Figure 1

Gating Strategy for FACS analysis

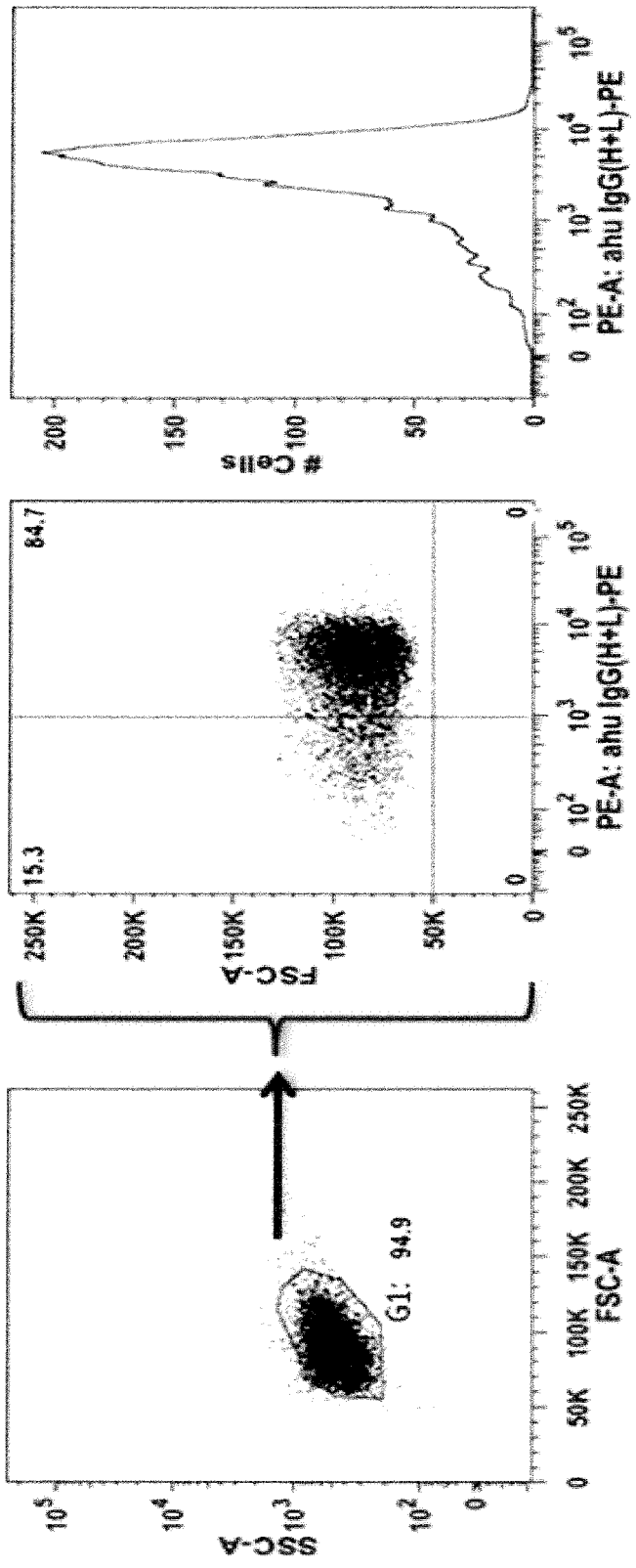


Figure 2

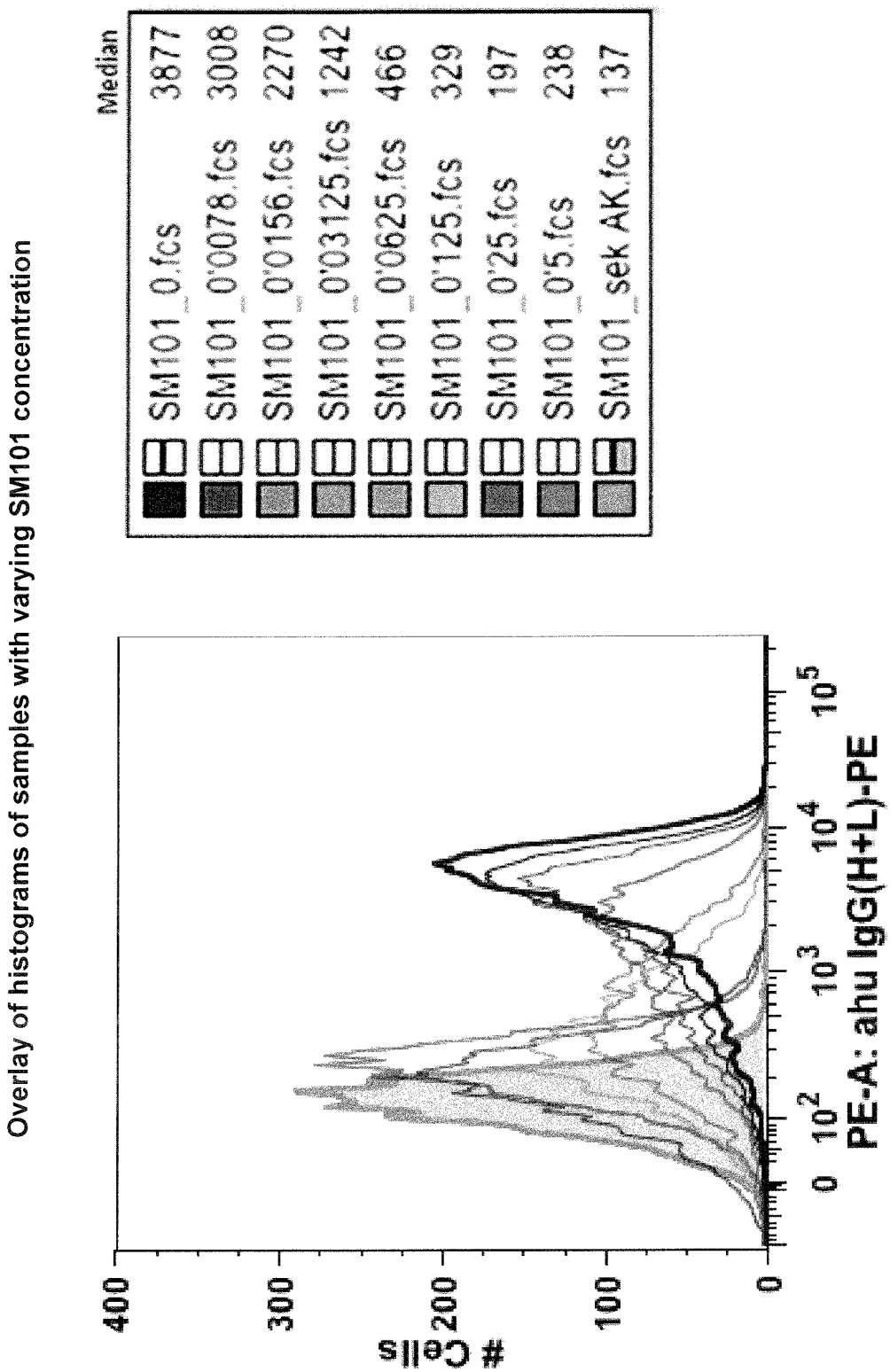

Overlay of histograms of samples with varying SM101 concentration
Median
SM101_0.fcs 3877
SM101_0'0078.fcs 3008
SM101_0'0156.fcs 2270
SM101_0'03125.fcs 1242
SM101_0'0625.fcs 466
SM101_0'125.fcs 329
SM101_0'25.fcs 197
SM101_0'5.fcs 238
SM101_sek AK.fcs 137
Cells
400
300
200
100
0
0
10^2
10^3
10^4
10^5
PE-A: ahu IgG(H+L)-PE

Figure 3

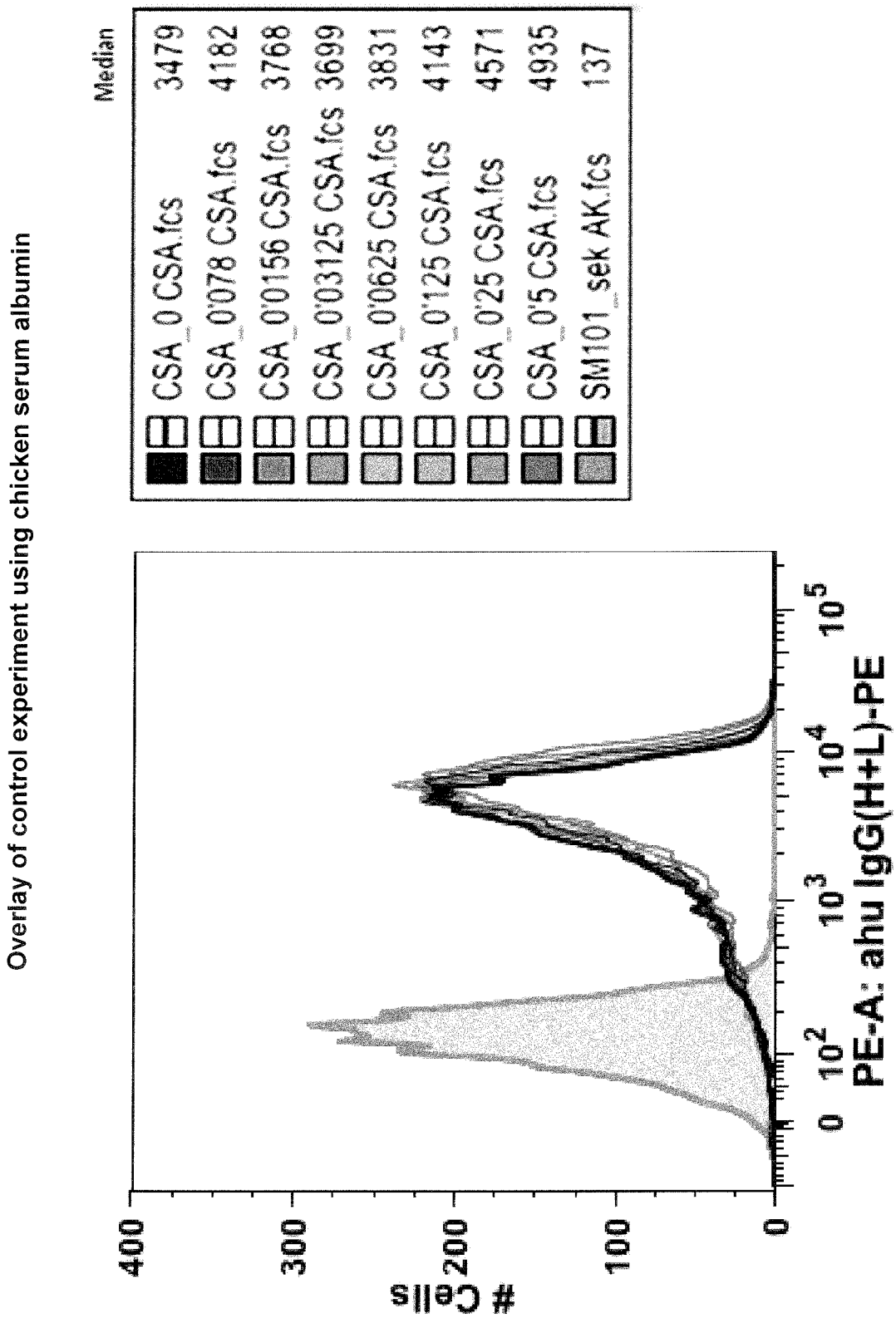

Overlay of control experiment using chicken serum albumin
Median
CSA_0 CSA.fcs 3479
CSA_0'078 CSA.fcs 4182
CSA_0'0156 CSA.fcs 3768
CSA_0'03125 CSA.fcs 3699
CSA_0'0625 CSA.fcs 3831
CSA_0'125 CSA.fcs 4143
CSA_0'25 CSA.fcs 4571
CSA_0'5 CSA.fcs 4935
SM101_sek AK.fcs 137
Cells
400
300
200
100
0
0
10^2
10^3
10^4
10^5
PE-A: ahu IgG(H+L)-PE

Figure 4

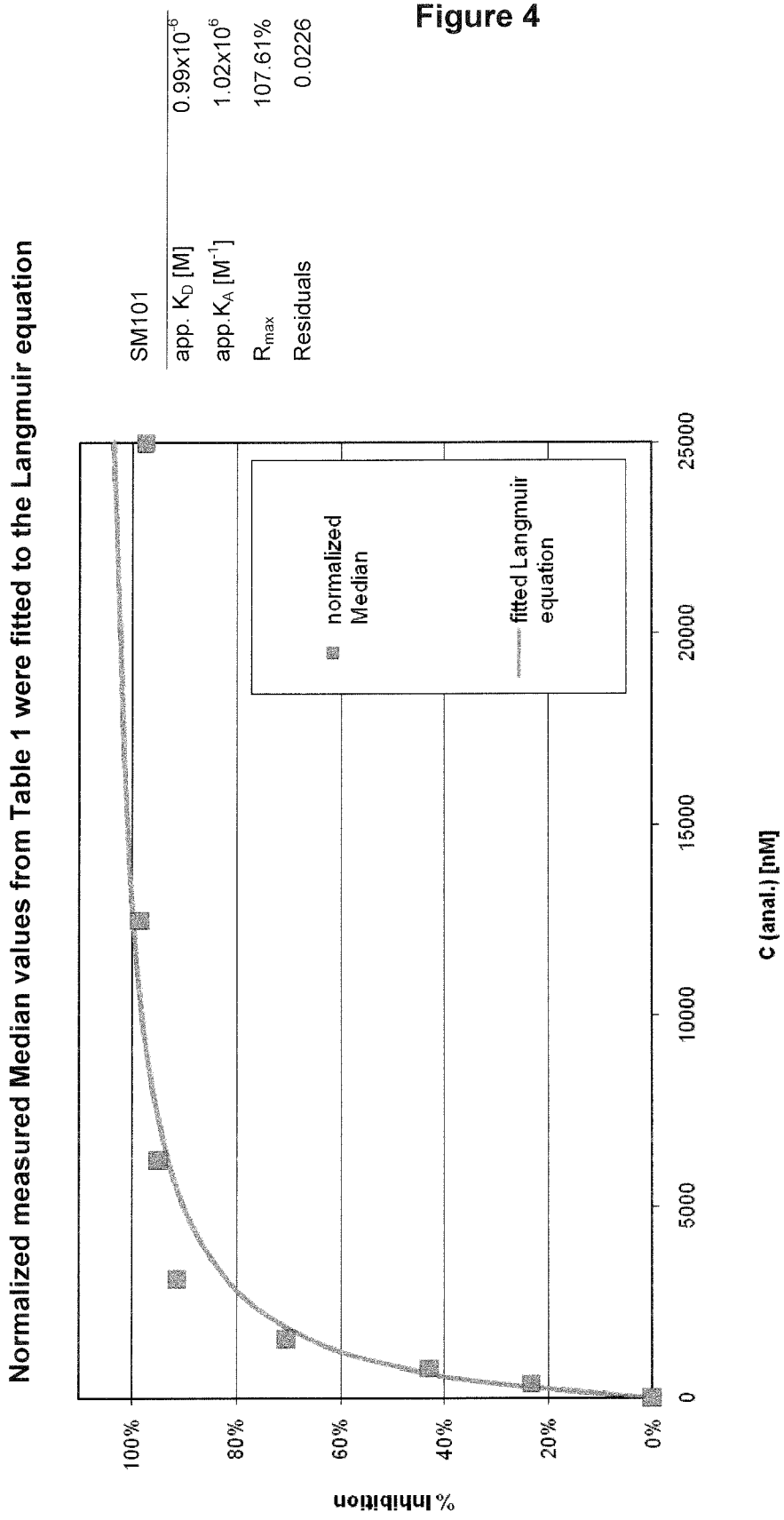

Normalized measured Median values from Table 1 were fitted to the Langmuir equation
SM101
app. K_D [M] 0.99x10^{-6}
app.K_A [M^{-1}] 1.02x10^{6}
R_{max} 107.61%
Residuals 0.0226
normalized Median
fitted Langmuir equation
% Inhibition
100%
80%
60%
40%
20%
0%
0
5000
10000
15000
20000
25000
C (anal.) [nM]

Figure 5

Data fitted to sigmoid logistic function showing %inhibition versus mass concentration of SM101

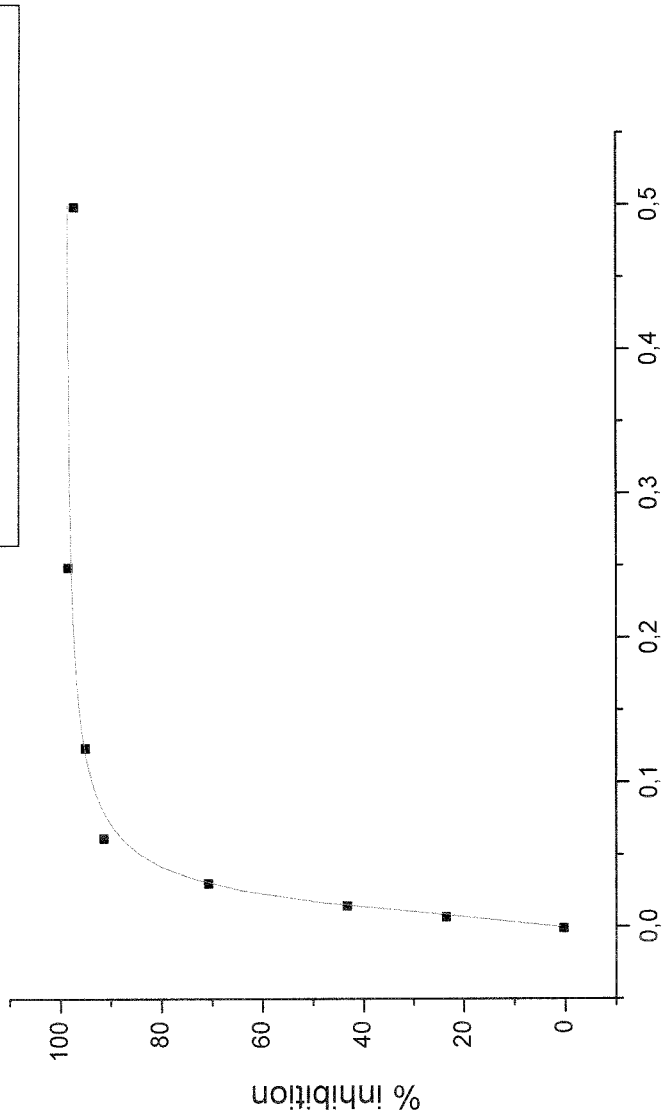


Figure 6

Langmuir diagram of data fitted to normalized measured Median values of reference and SM101

SM101	Ref. Std.	IMP
app.K_D [M]	0.74×10^{-6}	0.90×10^{-6}
app.K_A [M^{-1}]	1.35×10^{6}	1.11×10^{6}
R_{max}	105.64	107.21
Residuals	0.05	0.02
IC_{50} [µg/mL]	12.9	16.2

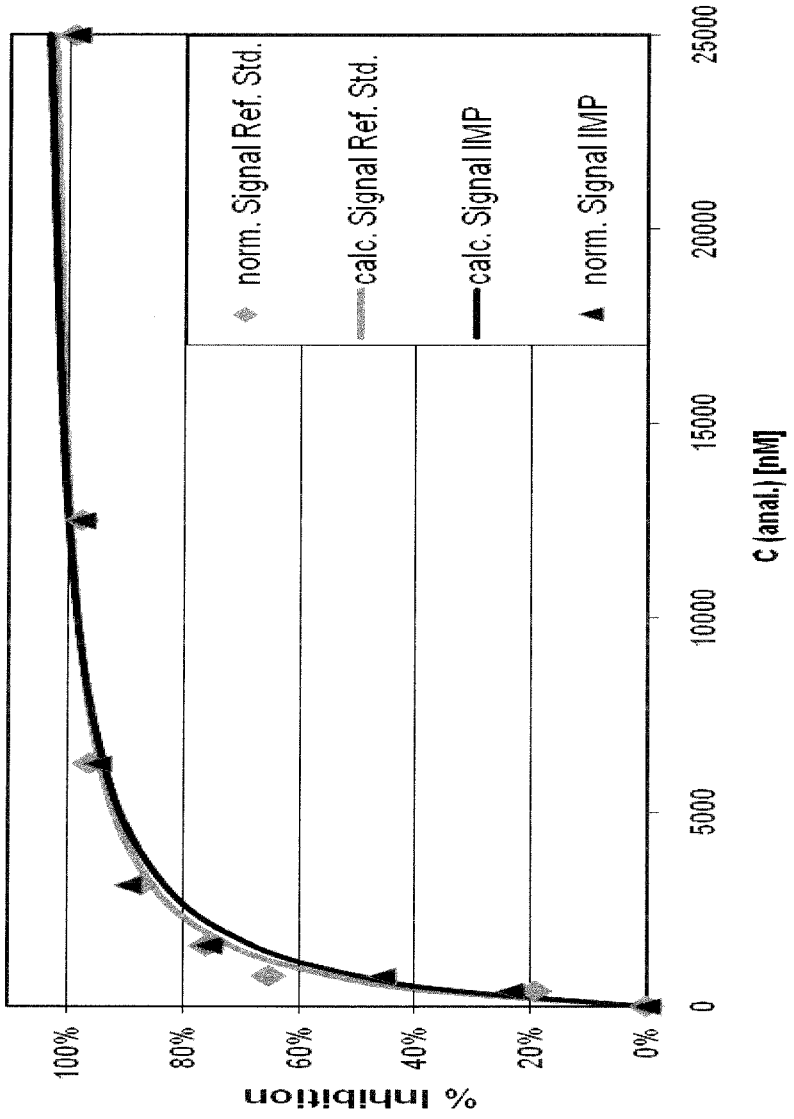


Figure 7

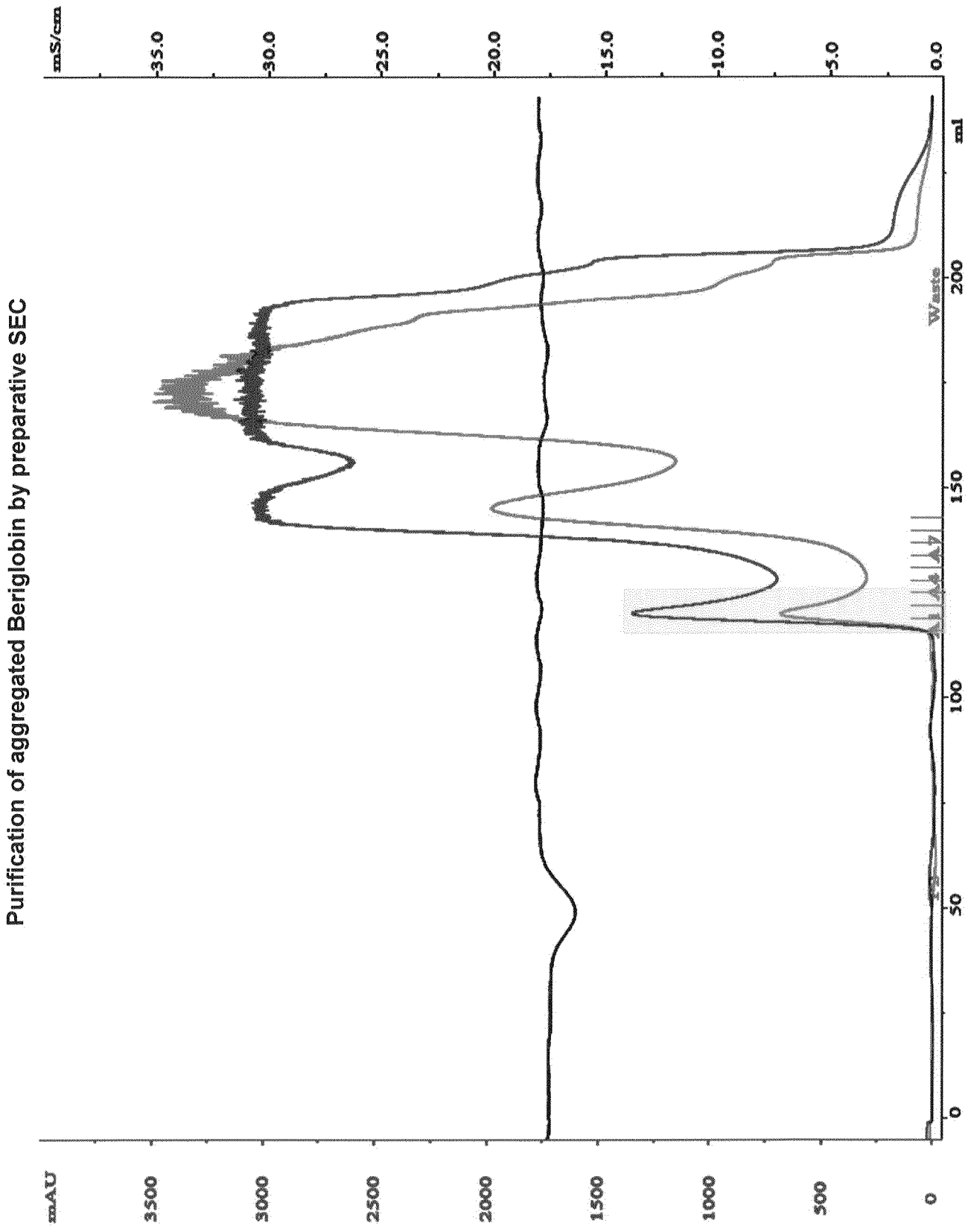

Purification of aggregated Beriglobin by preparative SEC
mS/cm
35.0
30.0
25.0
20.0
15.0
10.0
5.0
0.0
ml
Waste
200
150
100
50
0
mAU
3500
3000
2500
2000
1500
1000
500
0

Figure 8

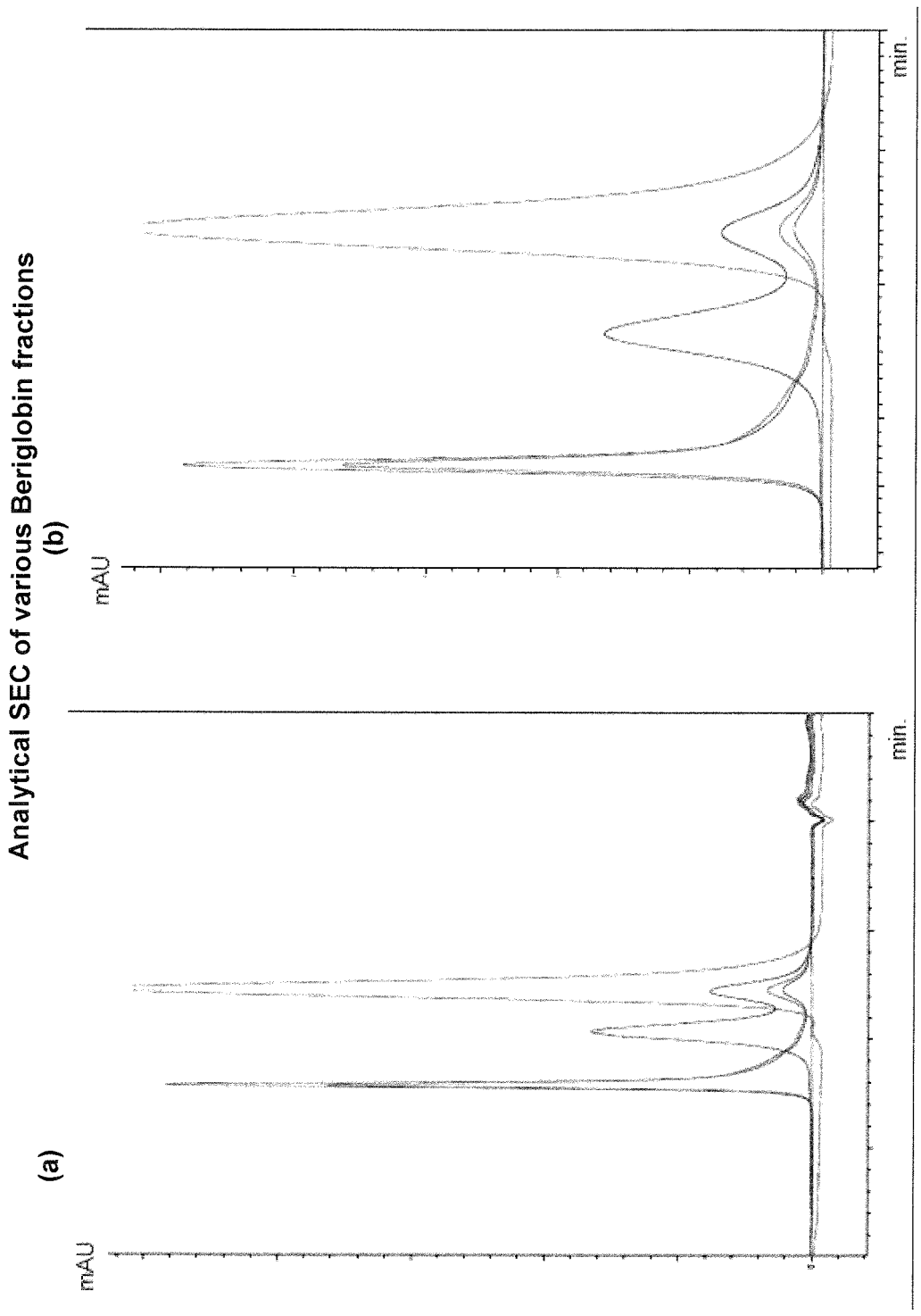
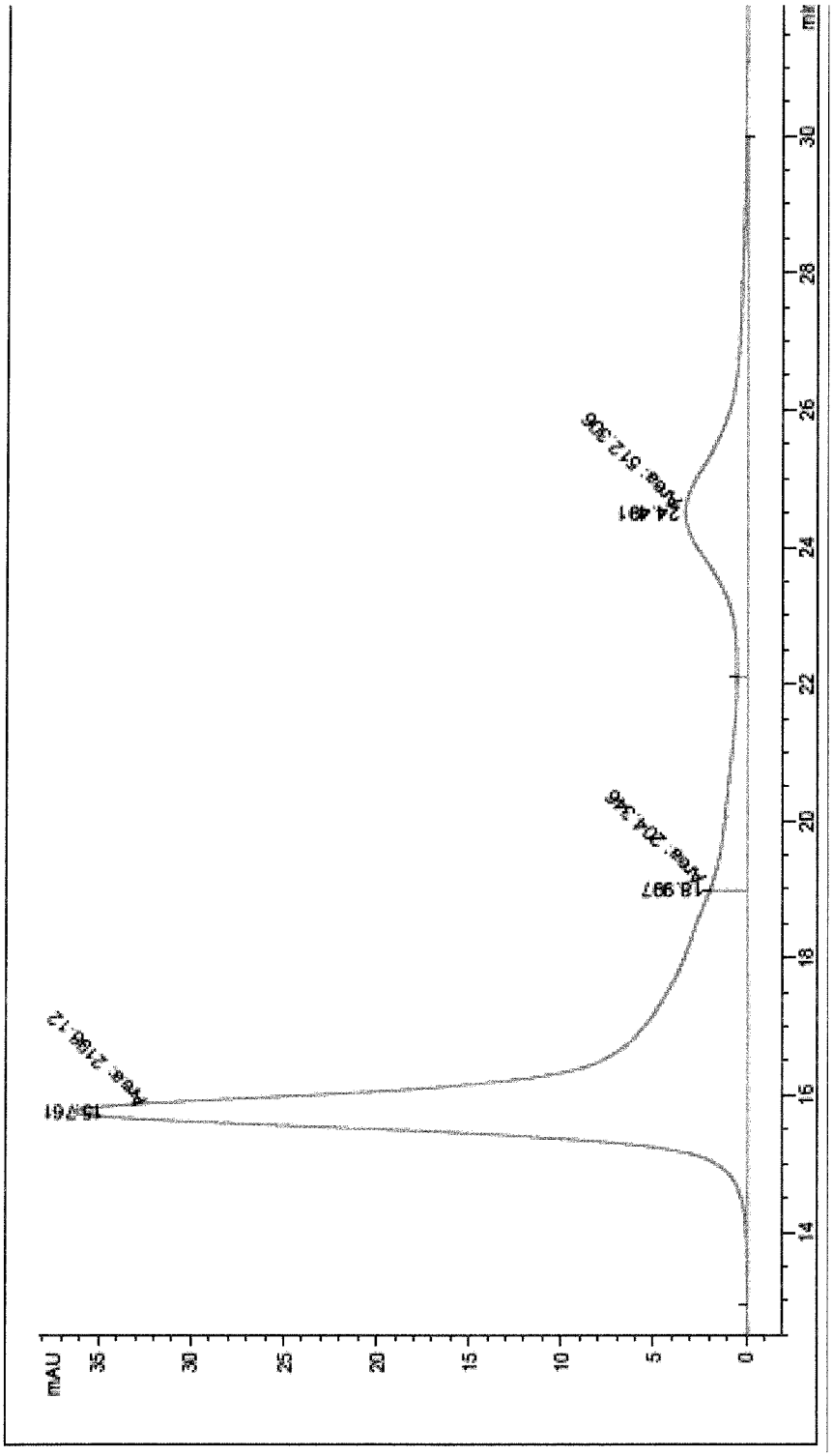
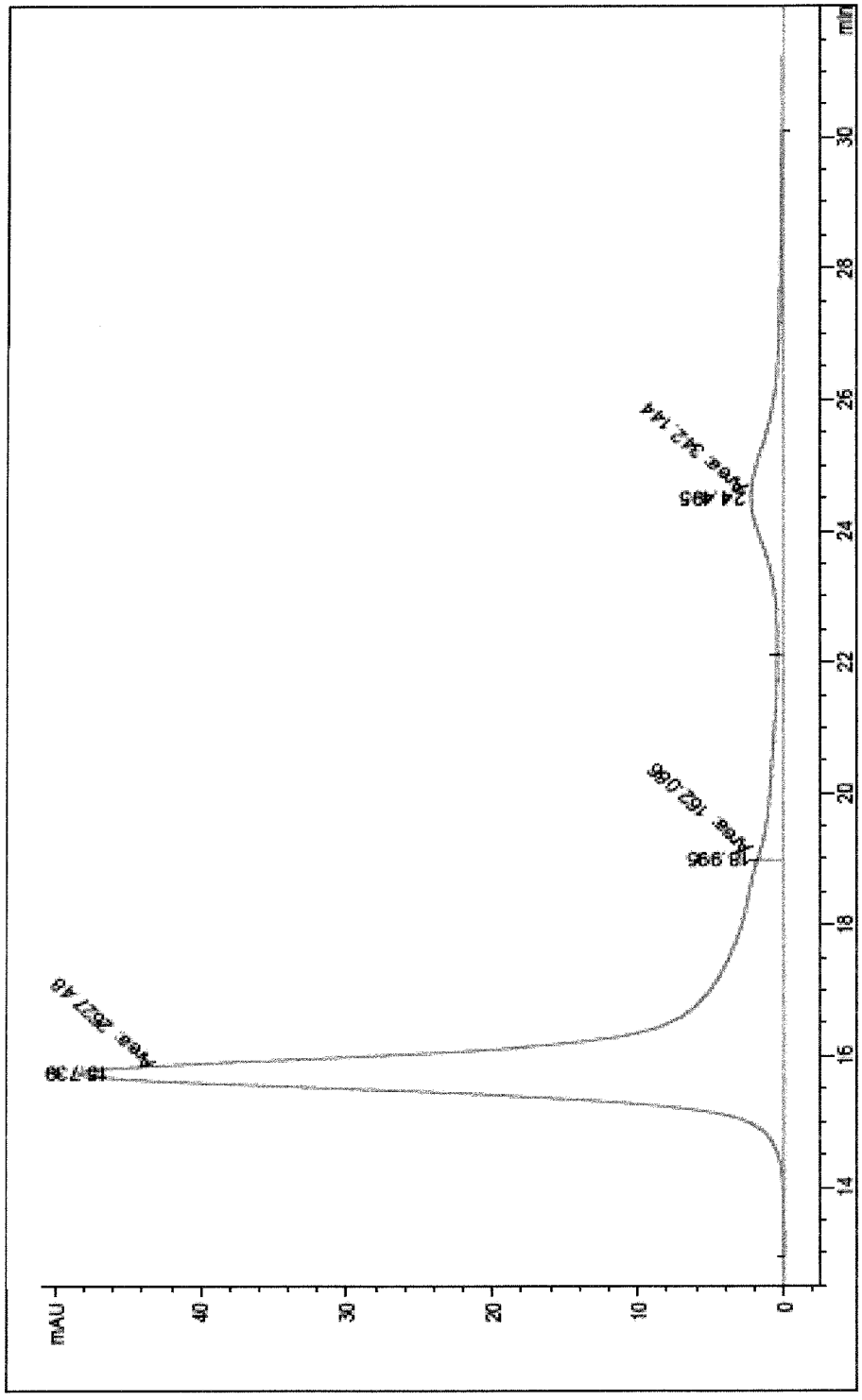

Analytical SEC of various Beriglobin fractions
(a)
mAU
min.
(b)
mAU
min.

Figure 9a



Beriglobin species	peak retention time [min]	Area, absolute [mAU·s]	Area, relative [%]
aggregated / oligomeric	15.8	2198	75.4
dimeric	n.a.	204	7.0
monomeric	24.5	512	17.6

Figure 9b



Beriglobin species	peak retention time [min]	Area, absolute [mAU·s]	Area, relative [%]
aggregated / oligomeric	15.7	2627	83.9
dimeric	n.a.	162	5.2
monomeric	24.5	342	10.9

Figure 10

FACS analysis of different batches and varying amounts of aggregated Beriglobin

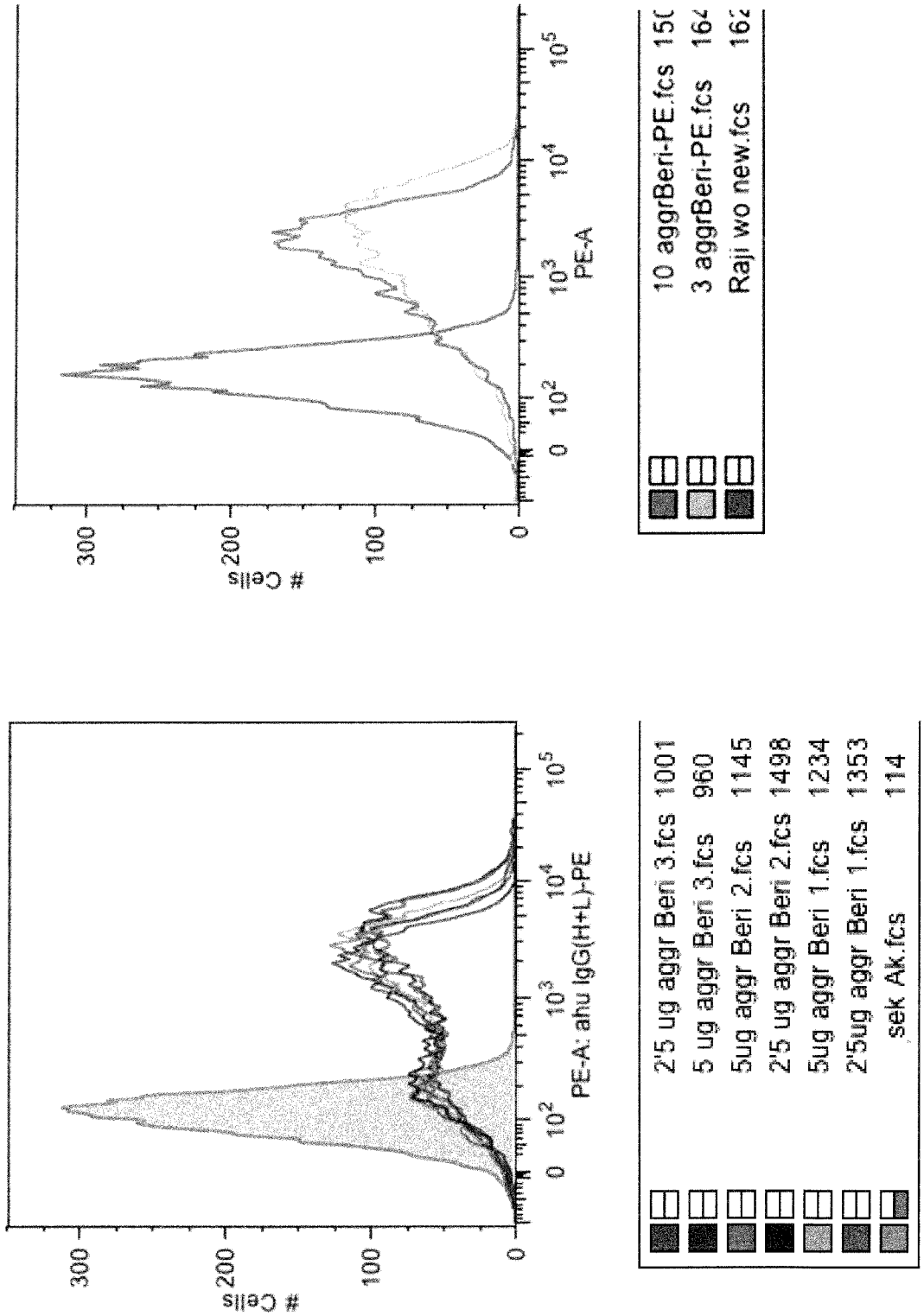


Figure 11a

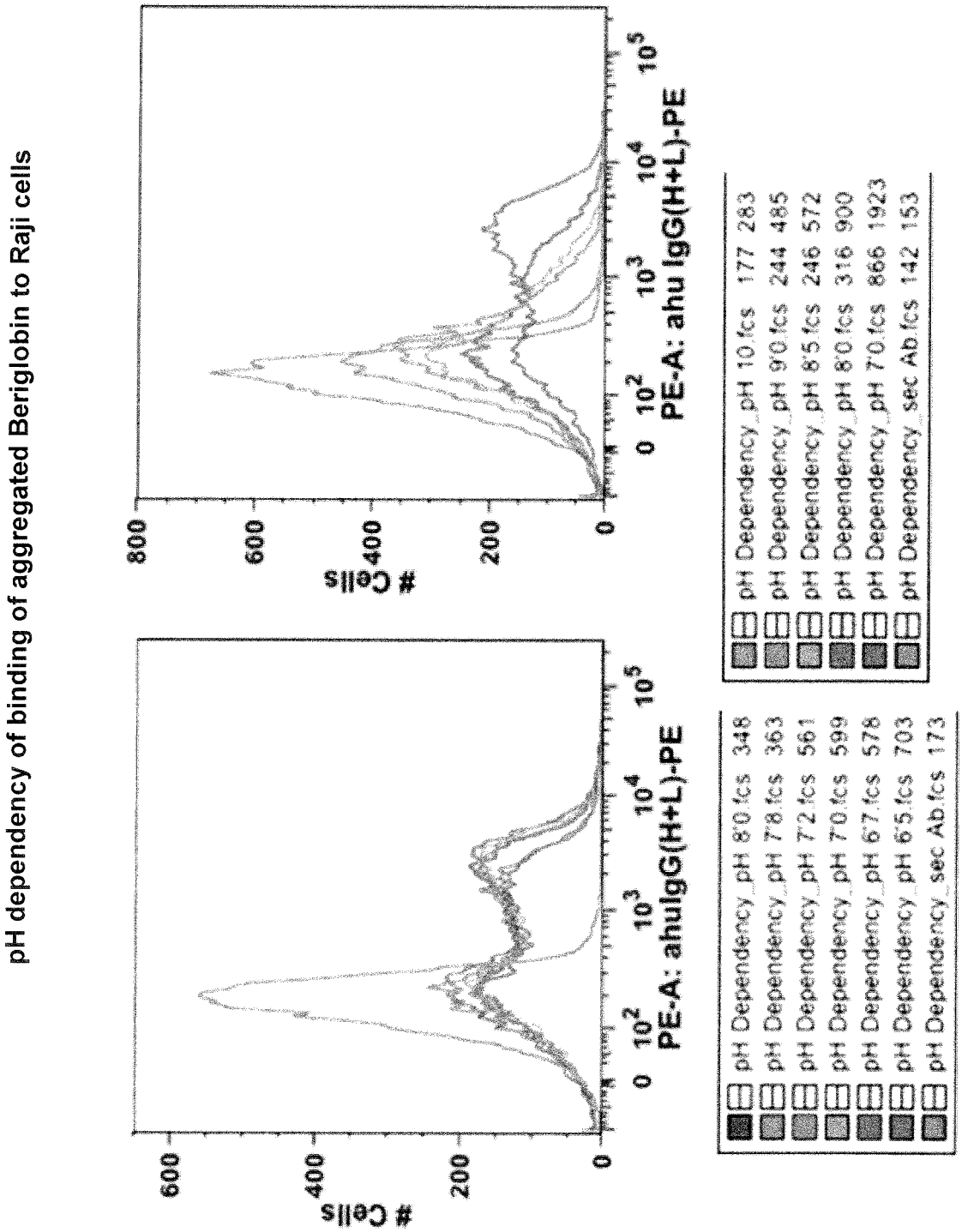
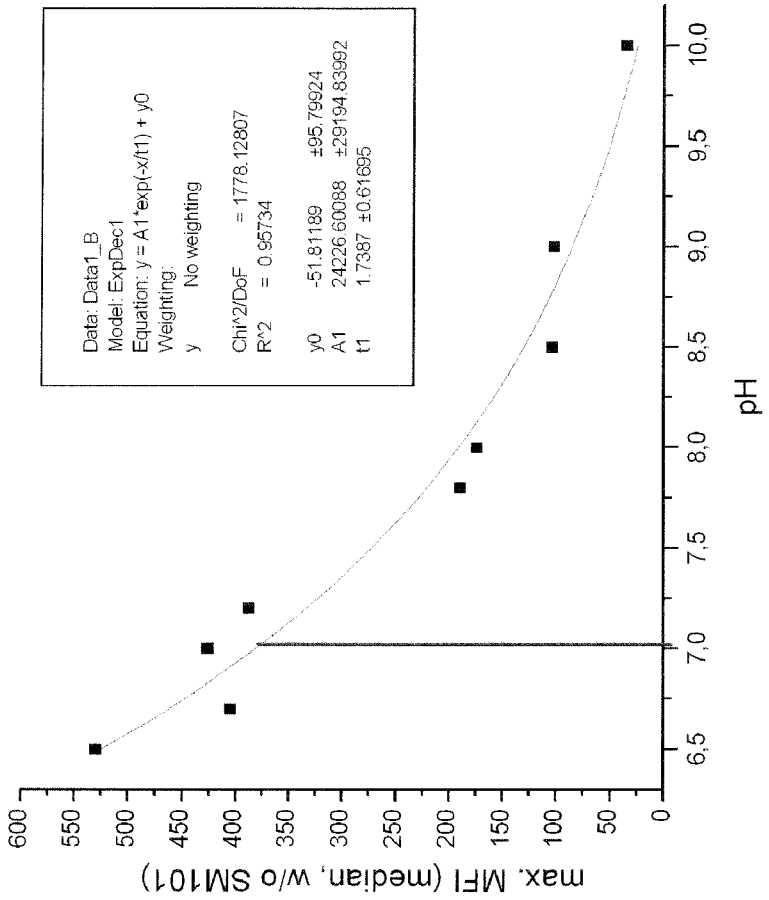

pH dependency of binding of aggregated Beriglobin to Raji cells
Cells
PE-A: ahuIgG(H+L)-PE
pH Dependency_pH 80.fcs 348
pH Dependency_pH 78.fcs 363
pH Dependency_pH 72.fcs 561
pH Dependency_pH 70.fcs 599
pH Dependency_pH 67.fcs 578
pH Dependency_pH 65.fcs 703
pH Dependency_sec Ab.fcs 173
Cells
PE-A: ahu IgG(H+L)-PE
pH Dependency_pH 10.fcs 177 283
pH Dependency_pH 90.fcs 244 485
pH Dependency_pH 85.fcs 246 572
pH Dependency_pH 80.fcs 316 900
pH Dependency_pH 70.fcs 866 1923
pH Dependency_sec Ab.fcs 142 153

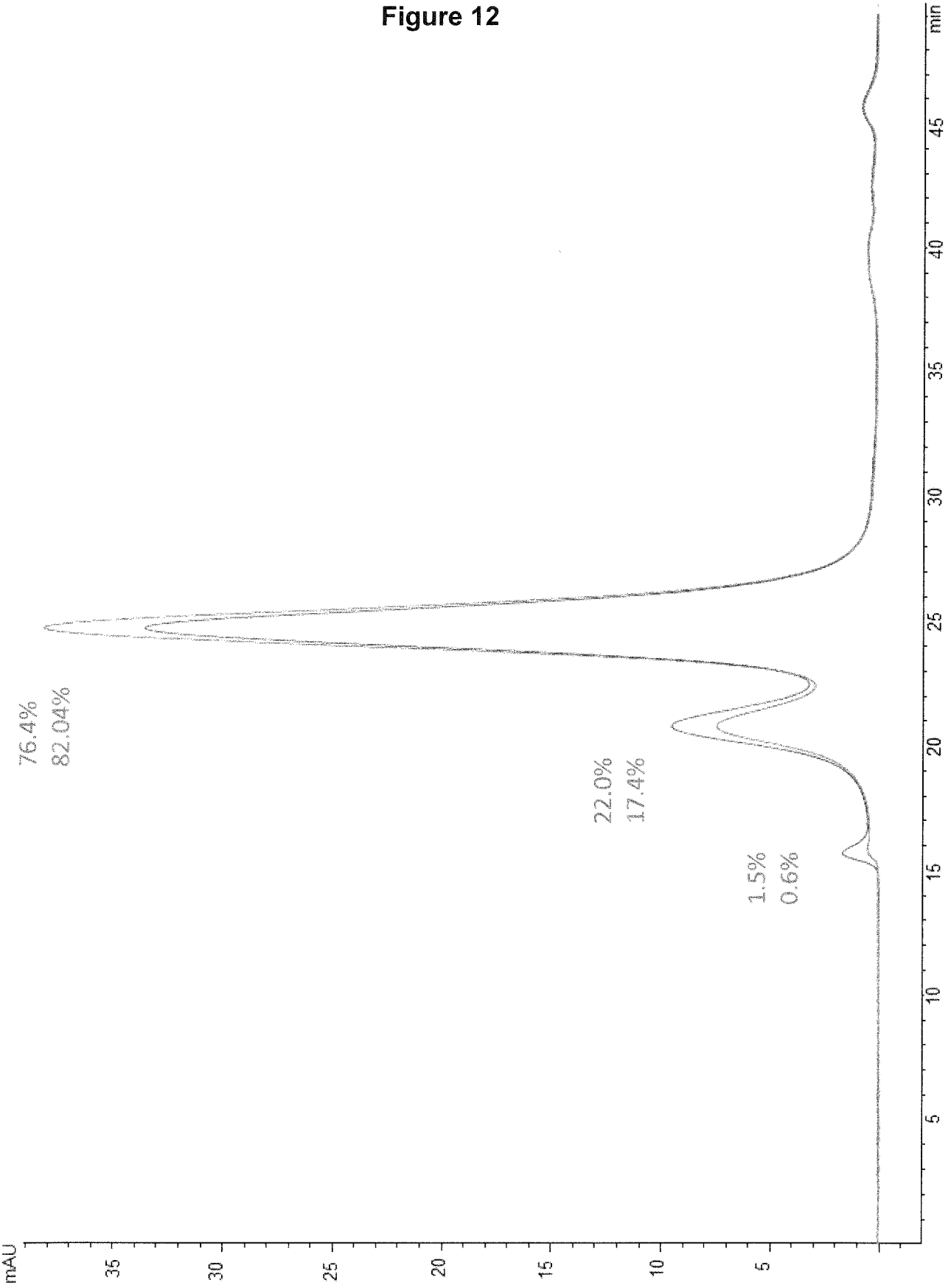
Figure 11b

pH dependency of binding of aggregated Beriglobin to Raji cell



pH	Median MFI
6.5	703
6.7	578
7	599
7.2	561
7.8	363
8	348
8.5	246
9	244
10	177

Figure 12


mAU
35
30
25
20
15
10
5
min
5
10
15
20
25
30
35
40
45
76.4%
82.04%
22.0%
17.4%
1.5%
0.6%