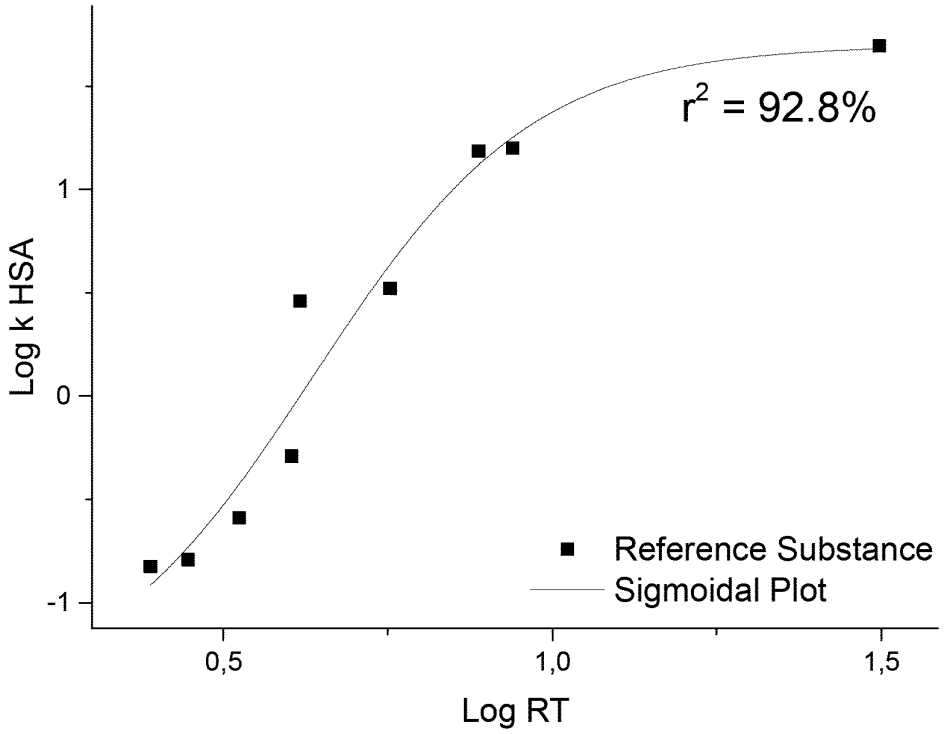

r² = 92.8%
Log k HSA
Log RT
Reference Substance
Sigmoidal Plot
1
0
-1
0,5
1,0
1,5

Fig. 1

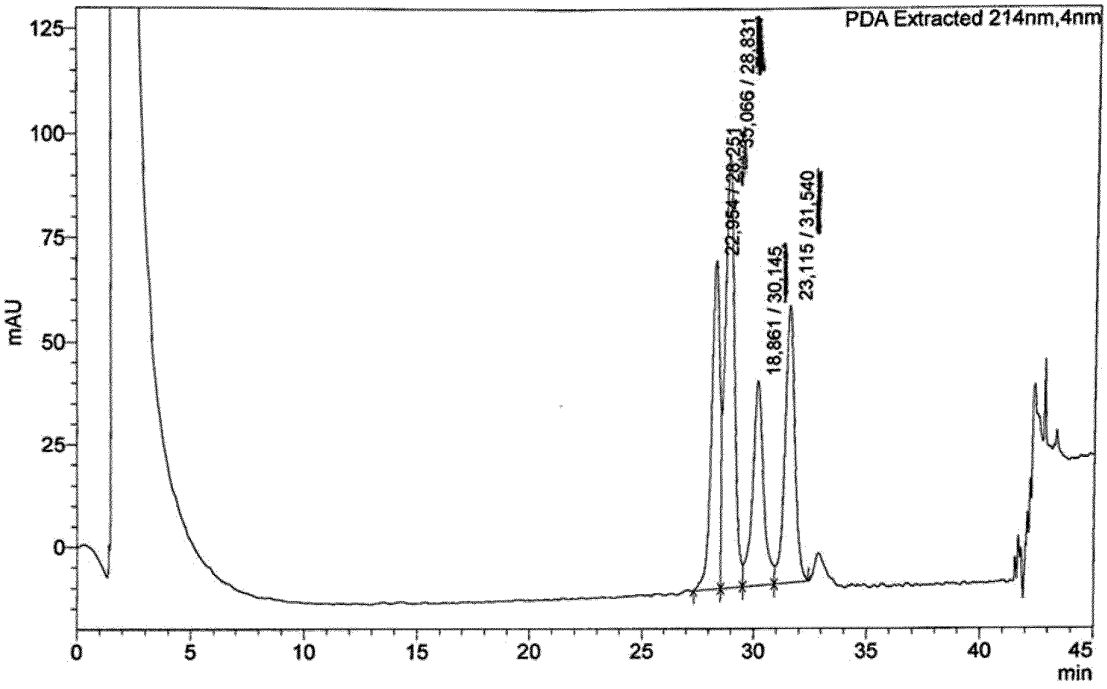

PDA Extracted 214nm,4nm
mAU
min
18,861 / 30,145
23,115 / 31,540

Fig. 2a

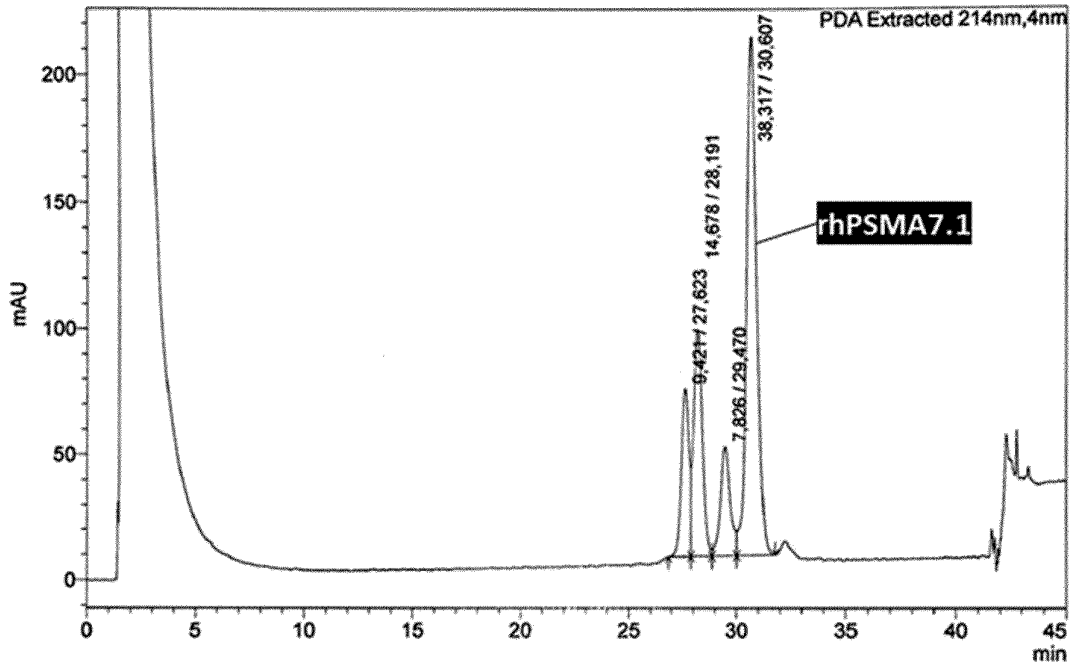

PDA Extracted 214nm,4nm
38,317 / 30,607
14,678 / 28,191
9,421 / 27,623
7,826 / 29,470
rhPSMA7.1
mAU
200
150
100
50
0
0
5
10
15
20
25
30
35
40
45
min

Fig. 2b

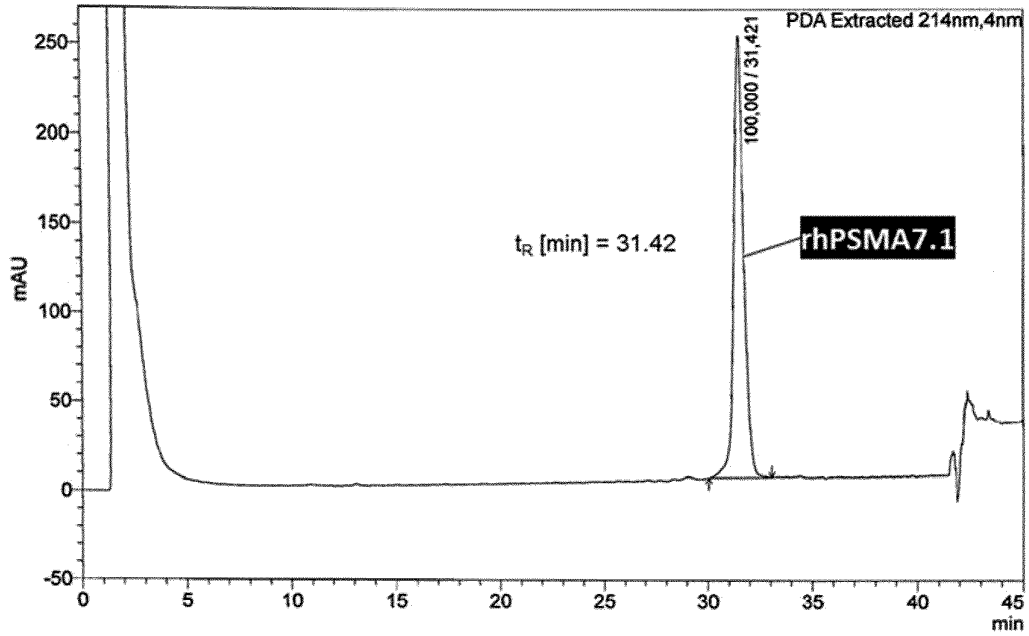

PDA Extracted 214nm,4nm
100,000 / 31,421
t_R [min] = 31.42
rhPSMA7.1
mAU
250
200
150
100
50
0
-50
0
5
10
15
20
25
30
35
40
45
min

Fig. 2c

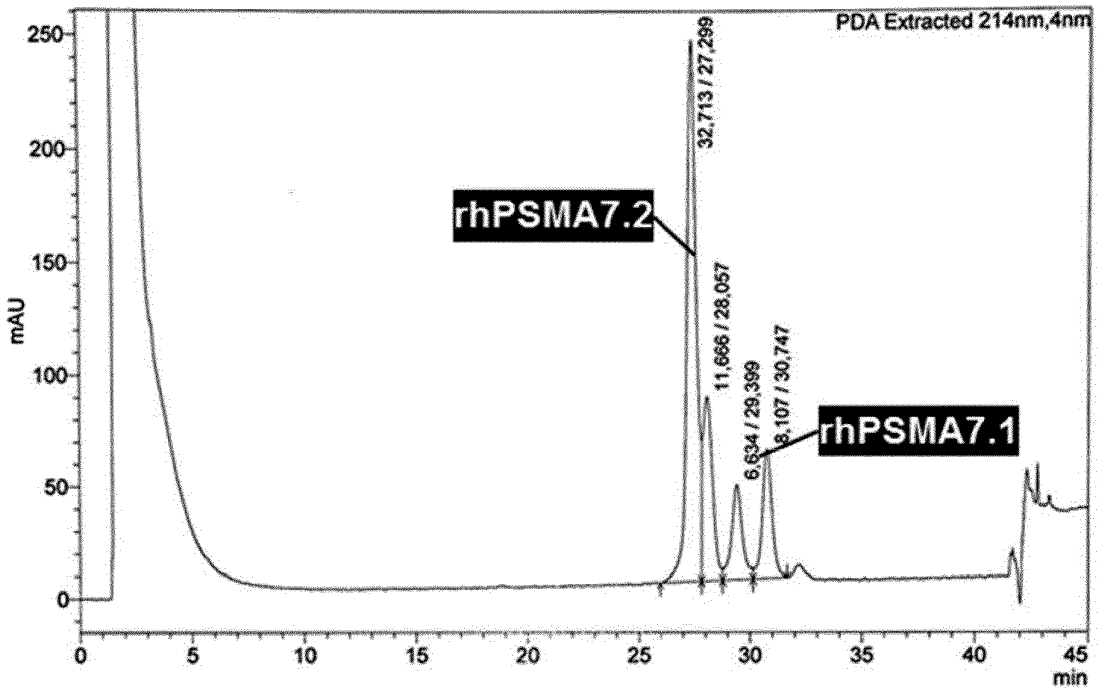

PDA Extracted 214nm,4nm
32,713 / 27,299
rhPSMA7.2
11,666 / 28,057
8,107 / 30,747
6,634 / 29,399
rhPSMA7.1
mAU
min

Fig. 3a

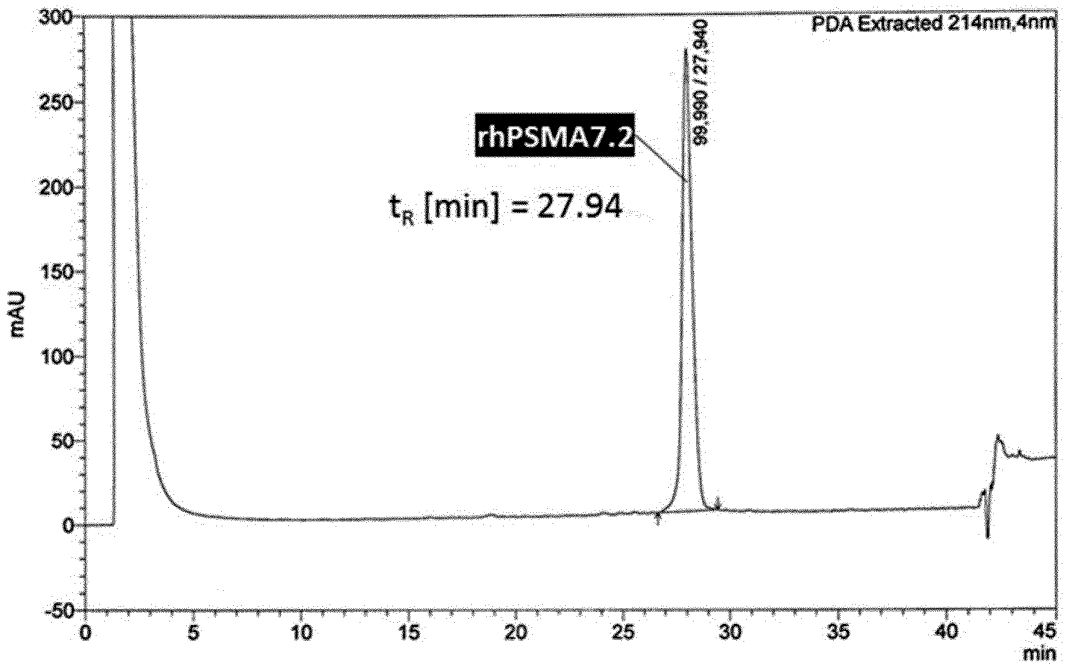

PDA Extracted 214nm,4nm
99,990 / 27,940
rhPSMA7.2
t_R [min] = 27.94
mAU
min

Fig. 3b

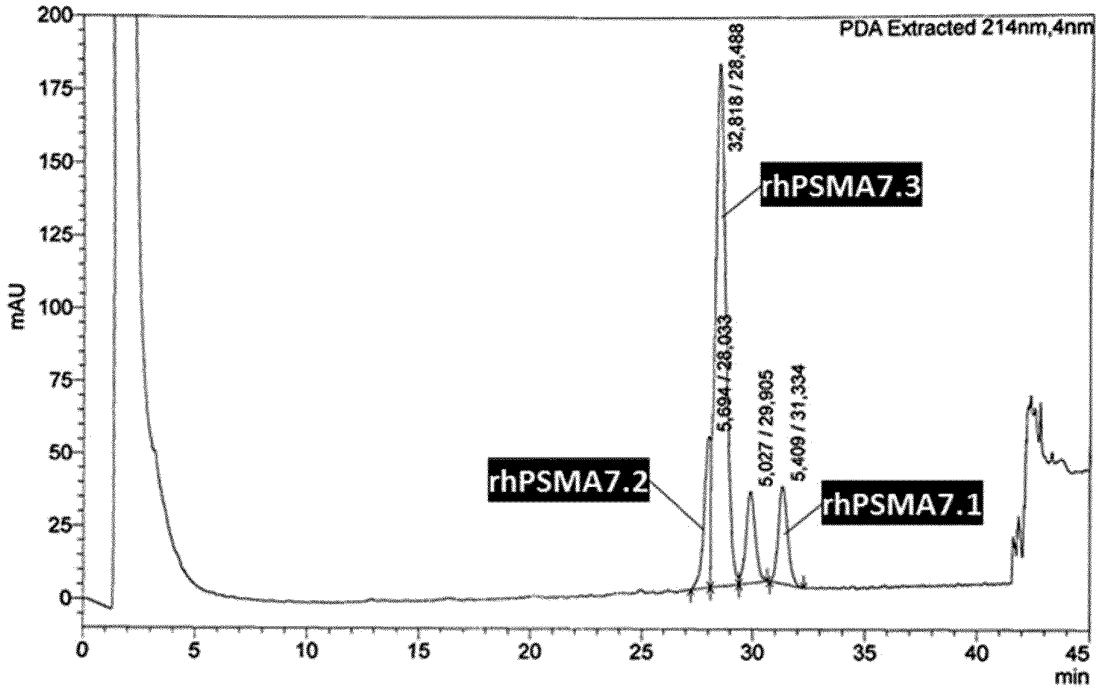

PDA Extracted 214nm,4nm
32,818 / 28,488
5,694 / 28,033
5,027 / 29,905
5,409 / 31,334
rhPSMA7.3
rhPSMA7.2
rhPSMA7.1
mAU
min

Fig. 4a

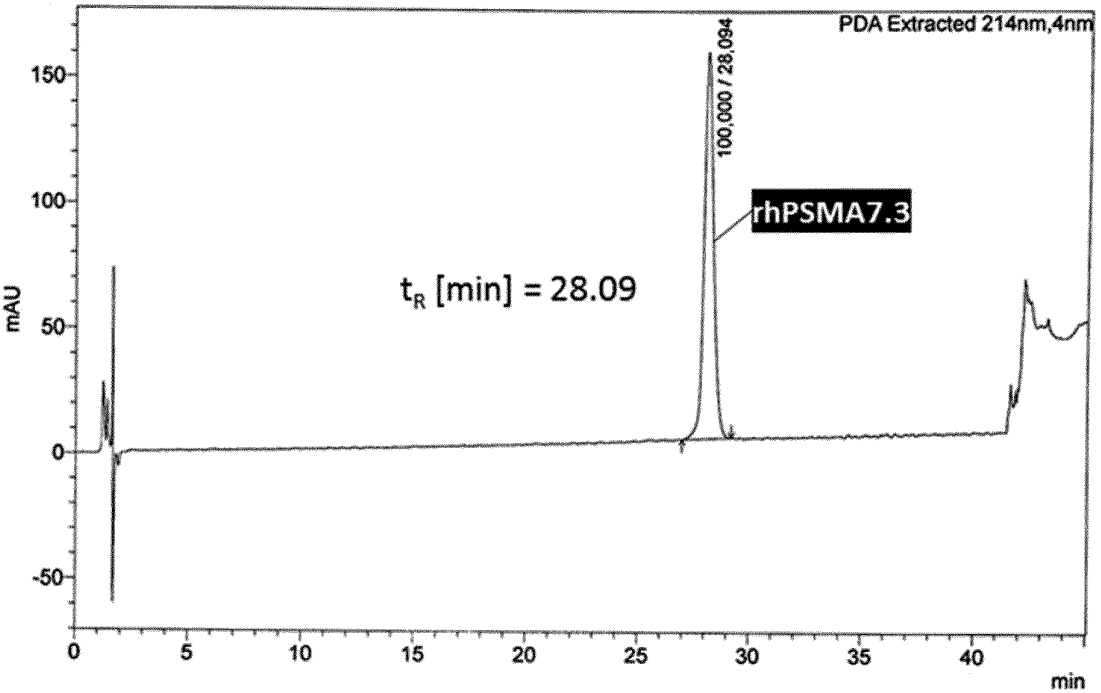

PDA Extracted 214nm,4nm
100,000 / 28,094
rhPSMA7.3
t_R [min] = 28.09
mAU
min

Fig. 4b

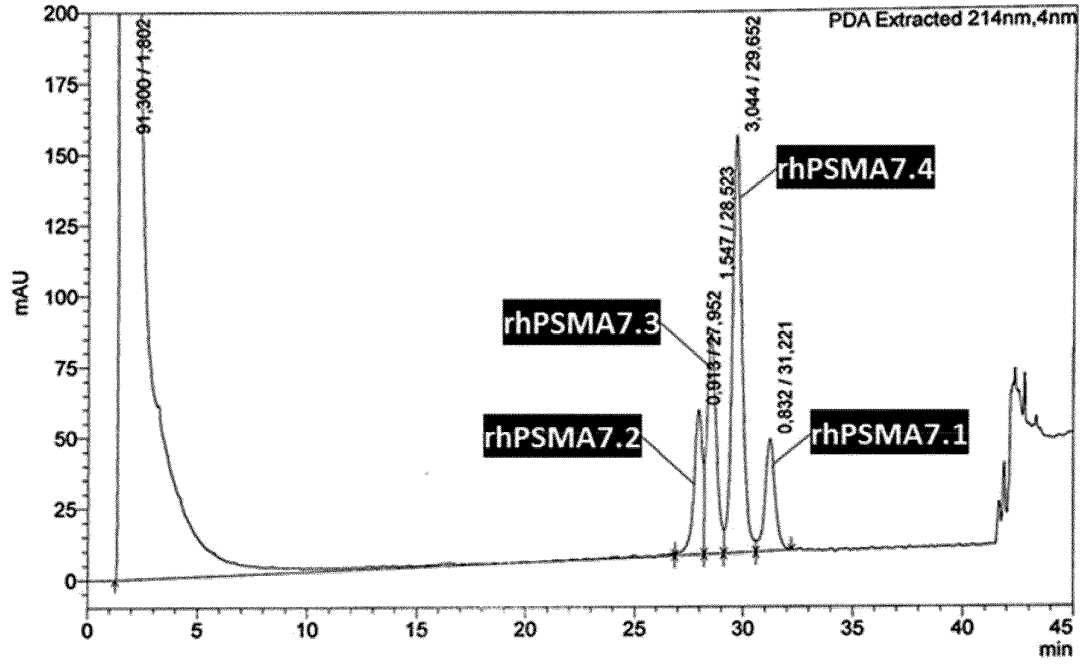

PDA Extracted 214nm,4nm
91,300 / 1,802
3,044 / 29,652
1,547 / 28,523
0,913 / 27,952
0,632 / 31,221
rhPSMA7.4
rhPSMA7.3
rhPSMA7.2
rhPSMA7.1
mAU
min

Fig. 5a

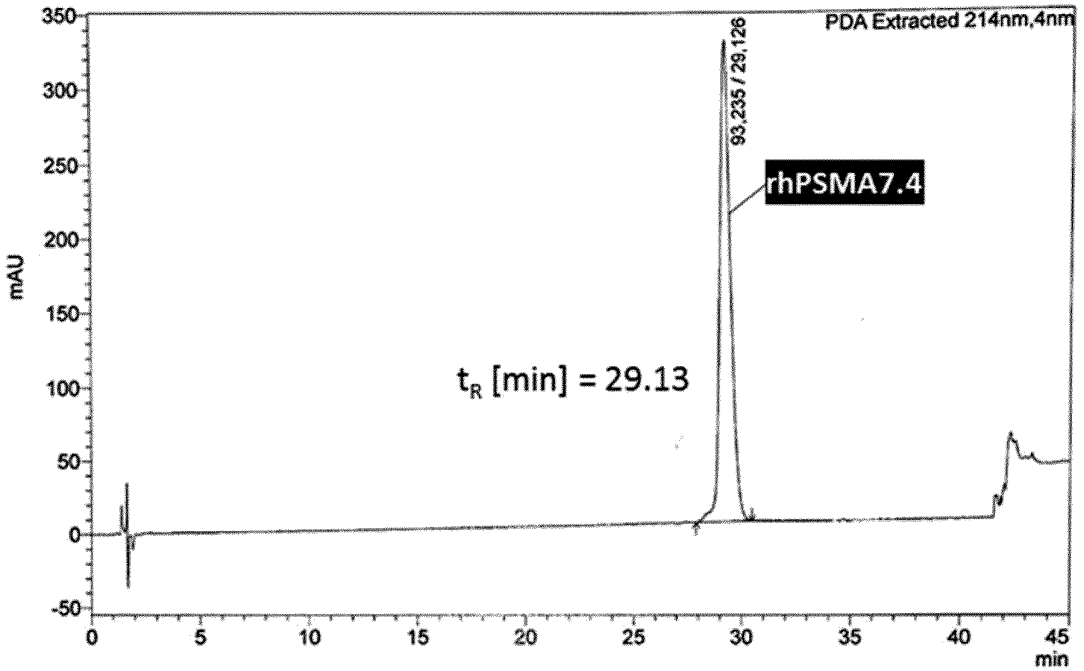

PDA Extracted 214nm,4nm
93,235 / 29,126
rhPSMA7.4
t_R [min] = 29.13
mAU
min

Fig. 5b

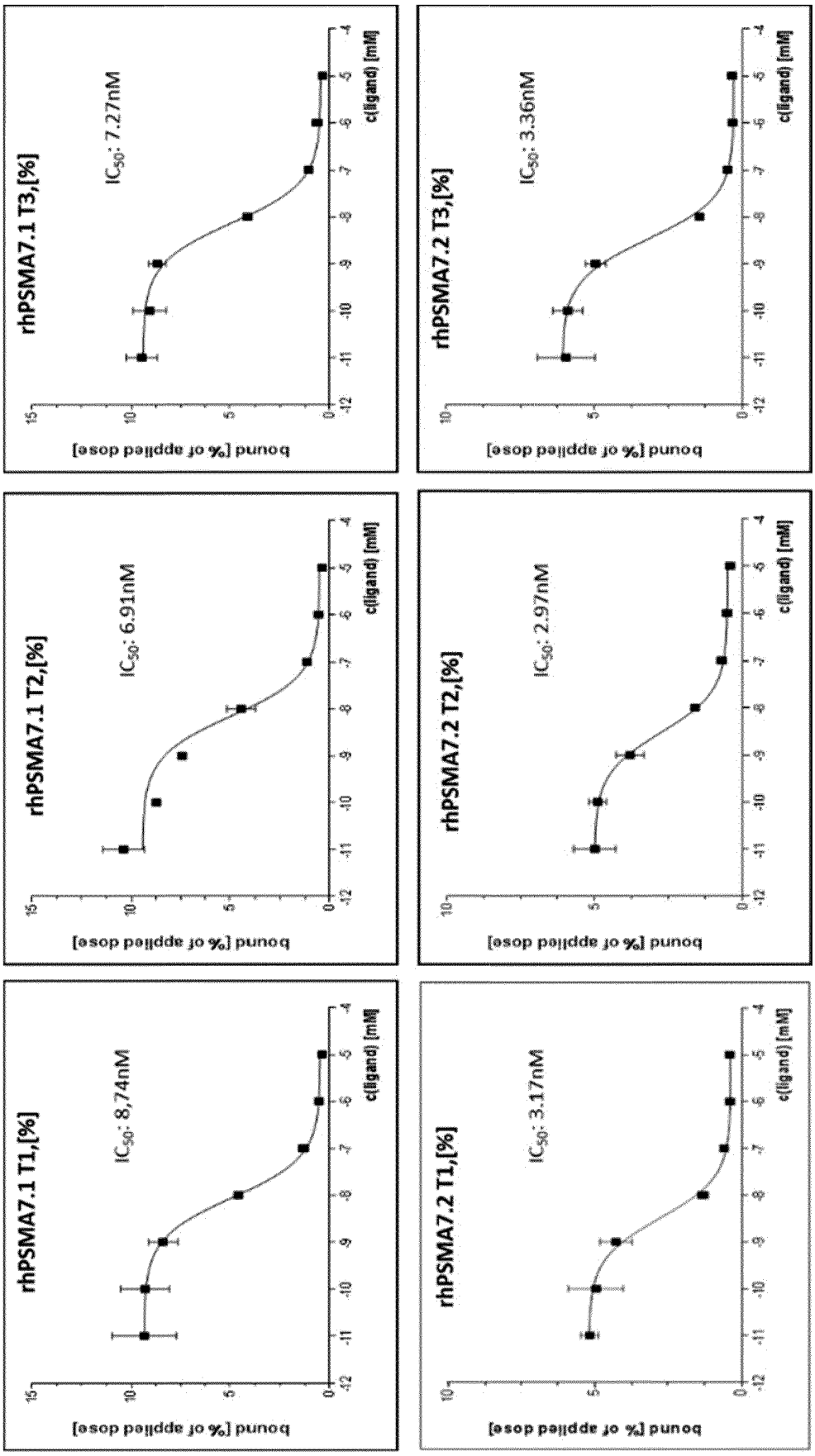

rhPSMA7.1 T1,[%]
IC50: 8,74nM
rhPSMA7.1 T2,[%]
IC50: 6.91nM
rhPSMA7.1 T3,[%]
IC50: 7.27nM
rhPSMA7.2 T1,[%]
IC50: 3.17nM
rhPSMA7.2 T2,[%]
IC50: 2.97nM
rhPSMA7.2 T3,[%]
IC50: 3.36nM
bound [% of applied dose]
c(ligand) [mM]

Fig. 6a

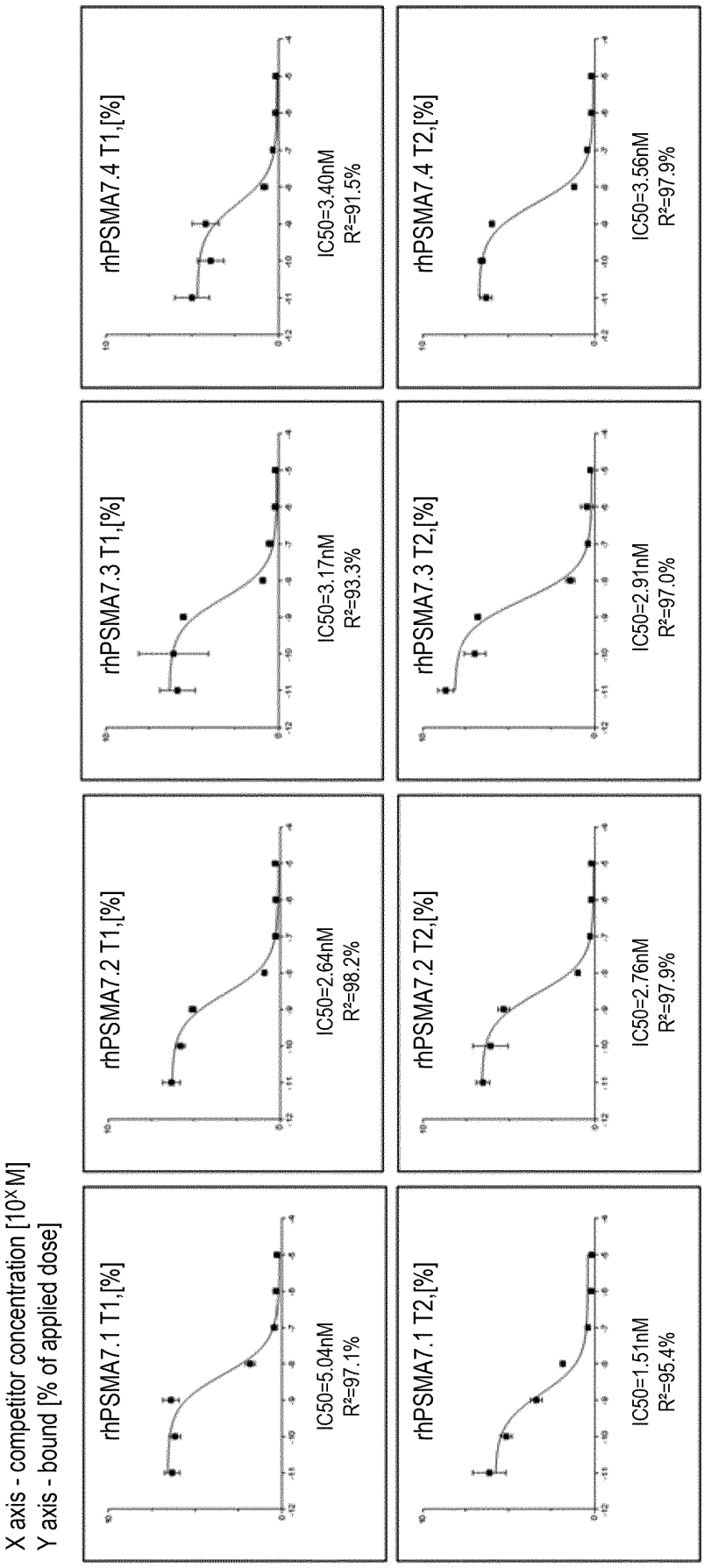

X axis - competitor concentration [10^X M]
Y axis - bound [% of applied dose]
rhPSMA7.1 T1,[%]
IC50=5.04nM
R²=97.1%
rhPSMA7.2 T1,[%]
IC50=2.64nM
R²=98.2%
rhPSMA7.3 T1,[%]
IC50=3.17nM
R²=93.3%
rhPSMA7.4 T1,[%]
IC50=3.40nM
R²=91.5%
rhPSMA7.1 T2,[%]
IC50=1.51nM
R²=95.4%
rhPSMA7.2 T2,[%]
IC50=2.76nM
R²=97.9%
rhPSMA7.3 T2,[%]
IC50=2.91nM
R²=97.0%
rhPSMA7.4 T2,[%]
IC50=3.56nM
R²=97.9%

Fig. 6b

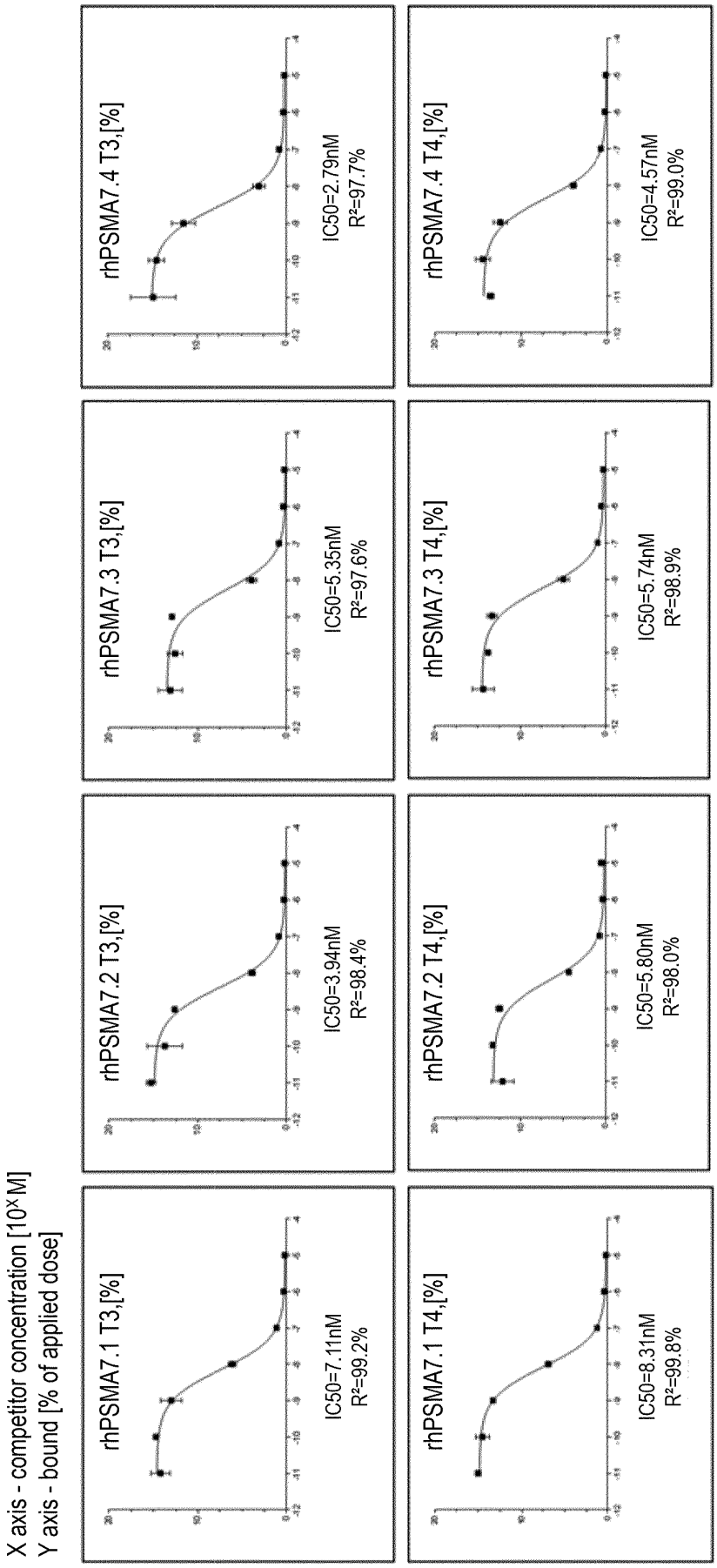


Fig. 6b (continued)

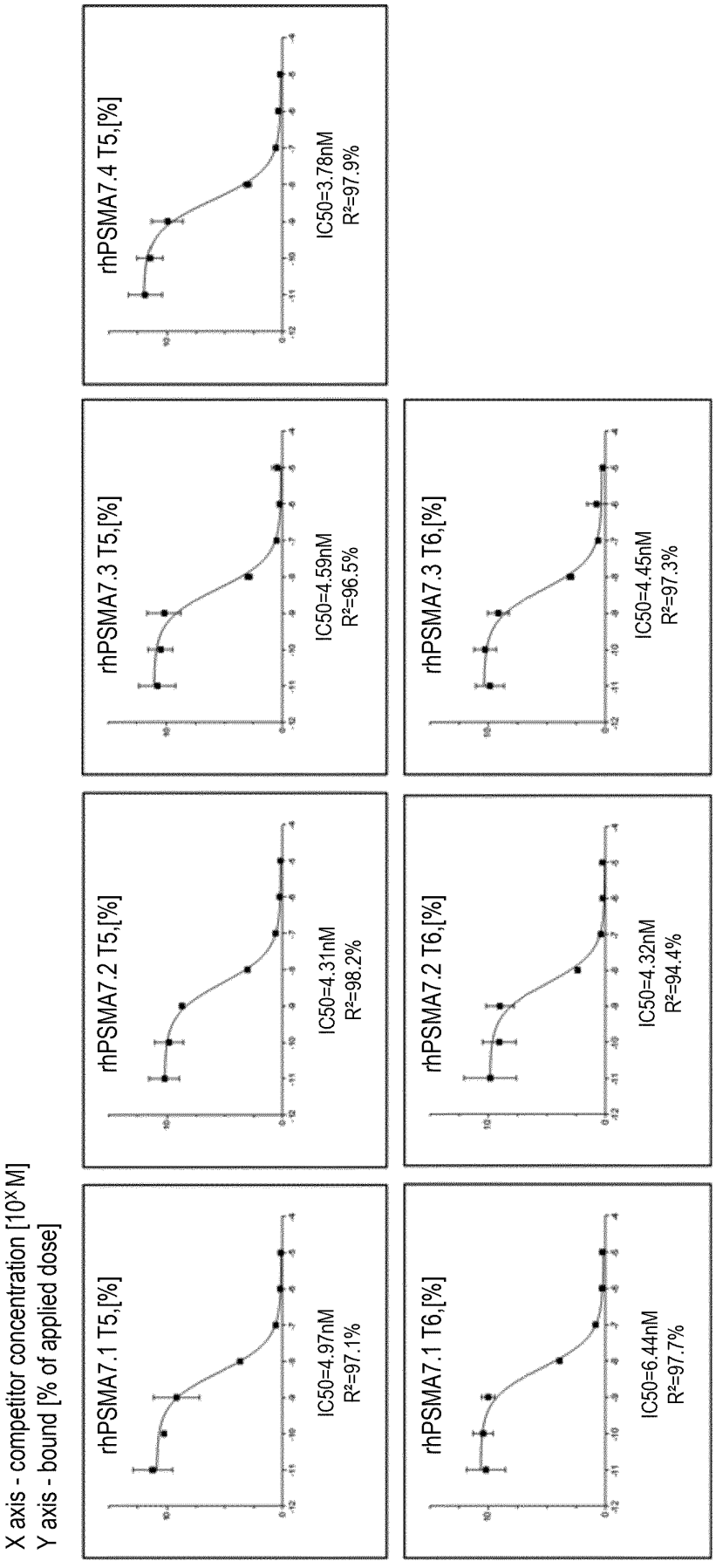


Fig. 6b (continued)

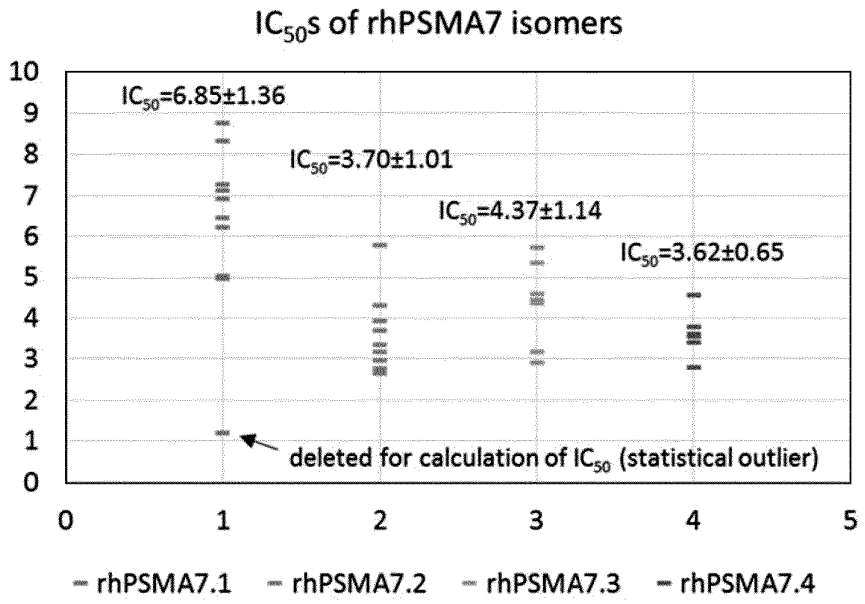

IC50s of rhPSMA7 isomers
IC50=6.85±1.36
IC50=3.70±1.01
IC50=4.37±1.14
IC50=3.62±0.65
deleted for calculation of IC50 (statistical outlier)
10
9
8
7
6
5
4
3
2
1
0
0
1
2
3
4
5
rhPSMA7.1
rhPSMA7.2
rhPSMA7.3
rhPSMA7.4

Fig. 7

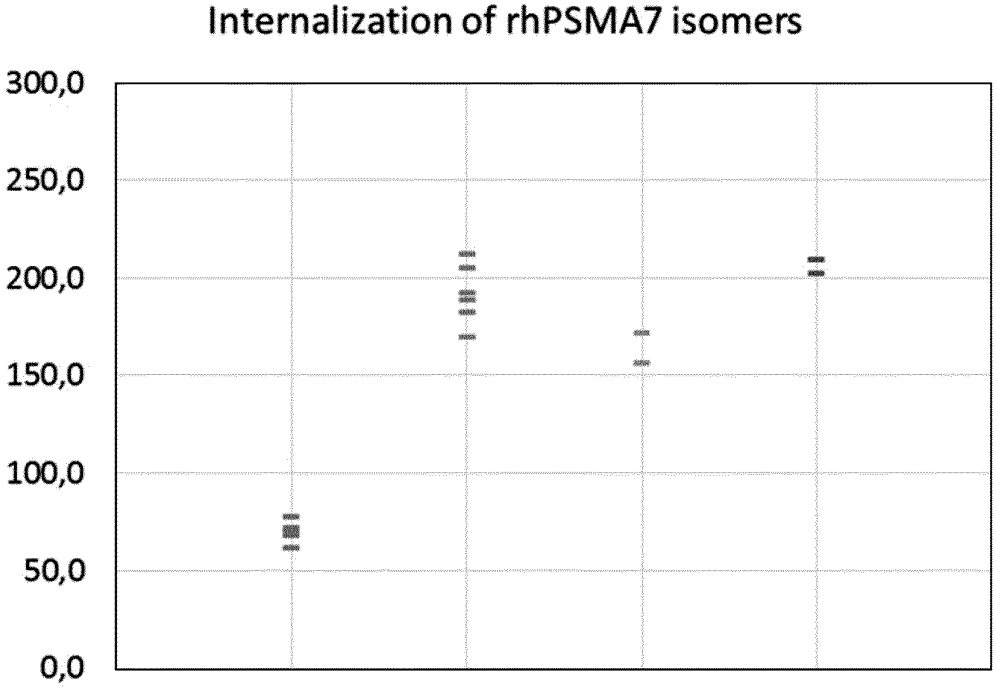

Internalization of rhPSMA7 isomers
300,0
250,0
200,0
150,0
100,0
50,0
0,0

Fig. 8

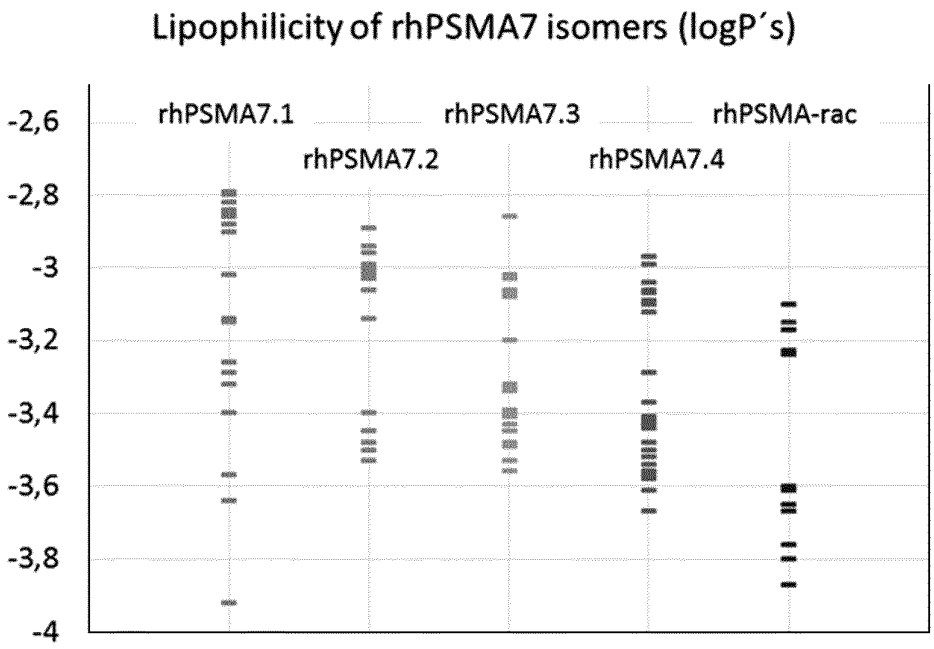

Lipophilicity of rhPSMA7 isomers (logP´s)
rhPSMA7.1
rhPSMA7.2
rhPSMA7.3
rhPSMA7.4
rhPSMA-rac
-2,6
-2,8
-3
-3,2
-3,4
-3,6
-3,8
-4

Fig. 9

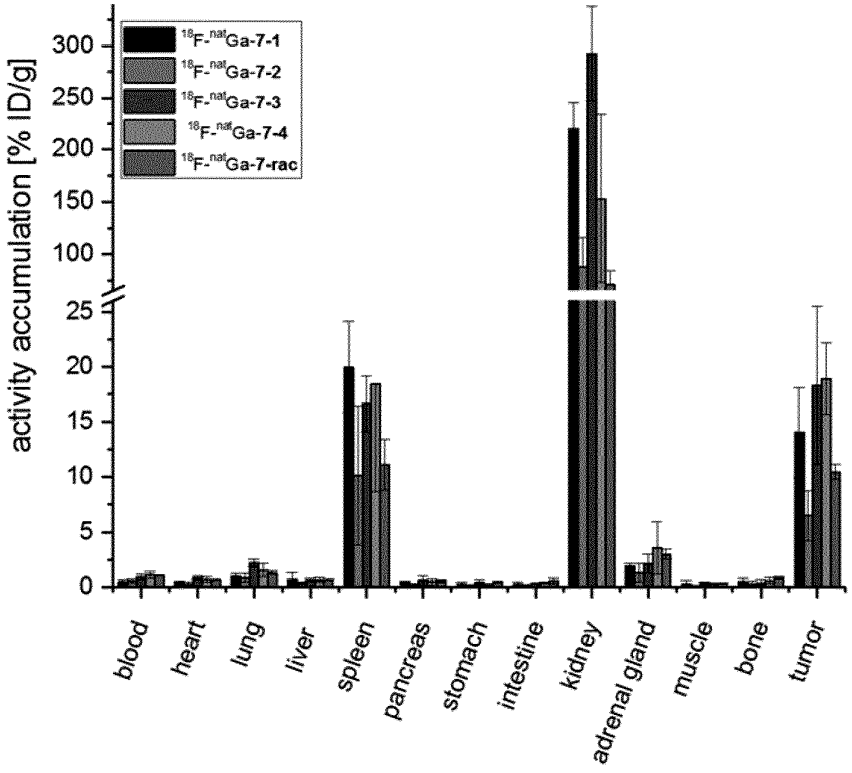

activity accumulation [% ID/g]
18F-natGa-7-1
18F-natGa-7-2
18F-natGa-7-3
18F-natGa-7-4
18F-natGa-7-rac
300
250
200
150
100
25
20
15
10
5
0
blood
heart
lung
liver
spleen
pancreas
stomach
intestine
kidney
adrenal gland
muscle
bone
tumor

Fig. 10

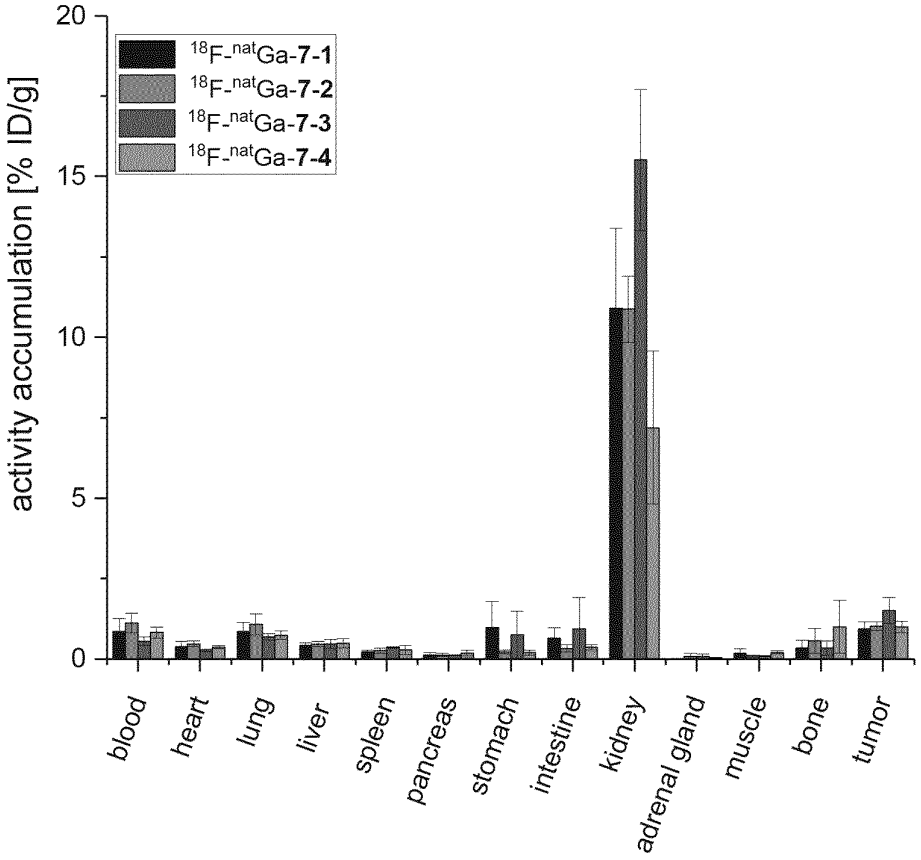

activity accumulation [% ID/g]
20
15
10
5
0
18F-natGa-7-1
18F-natGa-7-2
18F-natGa-7-3
18F-natGa-7-4
blood
heart
lung
liver
spleen
pancreas
stomach
intestine
kidney
adrenal gland
muscle
bone
tumor

Fig. 11

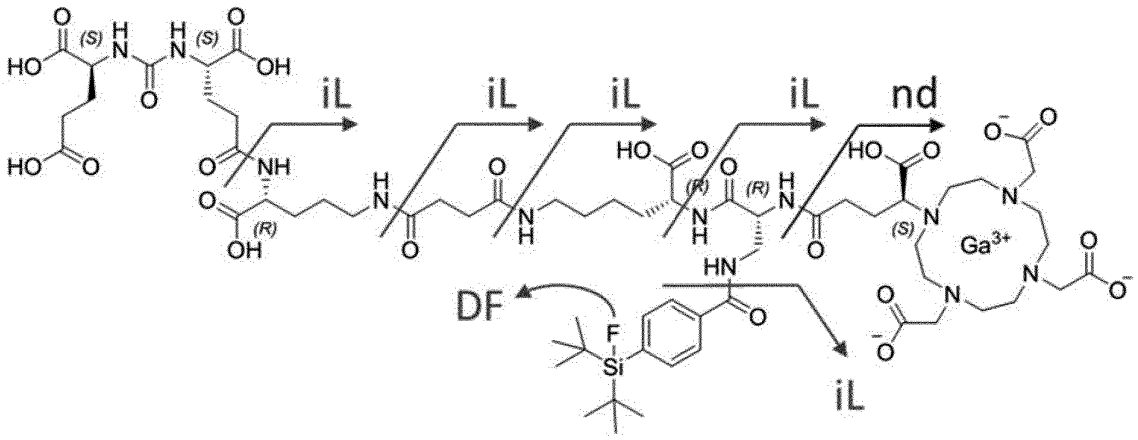

iL
iL
iL
iL
nd
DF
iL
Ga3+

Fig. 12

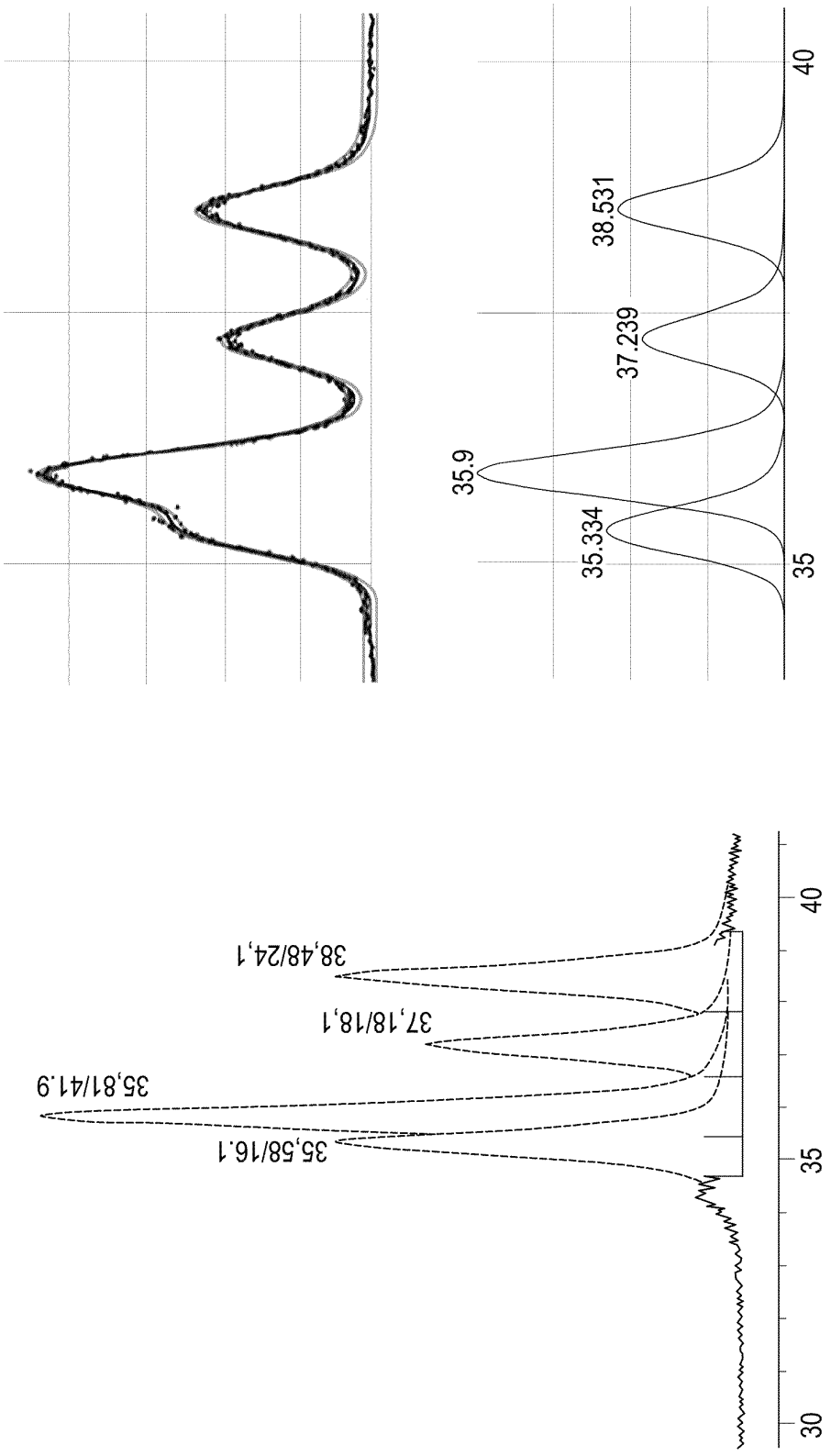

38.531
37.239
35.9
35.334
40
35
35,58/16,1
35,81/41,9
37,18/18,1
38,48/24,1
40
35
30

Fig.13

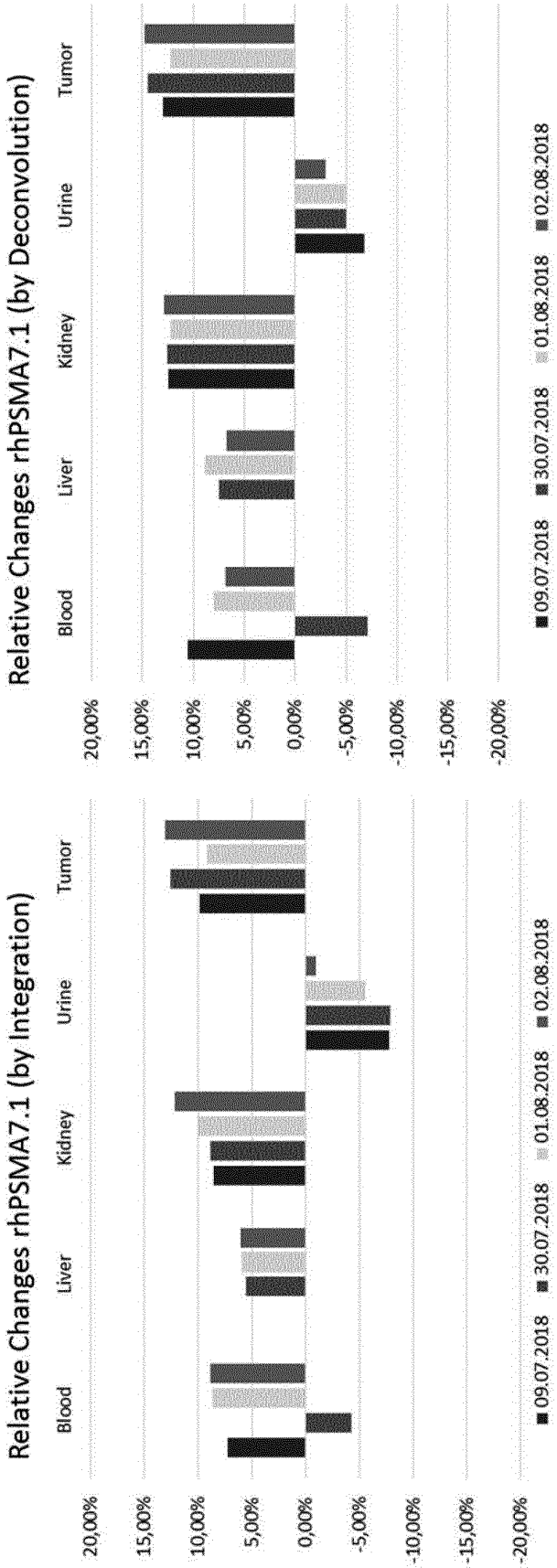

Relative Changes rhPSMA7.1 (by Deconvolution)
Blood
Liver
Kidney
Urine
Tumor
20,00%
15,00%
10,00%
5,00%
0,00%
-5,00%
-10,00%
-15,00%
-20,00%
09.07.2018
30.07.2018
01.08.2018
02.08.2018
Relative Changes rhPSMA7.1 (by Integration)
Blood
Liver
Kidney
Urine
Tumor
20,00%
15,00%
10,00%
5,00%
0,00%
-5,00%
-10,00%
-15,00%
-20,00%
09.07.2018
30.07.2018
01.08.2018
02.08.2018

Fig. 14a

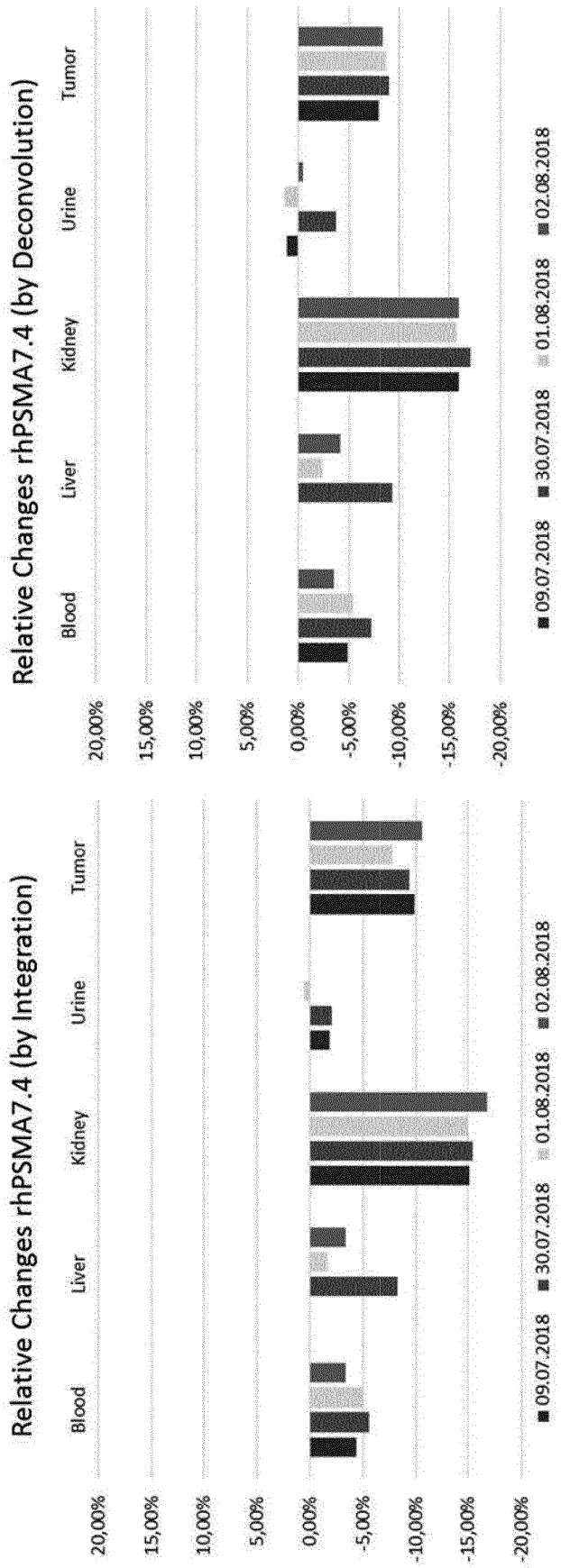

Relative Changes rhPSMA7.4 (by Deconvolution)
Blood
Liver
Kidney
Urine
Tumor
20,00%
15,00%
10,00%
5,00%
0,00%
-5,00%
-10,00%
-15,00%
-20,00%
09.07.2018
30.07.2018
01.08.2018
02.08.2018
Relative Changes rhPSMA7.4 (by Integration)
Blood
Liver
Kidney
Urine
Tumor
20,00%
15,00%
10,00%
5,00%
0,00%
-5,00%
-10,00%
-15,00%
-20,00%
09.07.2018
30.07.2018
01.08.2018
02.08.2018

Fig. 14b

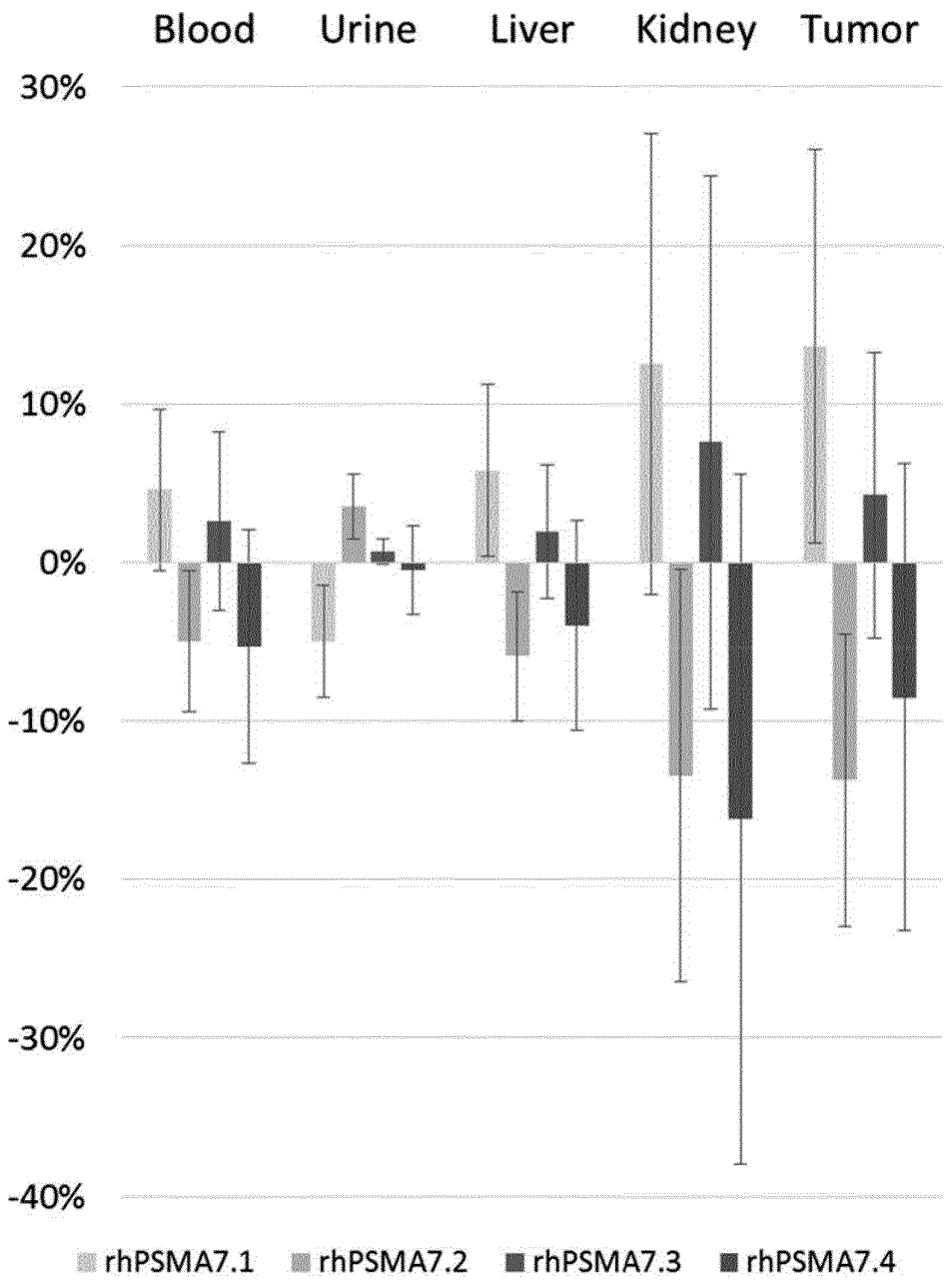

Blood
Urine
Liver
Kidney
Tumor
30%
20%
10%
0%
-10%
-20%
-30%
-40%
rhPSMA7.1
rhPSMA7.2
rhPSMA7.3
rhPSMA7.4

Fig. 15

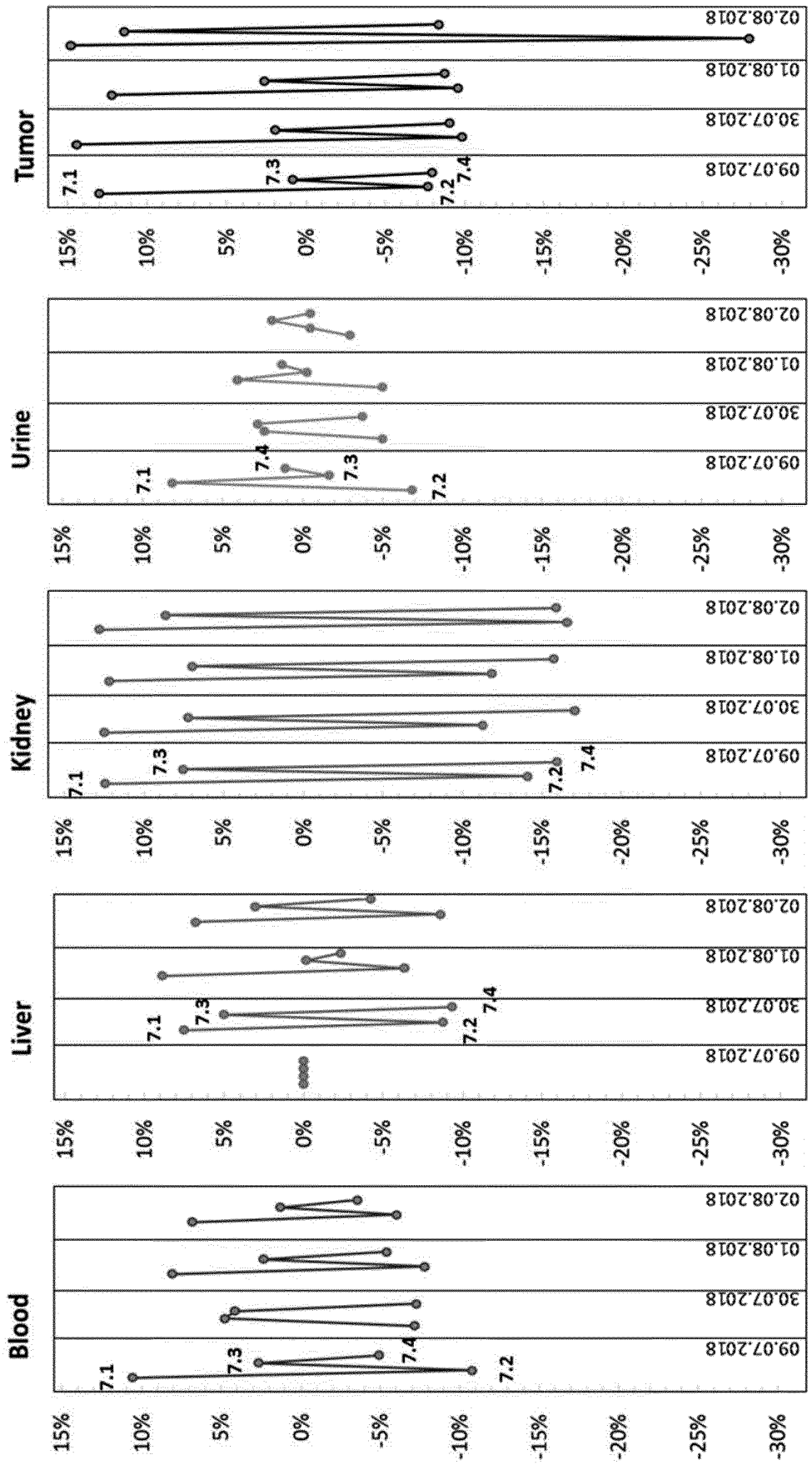

Tumor
Urine
Kidney
Liver
Blood
09.07.2018
30.07.2018
01.08.2018
02.08.2018
15%
10%
5%
0%
-5%
-10%
-15%
-20%
-25%
-30%
7.1
7.2
7.3
7.4

Fig. 16

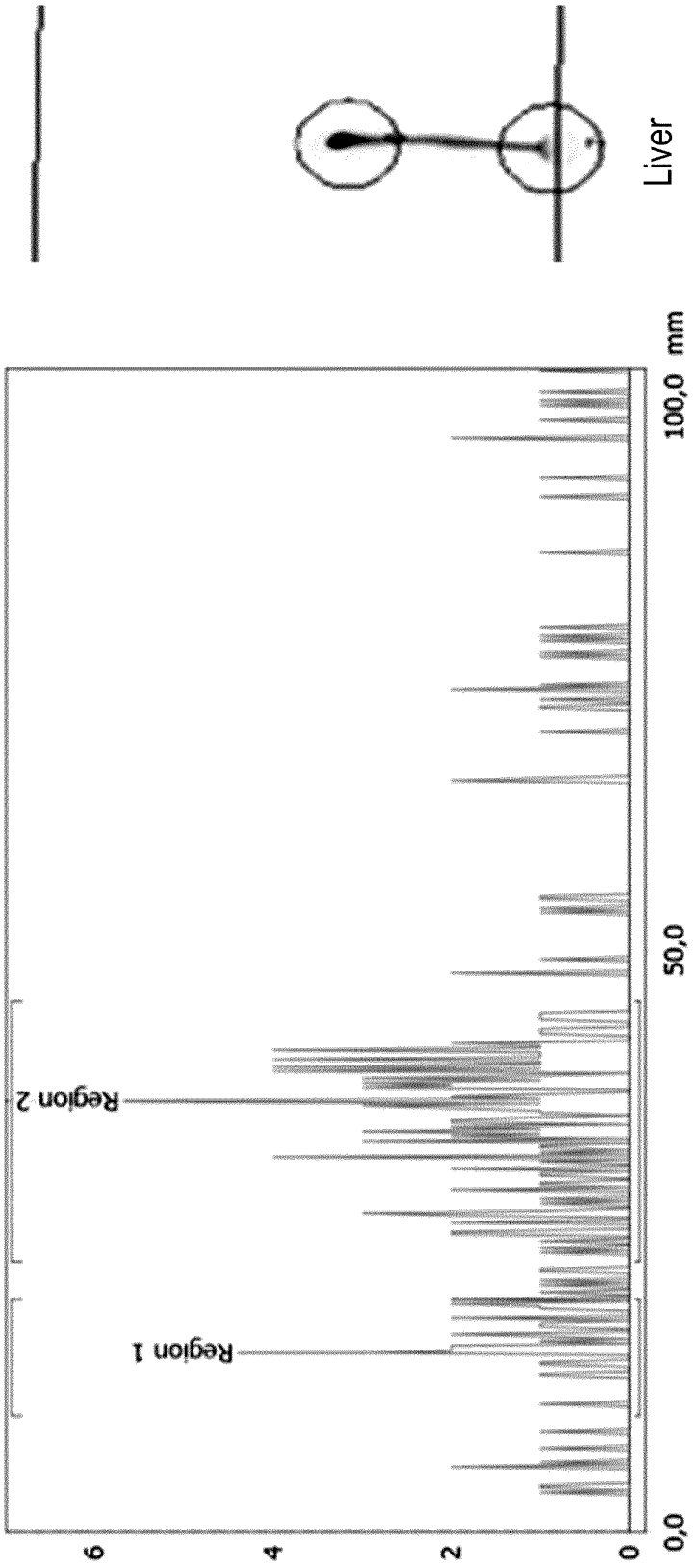
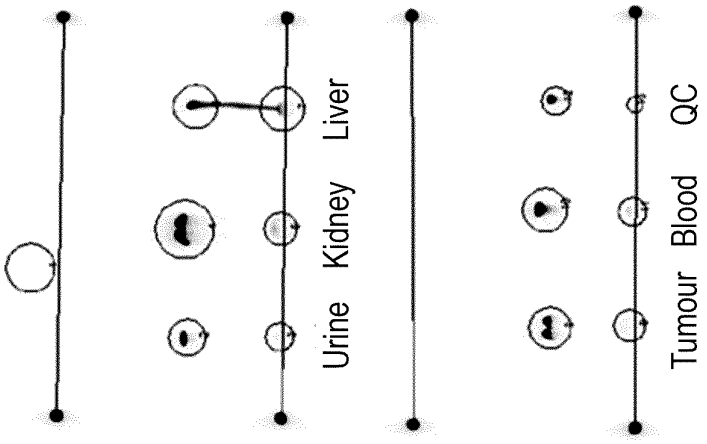


Fig. 17


Urine
Kidney
Liver
Tumour
Blood
QC

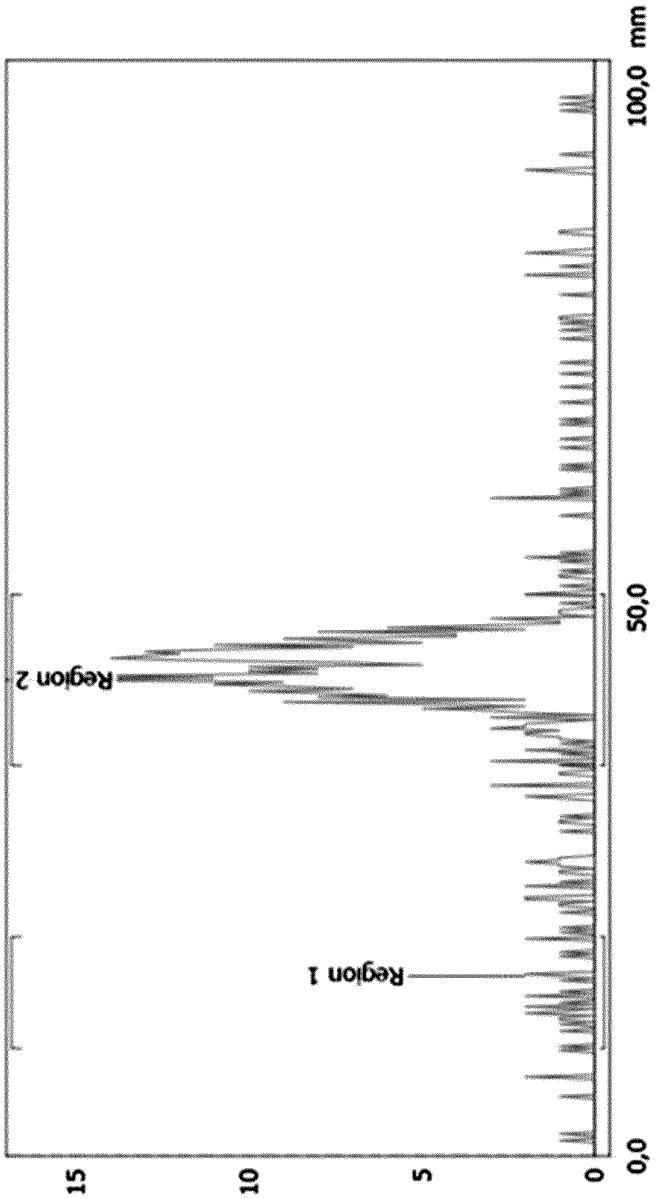
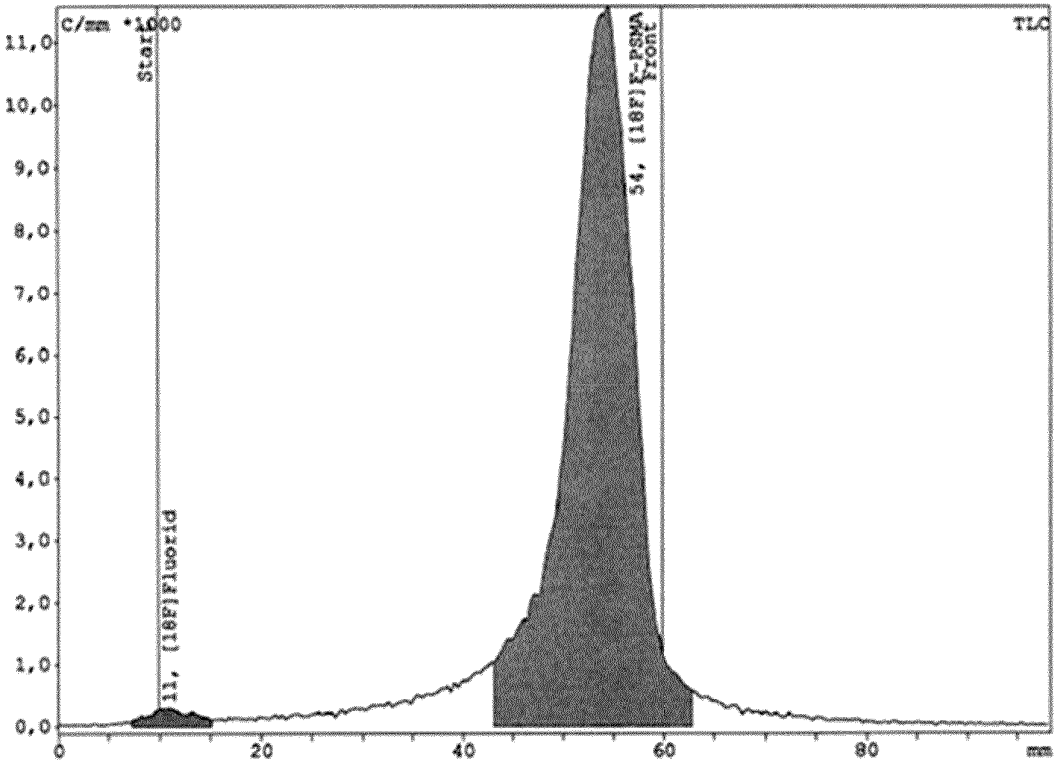

15
10
5
0
0,0
50,0
100,0 mm
Region 1
Region 2

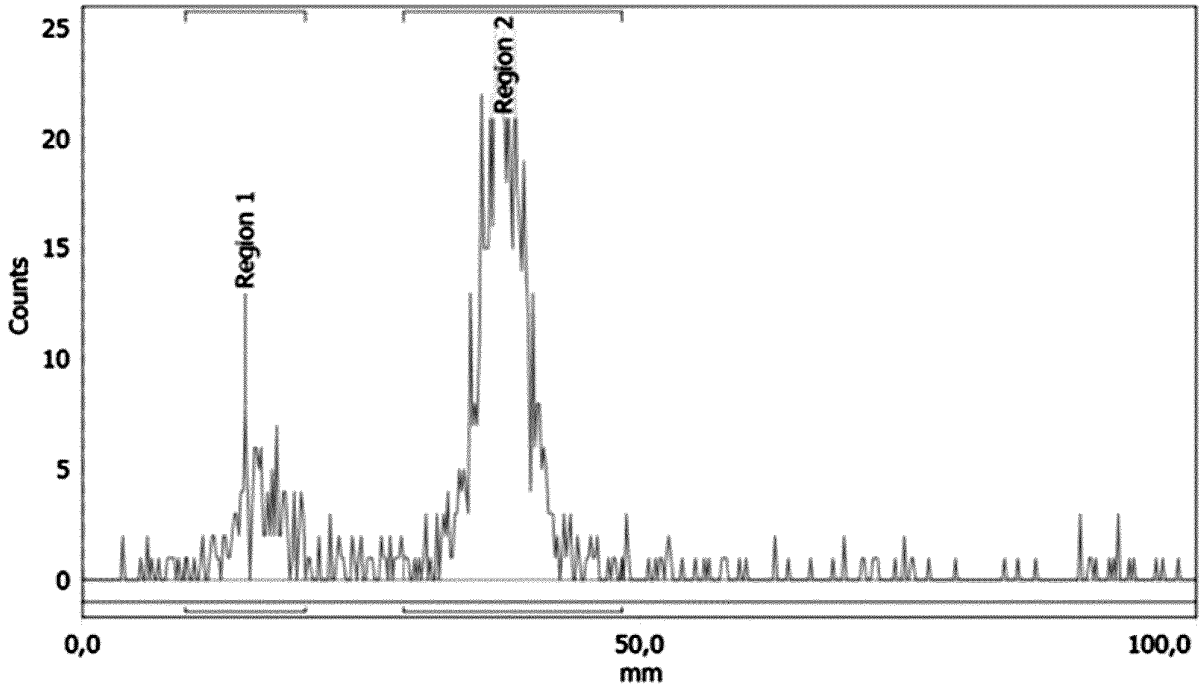
Fig. 18



Integration TLC

Substance	RF	%Total %	Typ	Area Counts	%Area %	Instrument	Ret mm	S/N ratio
[18F]Fluoride	0,013	1,50	DD(	1614,00	1,74	TLC	10,52	6,3
[18F]F-PSMA	0,888	84,68	DD(	91023,00	98,26	TLC	54,27	167,5
Total in ROI (region of interest)				92637,00	100,00			
Total Area				107492,00				
Area (Total) RF				99480,00				

Fig. 19



Regions: ^{18}F Detector: PMT

Name	Start (mm)	End (mm)	Retention (RF)	Area (Counts)	%ROI (%)	%Total (%)
Region 1	9,2	20,0	0,073	127	17,49	14,02
Region 2	28,8	48,4	0,189	599	82,51	66,11
2 Peaks				726	100,00	80,13

Fig. 20

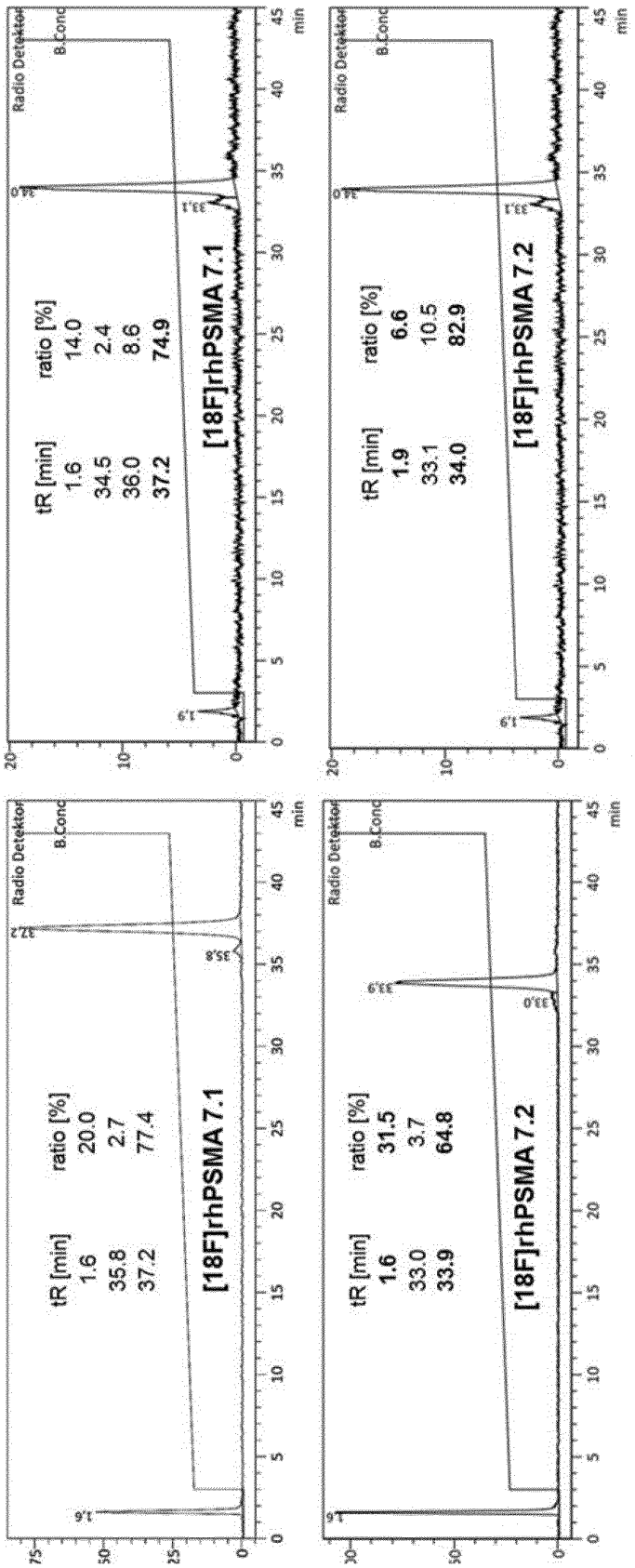

[18F]rhPSMA 7.1
tR [min] ratio [%]
1.6 14.0
34.5 2.4
36.0 8.6
37.2 74.9
[18F]rhPSMA 7.2
tR [min] ratio [%]
1.9 6.6
33.1 10.5
34.0 82.9
[18F]rhPSMA 7.1
tR [min] ratio [%]
1.6 20.0
35.8 2.7
37.2 77.4
[18F]rhPSMA 7.2
tR [min] ratio [%]
1.6 31.5
33.0 3.7
33.9 64.8
Radio Detektor
B.Conc
min

Fig. 21

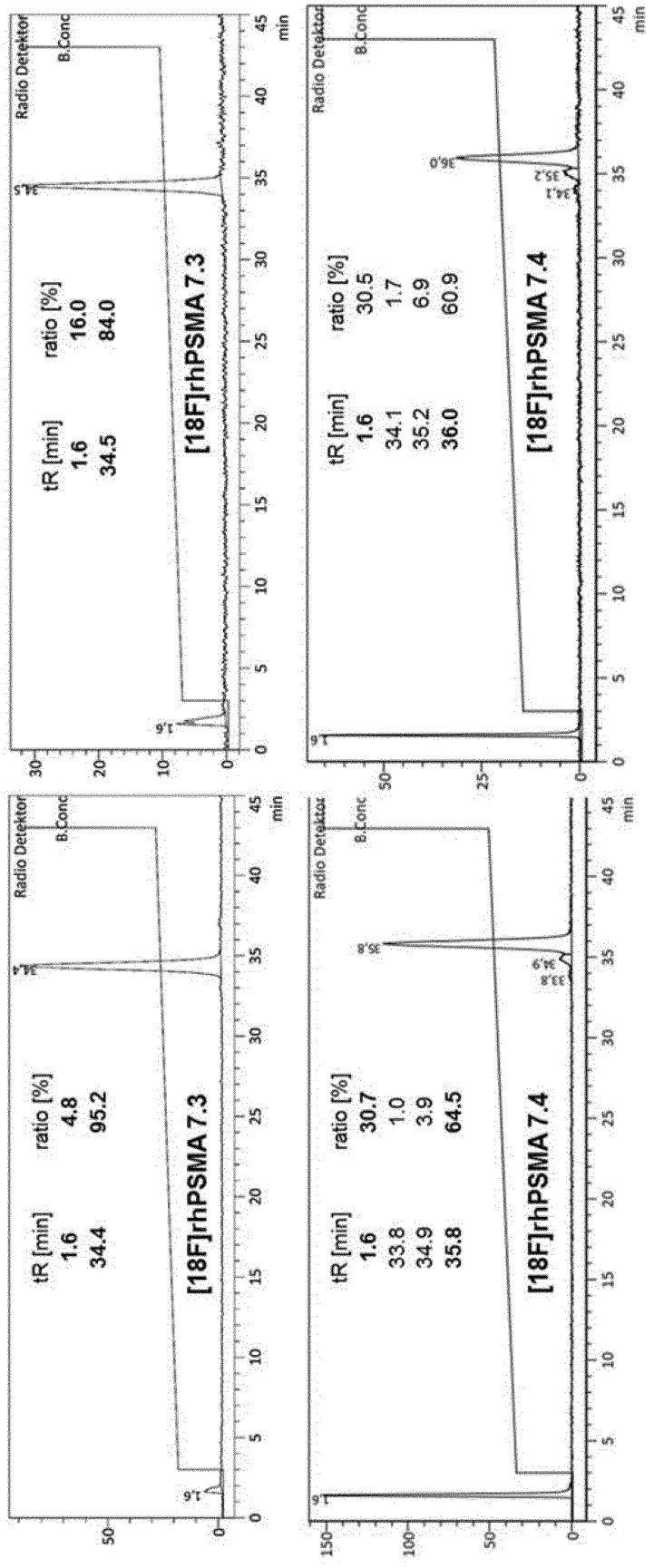


Fig. 21
(continued)

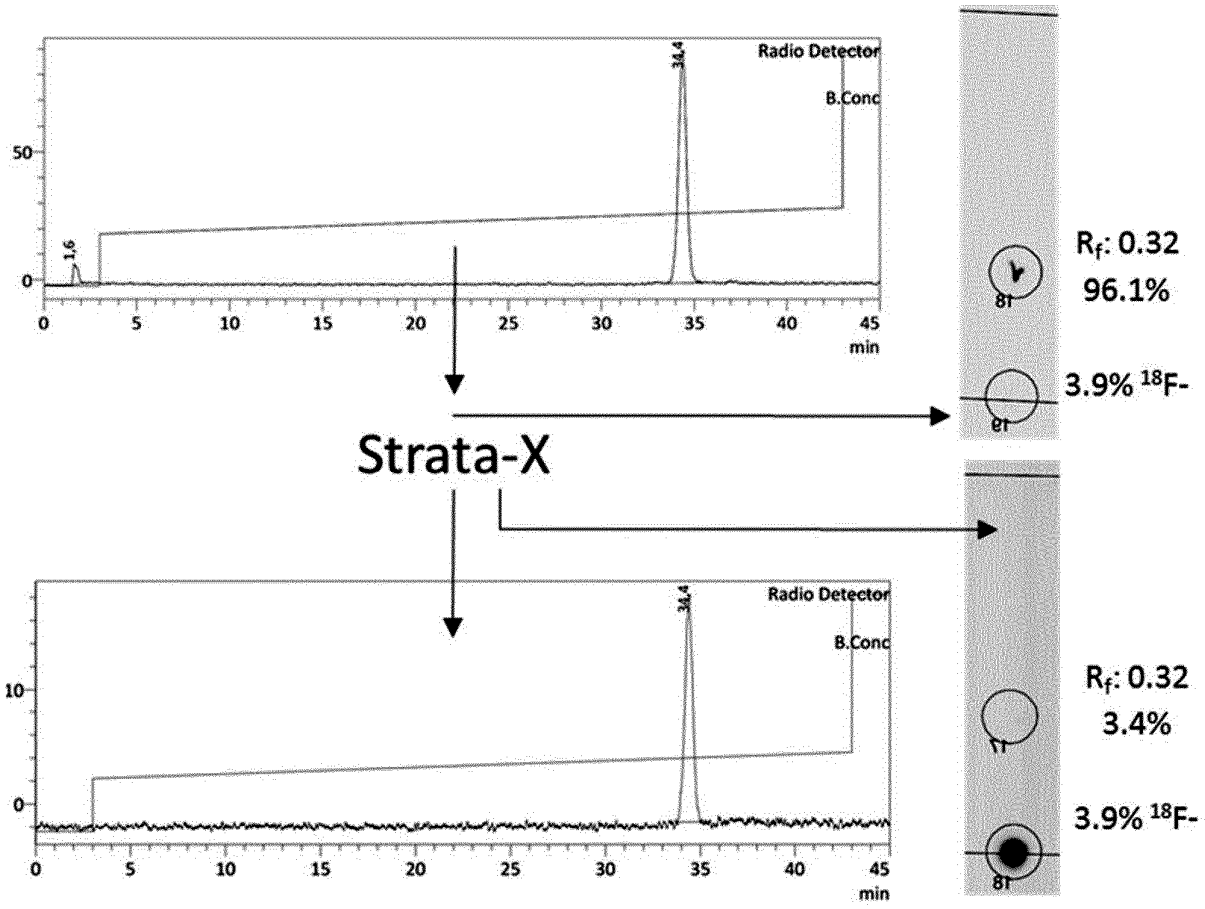

Radio Detector
B.Conc
34.4
1.6
50
0
0 5 10 15 20 25 30 35 40 45
min
Strata-X
Radio Detector
B.Conc
34.4
10
0
0 5 10 15 20 25 30 35 40 45
min
Rf: 0.32
96.1%
3.9% 18F-
Rf: 0.32
3.4%
3.9% 18F-

Fig. 22

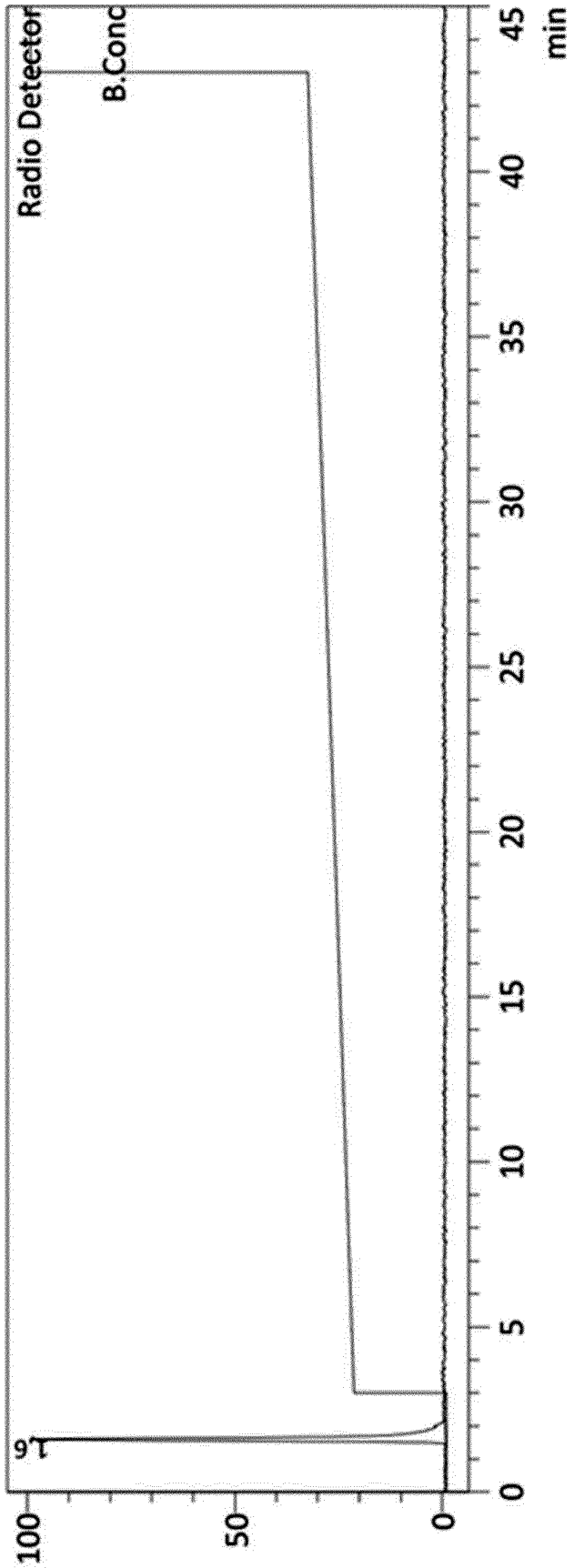


Fig. 23

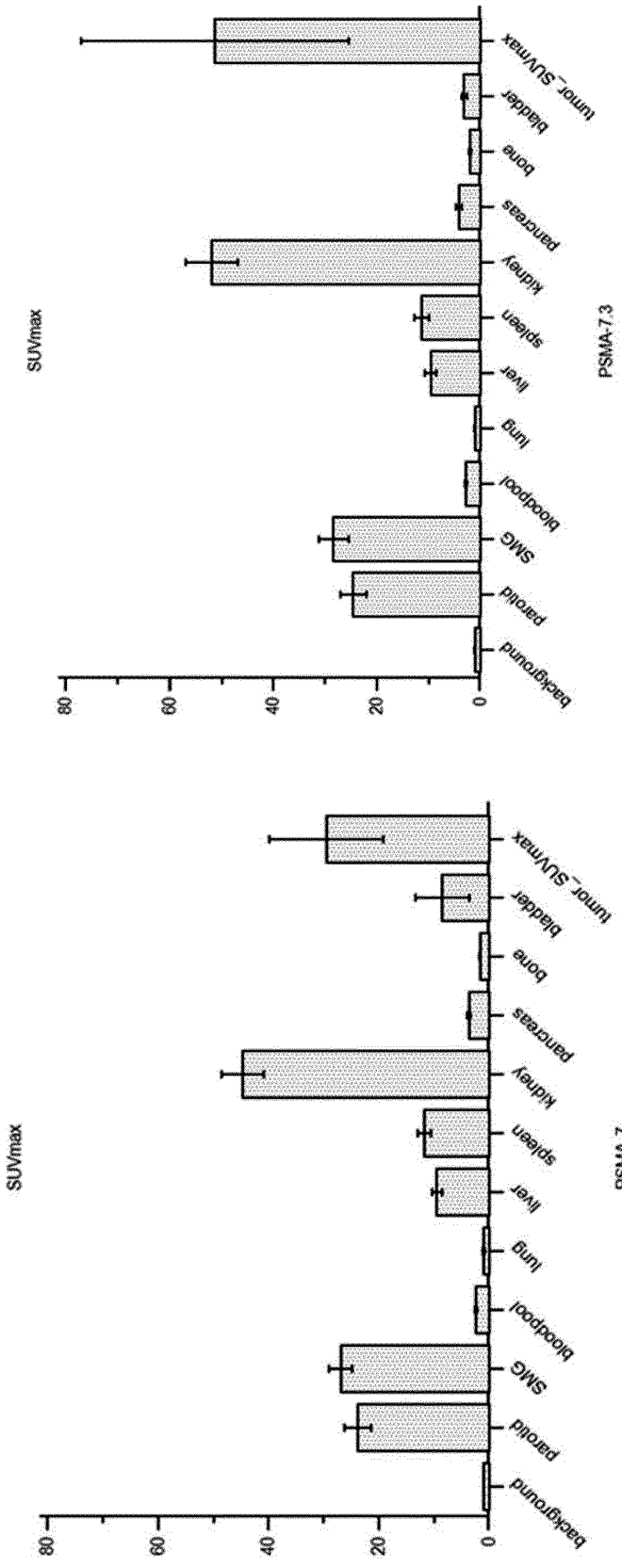

PSMA-7.3
PSMA-7
SUVmax
tumor_SUVmax
bladder
bone
pancreas
kidney
spleen
liver
lung
bloodpool
SMG
parotid
background
0
20
40
60
80

Fig. 24

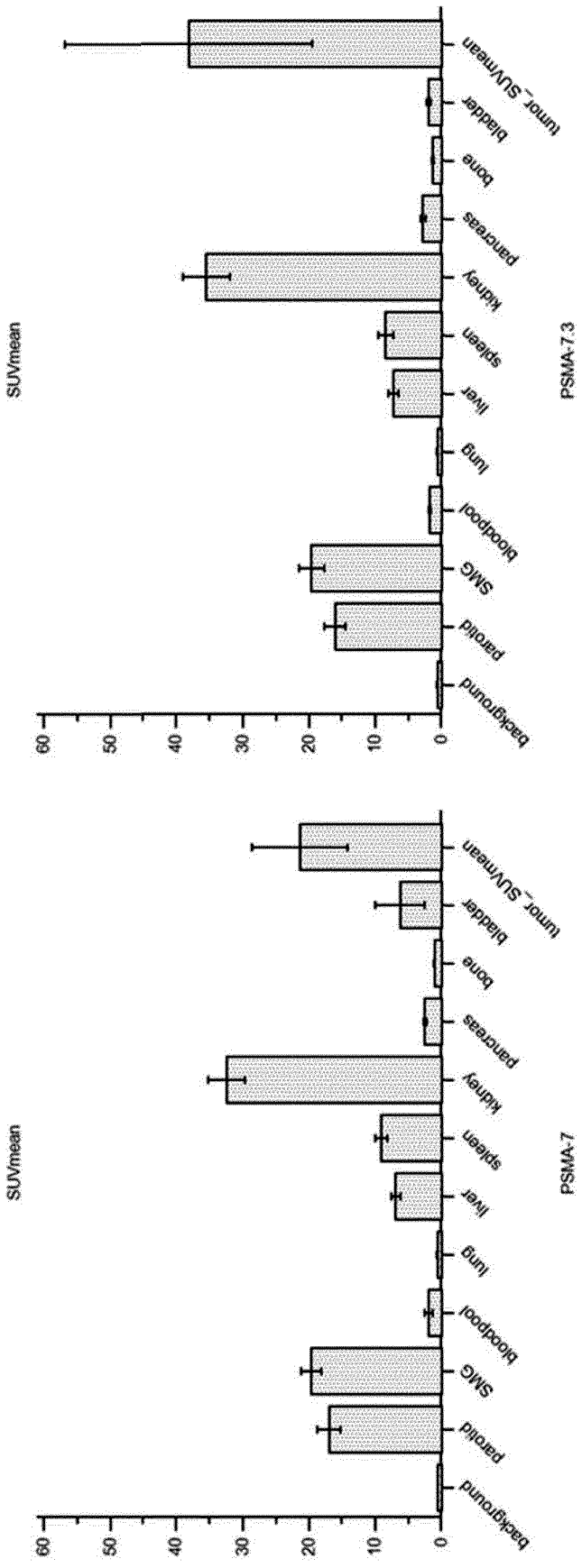

SUVmean
PSMA-7.3
tumor_SUVmean
bladder
bone
pancreas
kidney
spleen
liver
lung
bloodpool
SMG
parotid
background
0
10
20
30
40
50
60
SUVmean
PSMA-7
tumor_SUVmean
bladder
bone
pancreas
kidney
spleen
liver
lung
bloodpool
SMG
parotid
background
0
10
20
30
40
50
60

Fig. 25

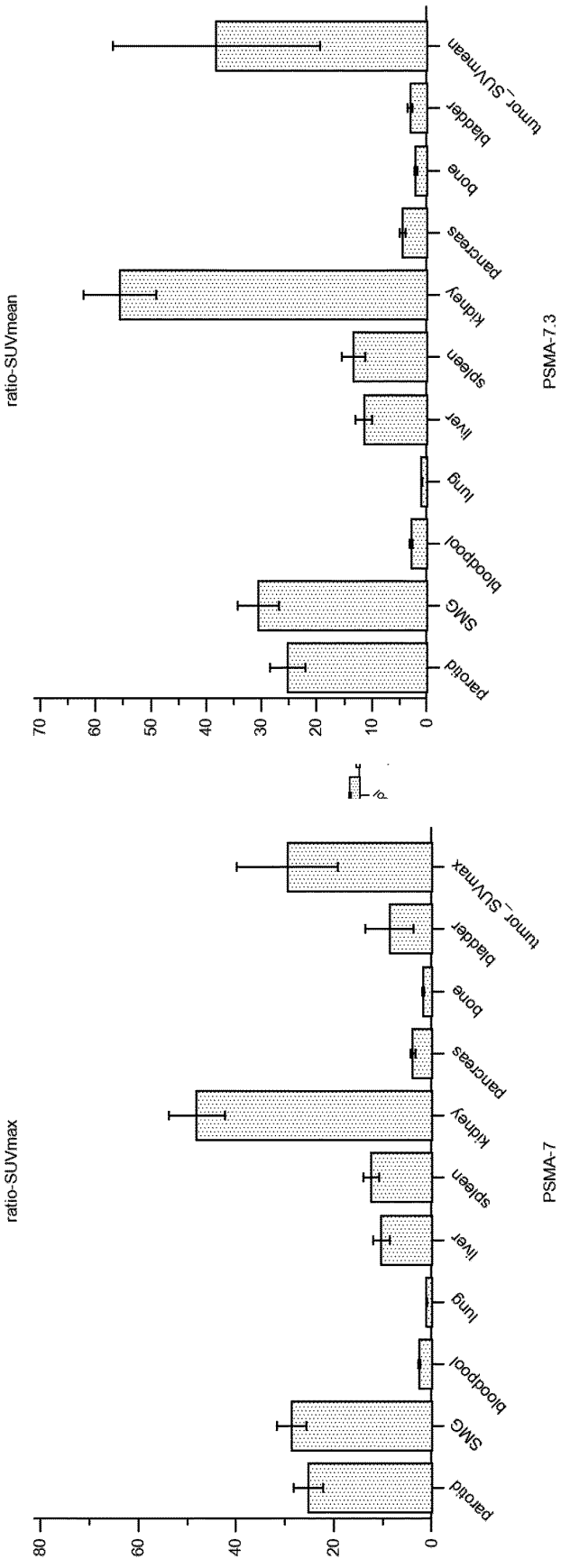

ratio-SUVmean
PSMA-7.3
70
60
50
40
30
20
10
0
parotid
SMG
bloodpool
lung
liver
spleen
kidney
pancreas
bone
bladder
tumor_SUVmean
ratio-SUVmax
PSMA-7
80
60
40
20
0
parotid
SMG
bloodpool
lung
liver
spleen
kidney
pancreas
bone
bladder
tumor_SUVmax

Fig. 26

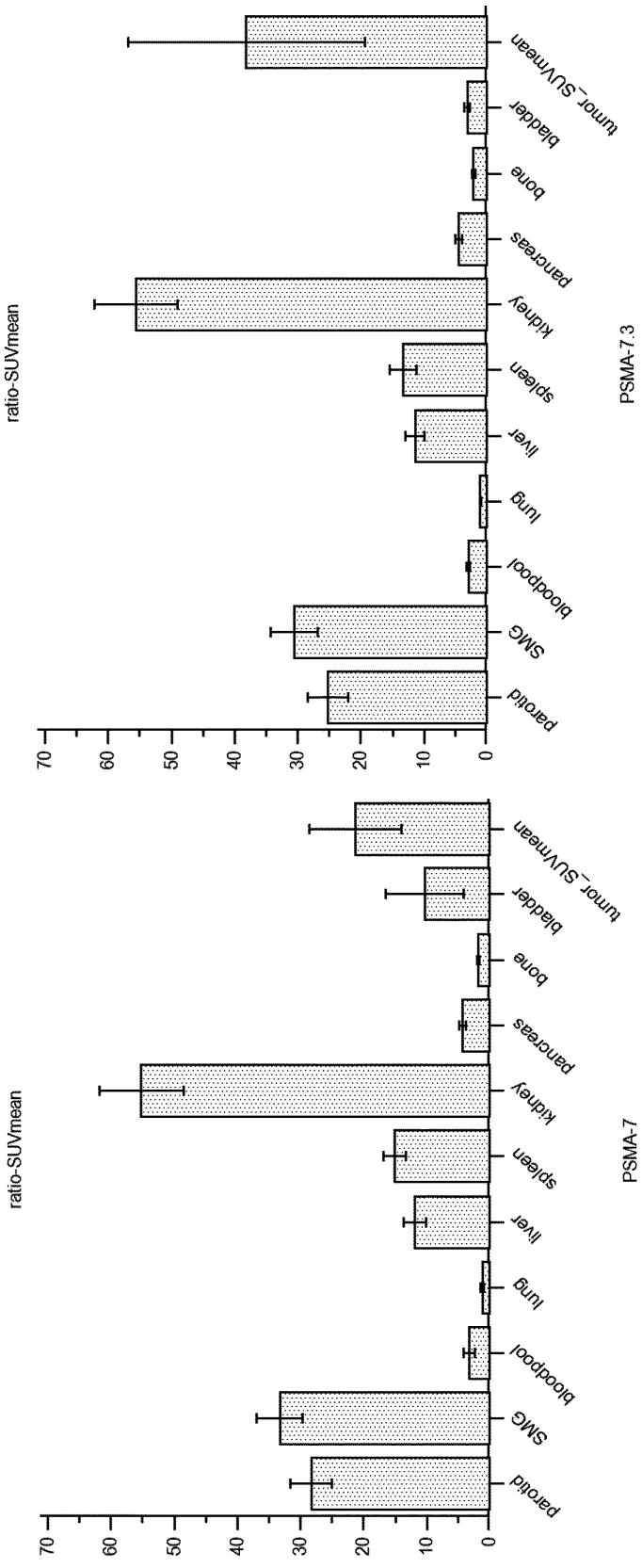

ratio-SUVmean
70
60
50
40
30
20
10
0
parotid
SMG
bloodpool
lung
liver
spleen
kidney
pancreas
bone
bladder
tumor_SUVmean
PSMA-7
PSMA-7.3

Fig. 27

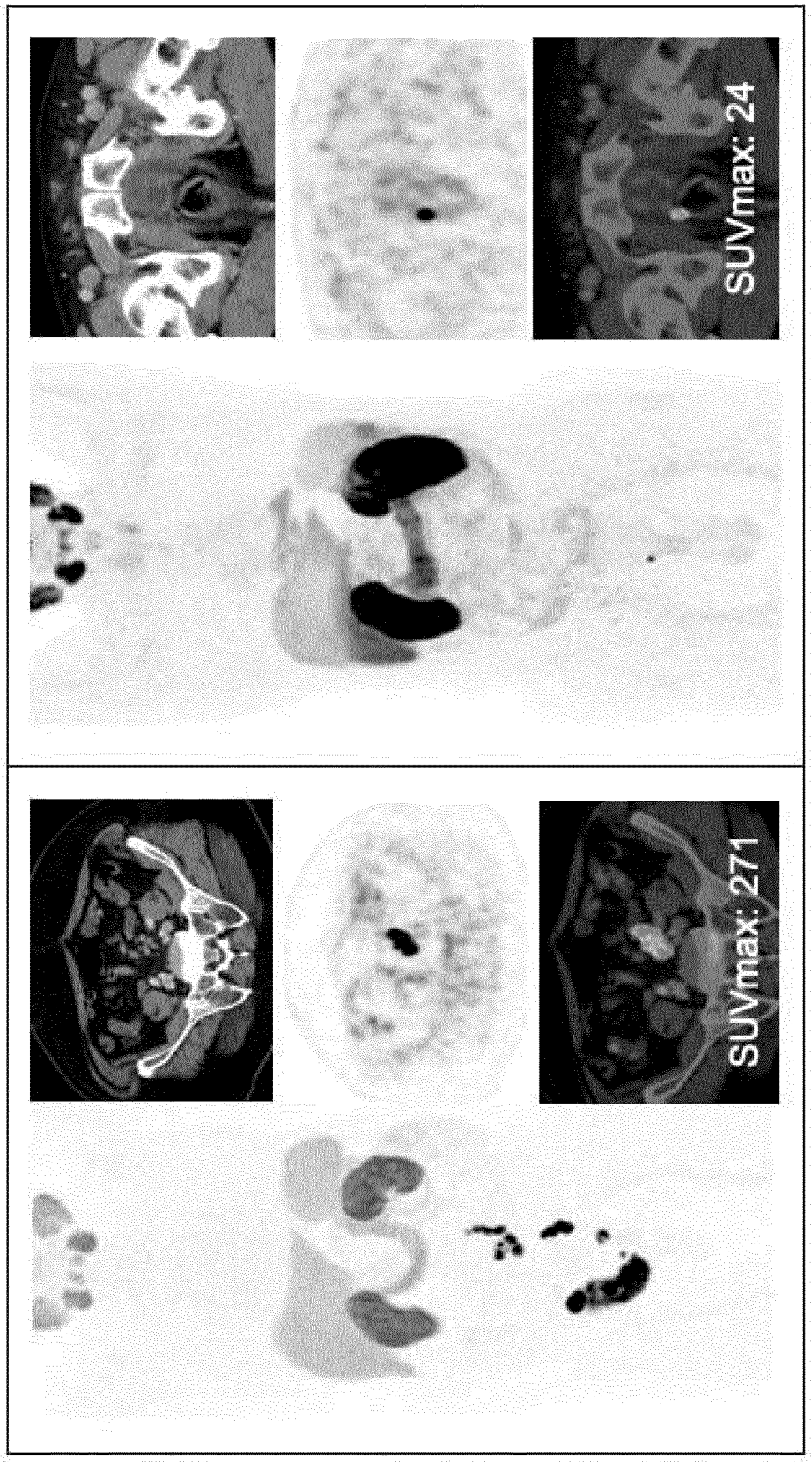


Fig. 28