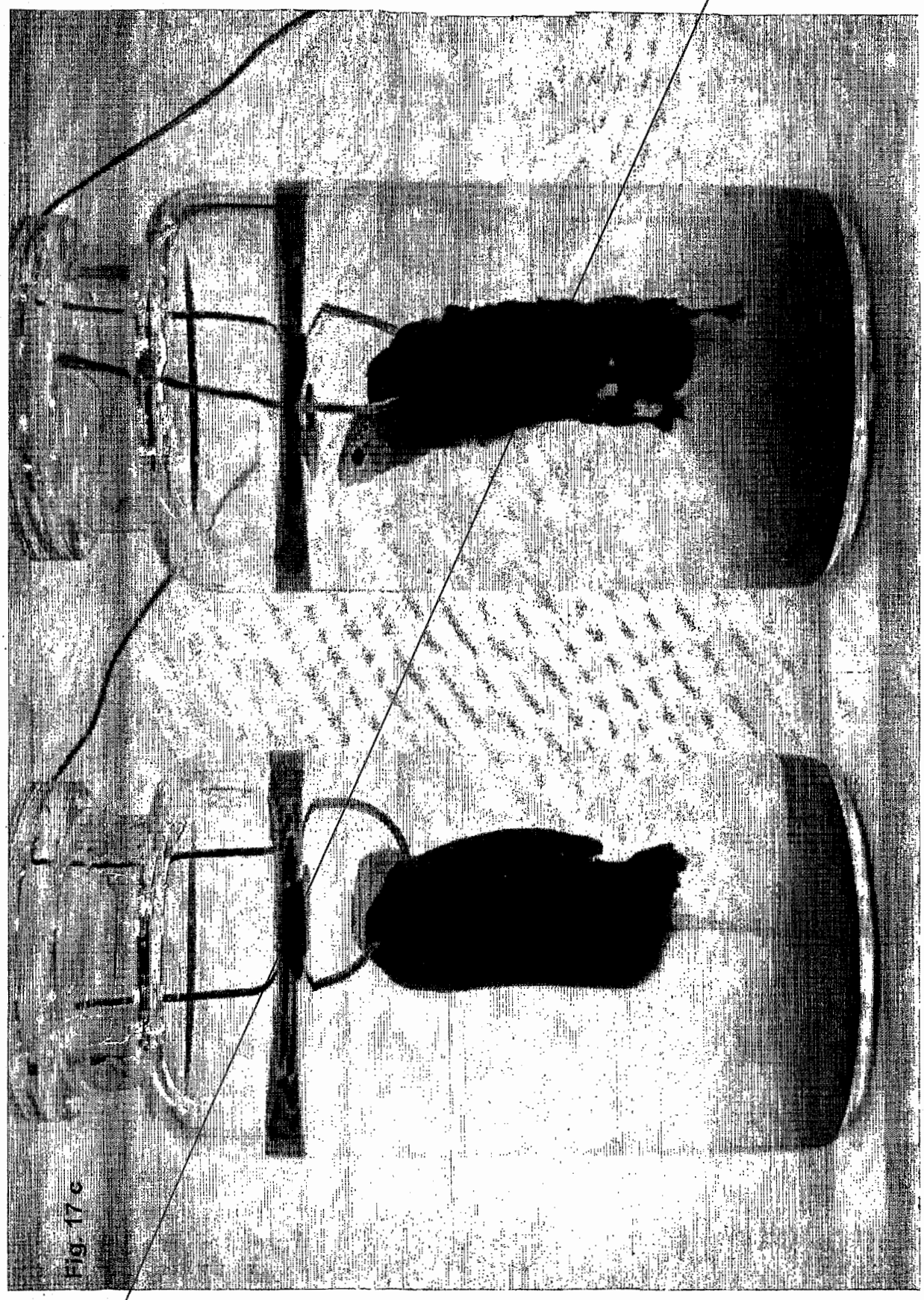


Fig 17c

REPLACEMENT SHEET
25 OCT 2006

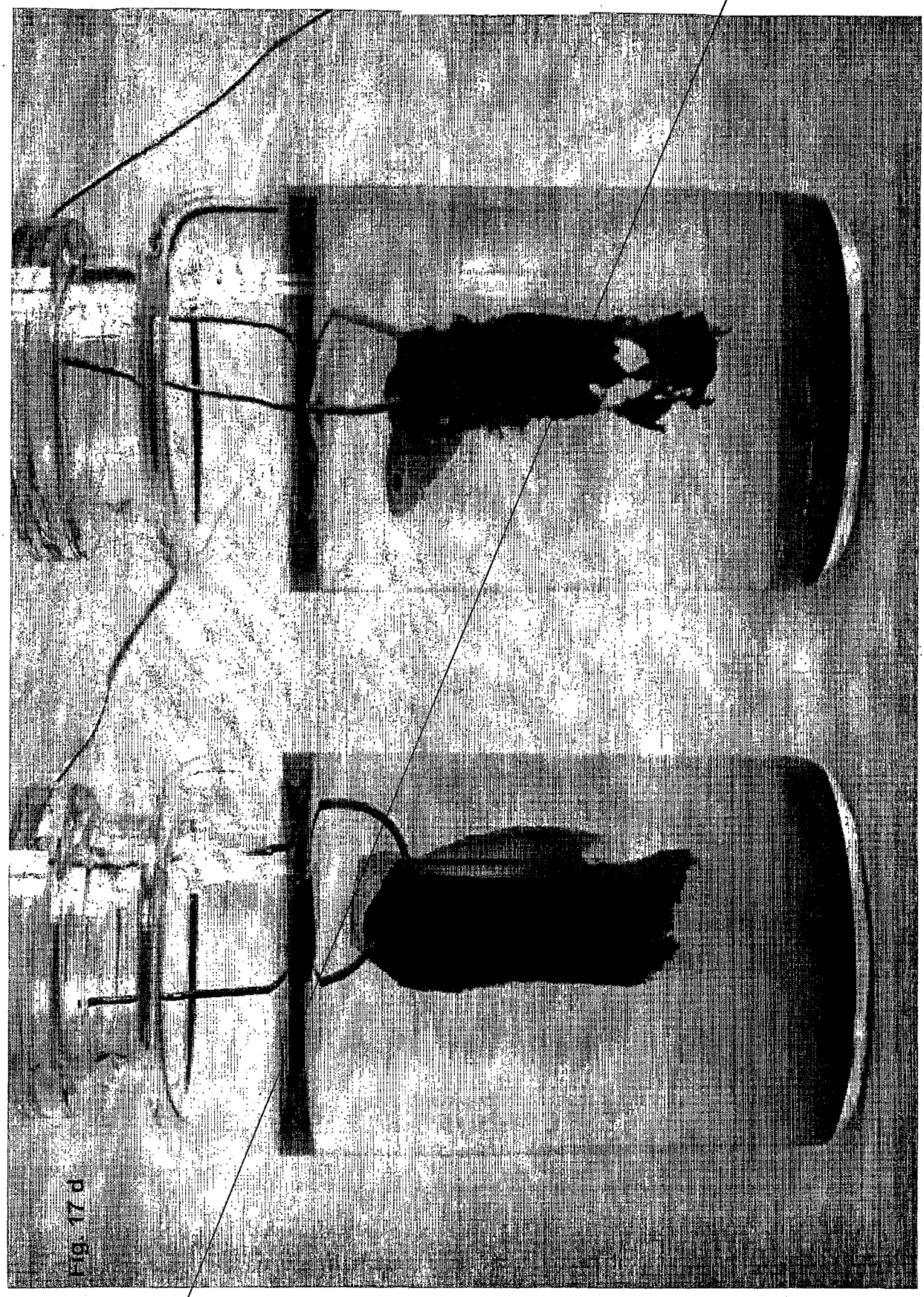


Fig. 17d

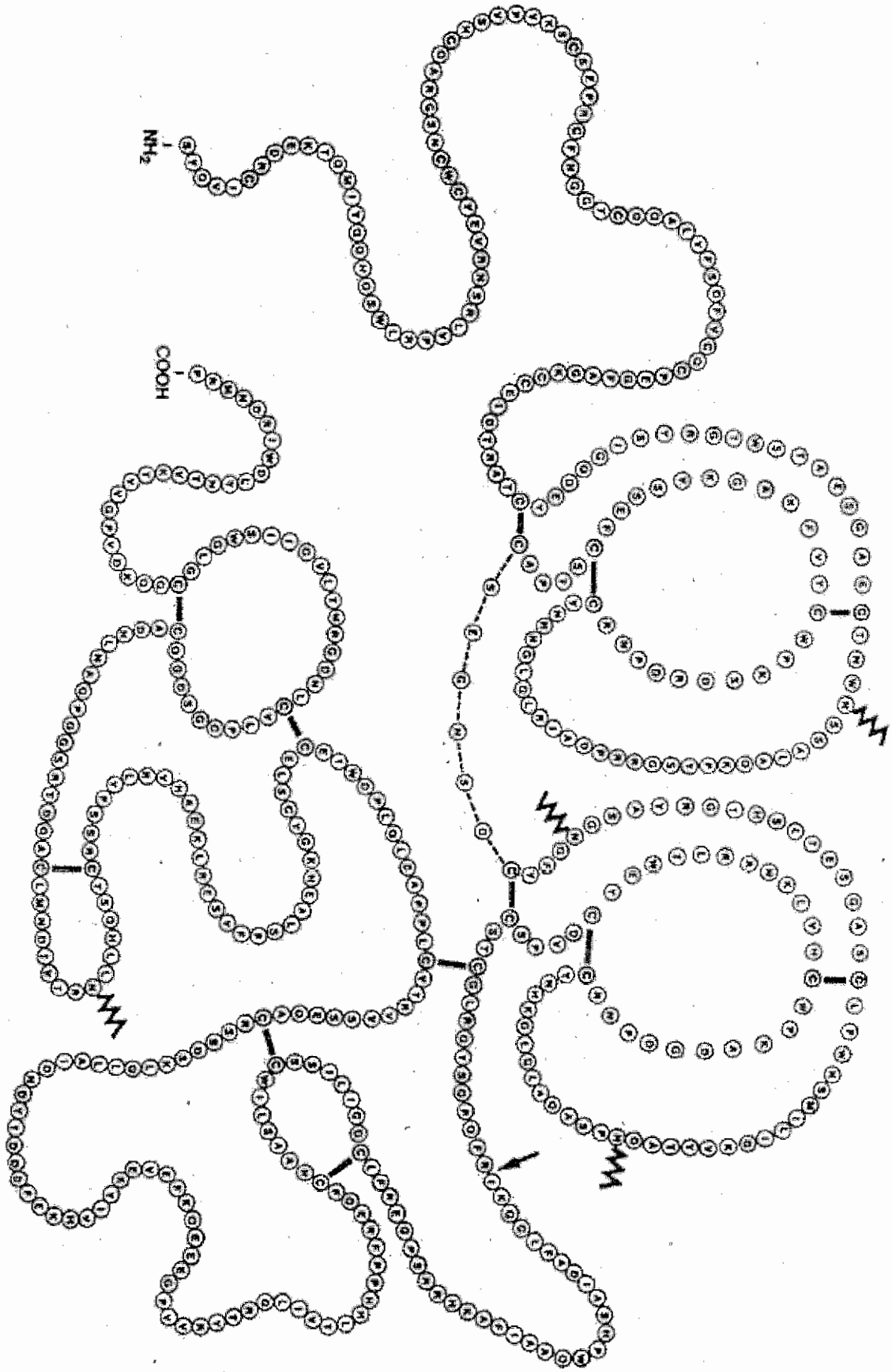


Fig. 1

REPLACEMENT SHEET
25 OCT 2006

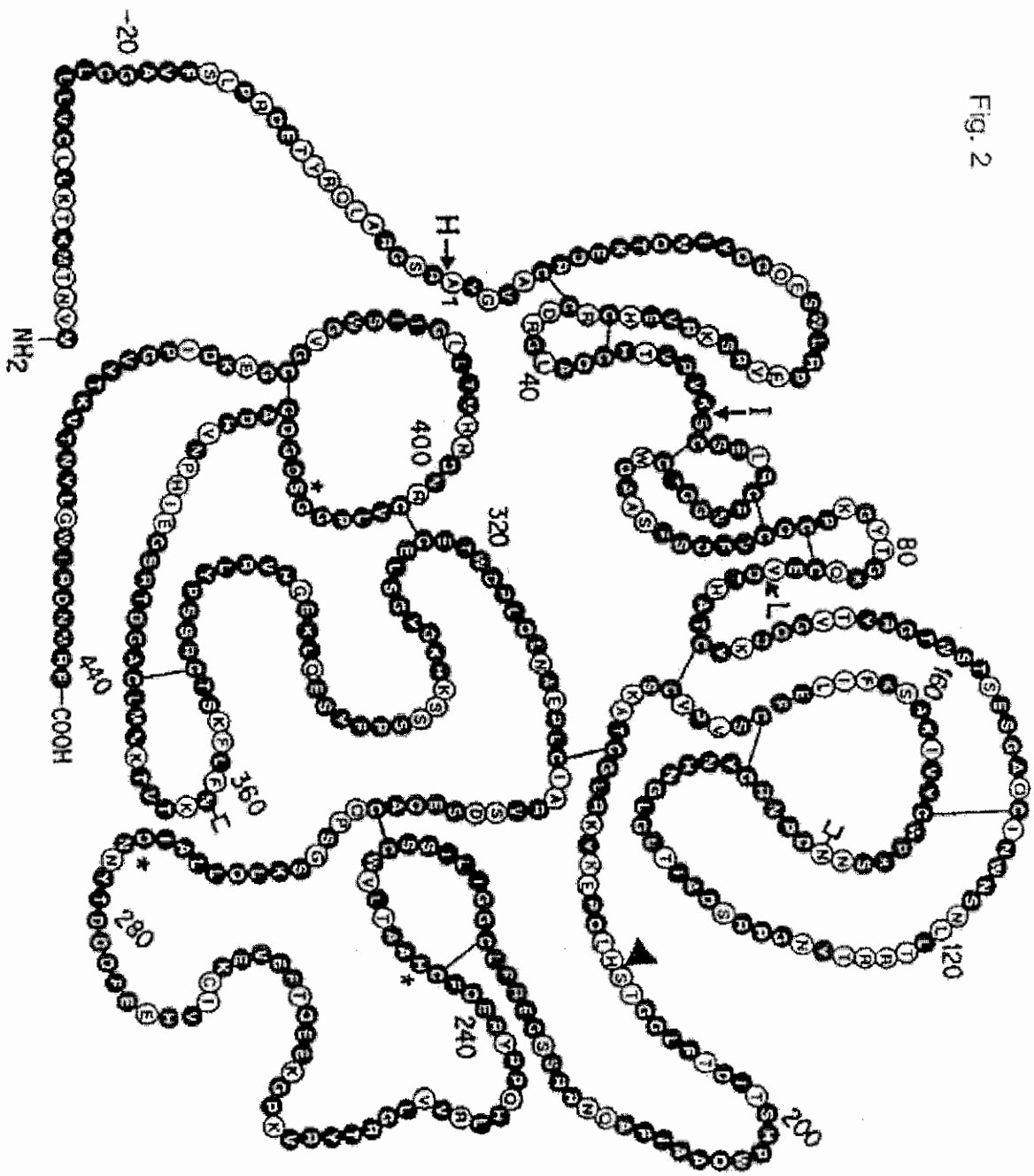


Fig. 2

REPLACEMENT SHEET
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Fig. 2b

[GENETYX-MAC: Multiple Alignment]
Date : 2003.08.23

tPA Isoform 1 vs DSPA alpha 1

```
tPA_AS      1 M-DAMKRGLCCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRP    59
DSPA_AS     1 MVNTMKTKLLCVLLLCGAVFSLPRQETYRQLARGSRAYGVACKDEITQMTYRRQESWLRP    60
              *   **  * **********  * **      ** * * * * * ** *** *    *****

tPA_AS     60 VLRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCC   119
DSPA_AS    61 EVRSKRVEHCQCDRGQARCHTVPVNSCSEPRCFNGGTCWQAVYFSDFVCQCPAGYTGKRC   120
                ** *** * *  * * ** *** ************ ** ********** *  ** *

tPA_AS    120 EIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYC   179
DSPA_AS   121 EVDTRATCYEGQGVTYRGTWSTAESRVECINWNSSLLTRRTYNGRMPDAFNLGLGNHNYC   180
              * ******** **  **********  ** ***** *    * ** ***  *********

tPA_AS    180 RNPDRDSKPWCYVFKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPW   239
DSPA_AS   181 RNPNGAPKPWCYVIKAGKFTSESCSVPVCSK----------------------------   204
              ***    ****** ****

tPA_AS    240 NSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTC   299
DSPA_AS   205 ------------------------------------------------------ATC   214
                                                                     **

tPA_AS    300 GLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCF   359
DSPA_AS   215 GLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCF   274
              *** *  **    **** ** **********  *** *************** * *****

tPA_AS    360 QERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRC   419
DSPA_AS   275 QESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNDIALLQLKSDSPQC   334
              **   *  * * ******* ****** * * ************ ************  *

tPA_AS    420 AQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQ   479
DSPA_AS   335 AQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPK   394
              ****  **  *** * ****************   ****** *** **********

tPA_AS    480 HLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQ   539
DSPA_AS   395 FLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGE   454
               * * *** ***********    * ************** **  *** ****** ***

tPA_AS    540 KDVPGVYTKVTNYLDWIRDNMRP                                       562
DSPA_AS   455 KDVPGVYTKVTNYLGWIRDNMHL                                       477
              ************** ******
```

Kringel 2

tPA Activation Site

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25 OCT 2006

Fig. 3

Humanised DSPA

Sequence is based on tPA Isoform 1 with
a) Deletion of Kringel 2
b) tPA activation site mutated to corresponding DSPA sequence

```
  1 mdamkrglcc vlllcgavfv spsqeiharf rrgarsyqvi crdektqmiy qqhqswlrpv
 61 lrsnrveycw cnsgraqchs vpvkscsepr cfnggtcqqa lyfsdfvcqc pegfagkcce
121 idtratcyed qgisyrgtws taesgaectn wnssalaqkp ysgrrpdair lglgnhnycr
181 npdrdskpw cyvfkagky ssefcstpa csegnsdst cglrqysqp qfhskgglf
241 adiashpwq aaifakhrr spgerflcg gilisscwi lsaahcfqe rfpphhltv
301 ilgrtyrvv pgeeeqkfe vekyivhke fdddtydnd iallqlksd ssrcaqess
361 vvrtvclpp adlqlpdwt ecelsgygk healspfys erlkeahvr lypssrcts
421 qhllnrtvt dnmlcagdt rsggpqanl hdacqgdsg gplvclndg rmtlvgiis
481 wglgcgqkd vpgvytkvt nyldwirdn mrp
```

Italics: Signal sequence

Kringel 2 Deletion: nsd-Kringel2-stc

mutated tPA Activation Site according to DSPA

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Conversion of OD405 into converted substrate
[Flavigen, µM] = (OD- 0.012)/0.00298
R^2 = 0.9996

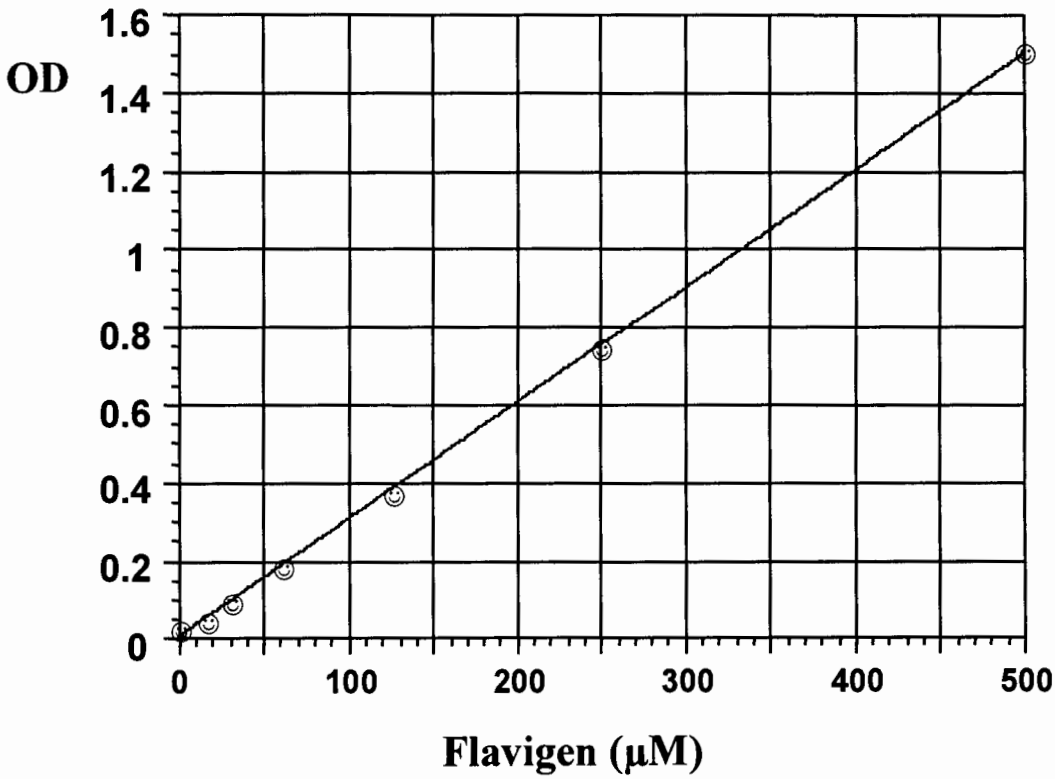


Figure 4a

REPLACEMENT SHEET
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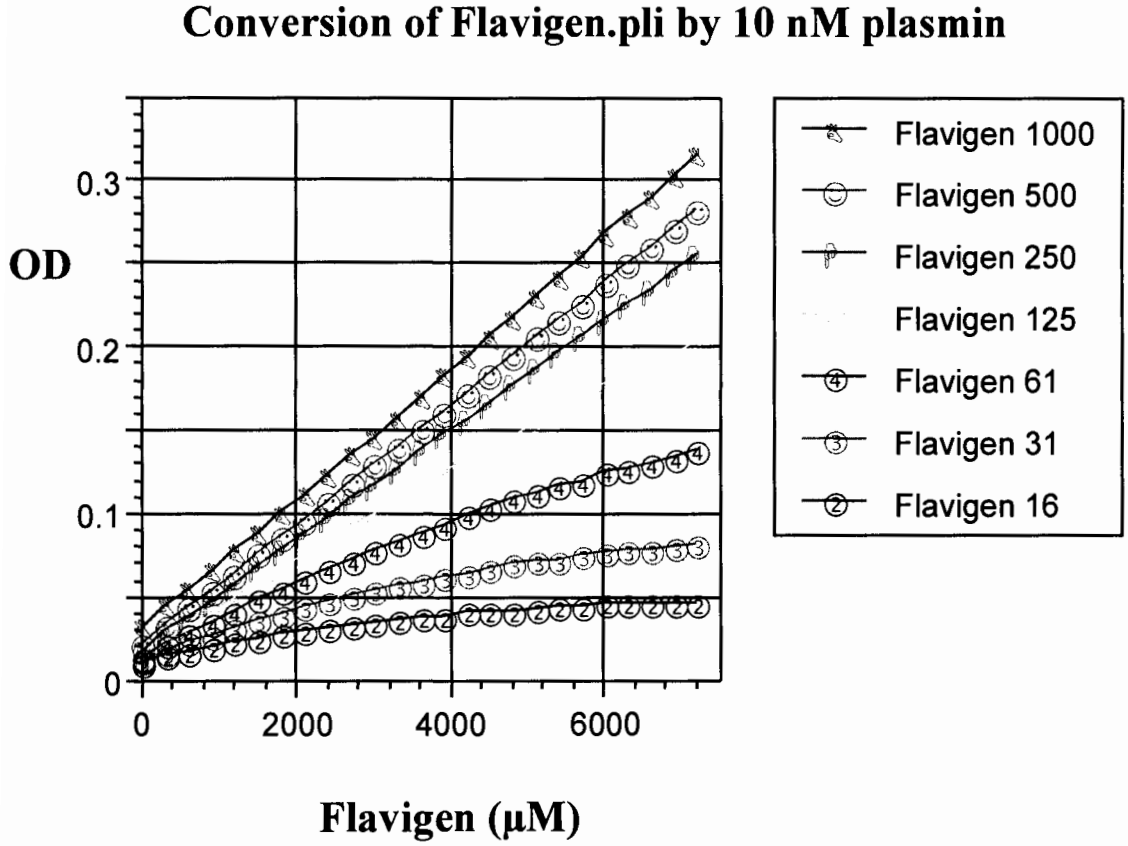


Figure 4b

REPLACEMENT SHEET
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Plot of pNA generation (nM/s) by 10 nM of plasmin as a function of Flavigen.pli concentration kcat = 1.36 s^{-1}; Km = 88.1 µM

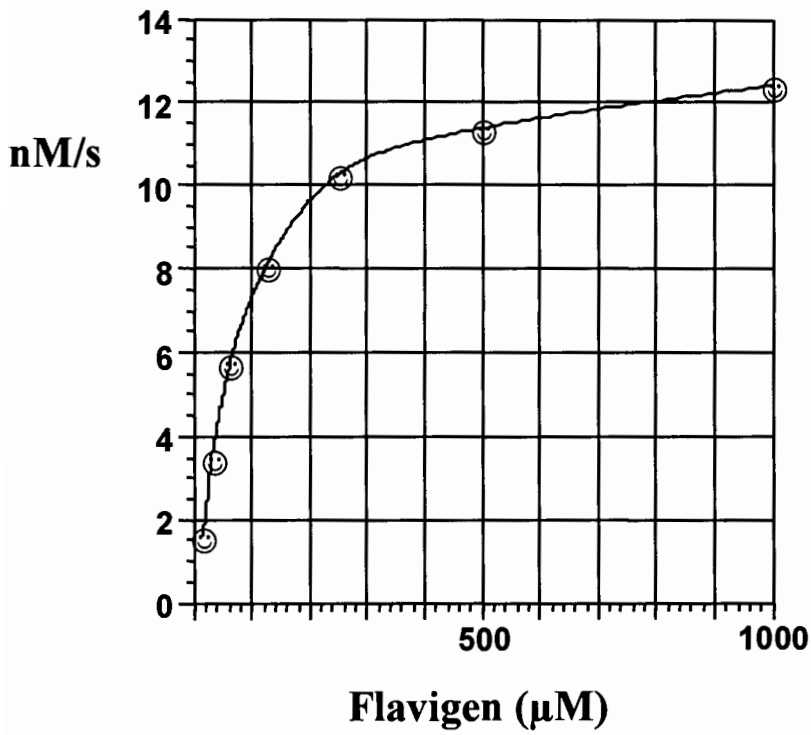
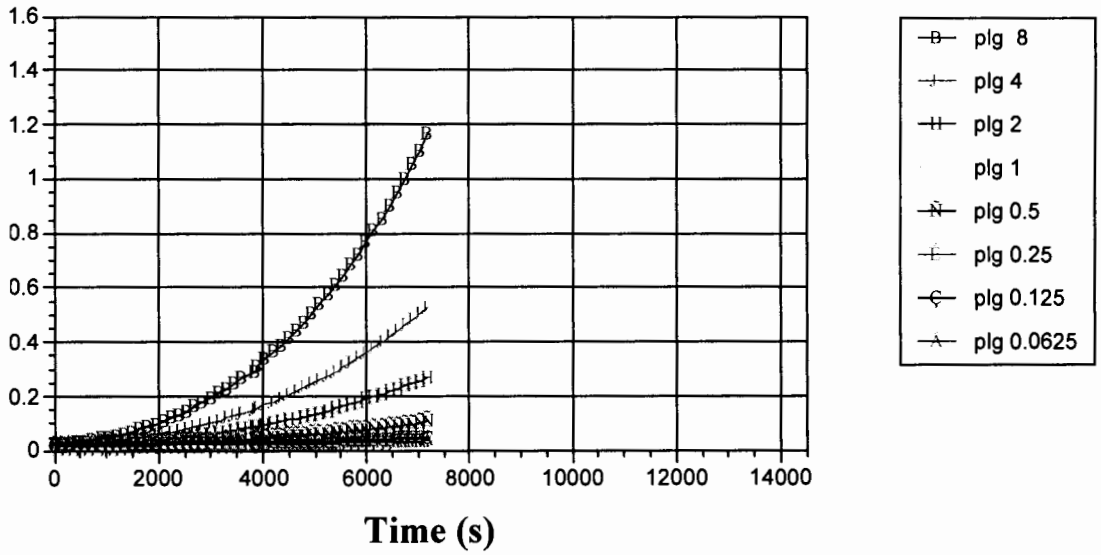


Figure 4c

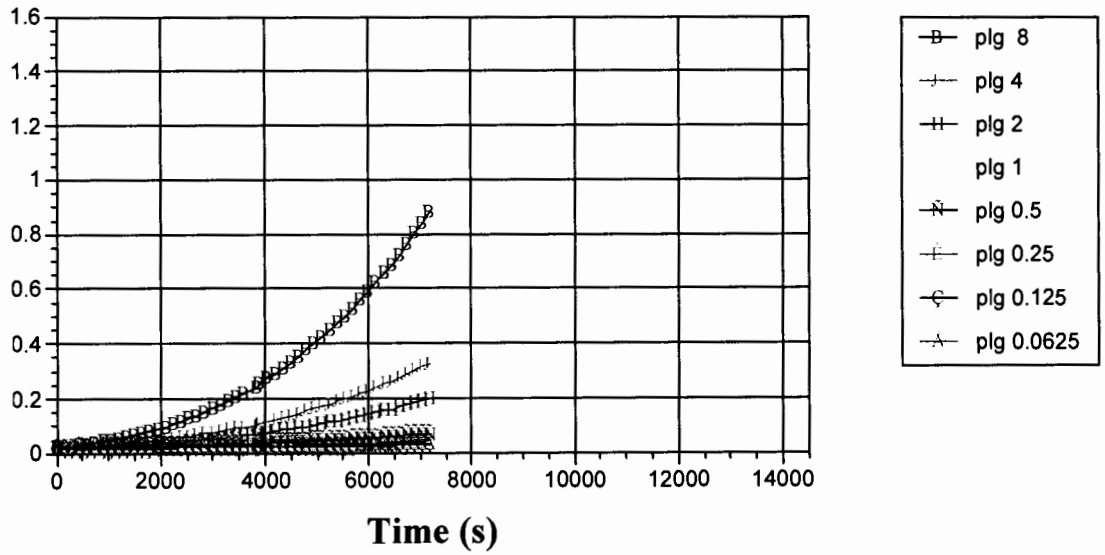
REPLACEMENT SHEET
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t-PA alone no cofactor

exp. 1



exp. 2



exp. 3

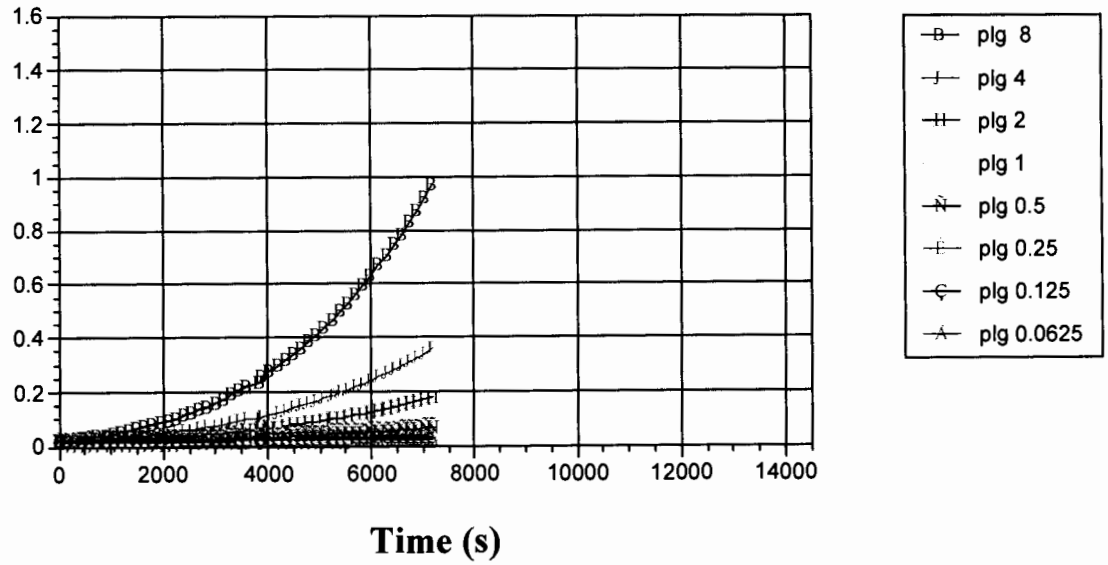
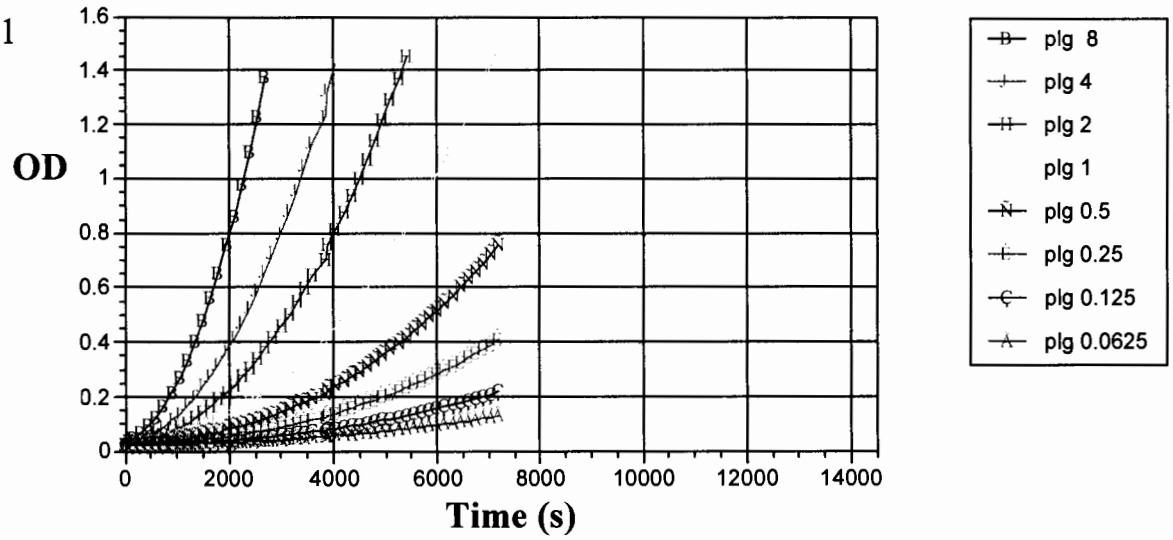


Figure 5a

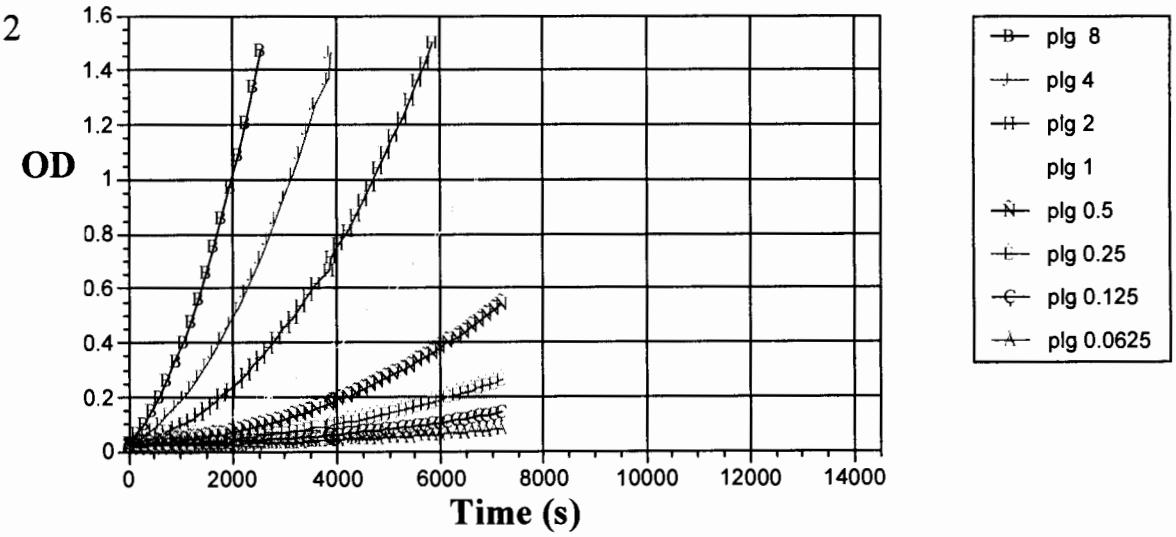
REPLACEMENT SHEET
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t-PA , b-amyloid

exp. 1



exp. 2



exp. 3

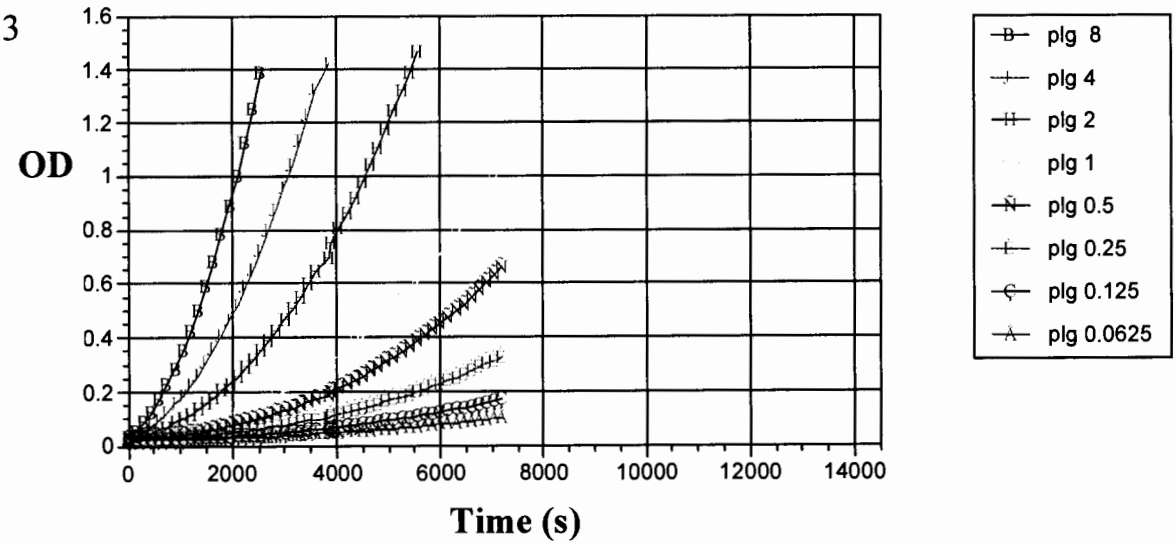
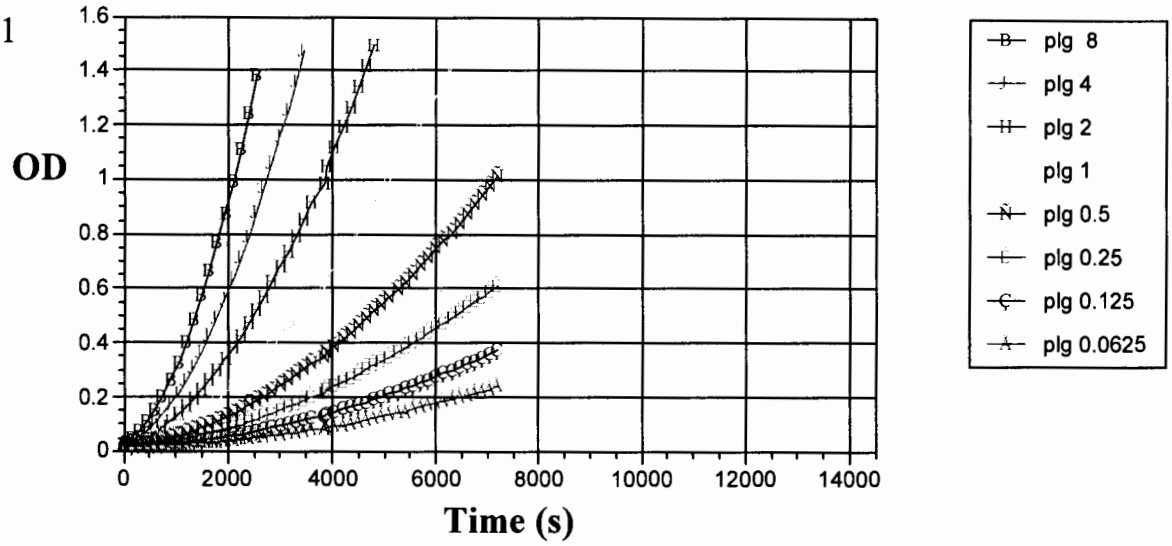


Figure 5b

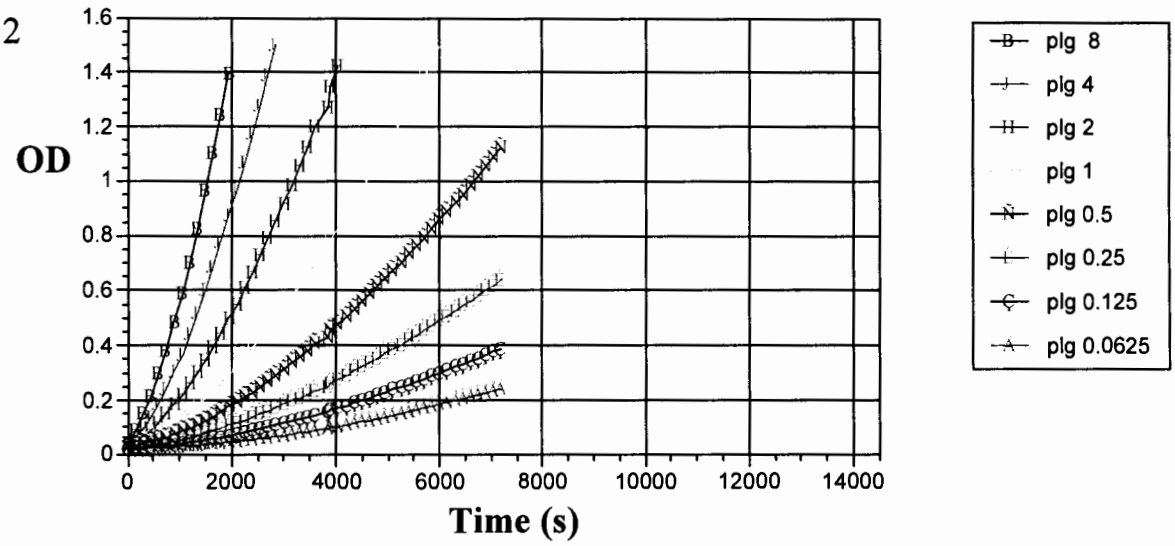
REPLACEMENT SHEET
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t-PA , fibrinogen

exp. 1



exp. 2



exp. 3

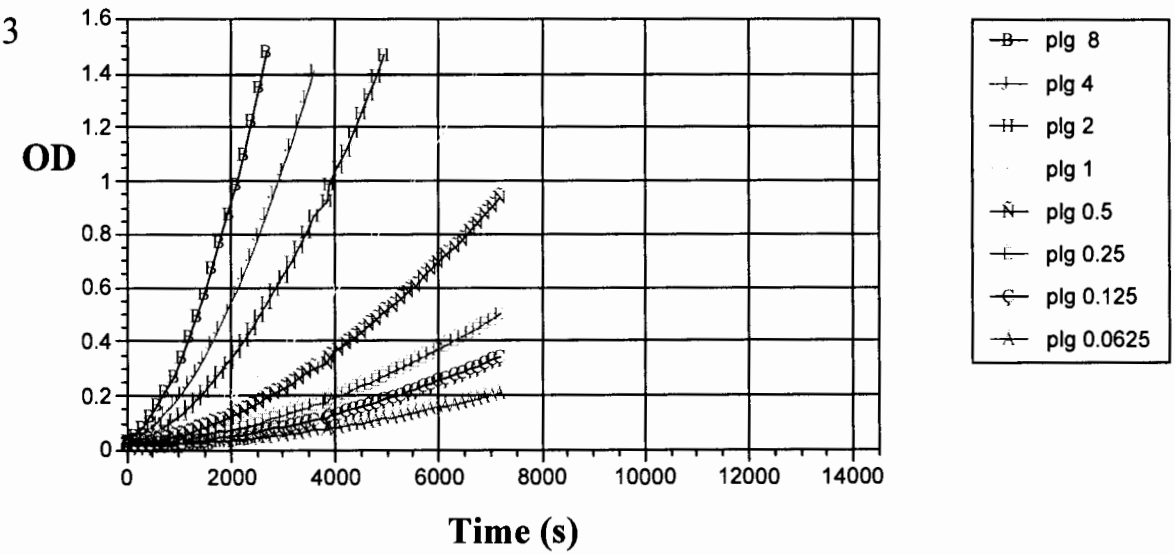
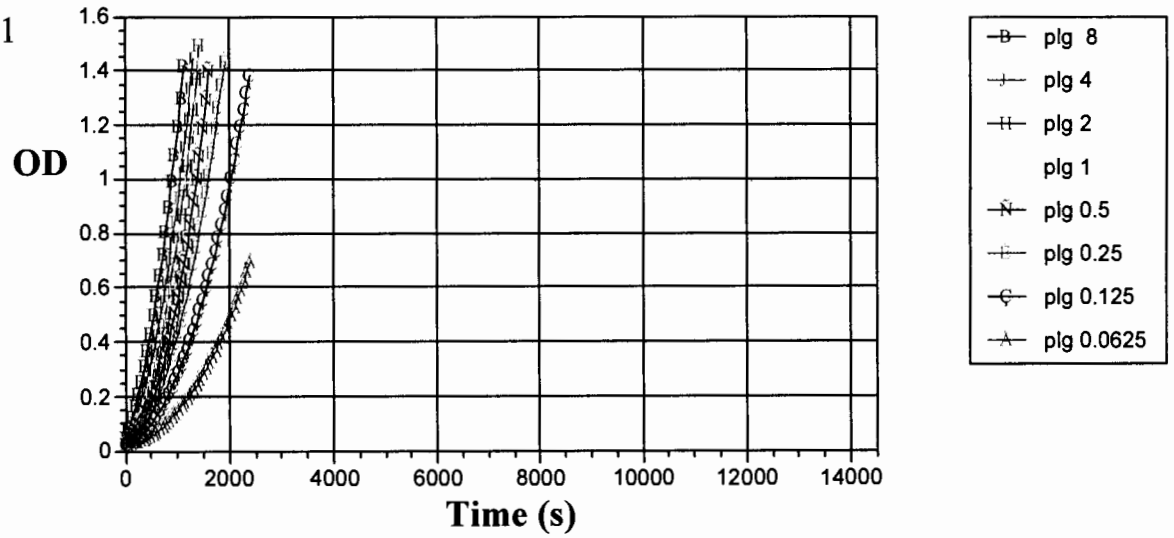


Figure 5c

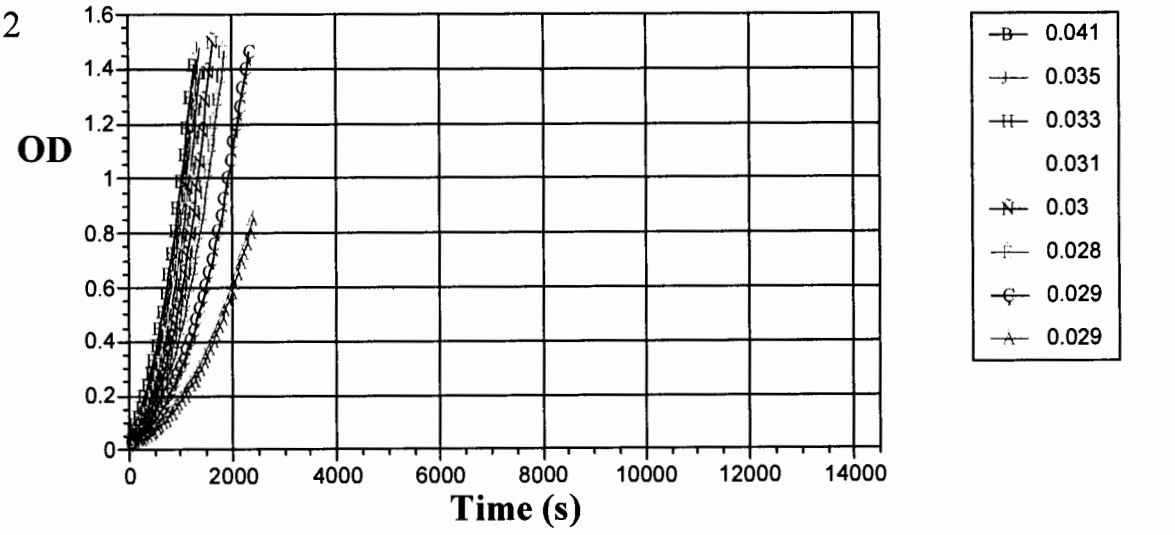
REPLACEMENT SHEET
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t-PA, fibrin

exp. 1



exp. 2



exp. 3

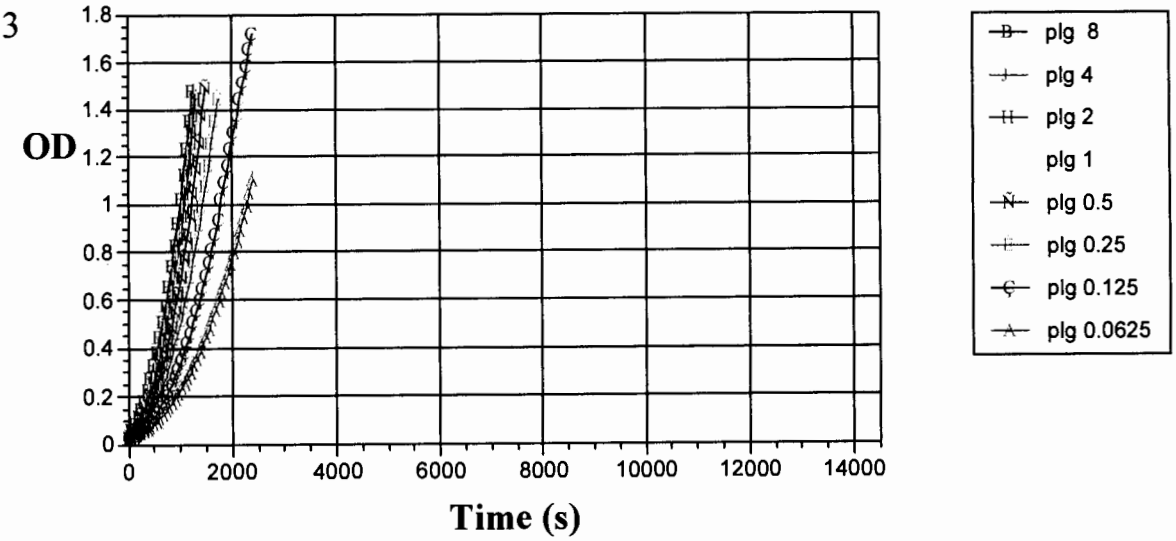
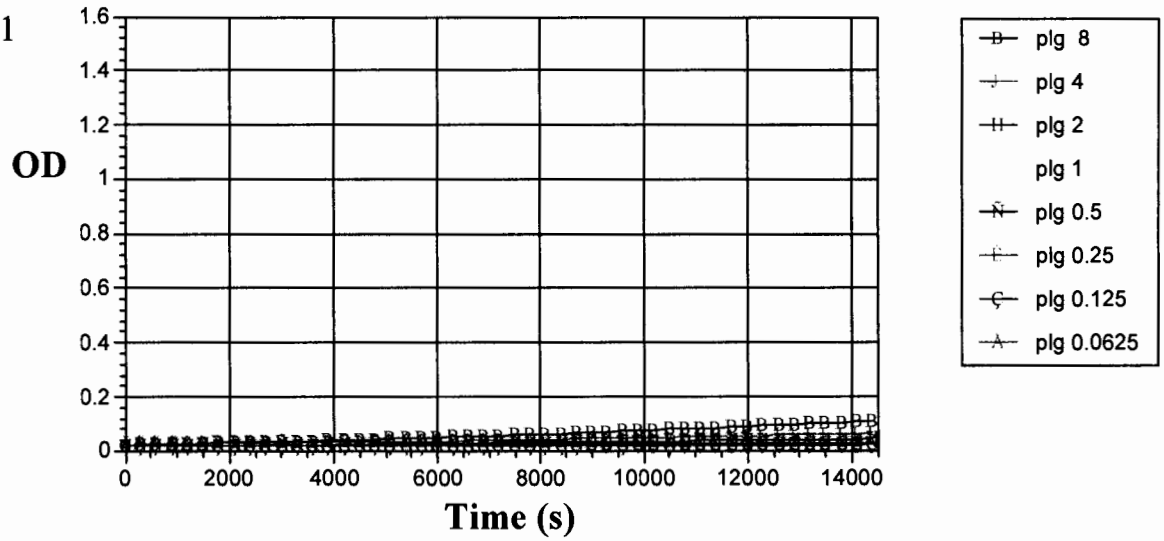


Figure 5d

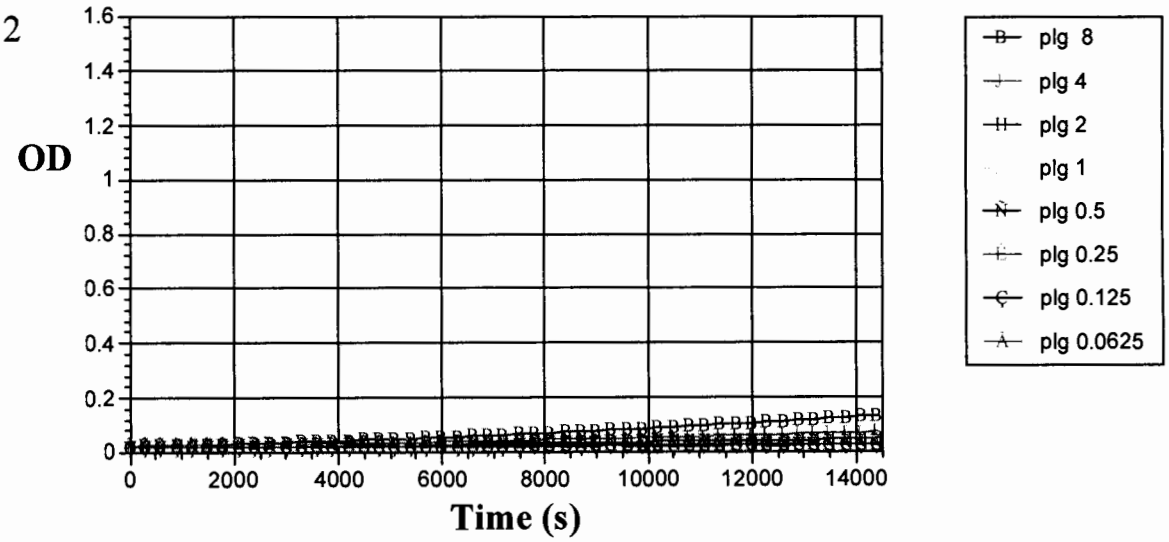
REPLACEMENT SHEET
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DSPA, no cofactor

exp. 1



exp. 2



exp. 3

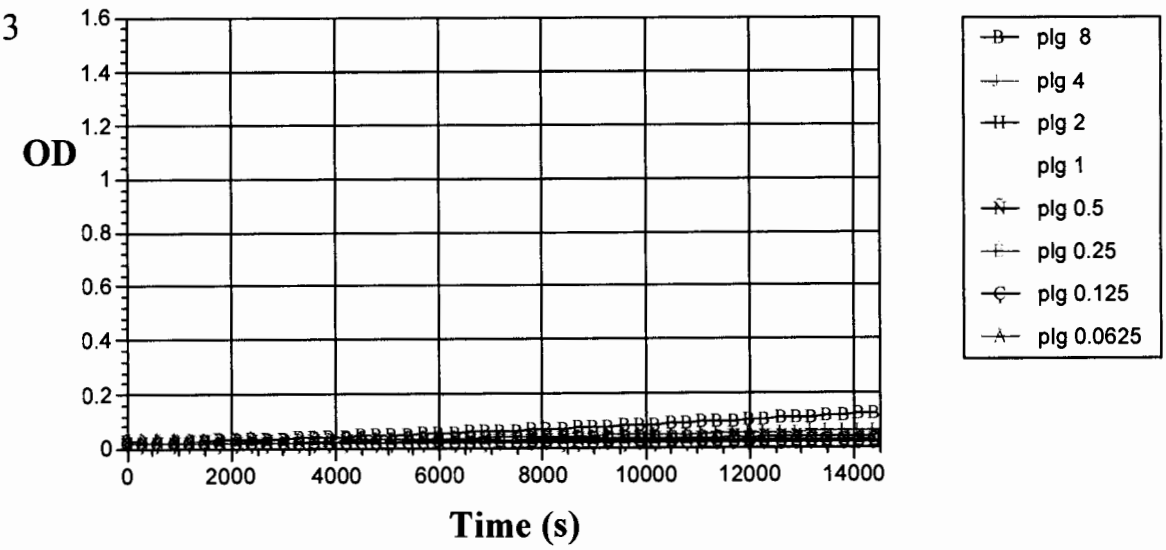
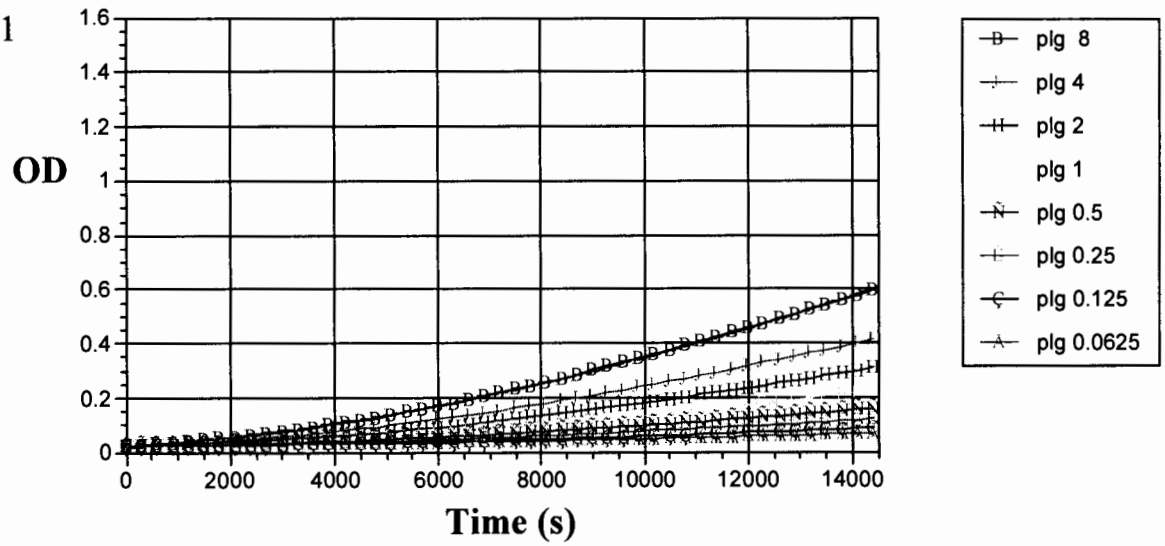


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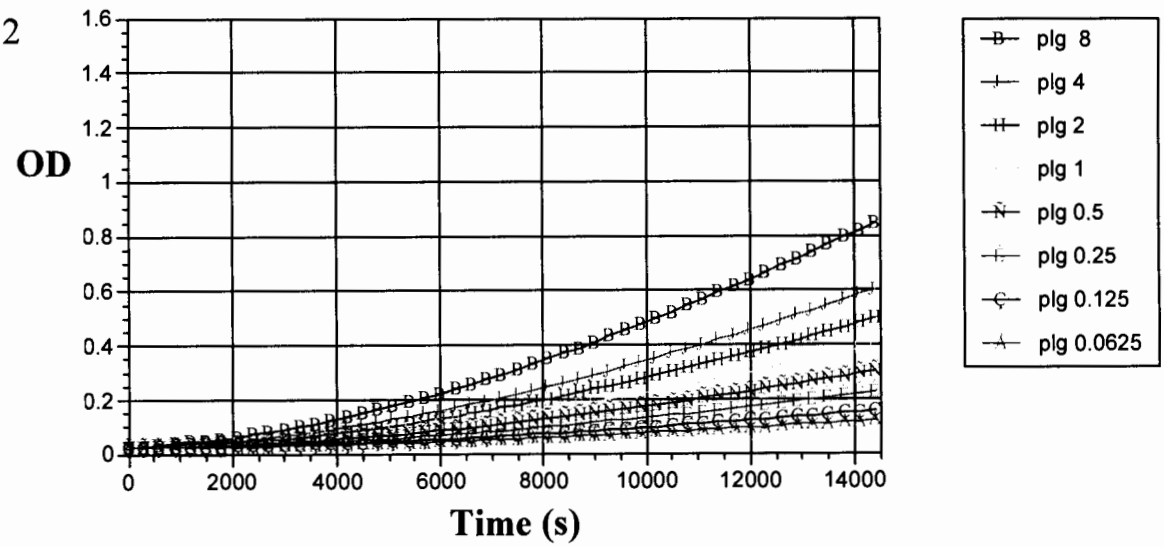
REPLACEMENT SHEET
25 OCT 2006

DSPA, b-amyloid

exp. 1



exp. 2



exp. 3

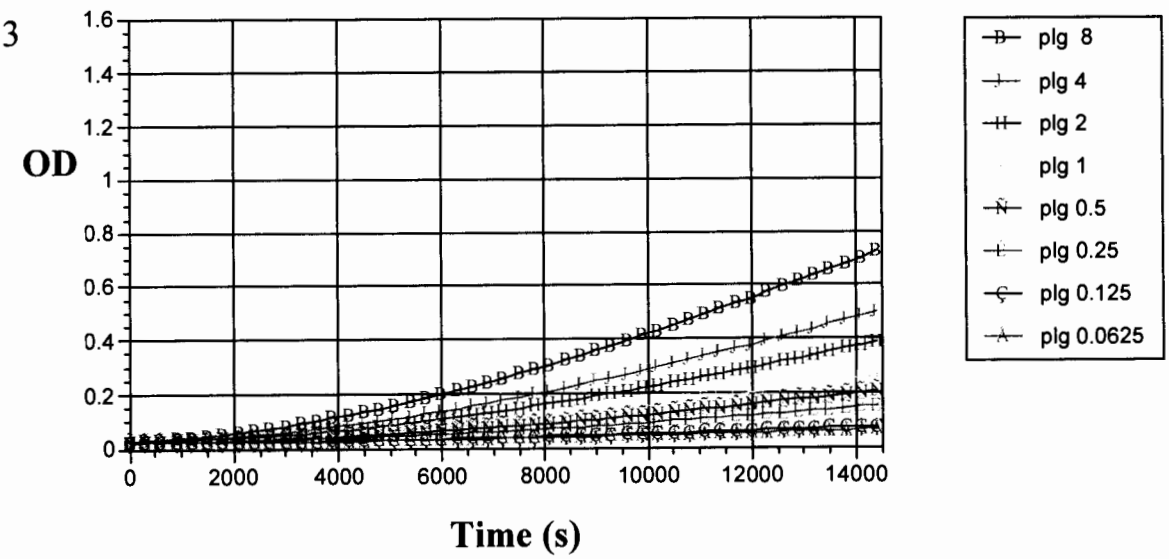
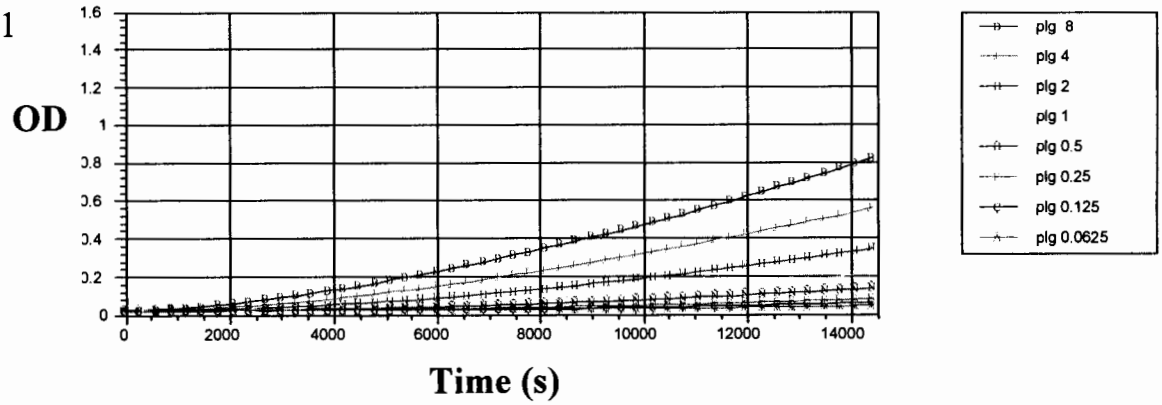


Figure 5f

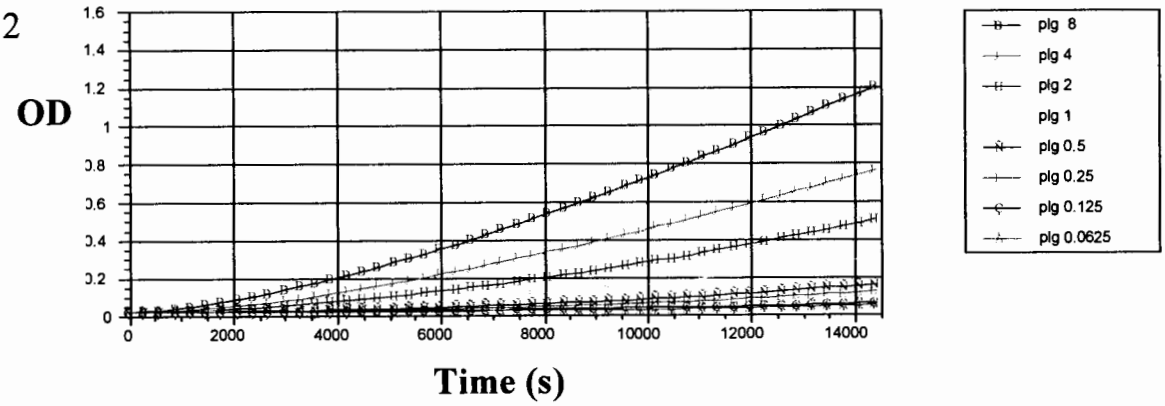
REPLACEMENT SHEET
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DSPA, fibrinogen

exp. 1



exp. 2



exp. 3

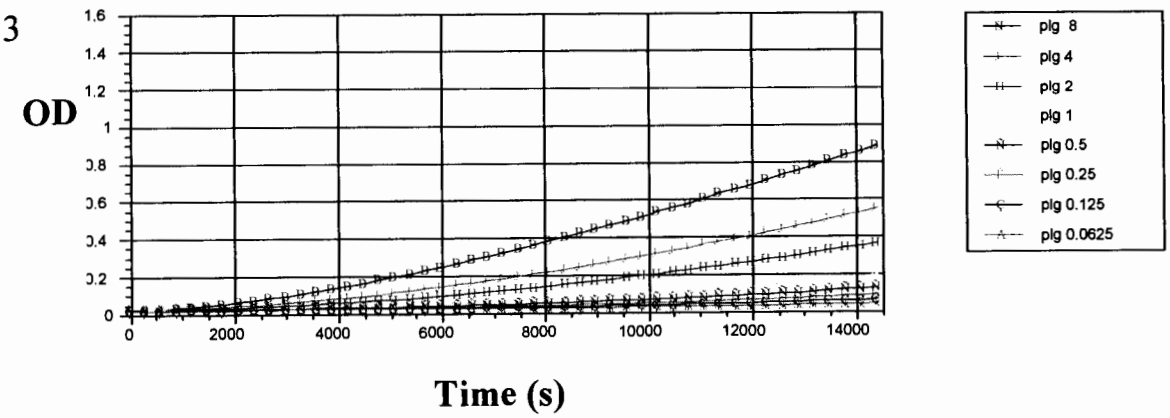
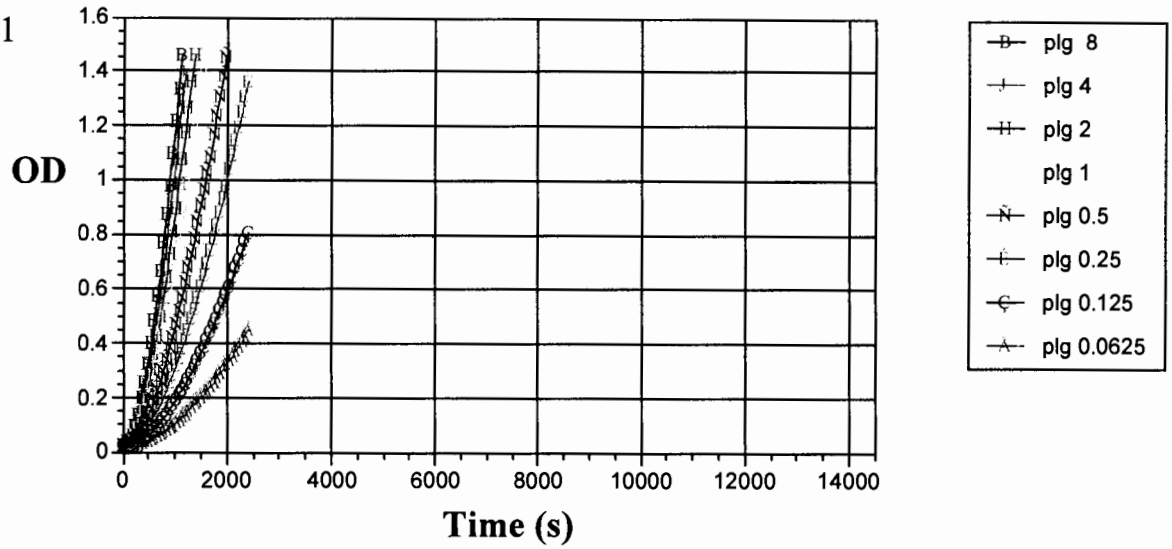


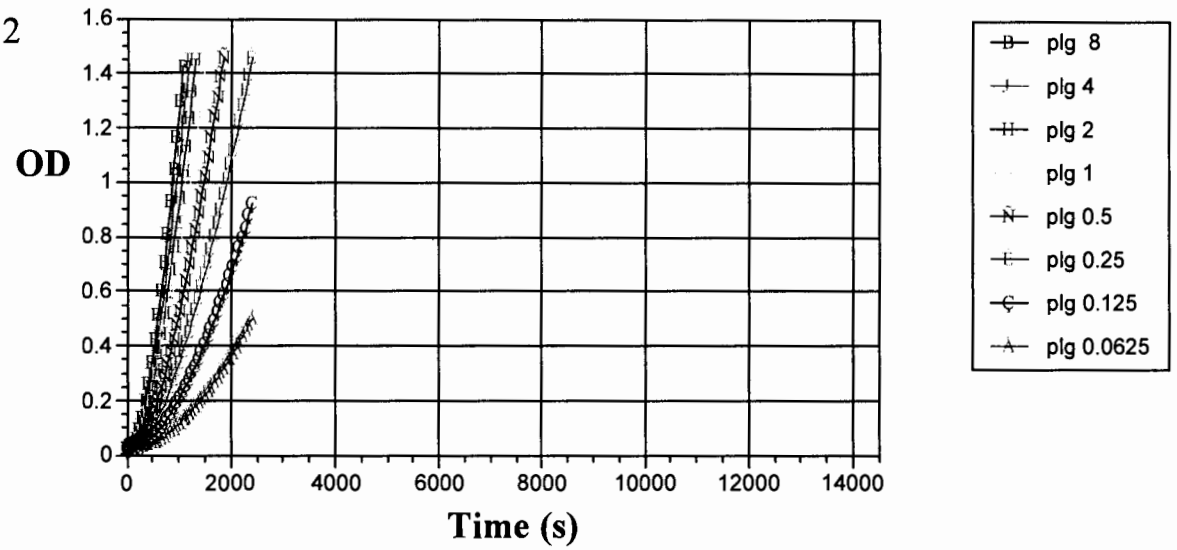
Figure 5g

DSPA , fibrin

exp. 1



exp. 2



exp. 3

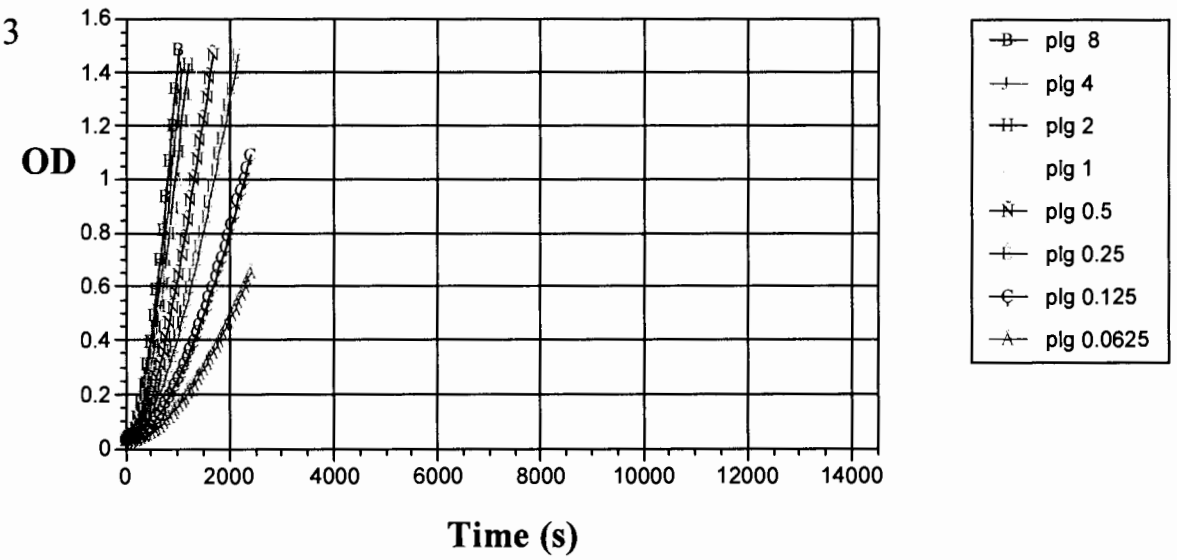
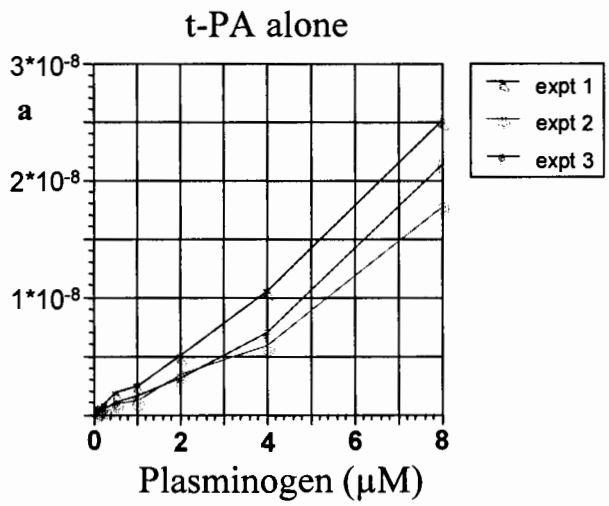
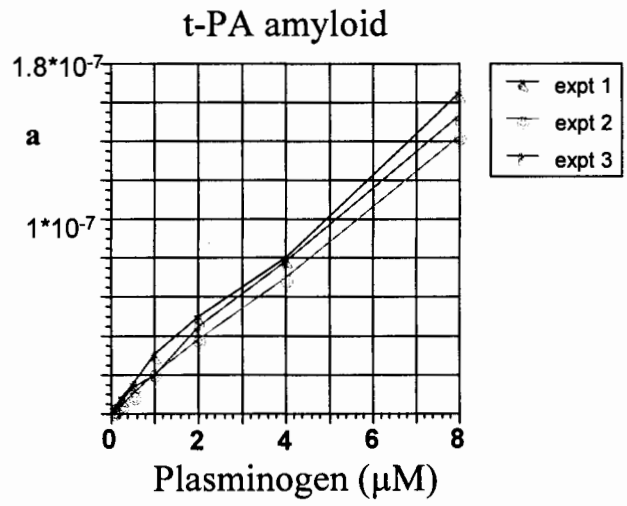


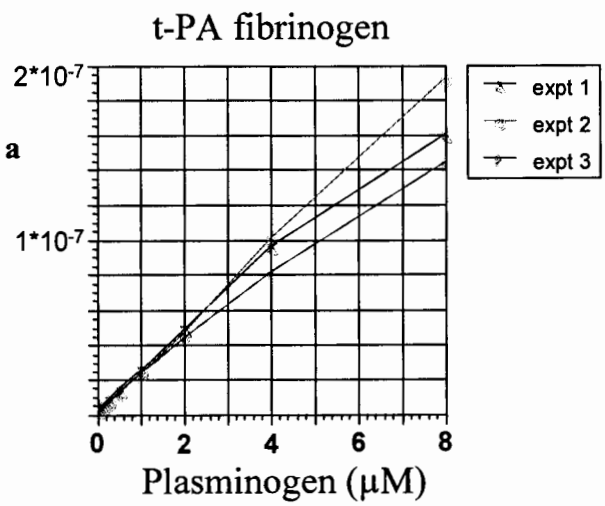
Figure 5h

REPLACEMENT SHEET
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Plots of **a** versus plasminogen concentration
a =ks.kcat.PA.E.P/(Km + P) The values were obtained by parabolic curve fitting to the equation OD (t) = a * t^2+ b * t + c







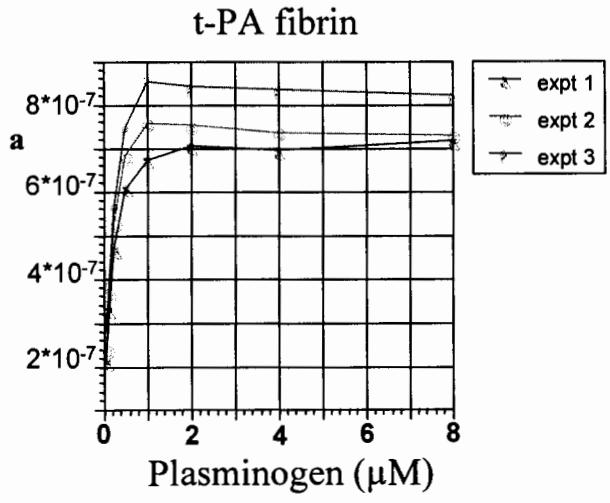
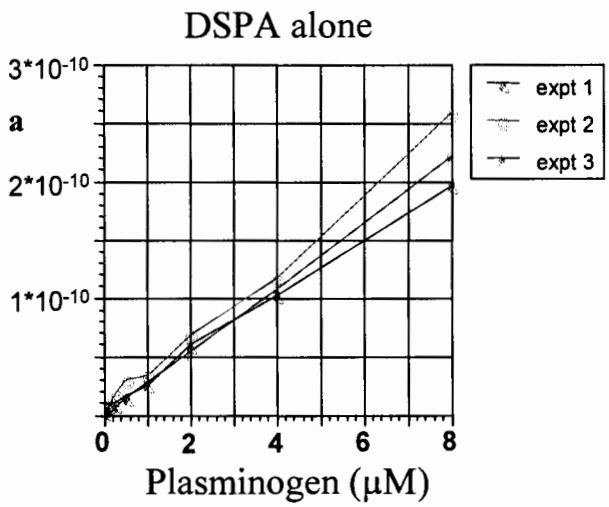
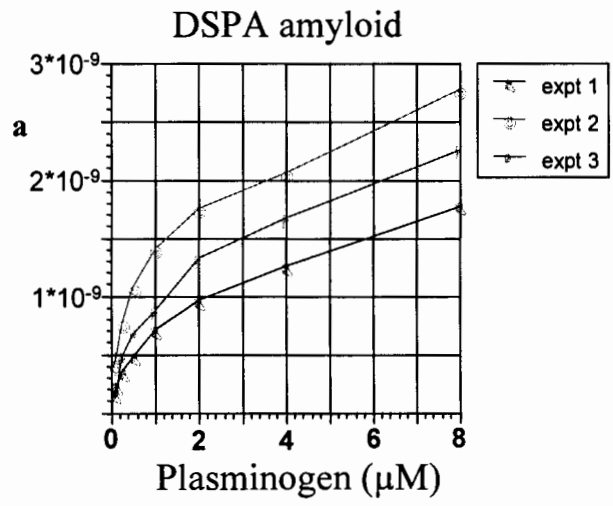


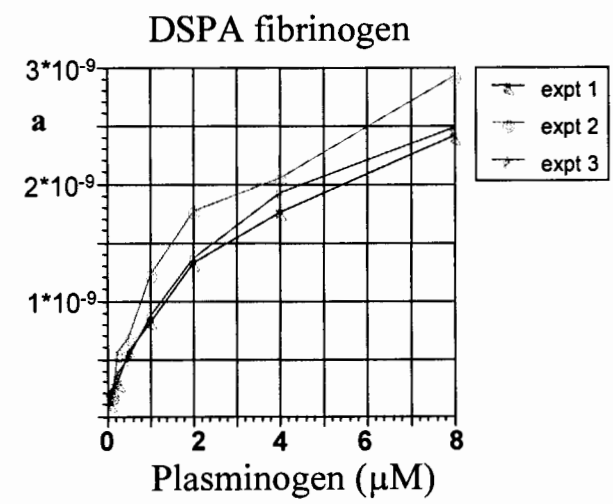
Figure 6a

REPLACEMENT SHEET
25 OCT 2006

Plots of a versus plasminogen concentration
a =ks.kcat.PA.E.P/(Km + P) The values were obtained by parabolic curve fitting to the equation OD (t) = a * t^2+ b * t + c







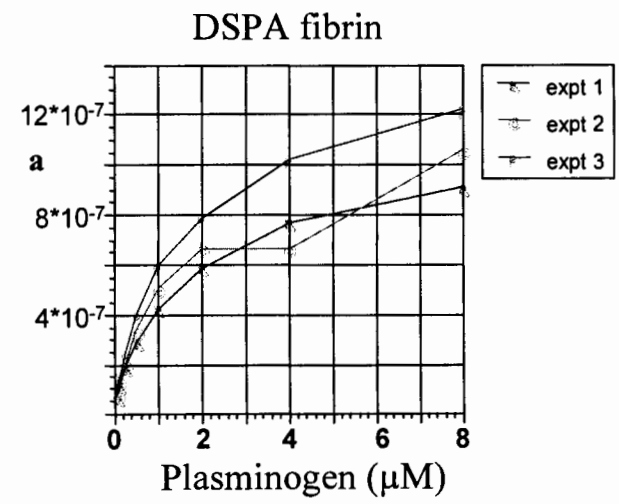
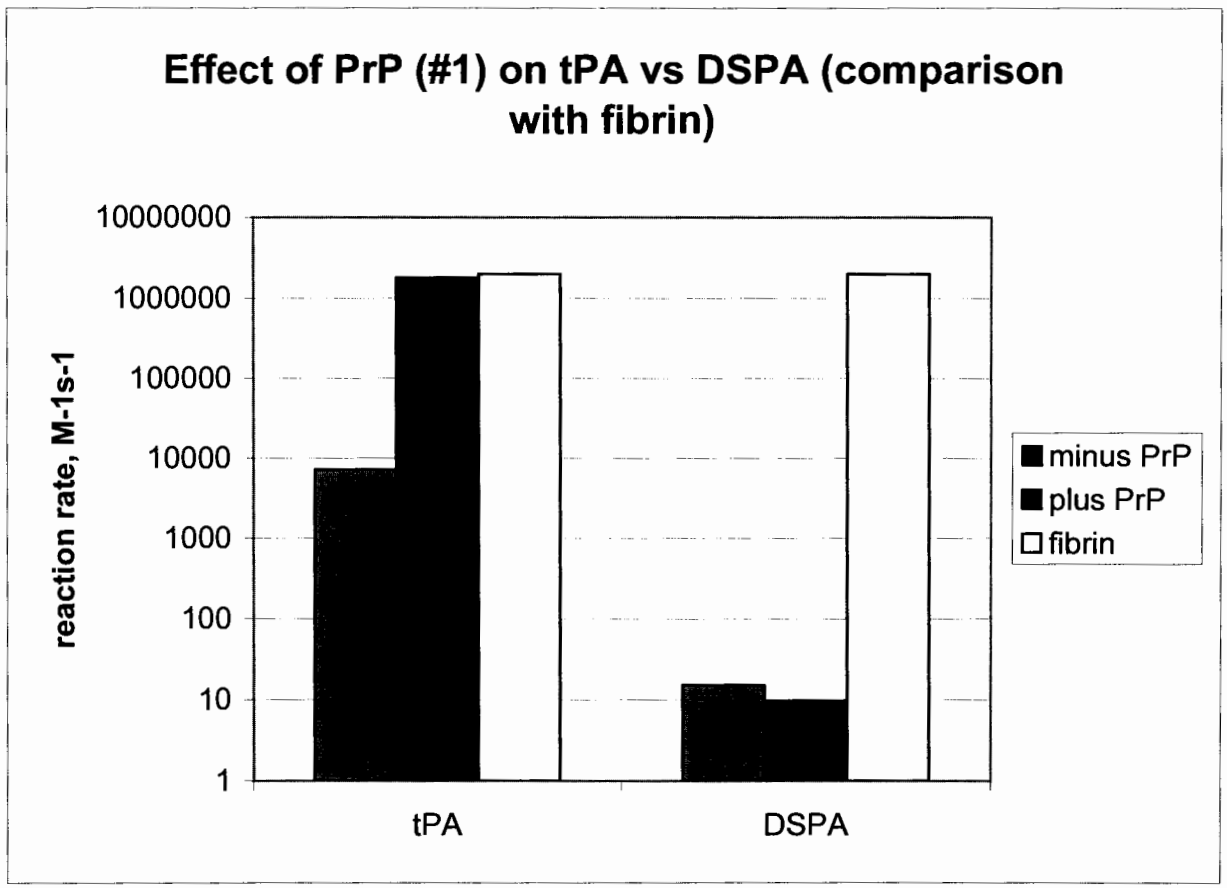


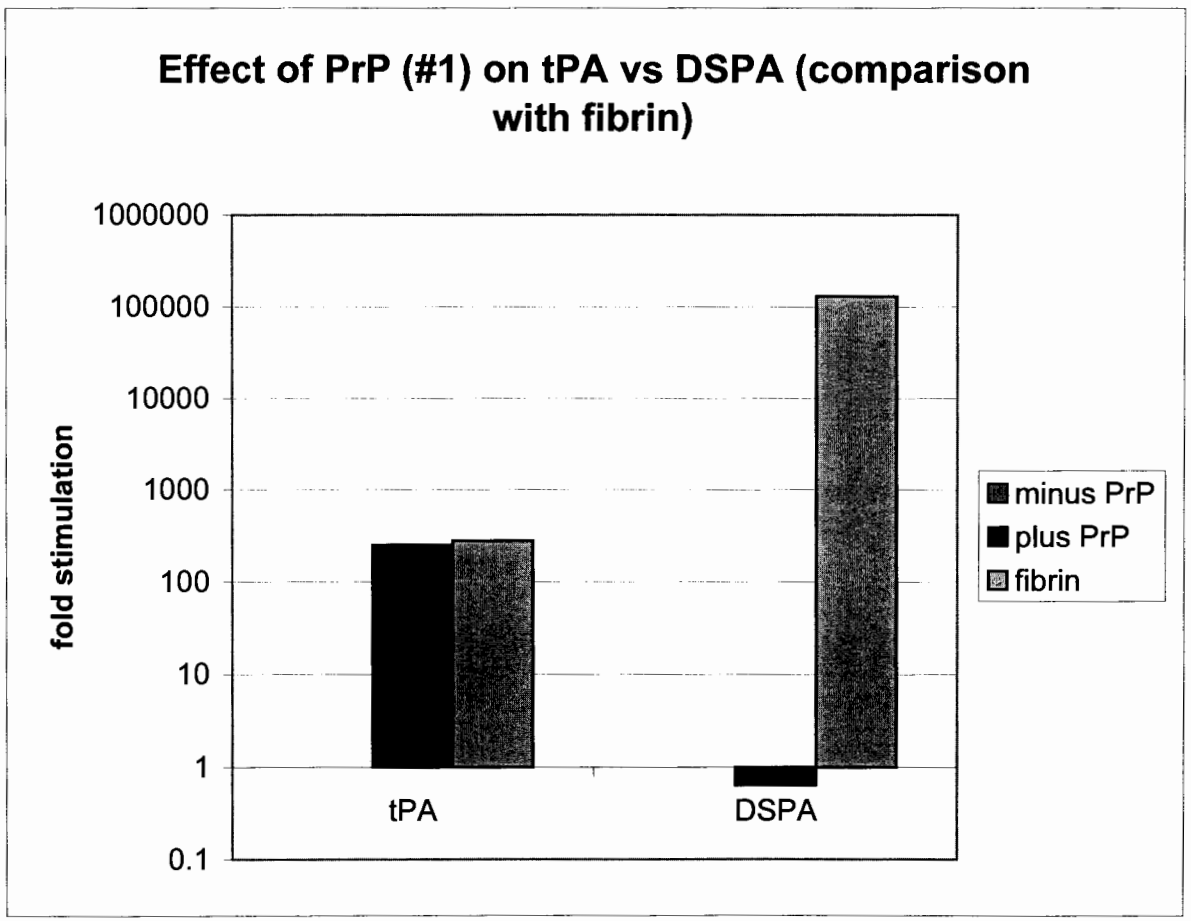
Figure 6b

Fig. 7



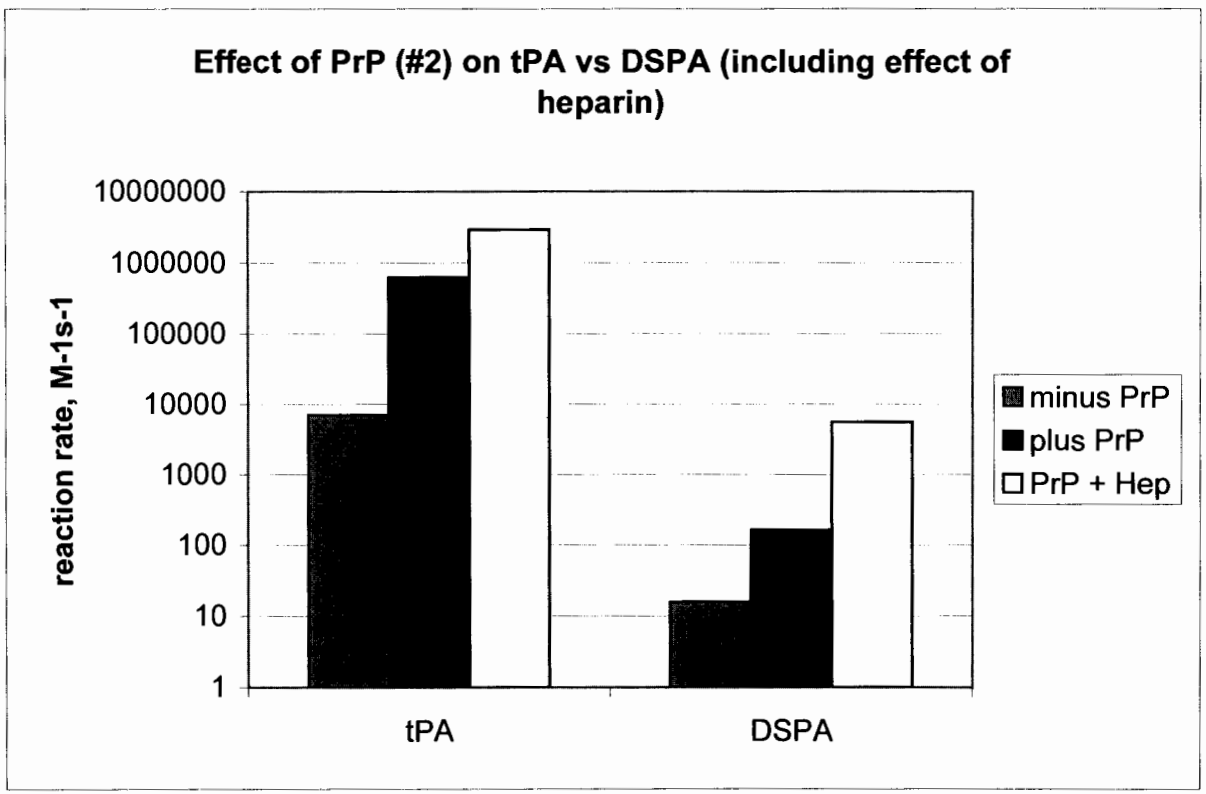
REPLACEMENT SHEET
25 OCT 2006

Fig. 8



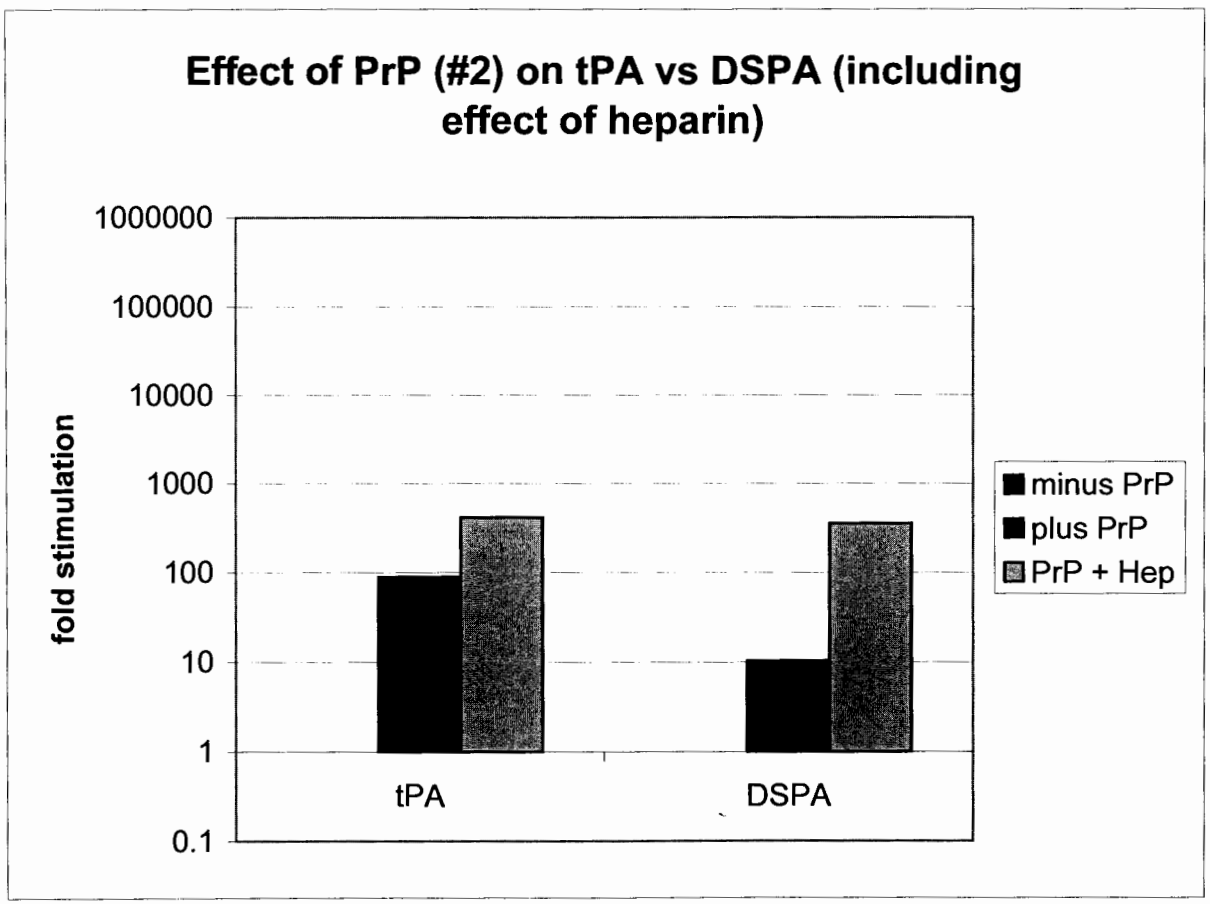
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25 OCT 2006

Fig. 9



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25 OCT 2006

Fig. 10



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Fig. 11

*MDAMKRGLCCVLLLCGAVFVSPS*QEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRPVLRSNRVEYCWCNSGRAQC
HSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCEIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSAL
AQKPYSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYVFKAGKYSSEFCSTPACSKATCGLRQYSQPQLHSTGGLFADIA
SHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEF
DDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRC
TSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLD
WIRDNMRP

Fig. 12

```
tPA       M-DAMKRGLCCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRP 59
Fig. 3    M-DAMKRGLCCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRP 59
Fig. 11   M-DAMKRGLCCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRP 59
DSPA_a1   MVNTMKTKLLCVLLLCGAVFSLPRQETYRQLARGSRAYGVACKDEITQMTYRRQESWLRP 60
          : ::**  * **********  * ** : :: **:*:* * *:** *** *::::*****

tPA       VLRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCC 119
Fig. 3    VLRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCC 119
Fig. 11   VLRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCC 119
DSPA_a1   EVRSKRVEHCQCDRGQARCHTVPVNSCSEPRCFNGGTCWQAVYFSDFVCQCPAGYTGKRC 120
           :**:***:* *: *:*:**:***:************ **:********** *::** *

tPA       EIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYC 179
Fig. 3    EIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYC 179
Fig. 11   EIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYC 179
DSPA_a1   EVDTRATCYEGQGVTYRGTWSTAESRVECINWNSSLLTRRTYNGRMPDAFNLGLGNHNYC 180
          *:********.**::********** .** ***** *:::.*.** ***:.*********

tPA       RNPDRDSKPWCYVFKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPW 239
Fig. 3    RNPDRDSKPWCYVFKAGKYSSEFCSTPACSEGNSD------------------------- 214
Fig. 11   RNPDRDSKPWCYVFKAGKYSSEFCSTPACSK---------------------------- 210
DSPA_a1   RNPNGAPKPWCYVIKAGKFTSESCSVPVCSK---------------------------- 211
          ***:  .******:****::** **.*.**:

tPA       NSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCSTC 299
Fig. 3    ----------------------------------------------------------STC 217
Fig. 11   ----------------------------------------------------------ATC 213
DSPA_a1   ----------------------------------------------------------ATC 214
                                                                      :**

tPA       GLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCF 359
Fig. 3    GLRQYSQPQFHSKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCF 277
Fig. 11   GLRQYSQPQLHSTGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCF 273
DSPA_a1   GLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCF 274
          ***:*.:**:: .****:**:**********::***.***************:*:*****

tPA       QERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRC 419
Fig. 3    QERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRC 337
Fig. 11   QERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRC 333
DSPA_a1   QESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNDIALLQLKSDSPQC 334
          ** : *.:*.*:******* ******.*:*:************:************.:*

tPA       AQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQ 479
Fig. 3    AQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQ 397
Fig. 11   AQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQ 393
DSPA_a1   AQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPK 394
          ****. **::*** *:****************:: ******:***.**********:.:

tPA       HLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQ 539
Fig. 3    HLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQ 457
Fig. 11   HLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQ 453
DSPA_a1   FLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGE 454
          .*:*:***:***********   .*:**************:**.:***:******:***:

tPA       KDVPGVYTKVTNYLDWIRDNMRP 562
Fig. 3    KDVPGVYTKVTNYLDWIRDNMRP 480
Fig. 11   KDVPGVYTKVTNYLDWIRDNMRP 476
DSPA_a1   KDVPGVYTKVTNYLGWIRDNMHL 477
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REPLACEMENT SHEET
25 OCT 2006

Fig. 13

MDAMKRGLCCVLLLCGAVFSLPSQETHRQLARGSRAYQVACRDEITQMIYQQHQSWLRPVLRSKRVEHCQCNRGQARC
HSVPVKSCSEPRCFNGGTCWQALYFSDFVCQCPEGYTGKCCEIDTRATCYEGQGISYRGTWSTAESRVECTNWNSSLL
TRRTYNGRMPDAFNLGLGNHNYCRNPNGAPKPWCYVIKAGKFSSESCSVPACSKATCGLRKYKEPQLHSTGGLFTDIA
SHPWQAAIFAQHRRSSGERFLCGGILISSCWILSAAHCFQESYLPDQLKVVLGRTYRVVPGEEEQTFKVKKYIVHKEF
DDDTYDNDIALLQLKSDSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHESSSPFYSEQLKEGHVRLYPSSRC
APKFLFNRTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLVGIISWGVGCGQKDVPGVYTKVTNYLG
WIRDNMHL

FIG 14

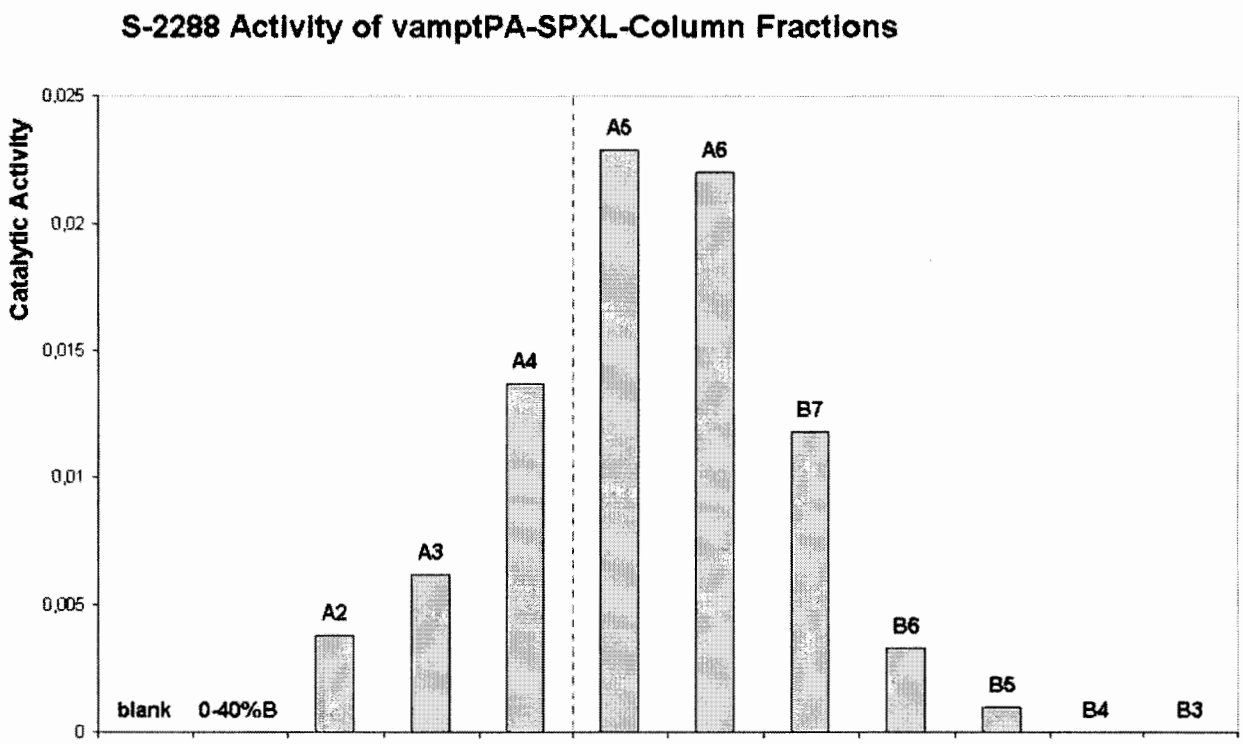

S-2288 Activity of vamptPA-SPXL-Column Fractions
Catalytic Activity
0,025
0,02
0,015
0,01
0,005
0
blank
0-40%B
A2
A3
A4
A5
A6
B7
B6
B5
B4
B3

FIG 15 a

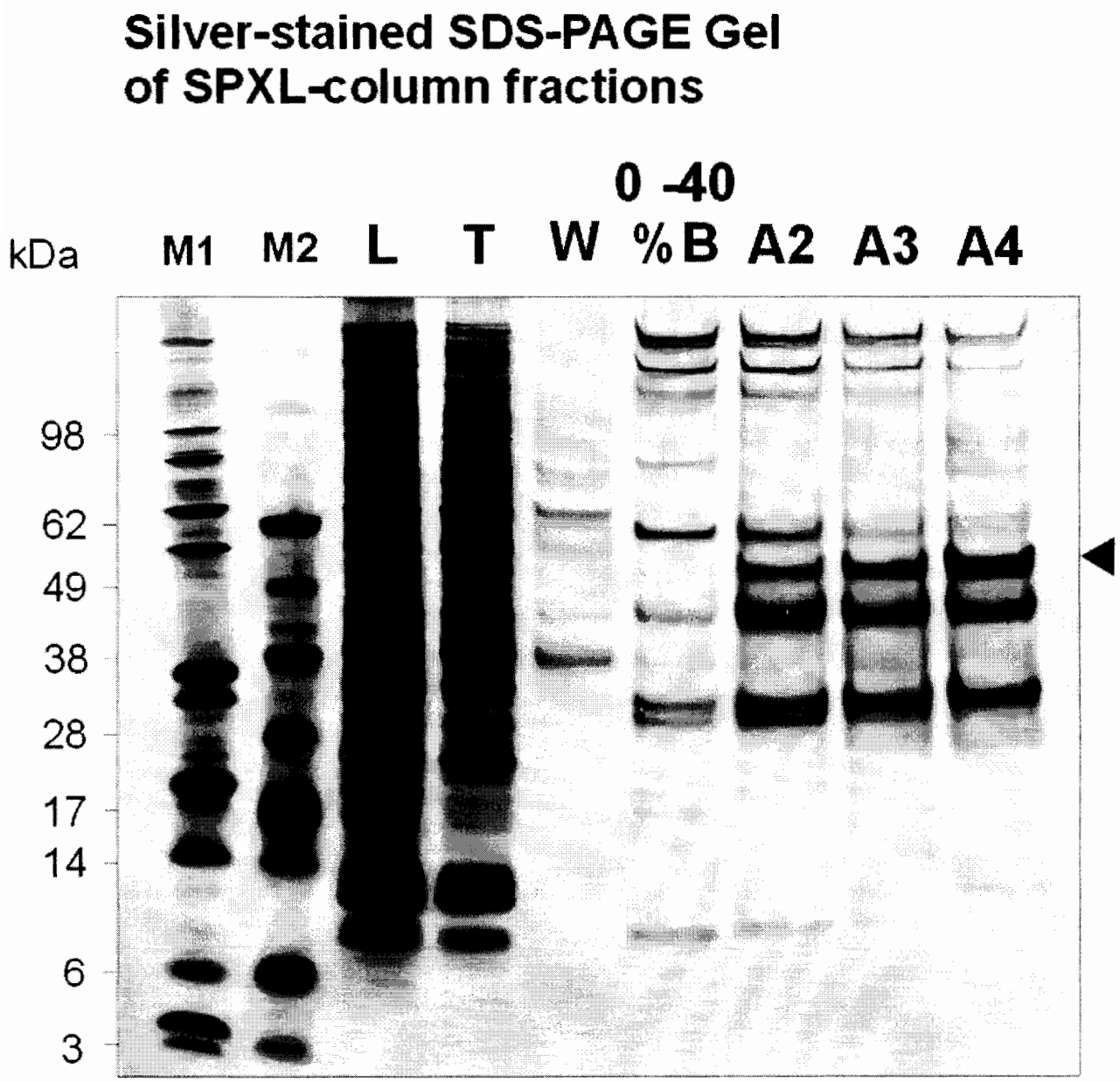
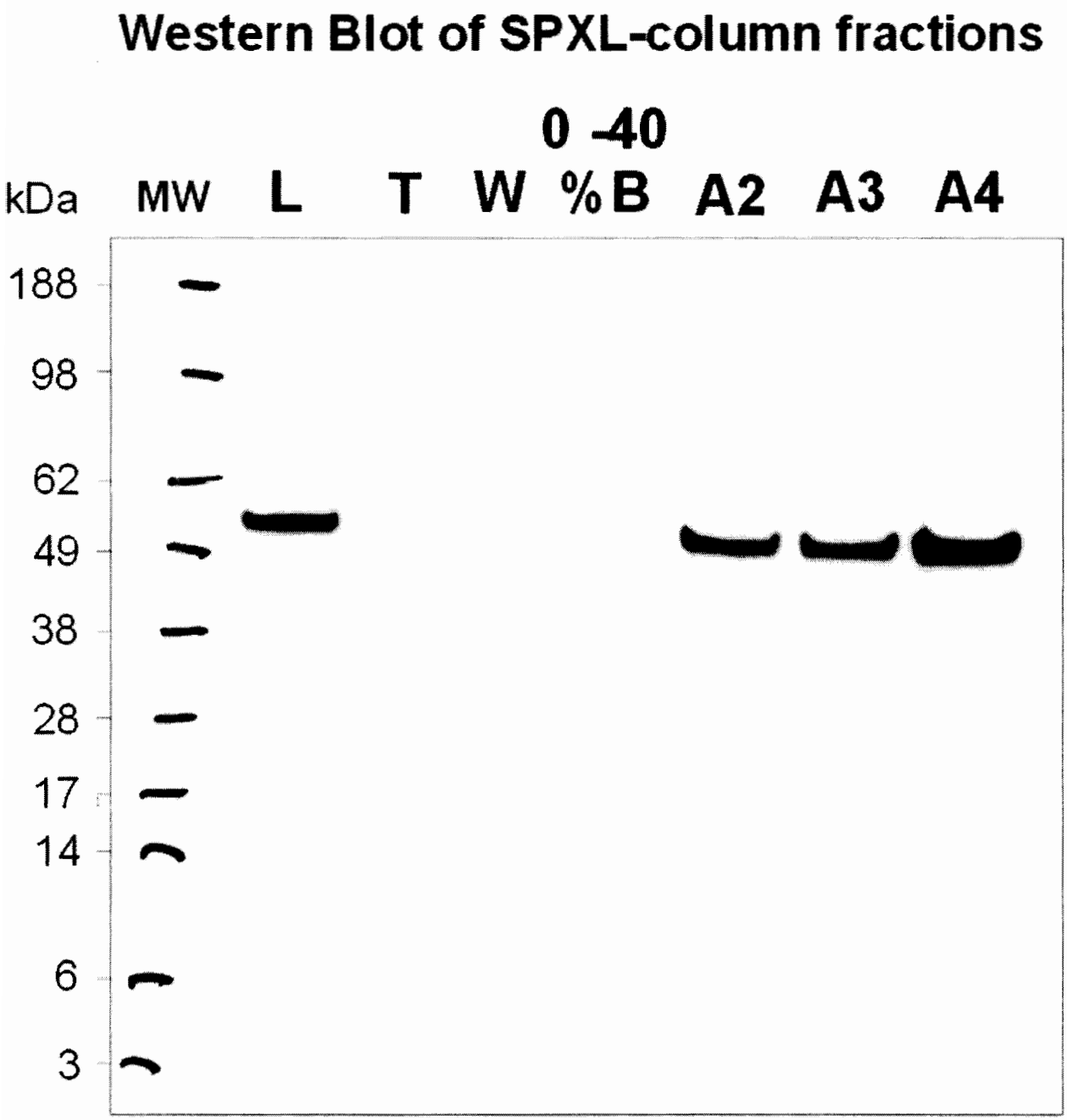
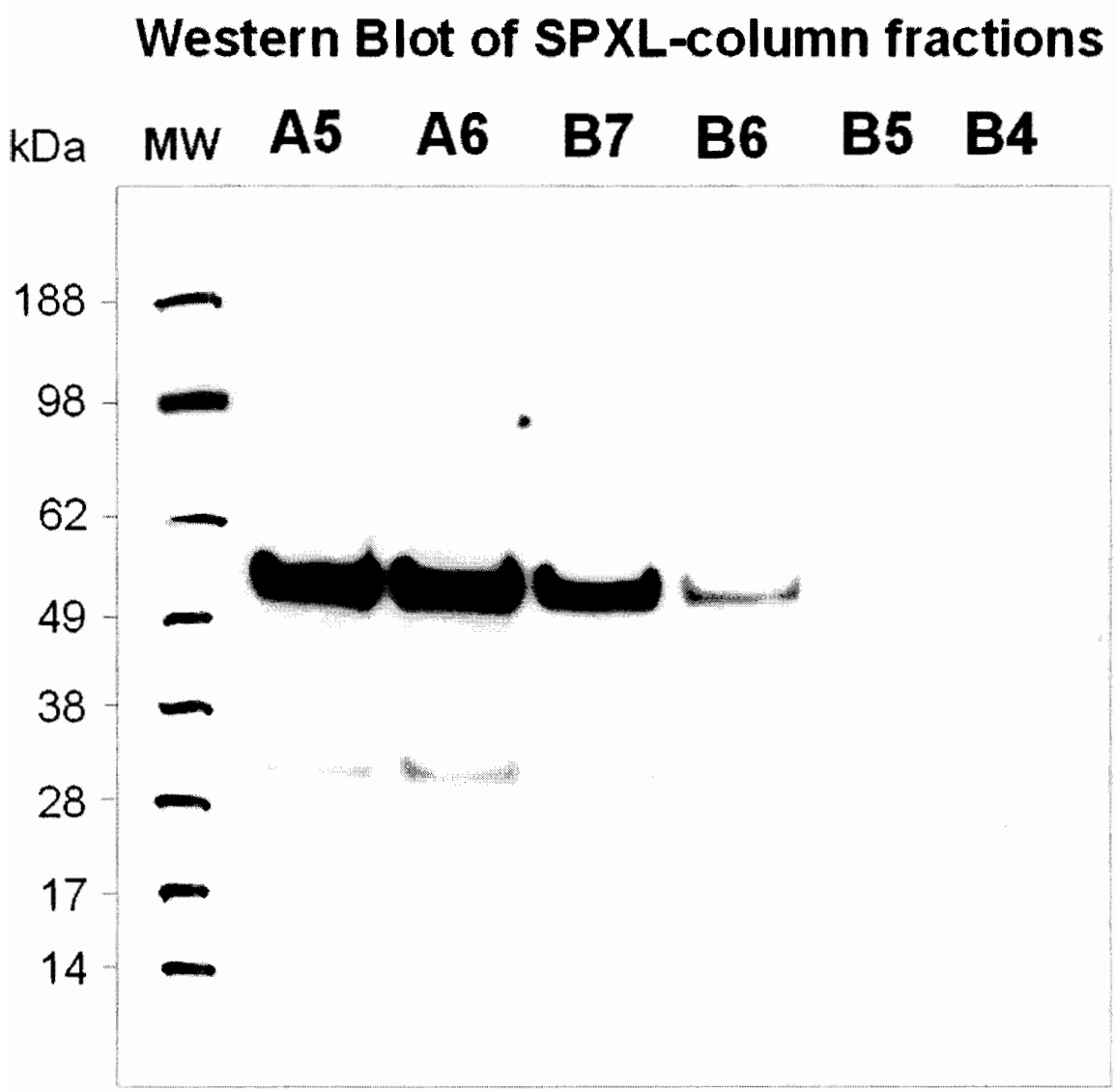

Silver-stained SDS-PAGE Gel
of SPXL-column fractions
0 -40
kDa
M1
M2
L
T
W
%B
A2
A3
A4
98
62
49
38
28
17
14
6
3

FIG 16 a


Western Blot of SPXL-column fractions
0 -40
kDa
MW
L
T
W
%B
A2
A3
A4
188
98
62
49
38
28
17
14
6
3

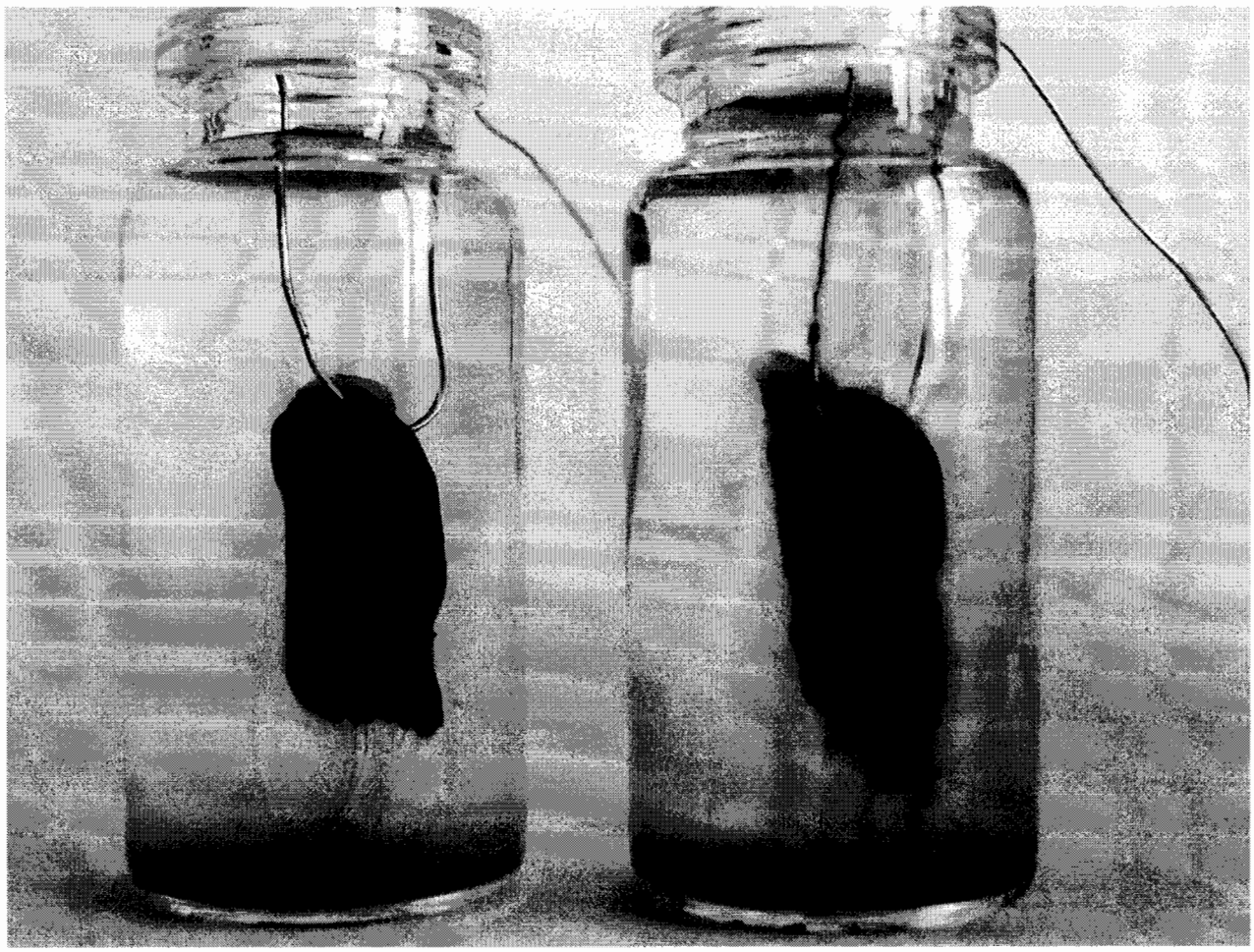
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25 OCT 2006

FIG 16 b



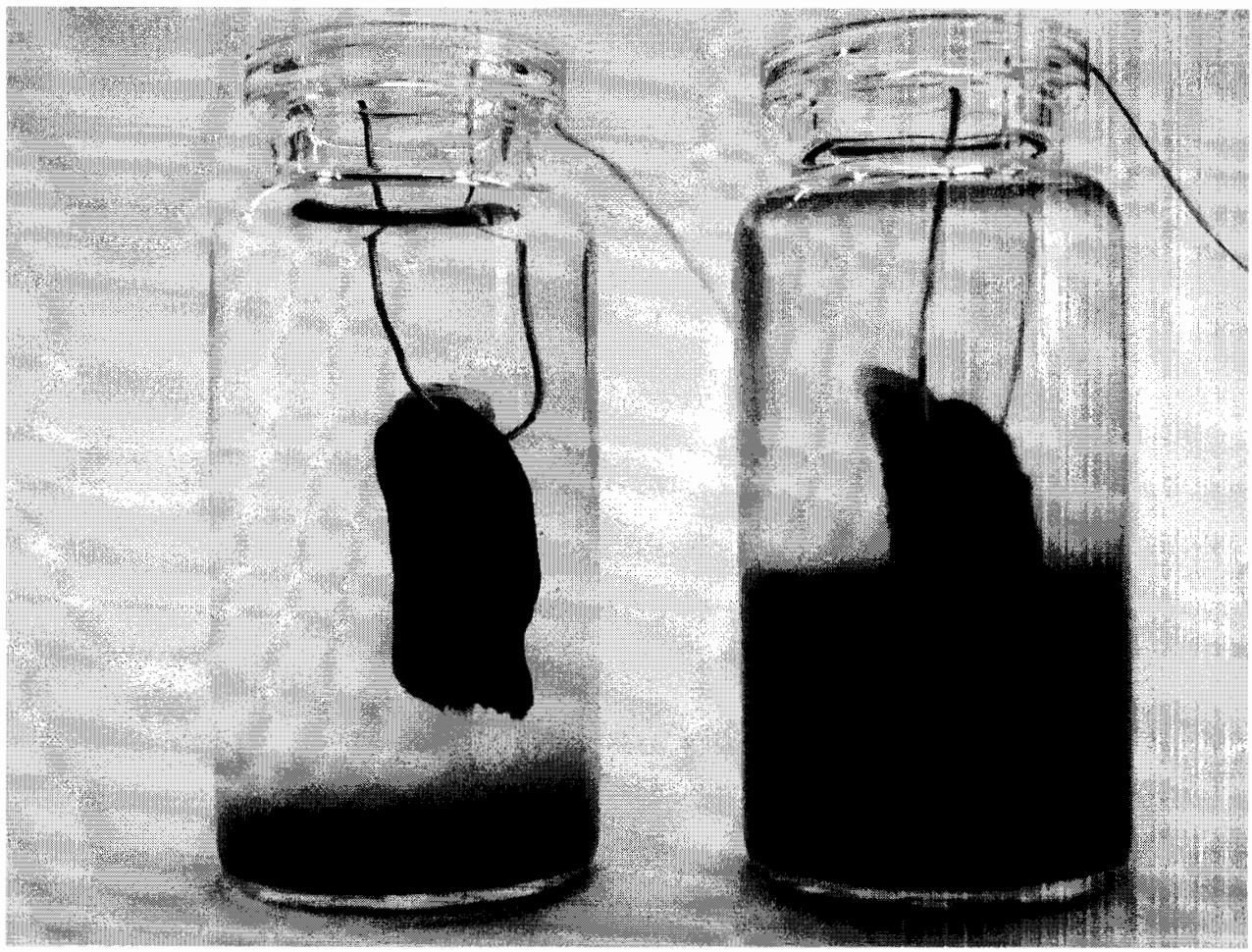
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25 OCT 2006

FIG 17 a



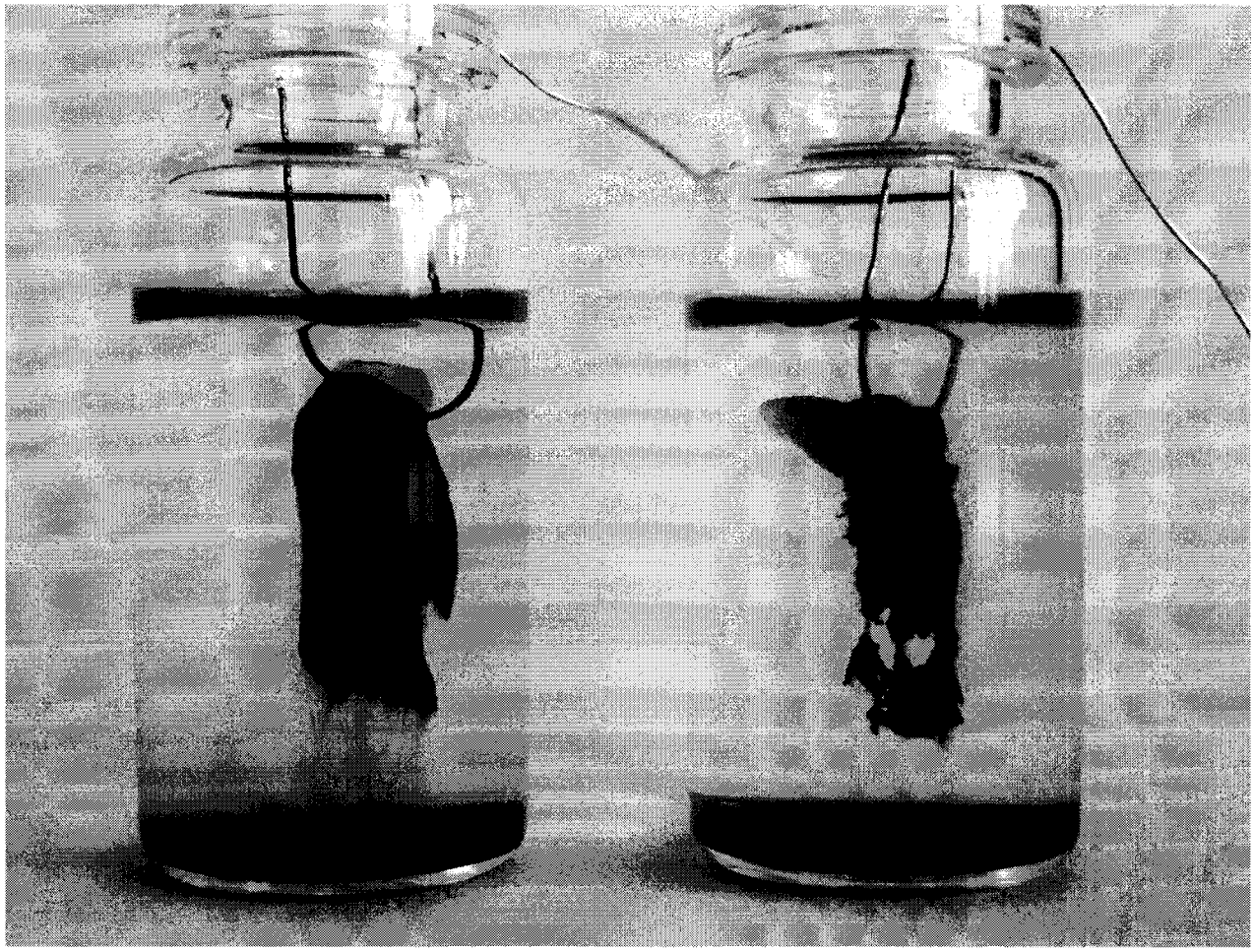
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25 OCT 2006

FIG 17 b



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FIG 17 c



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FIG 17 d

