Figure 1

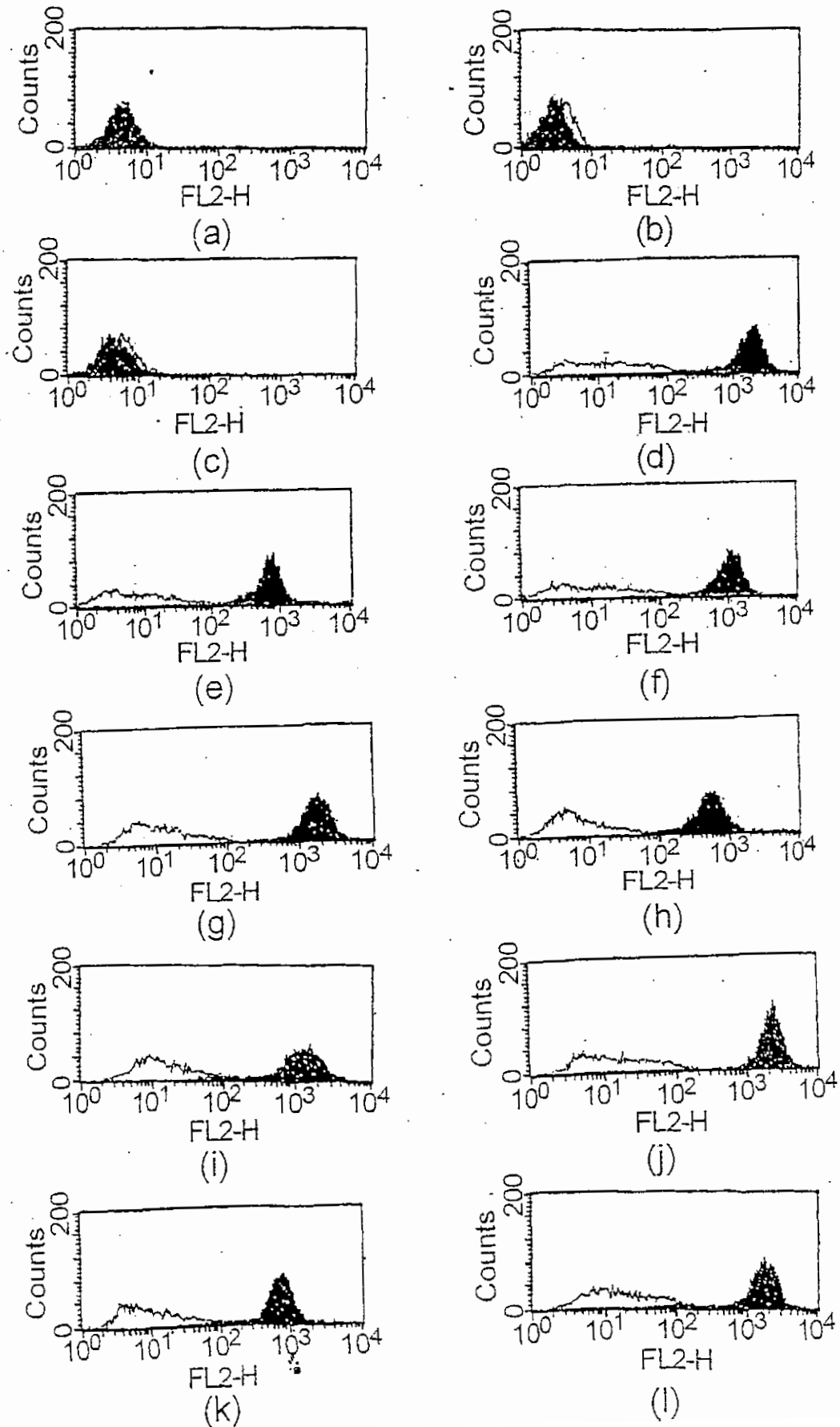


Figure 2

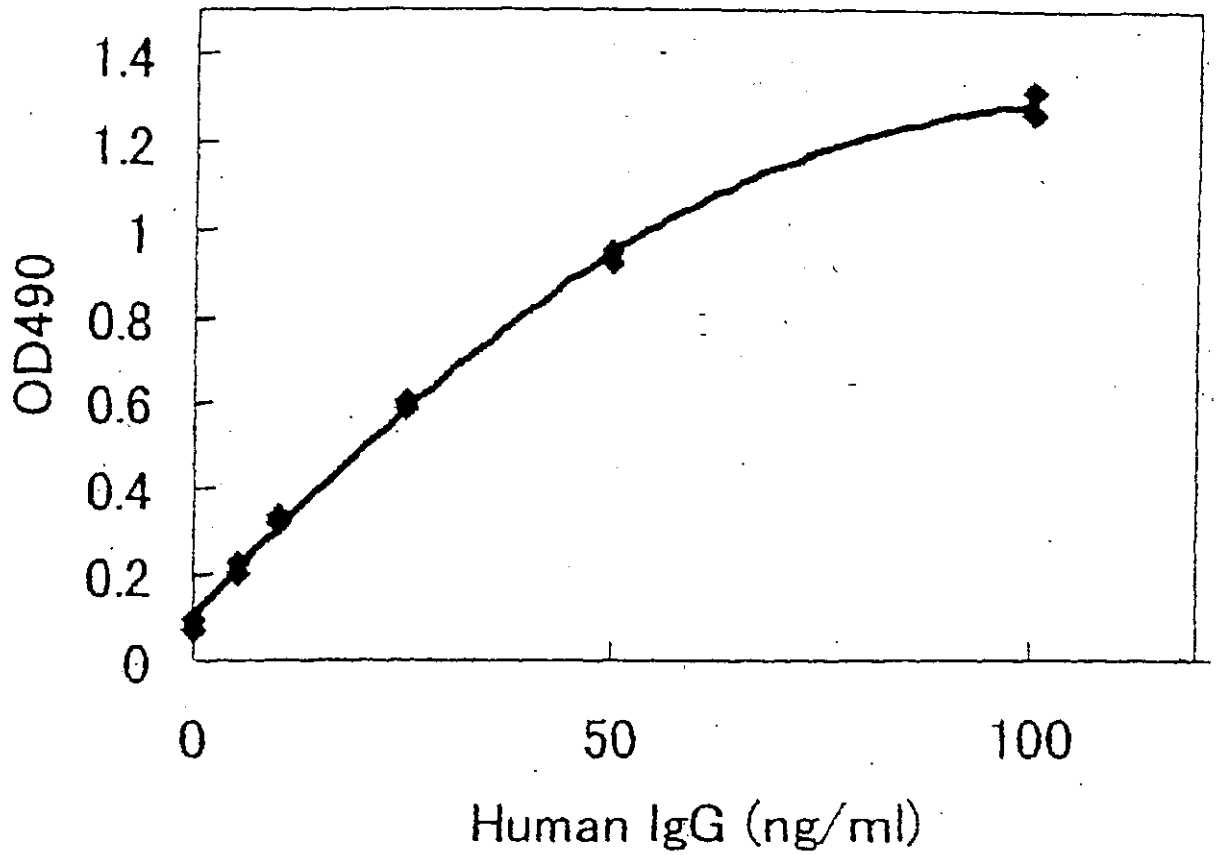


Figure 3

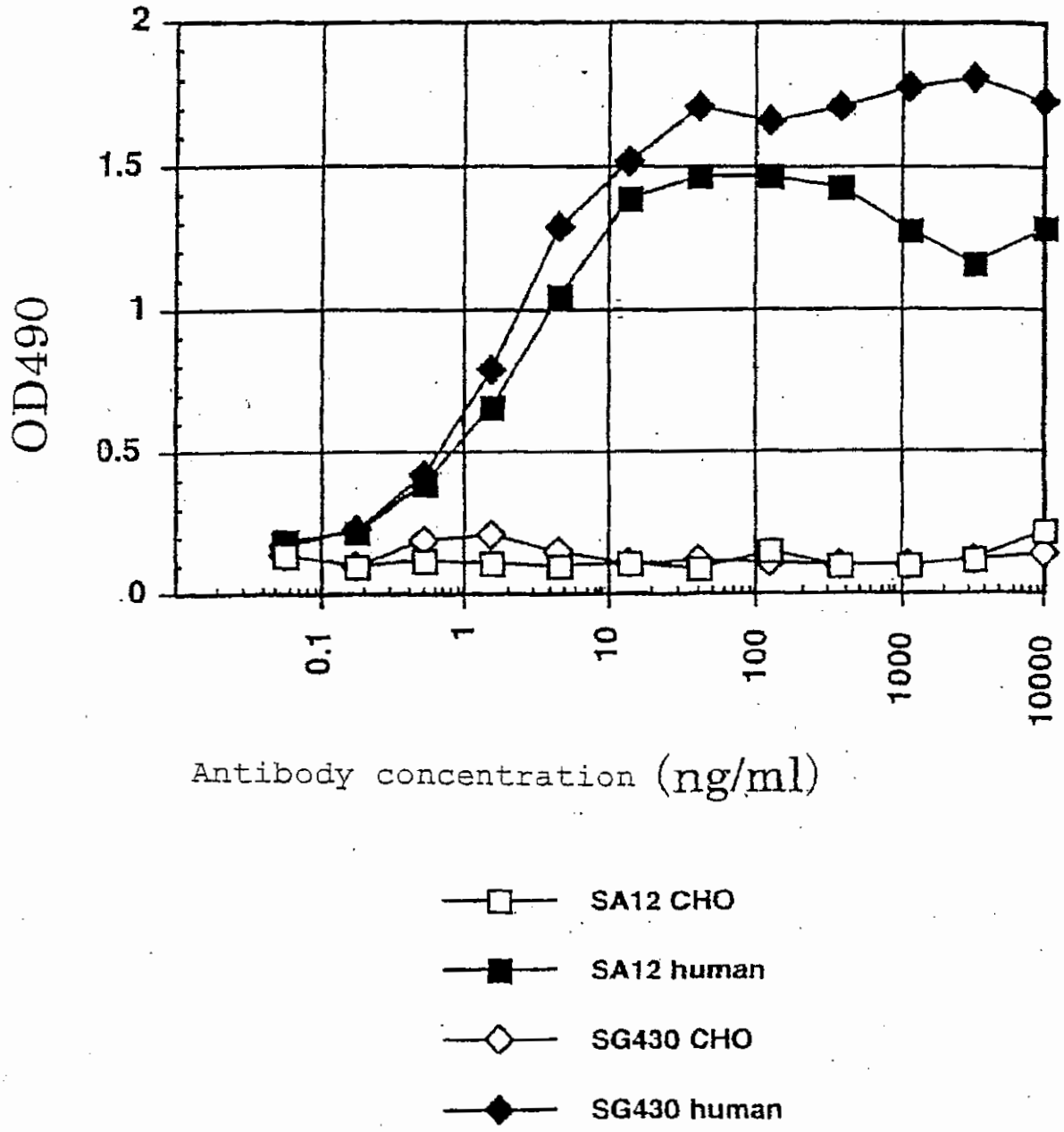

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
SA12 CHO
SA12 human
SG430 CHO
SG430 human

Figure 4

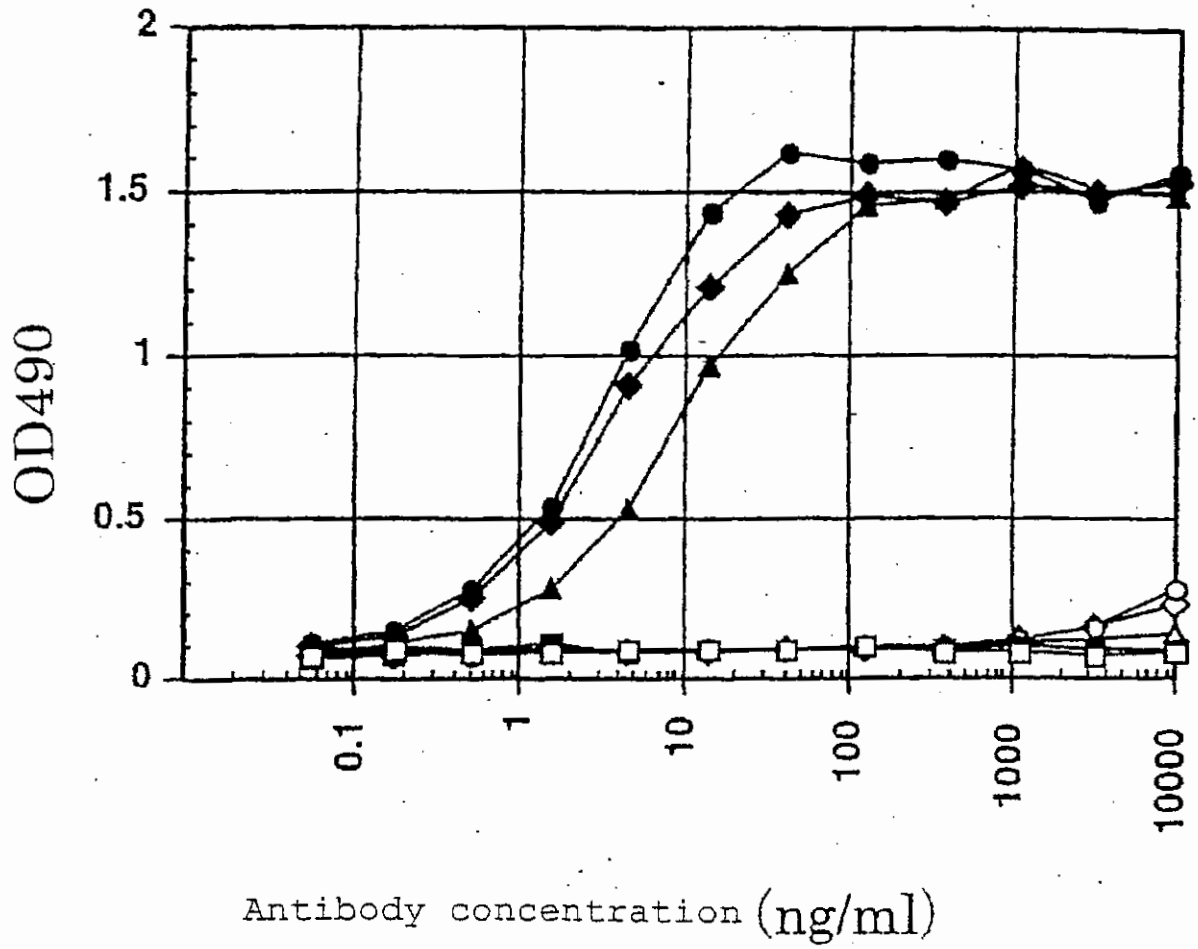

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
KLH CHO
KLH human
JMAb124 CHO
JMAb124 human
JMAb126 CHO
JMAb126 human
JMAb127 CHO
JMAb127 human

Figure 5

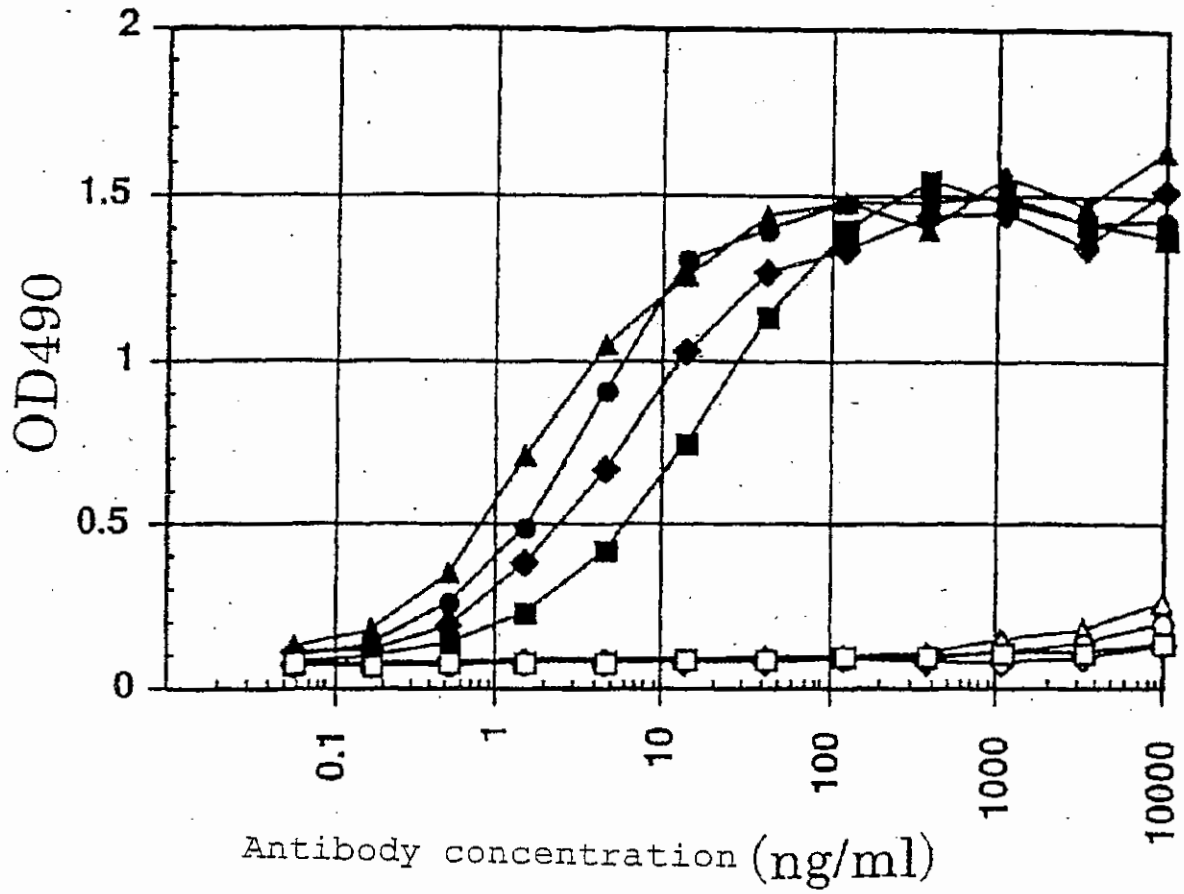

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
JMAb128 CHO
JMAb128 human
JMAb135 CHO
JMAb135 human
JMAb136 CHO
JMAb136 human
JMAb137 CHO
JMAb137 human

Figure 6

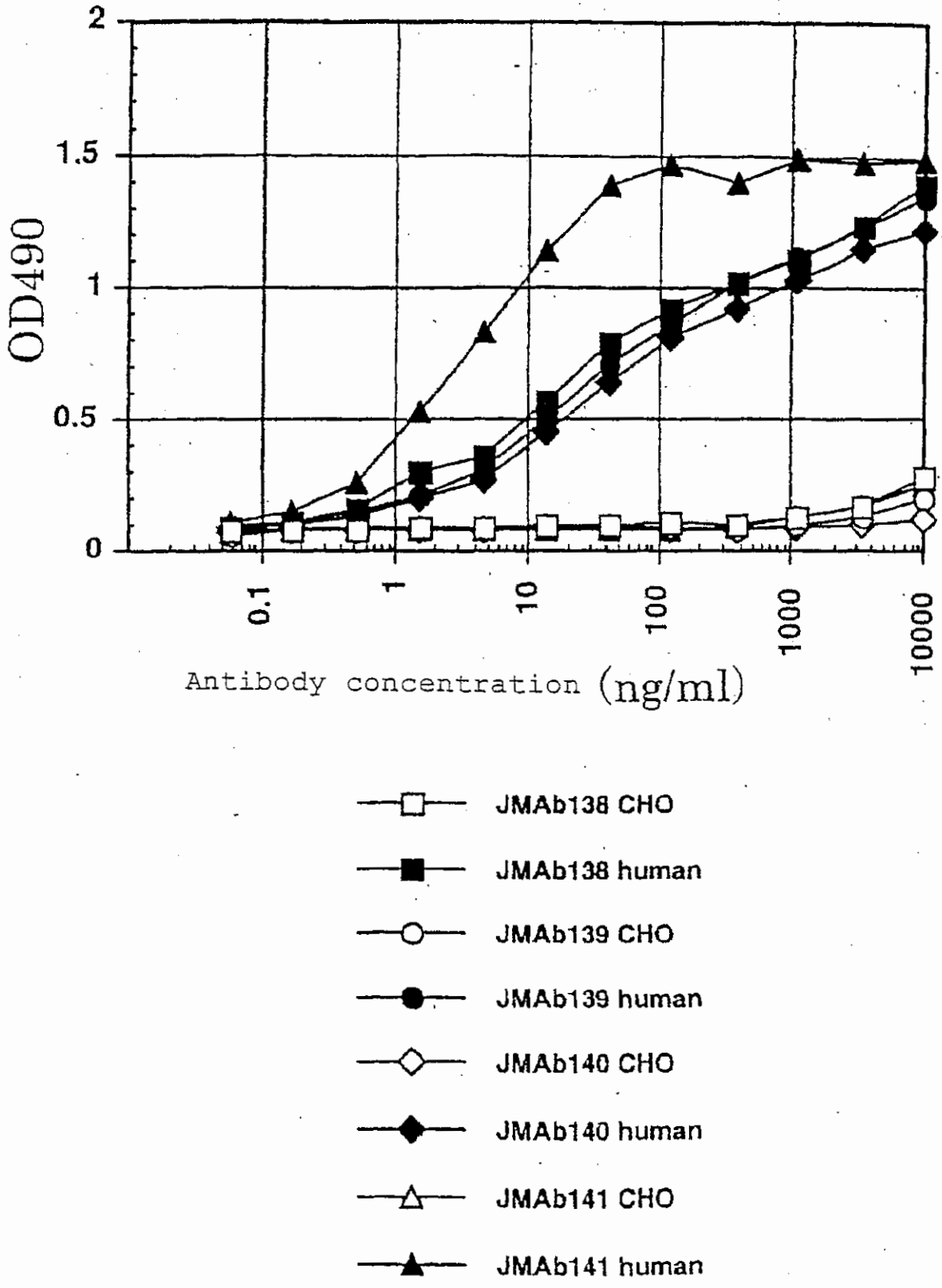

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
JMAb138 CHO
JMAb138 human
JMAb139 CHO
JMAb139 human
JMAb140 CHO
JMAb140 human
JMAb141 CHO
JMAb141 human

Figure 7

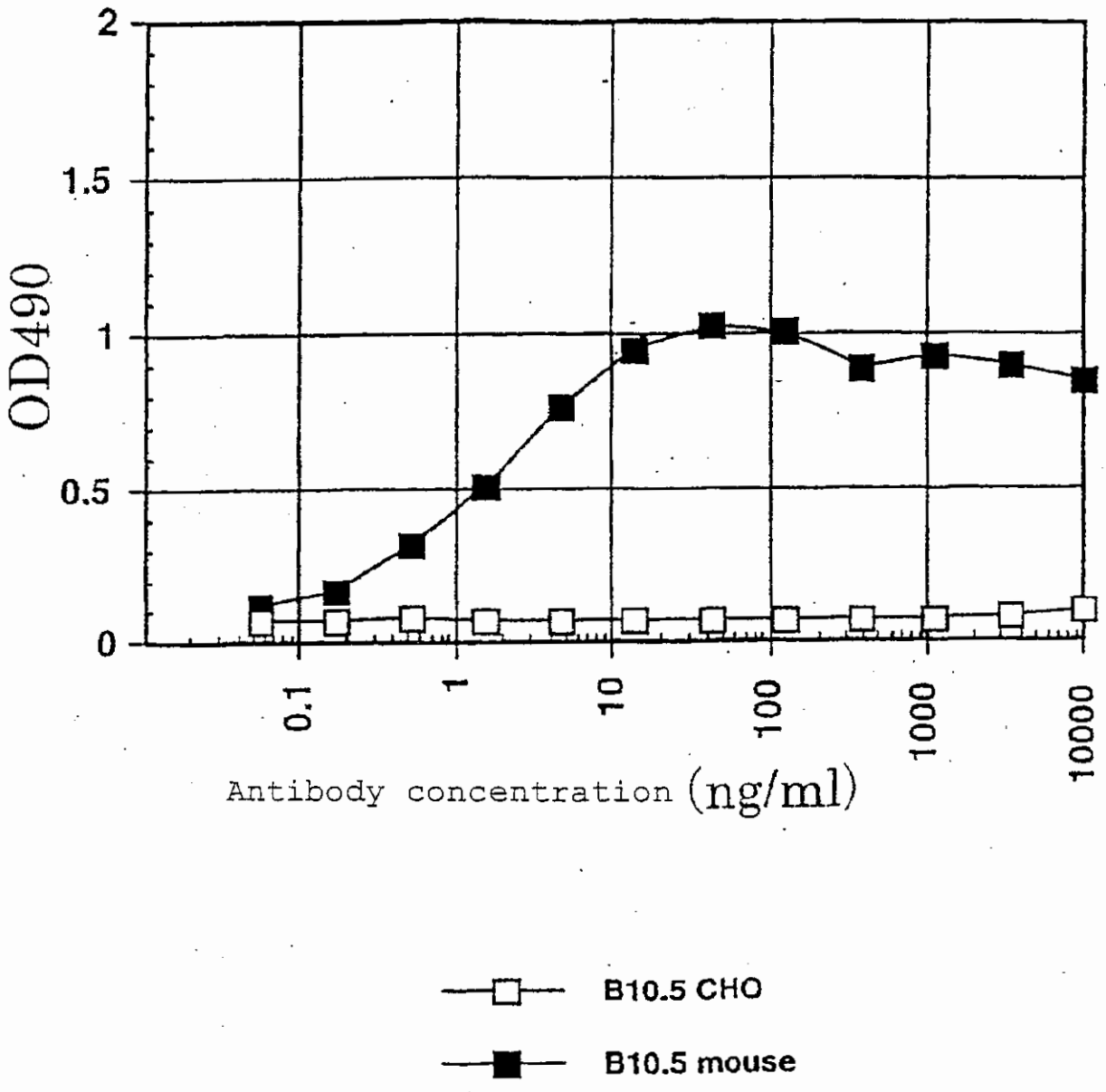

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
B10.5 CHO
B10.5 mouse

Figure 8

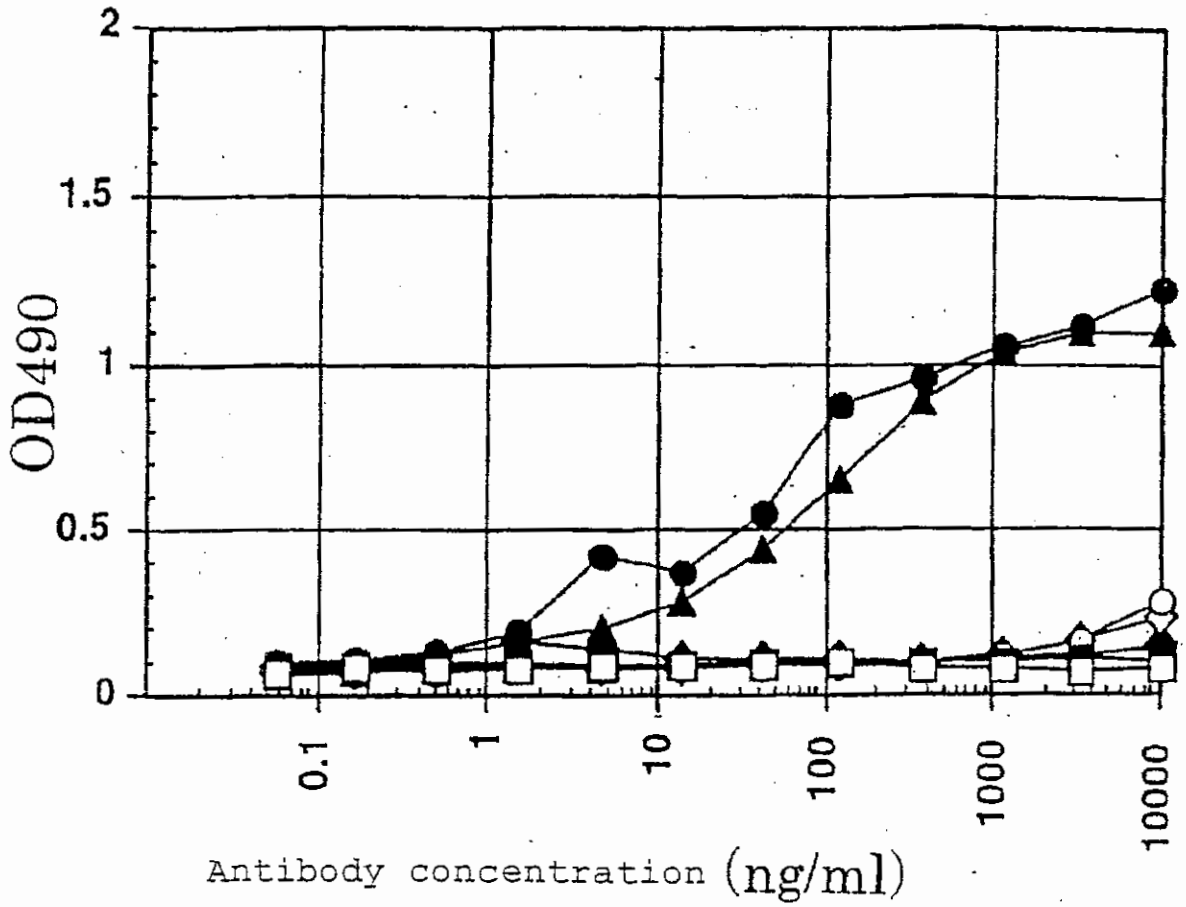

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
KLH CHO
KLH mouse
JMAb124 CHO
JMAb124 mouse
JMAb126 CHO
JMAb126 mouse
JMAb127 CHO
JMAb127 mouse

Figure 9

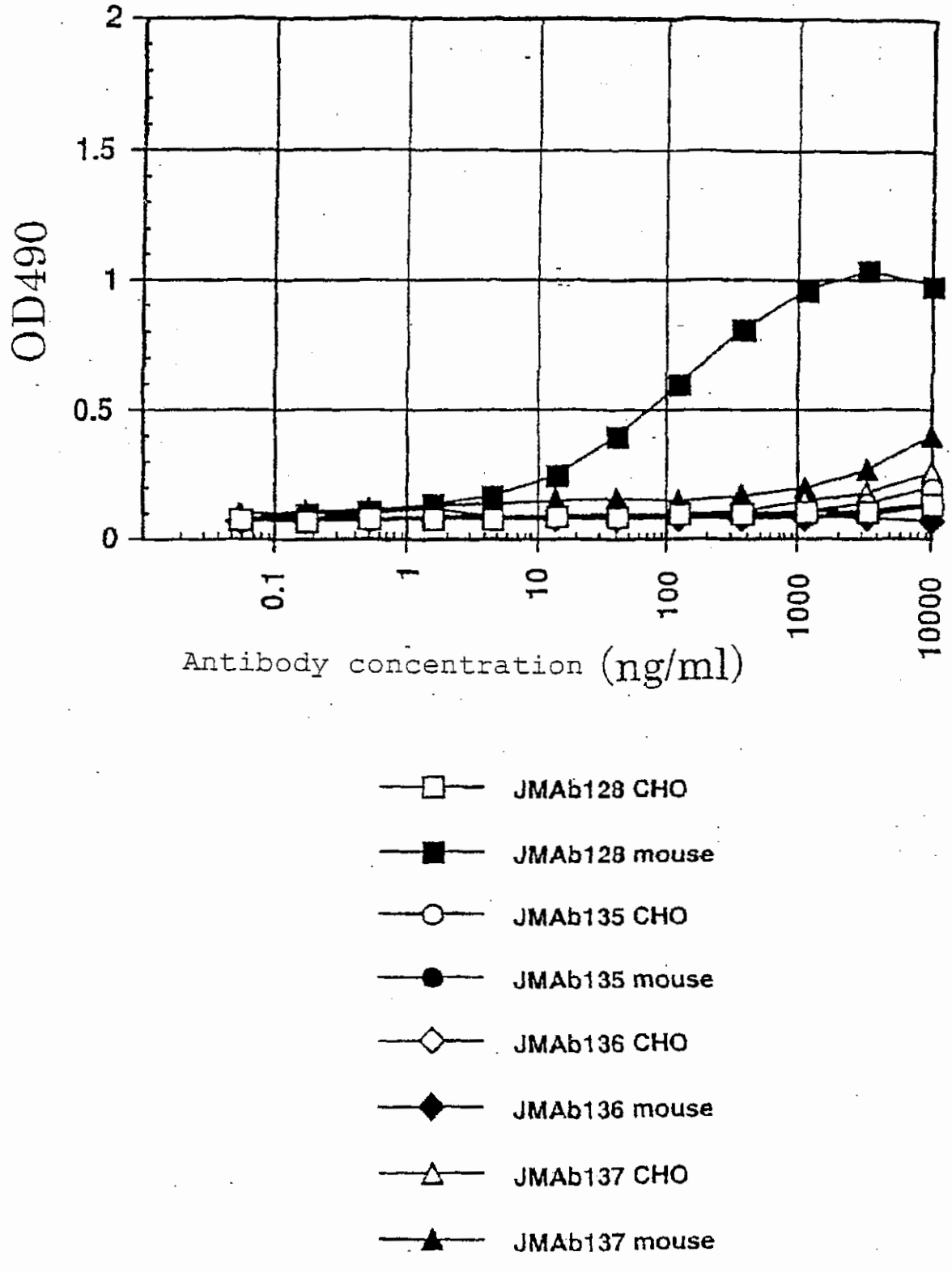
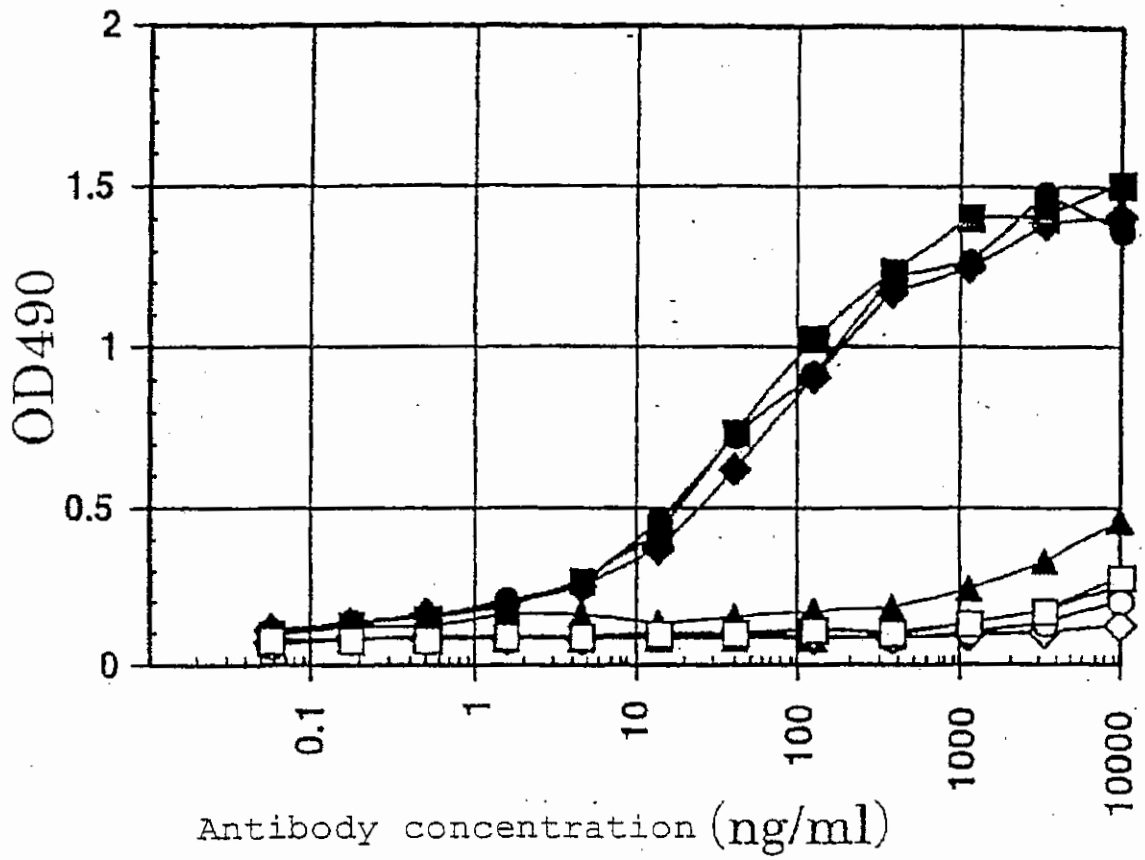

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
JMAb128 CHO
JMAb128 mouse
JMAb135 CHO
JMAb135 mouse
JMAb136 CHO
JMAb136 mouse
JMAb137 CHO
JMAb137 mouse

Figure 10



JMAB138 CHO
JMAb138 mouse
JMAb139 CHO
JMAb139 mouse
JMAb140 CHO
JMAb140 mouse
JMAb141 CHO
JMAb141 mouse

Figure 11

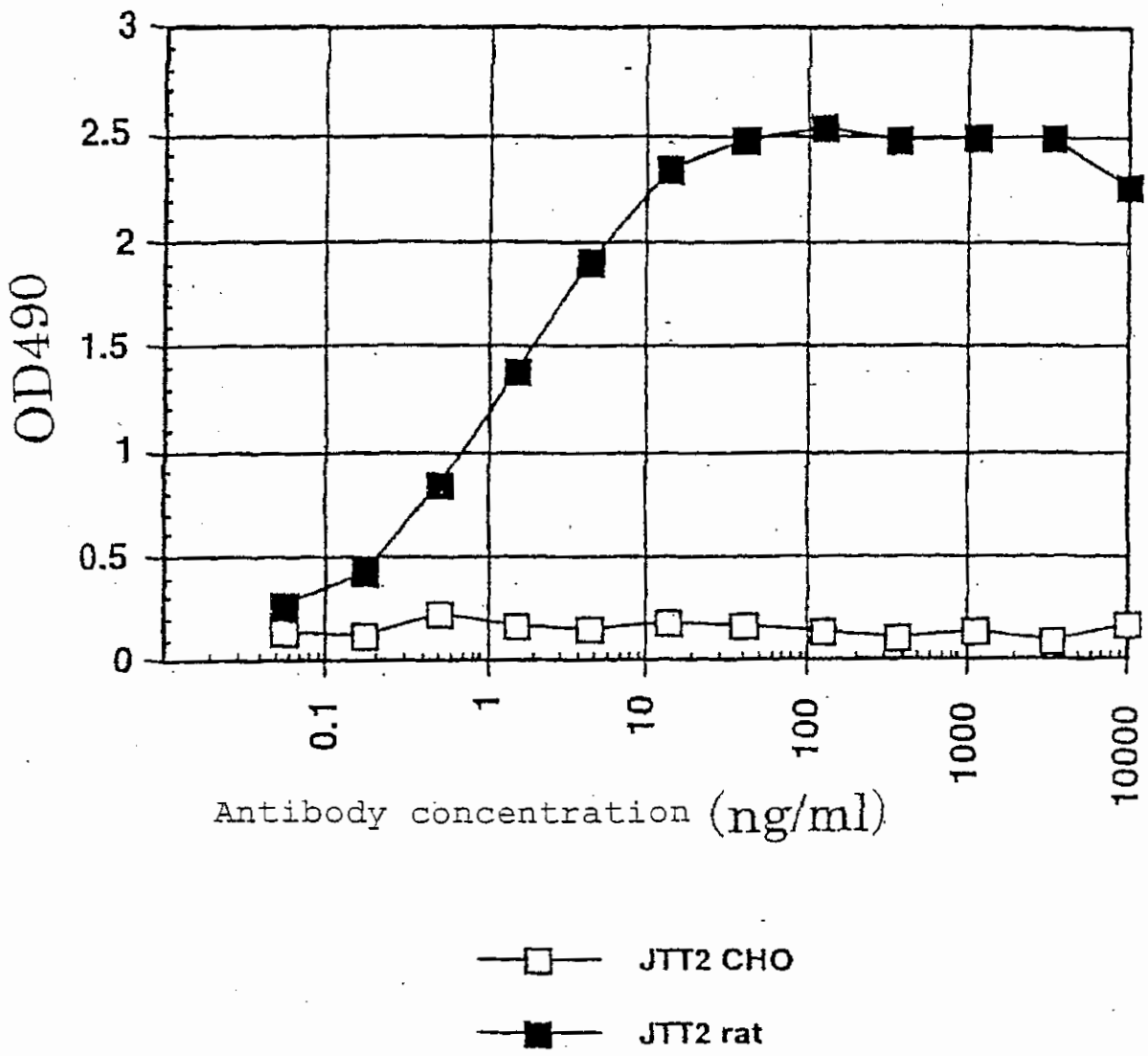

3
2.5
2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
JTT2 CHO
JTT2 rat

Figure 12

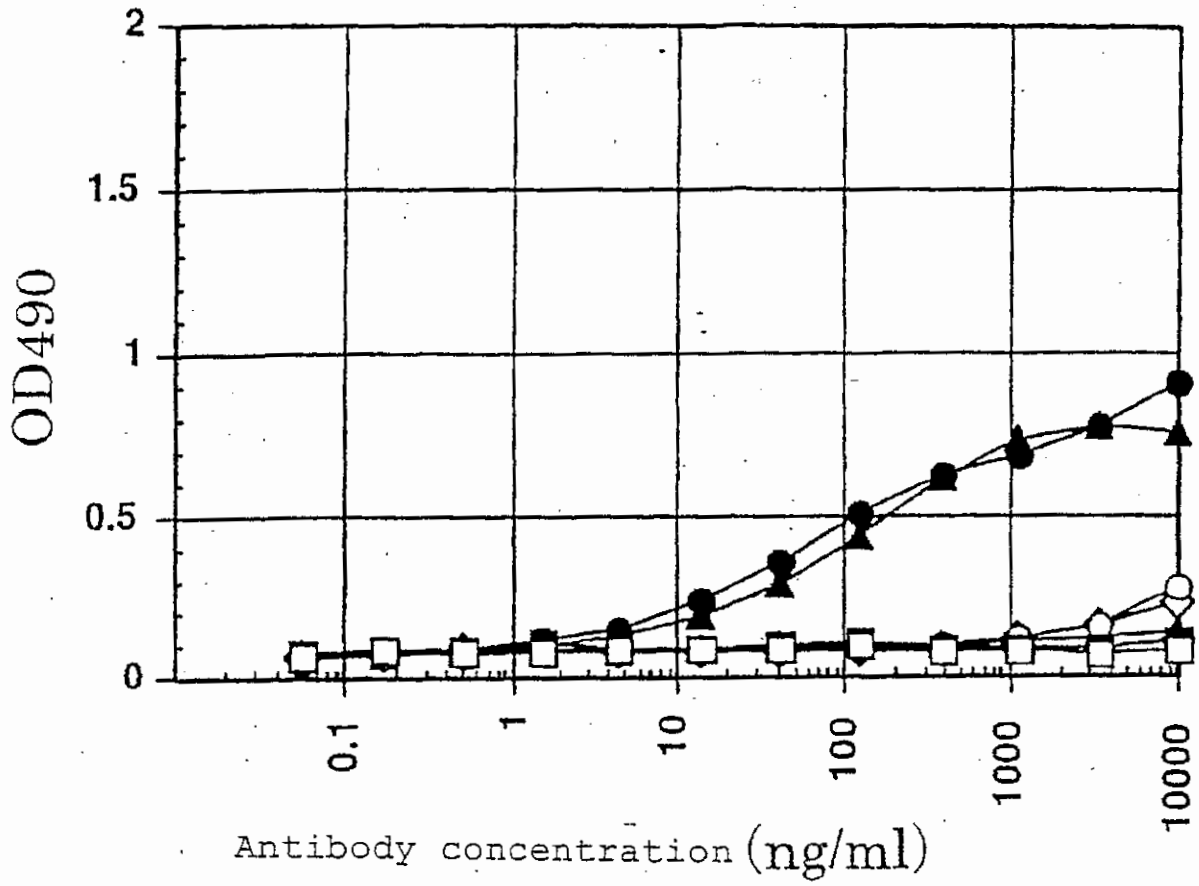

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
KLH CHO
KLH rat
JMAb124 CHO
JMAb124 rat
JMAb126 CHO
JMAb126 rat
JMAb127 CHO
JMAb127 rat

Figure 13

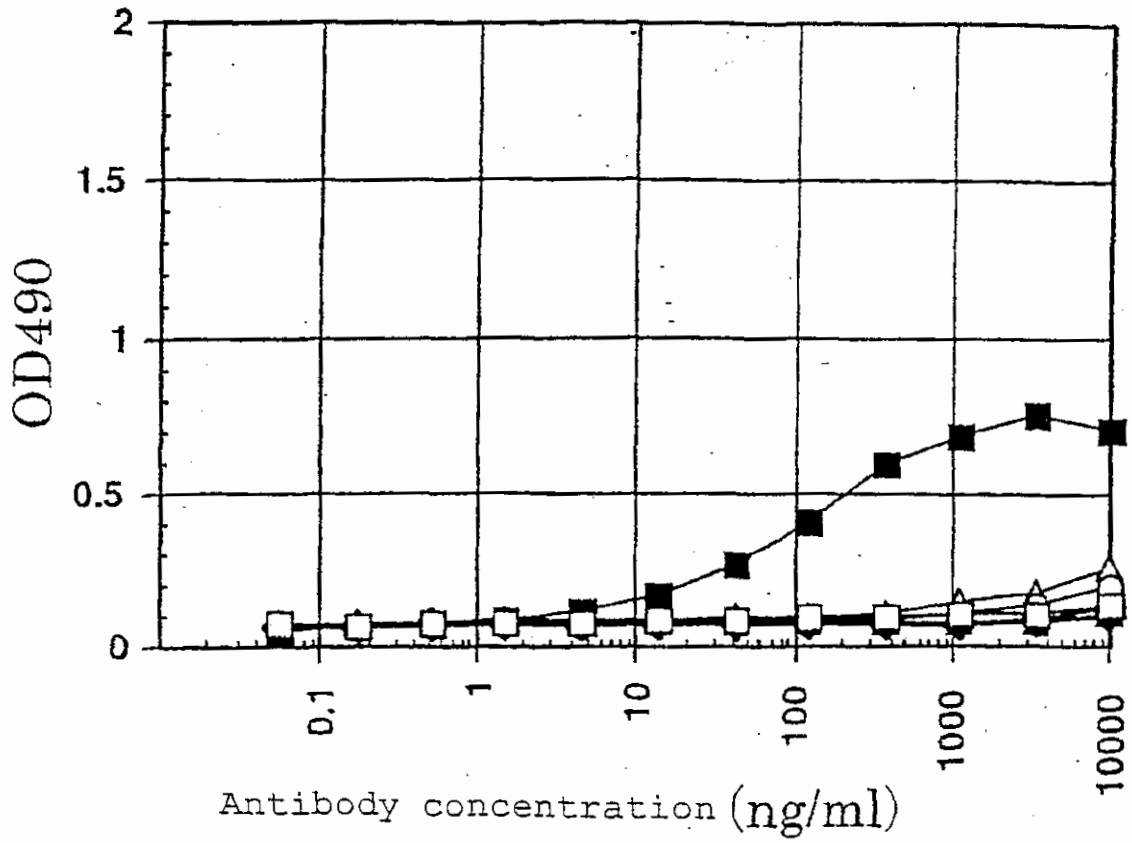

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
JMAb128 CHO
JMAb128 rat
JMAb135 CHO
JMAb135 rat
JMAb136 CHO
JMAb136 rat
JMAb137 CHO
JMAb137 rat

Figure 14

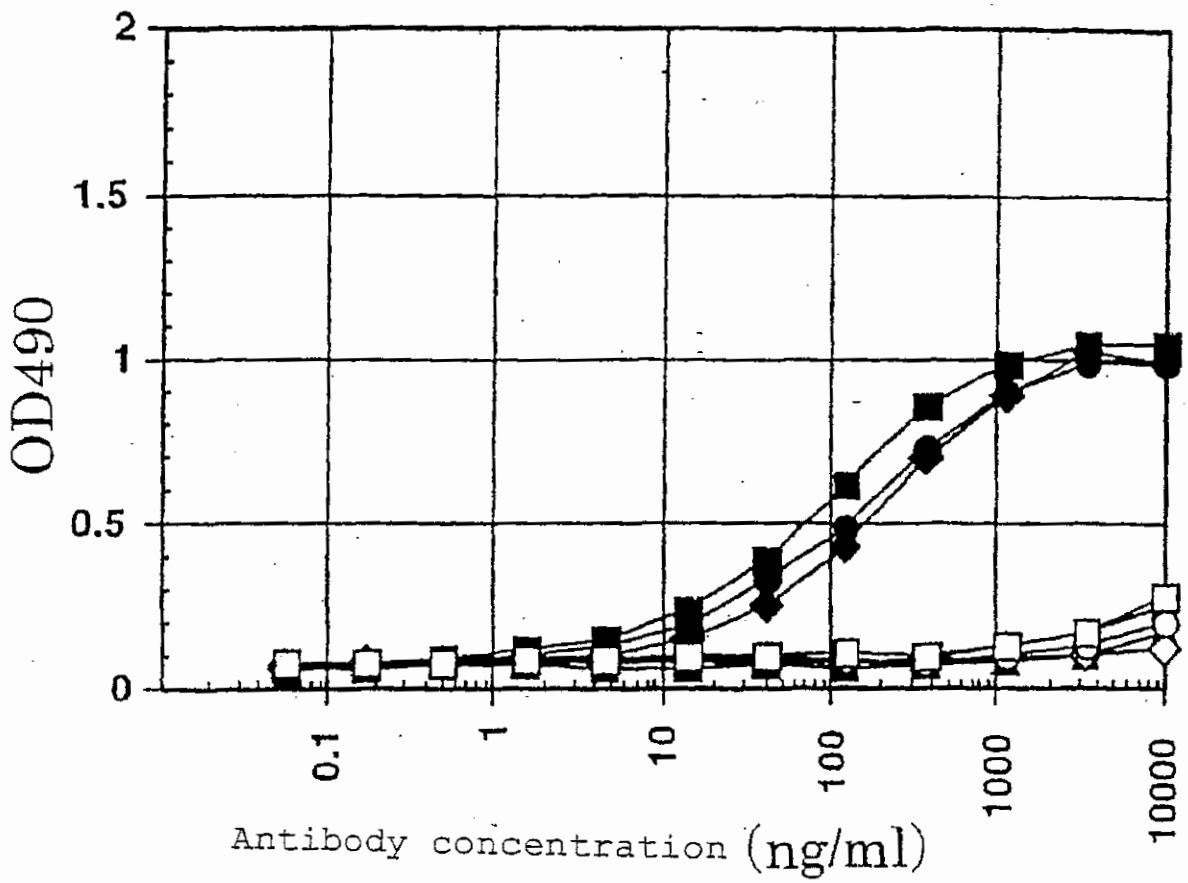

2
1.5
1
0.5
0
OD490
0.1
1
10
100
1000
10000
Antibody concentration (ng/ml)
JMAB138 CHO
JMAb138 rat
JMAb139 CHO
JMAb139 rat
JMAb140 CHO
JMAb140 rat
JMAb141 CHO
JMAb141 rat

Figure 15

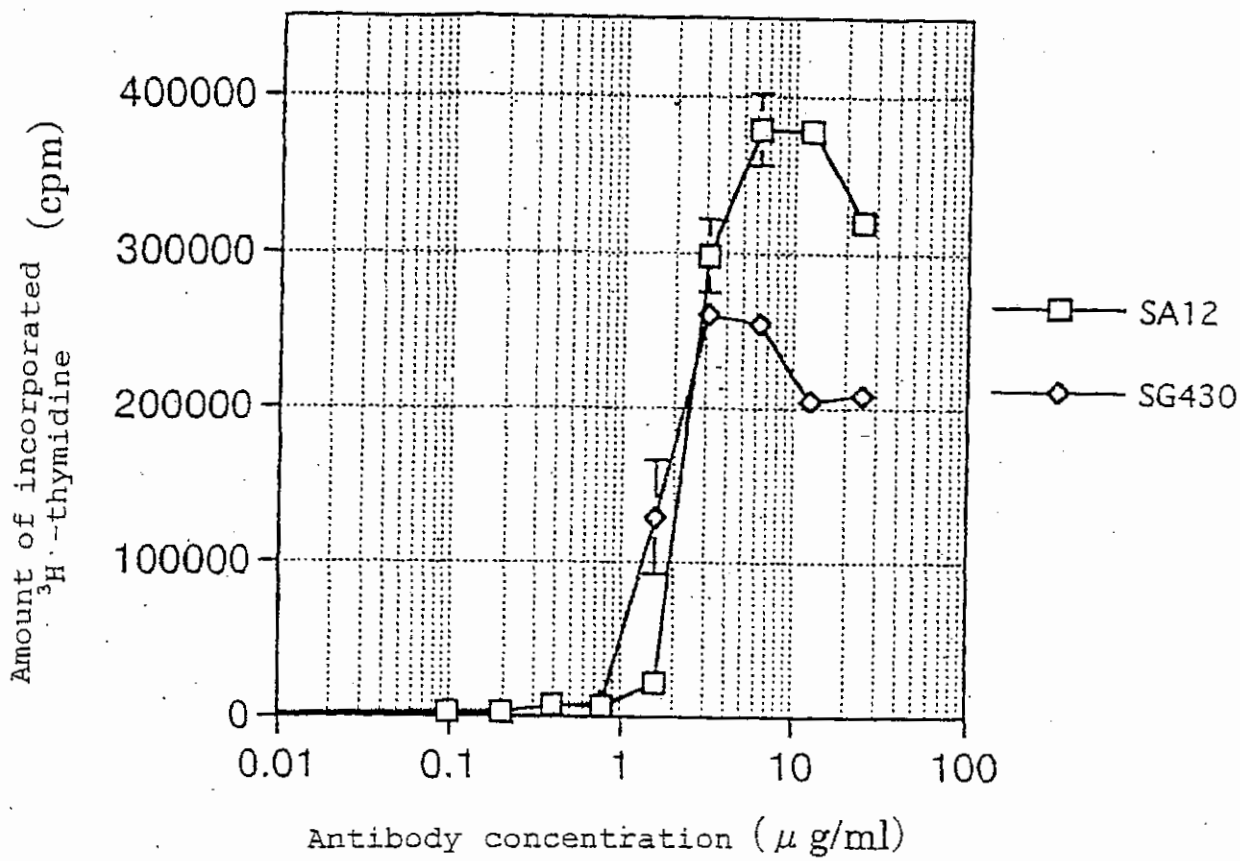

400000
300000
200000
100000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H-thymidine (cpm)
Antibody concentration (μg/ml)
SA12
SG430

Figure 16

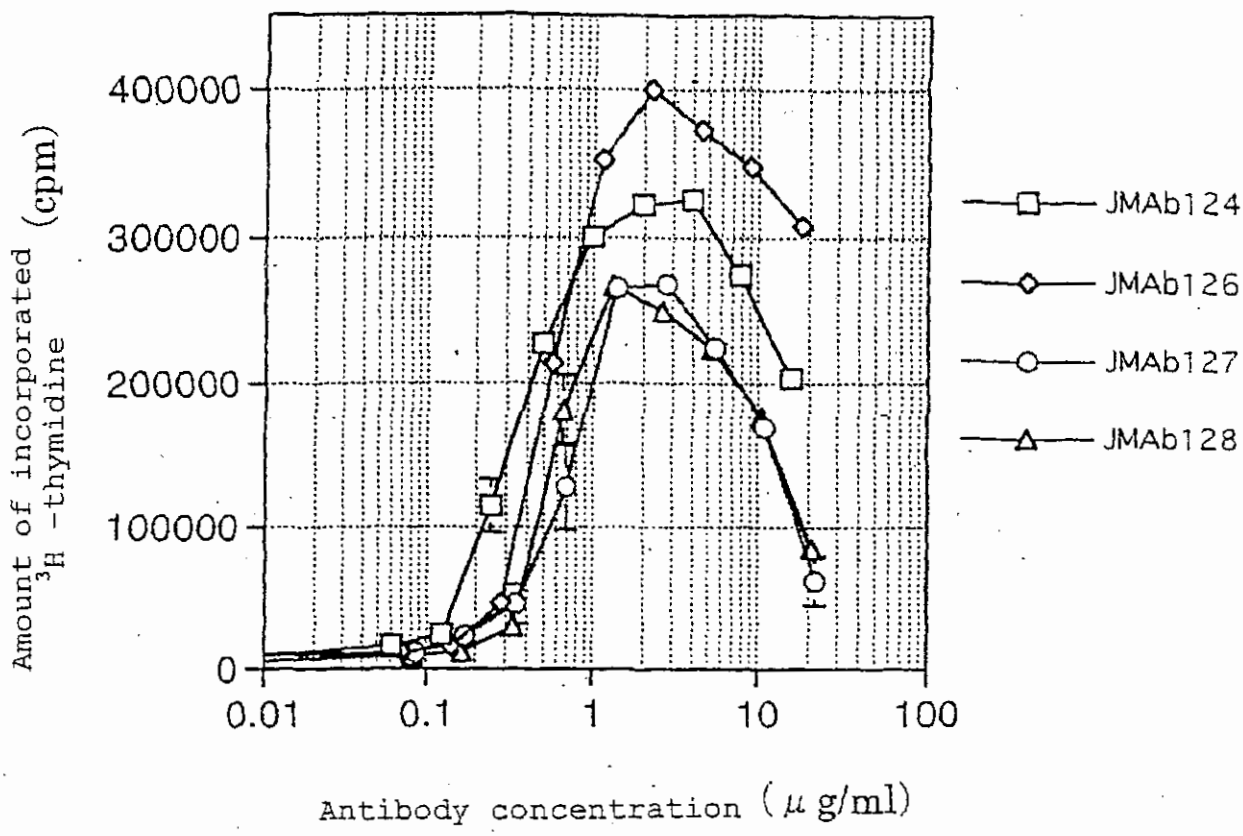

400000
300000
200000
100000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H -thymidine (cpm)
Antibody concentration (μg/ml)
JMAb124
JMAb126
JMAb127
JMAb128

Figure 17

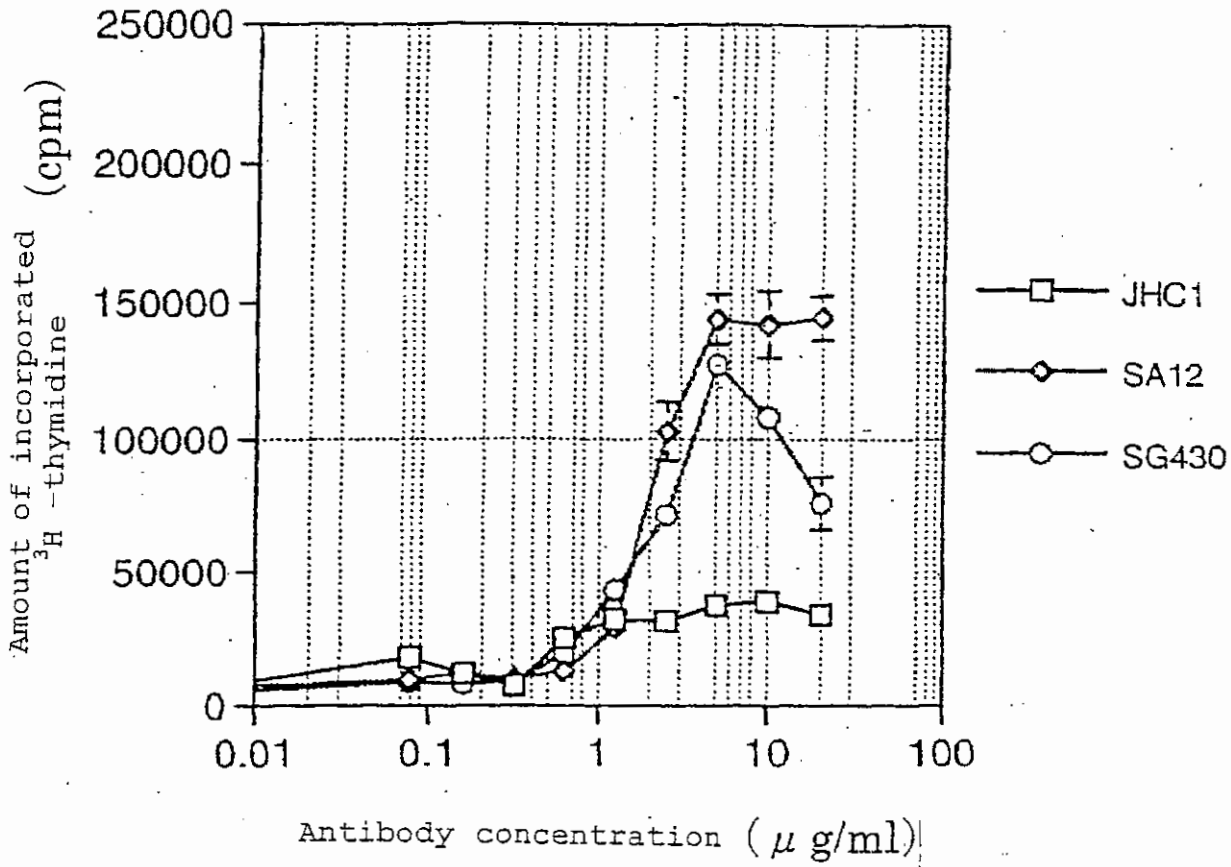

250000
200000
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H -thymidine (cpm)
Antibody concentration (μg/ml)
JHC1
SA12
SG430

Figure 18

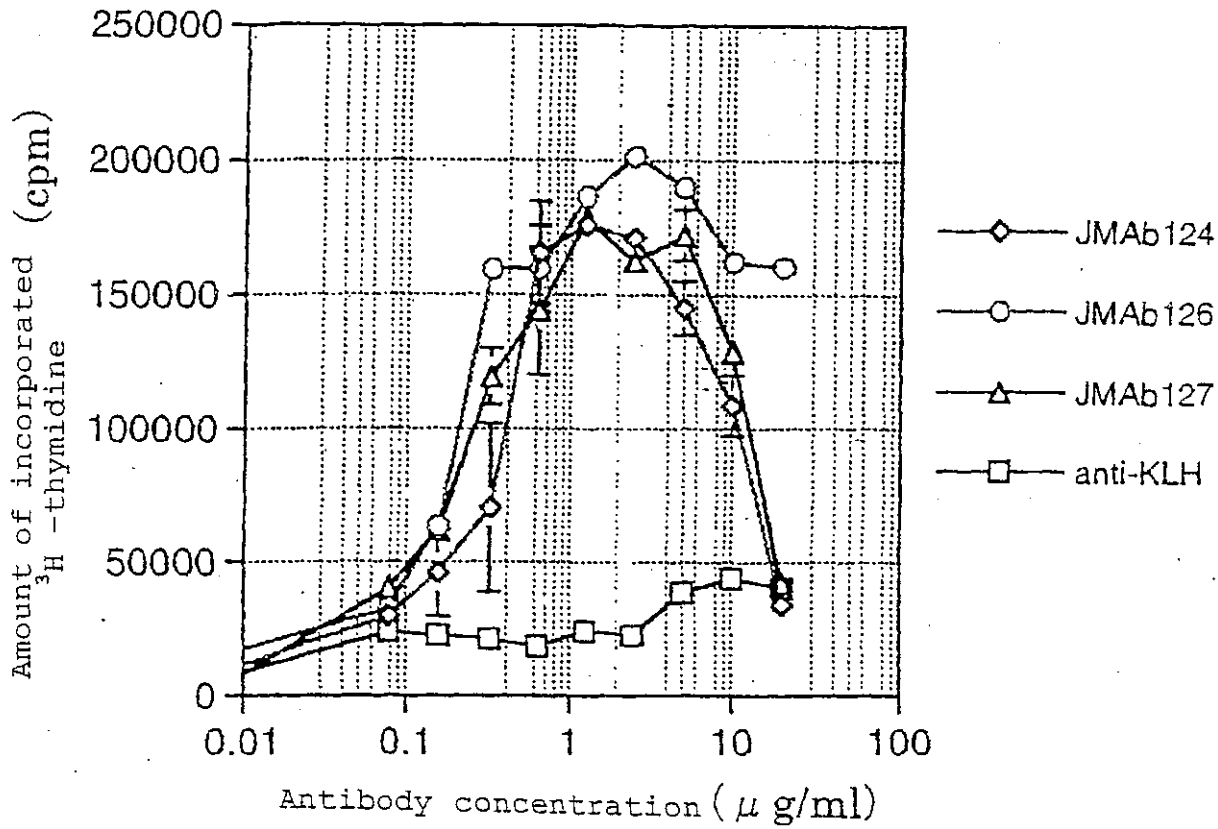

250000
200000
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H -thymidine (cpm)
Antibody concentration (μ g/ml)
JMAb124
JMAb126
JMAb127
anti-KLH

Figure 19

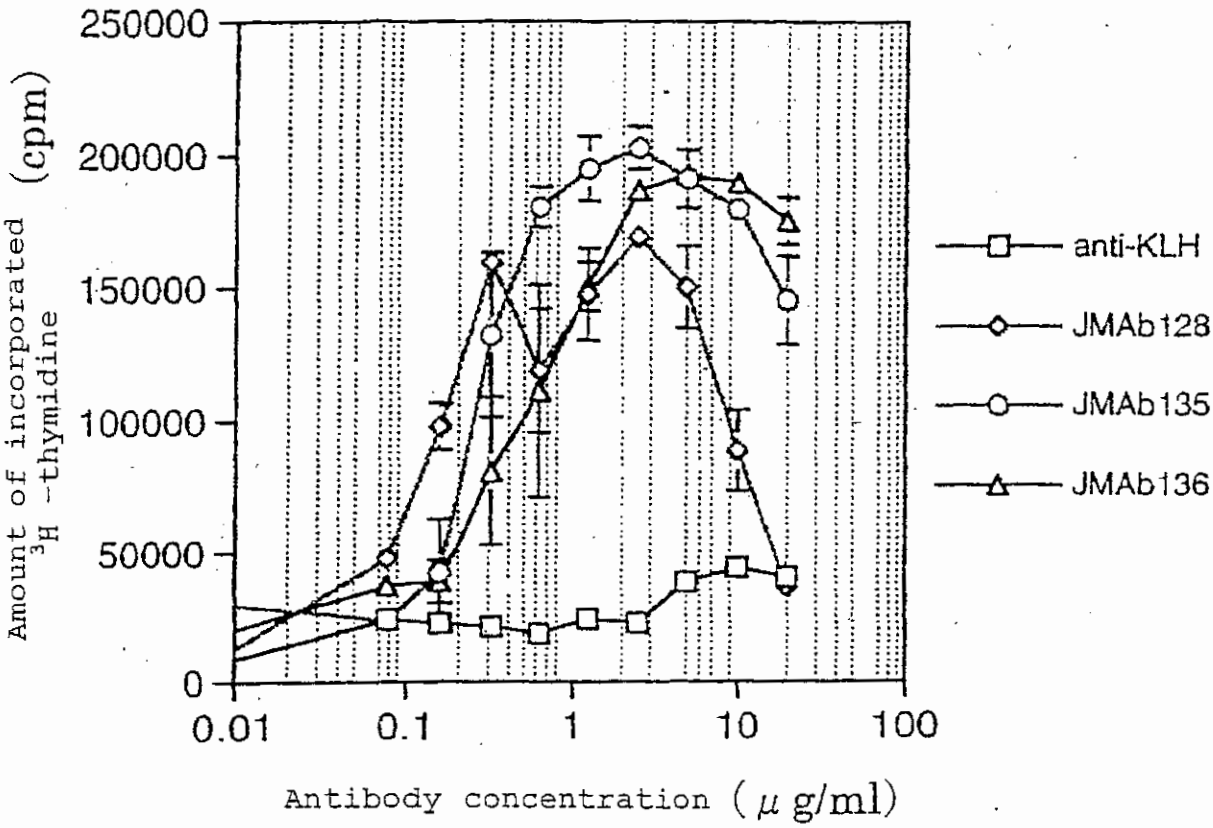

250000
200000
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H -thymidine (cpm)
Antibody concentration (μg/ml)
anti-KLH
JMAb128
JMAb135
JMAb136

Figure 20

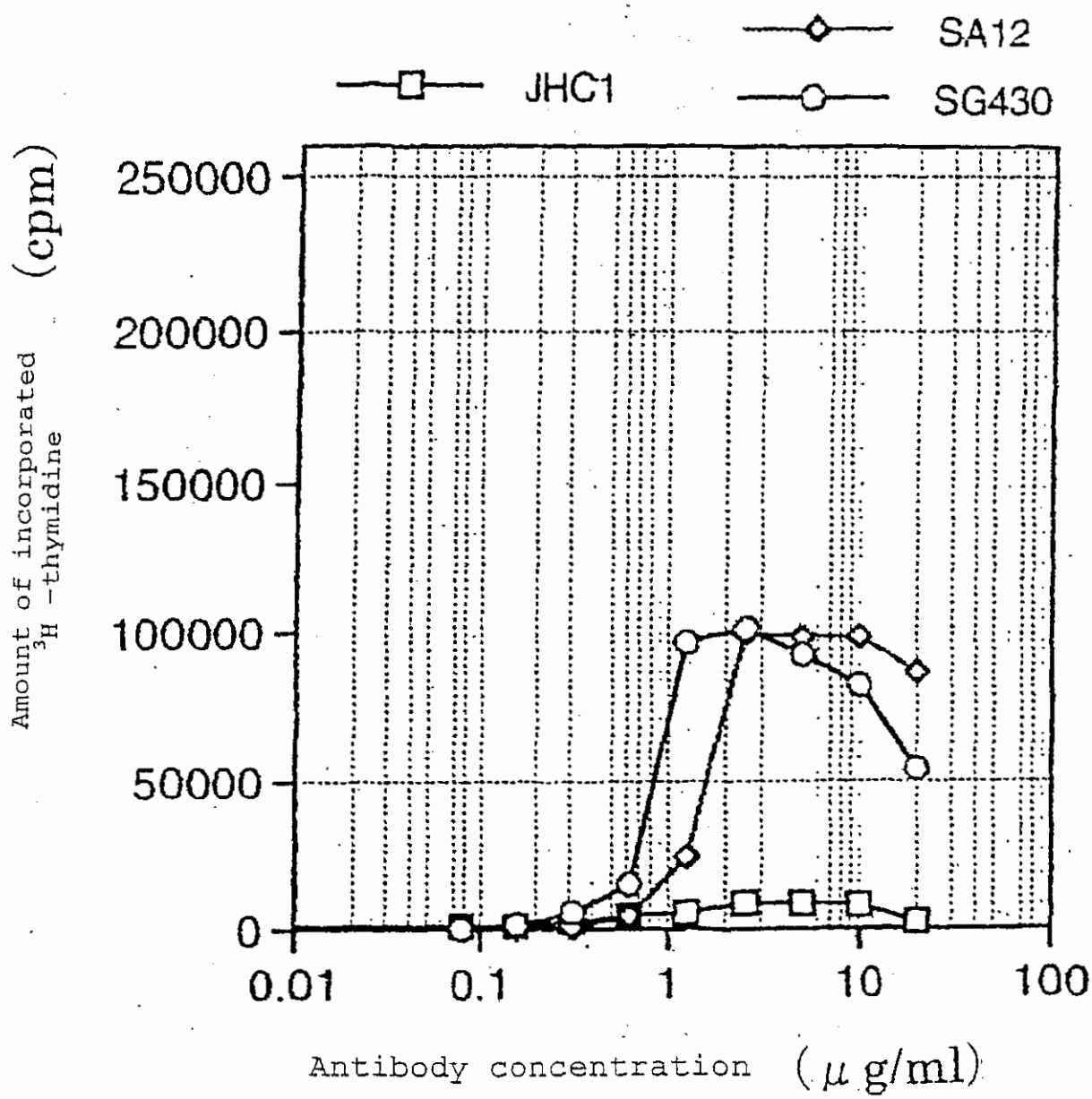

SA12
JHC1
SG430
Amount of incorporated ^{3}H -thymidine (cpm)
250000
200000
150000
100000
50000
0
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 21

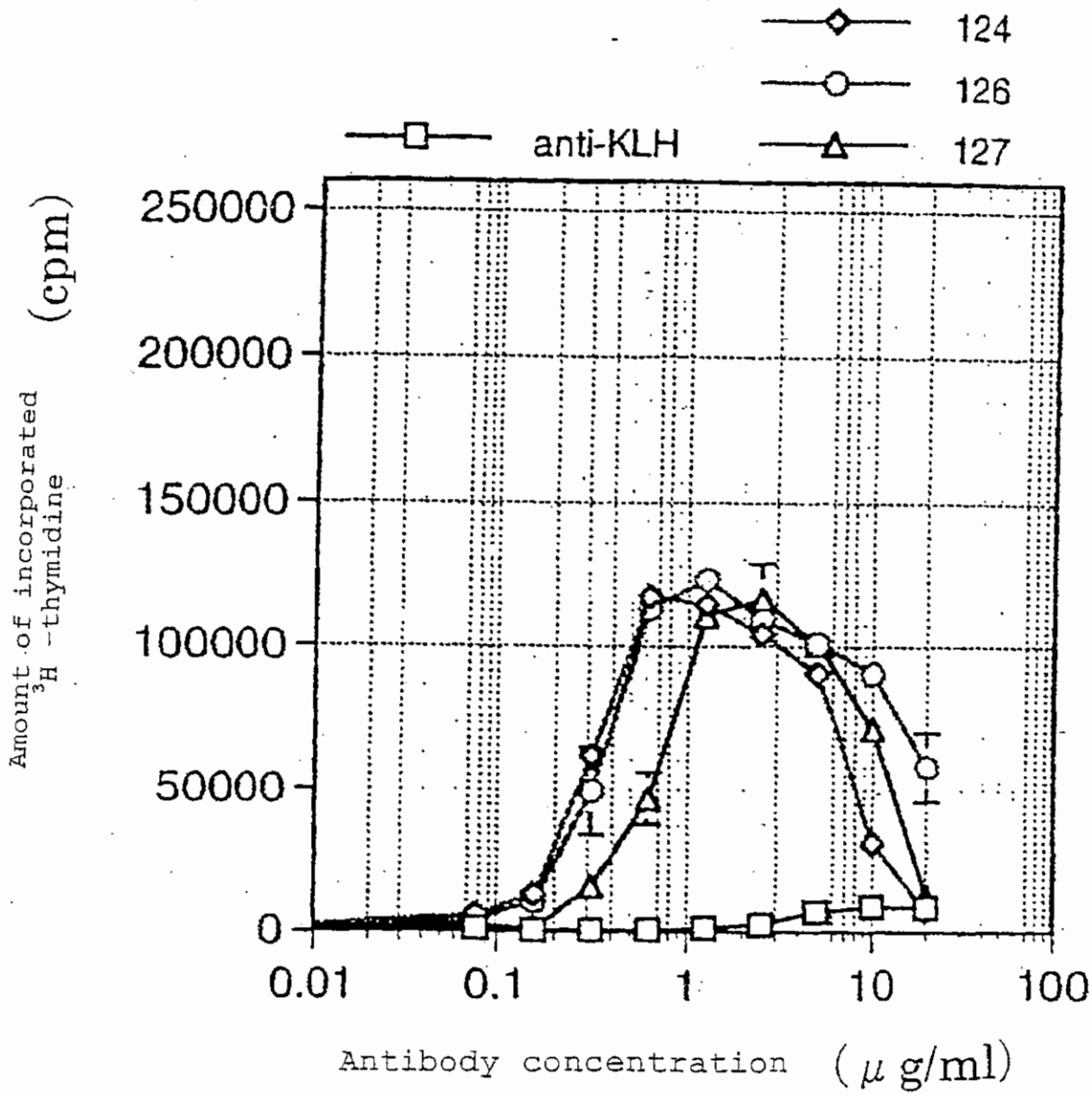

124
126
anti-KLH
127
250000
200000
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H -thymidine (cpm)
Antibody concentration (μg/ml)

Figure 22

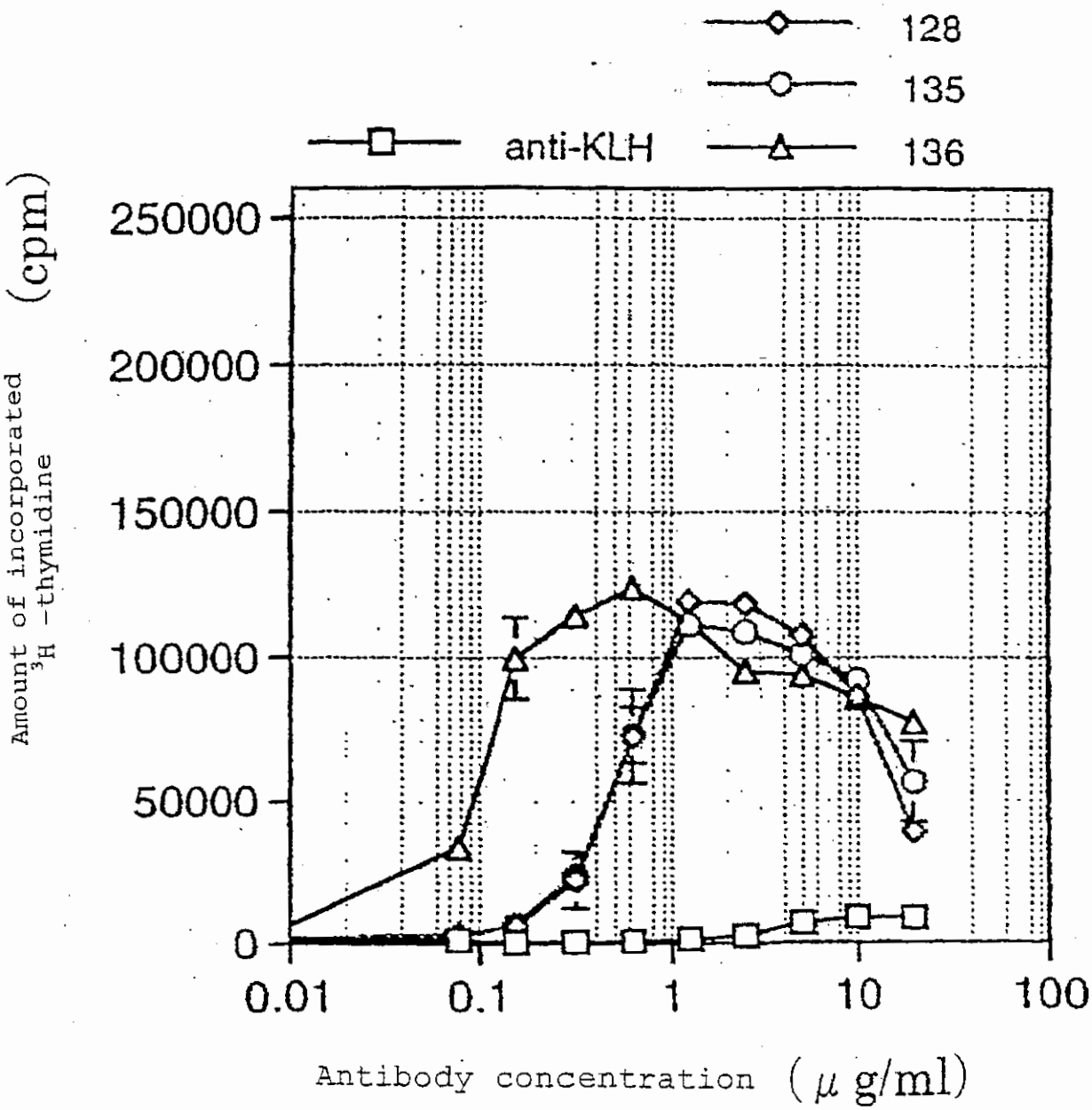

128
135
anti-KLH
136
Amount of incorporated ^{3}H -thymidine (cpm)
250000
200000
150000
100000
50000
0
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 23

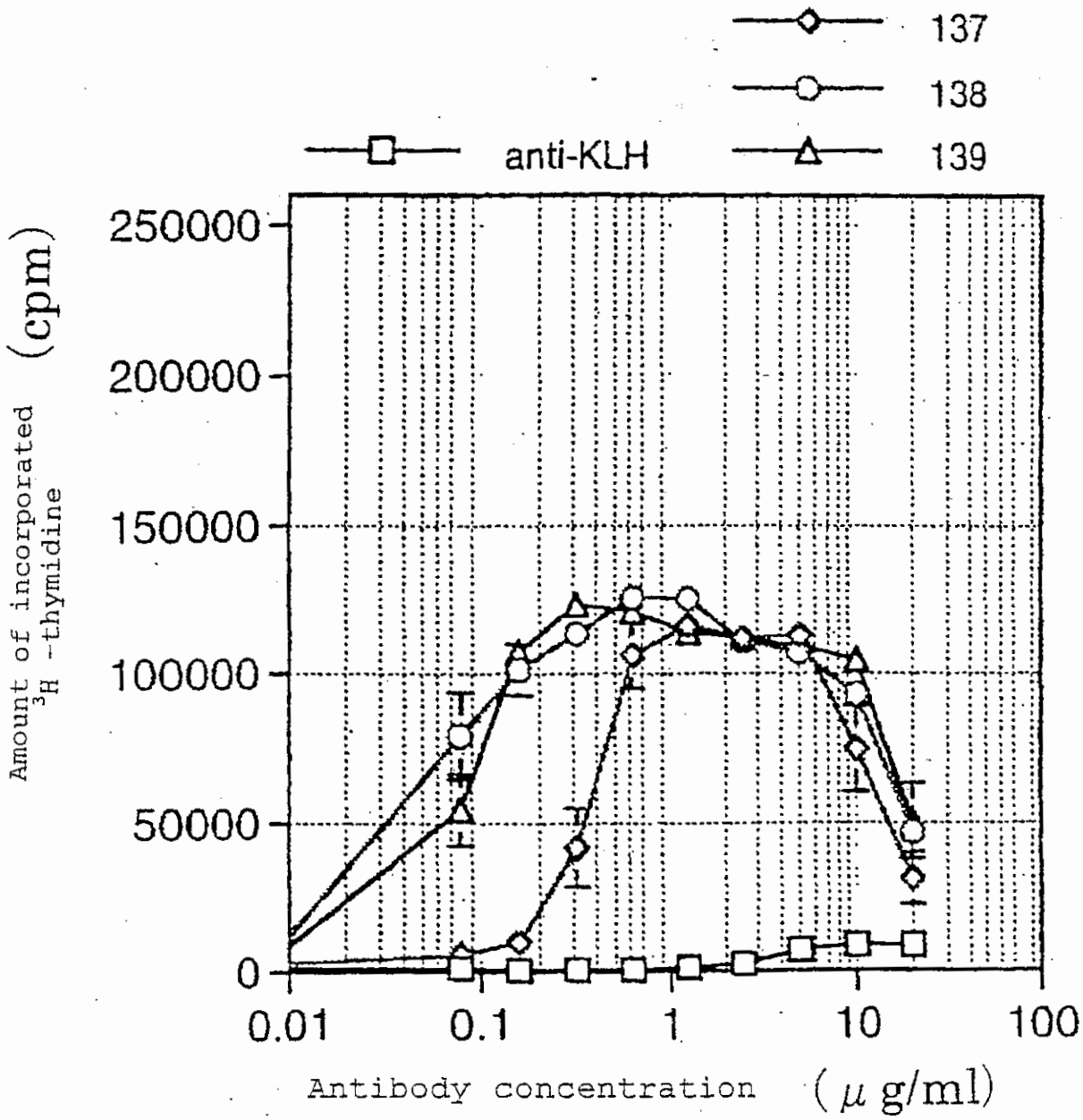

137
138
anti-KLH
139
250000
200000
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H -thymidine (cpm)
Antibody concentration (μg/ml)

Figure 24

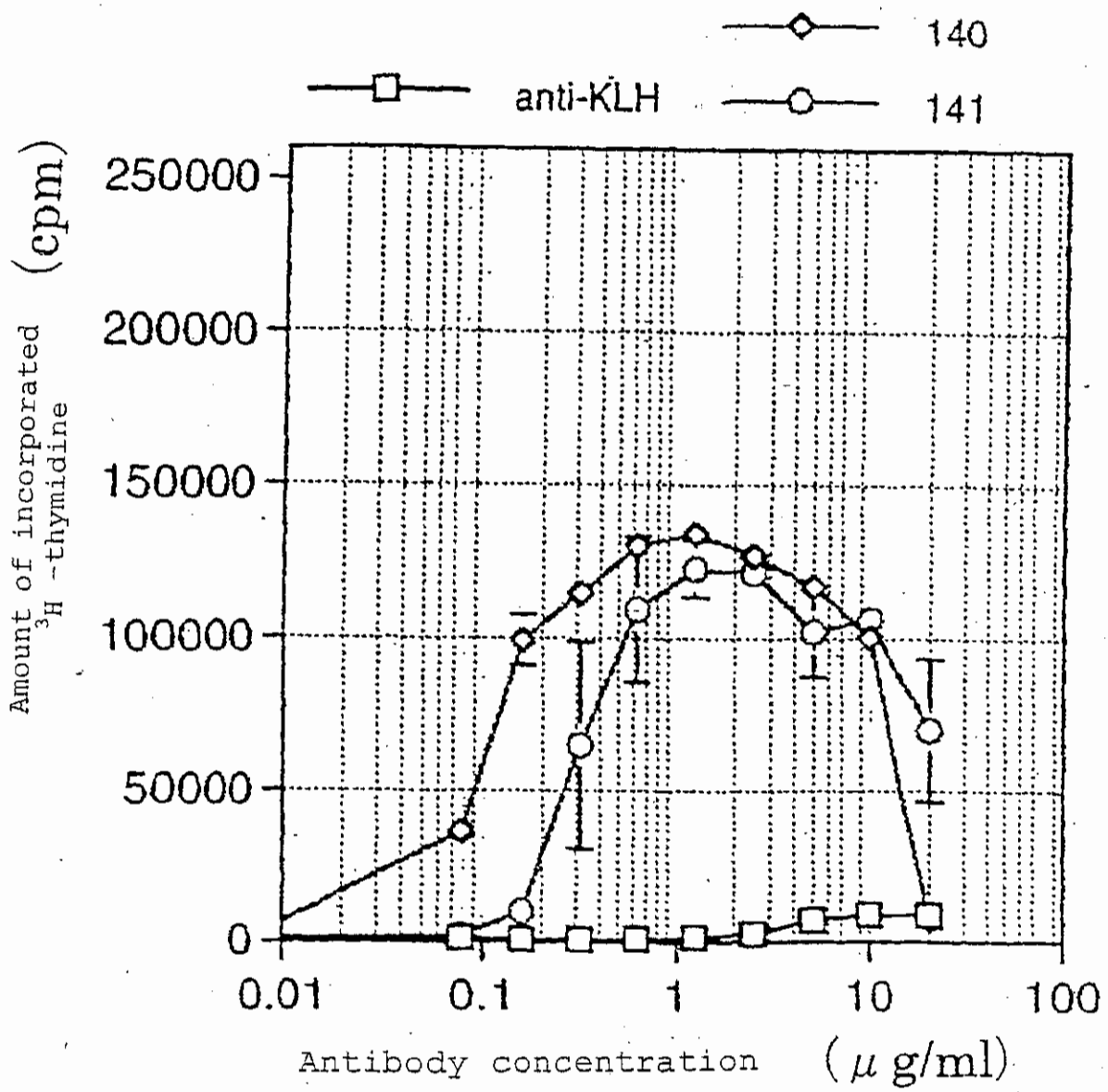

140
anti-KLH
141
Amount of incorporated ^{3}H -thymidine (cpm)
250000
200000
150000
100000
50000
0
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 25

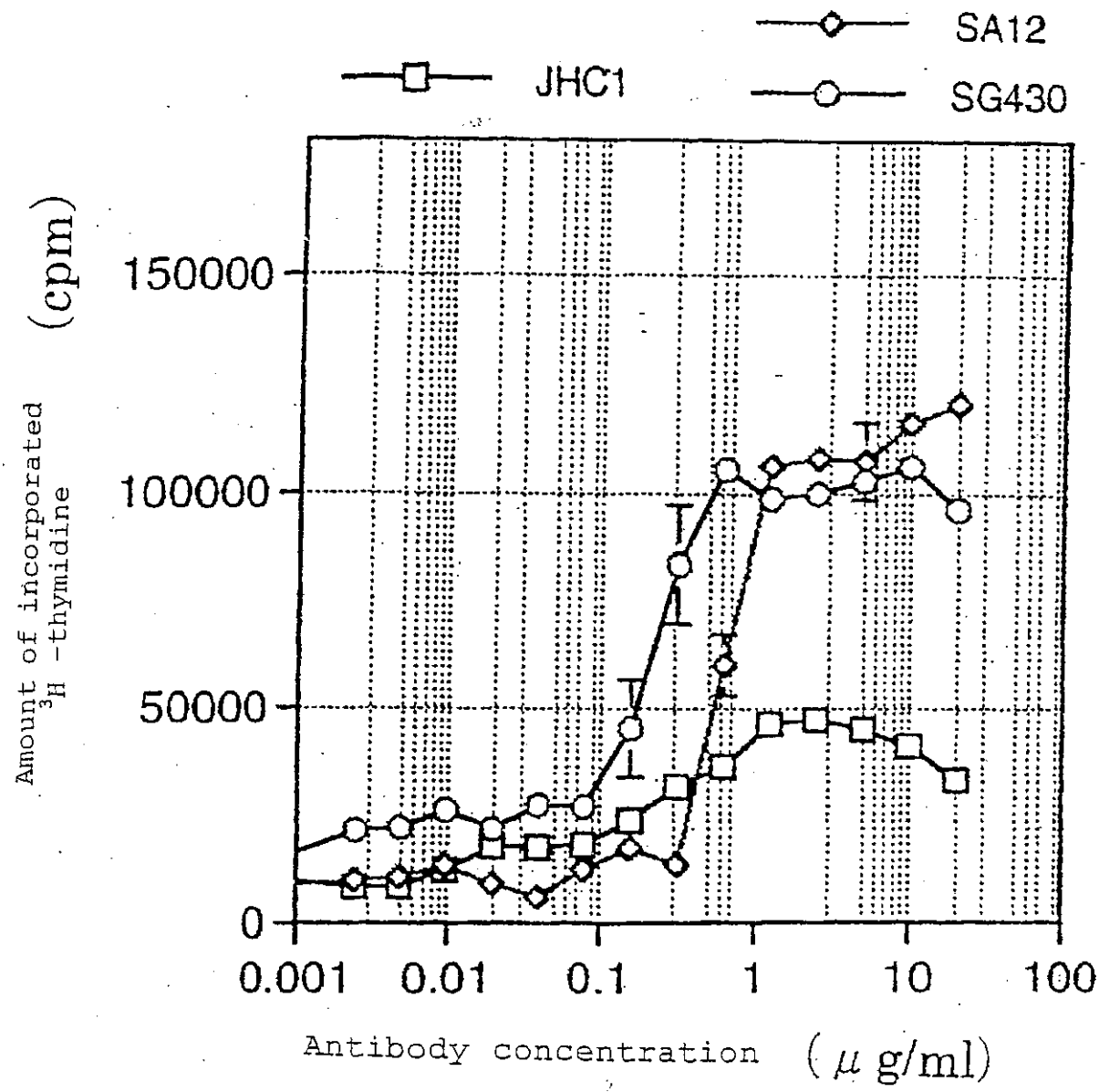

SA12
JHC1
SG430
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 26

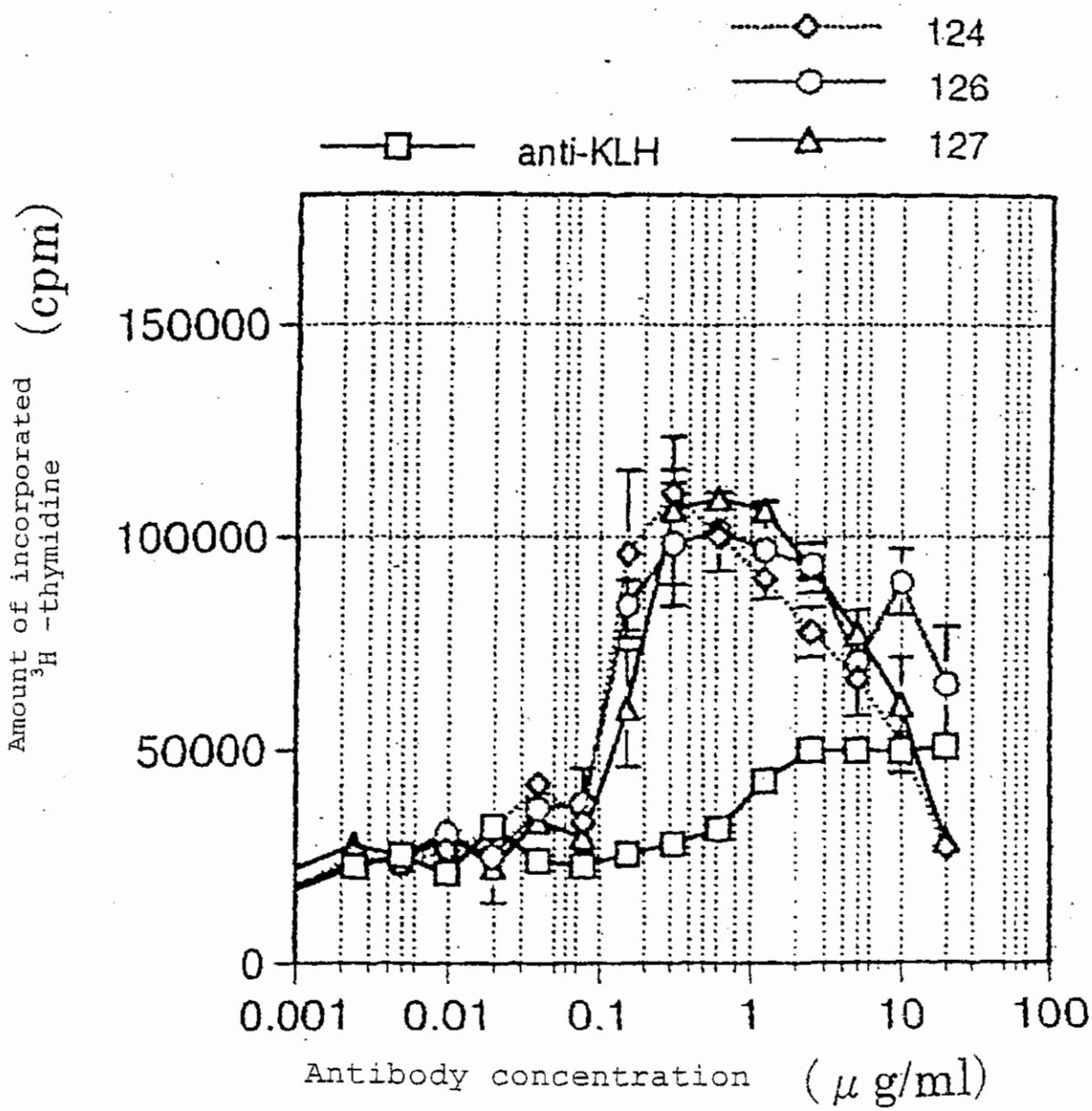

124
126
127
anti-KLH
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 27

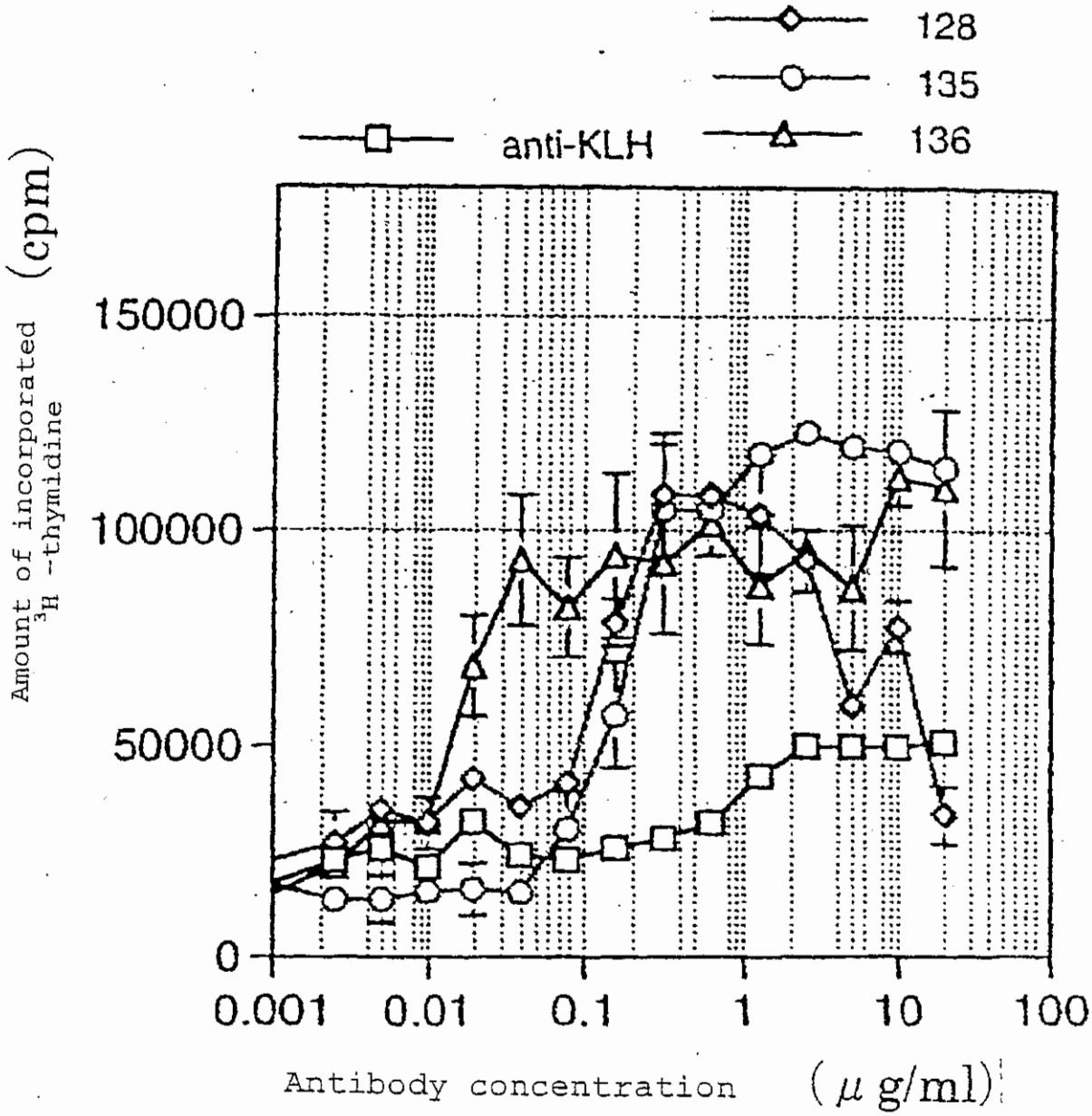

128
135
anti-KLH
136
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 28

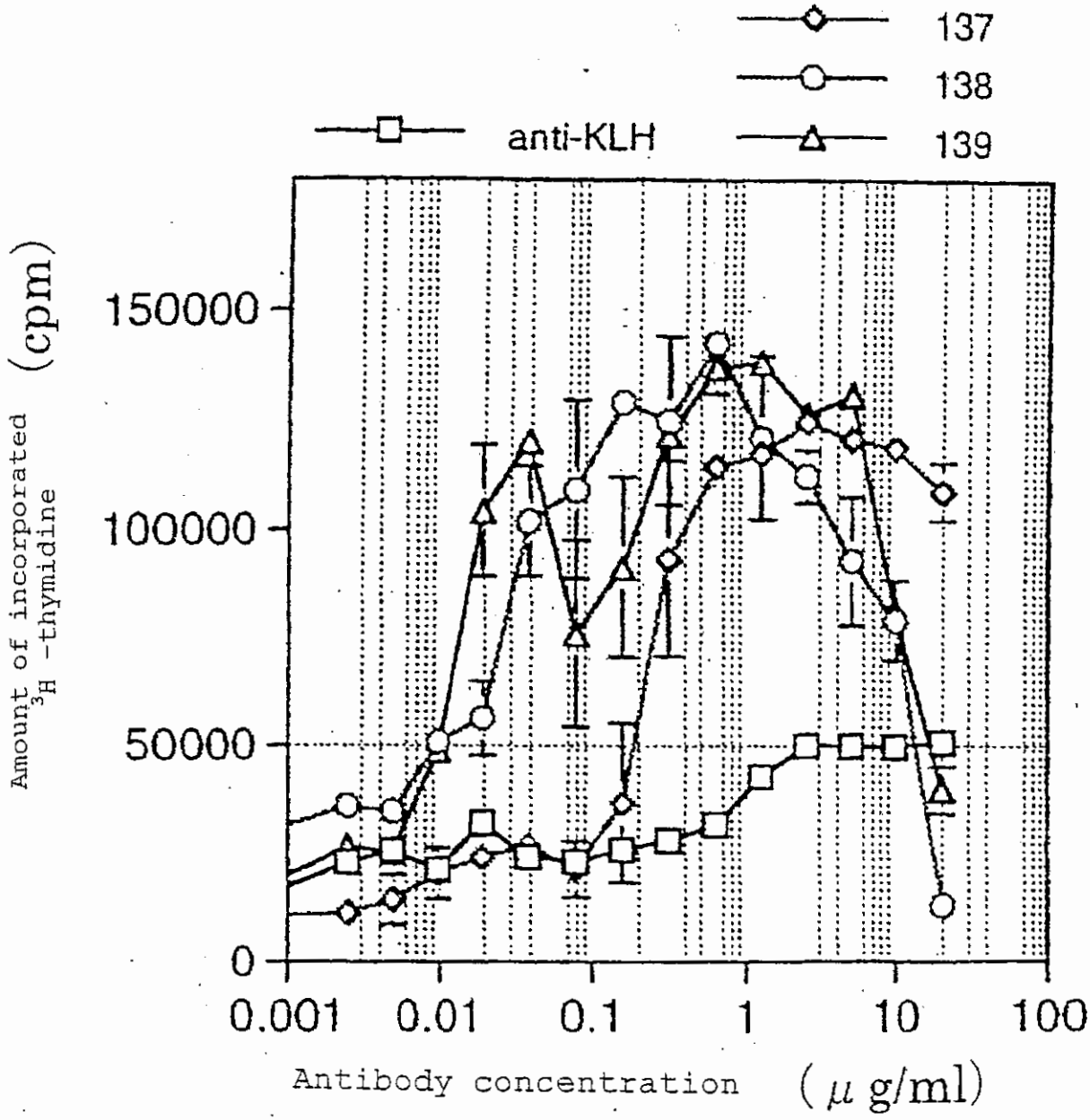

137
138
anti-KLH
139
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 29

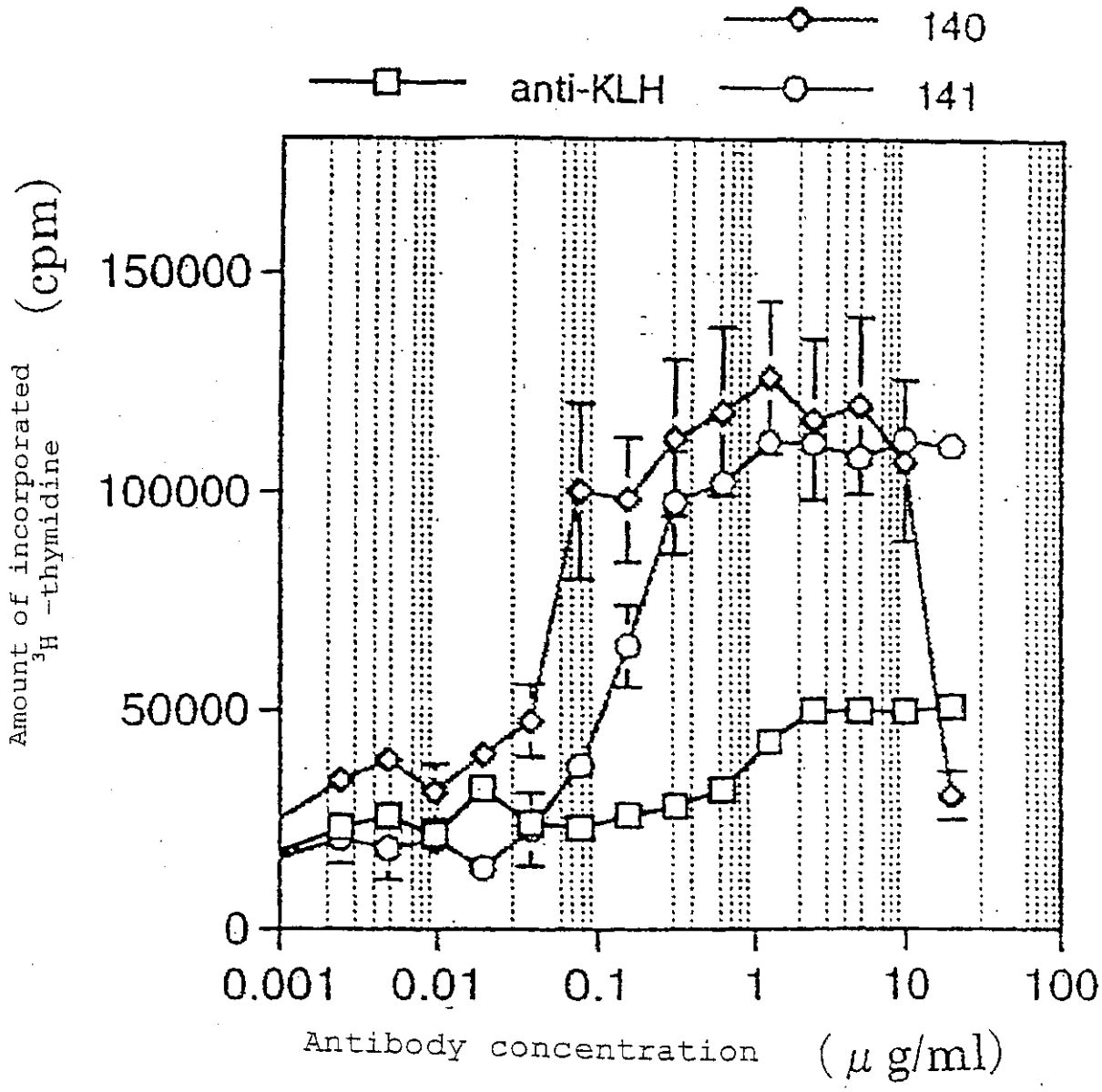

140
anti-KLH
141
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 30

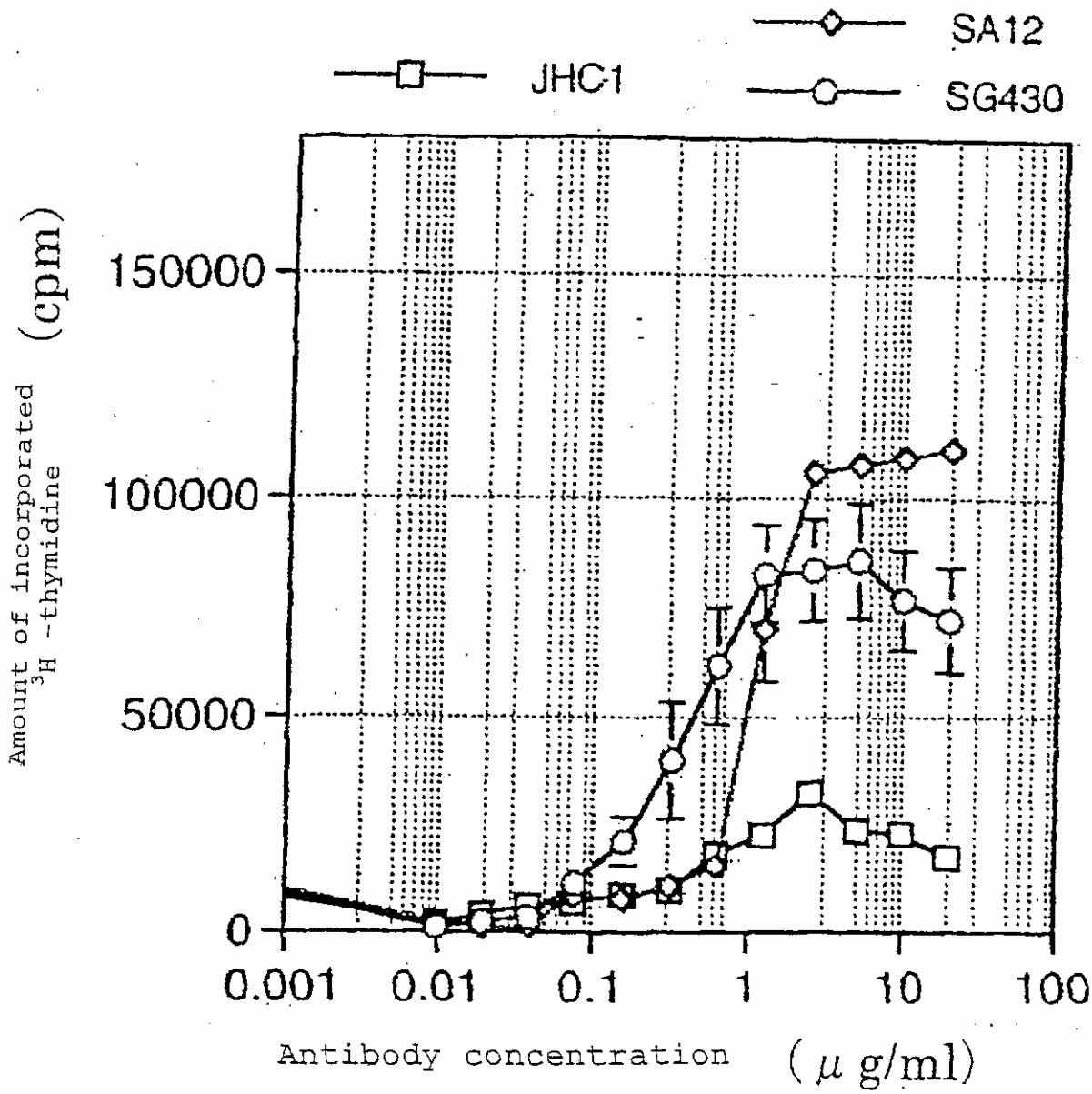

SA12
JHC1
SG430
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 31

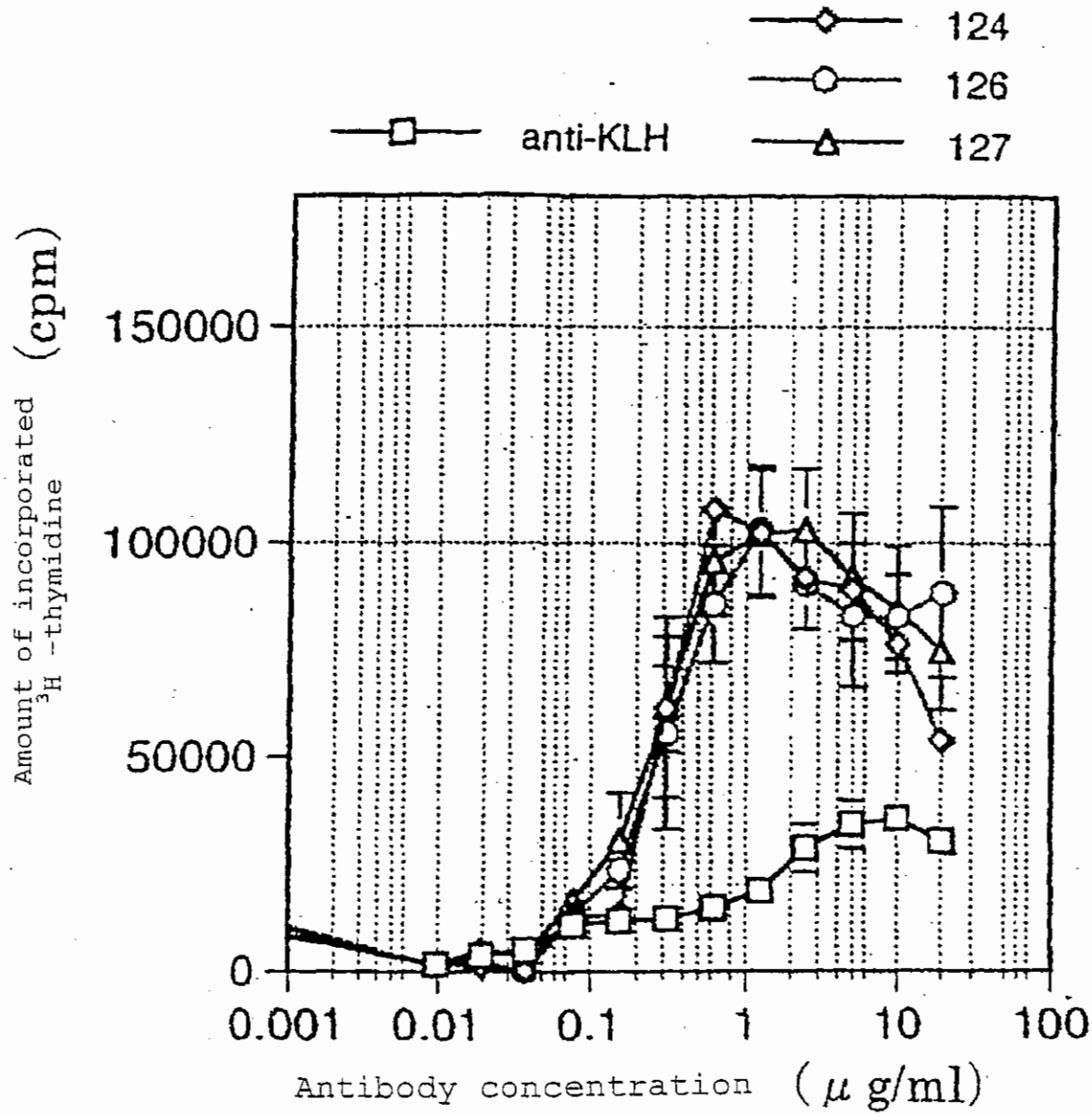

124
126
anti-KLH
127
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 32

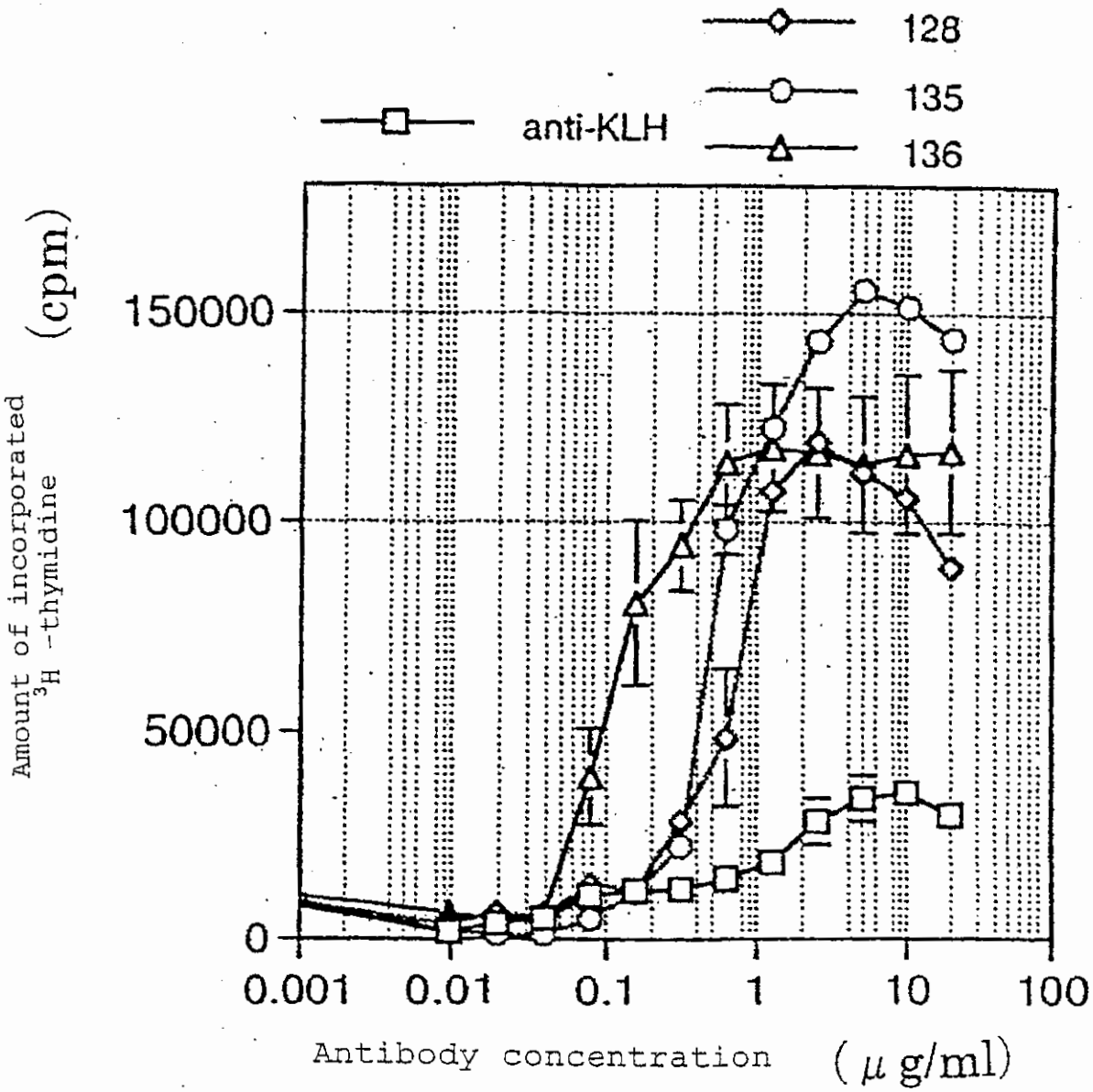

128
135
136
anti-KLH
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 33

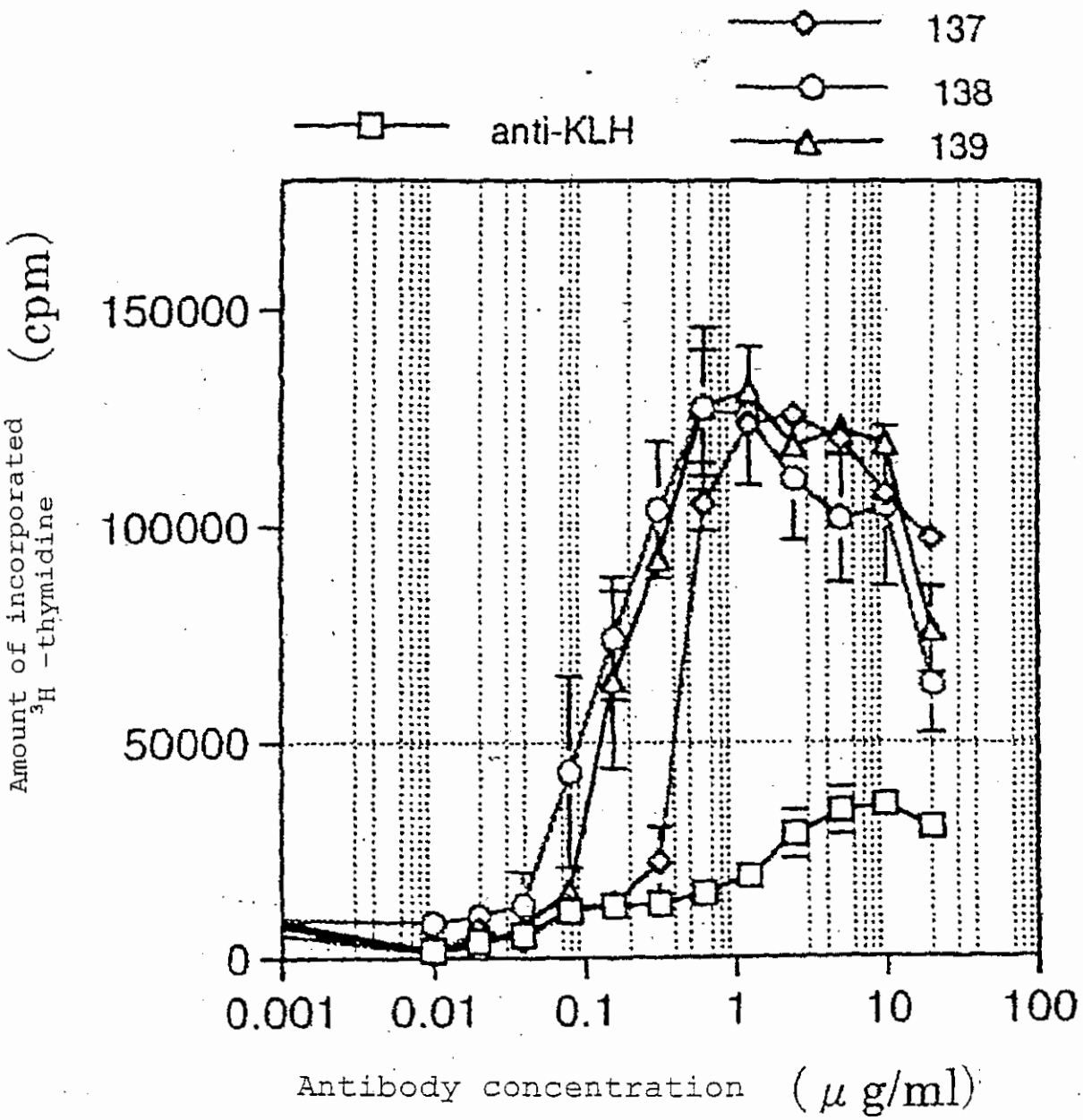

137
138
139
anti-KLH
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 34

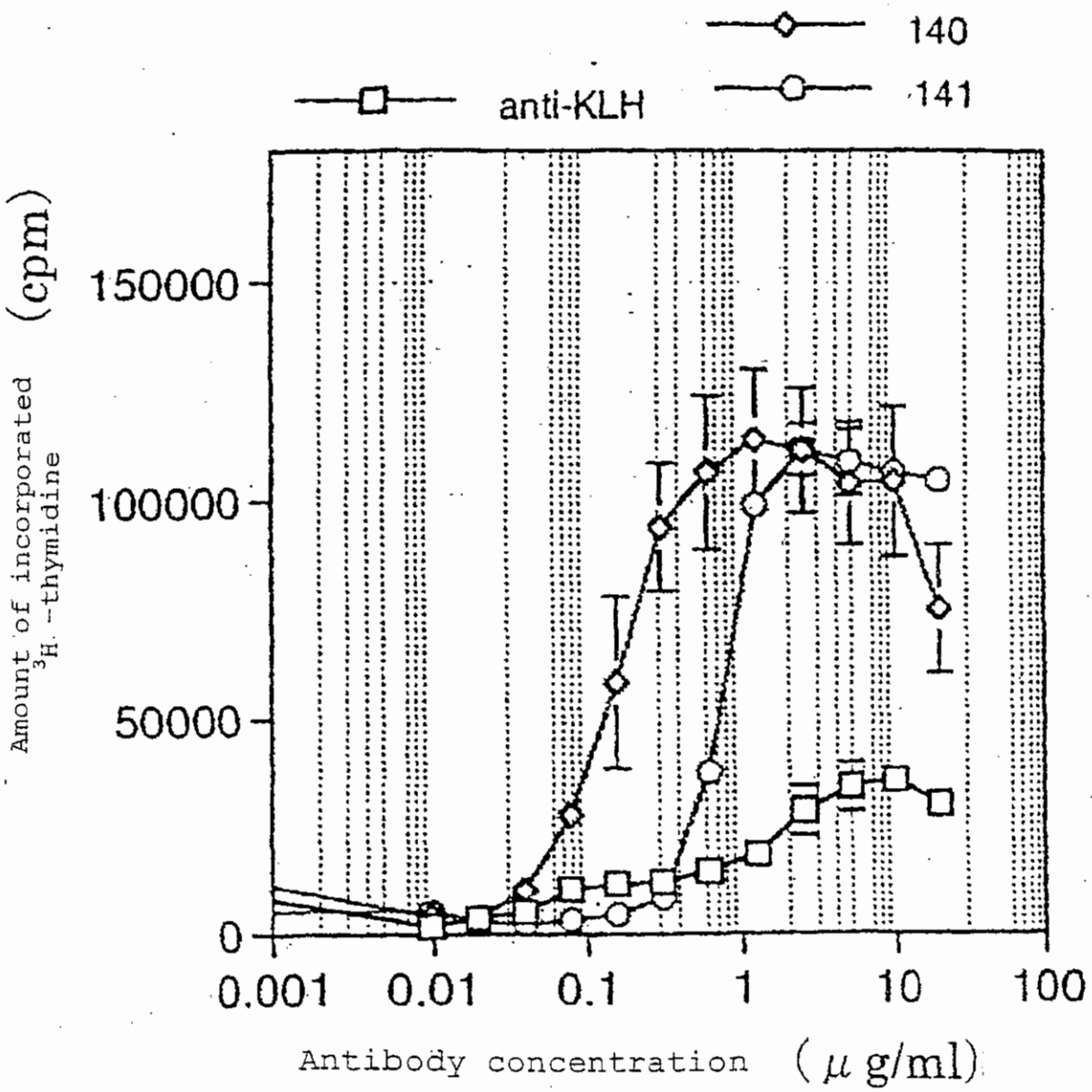

140
141
anti-KLH
Amount of incorporated ^{3}H-thymidine (cpm)
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 35

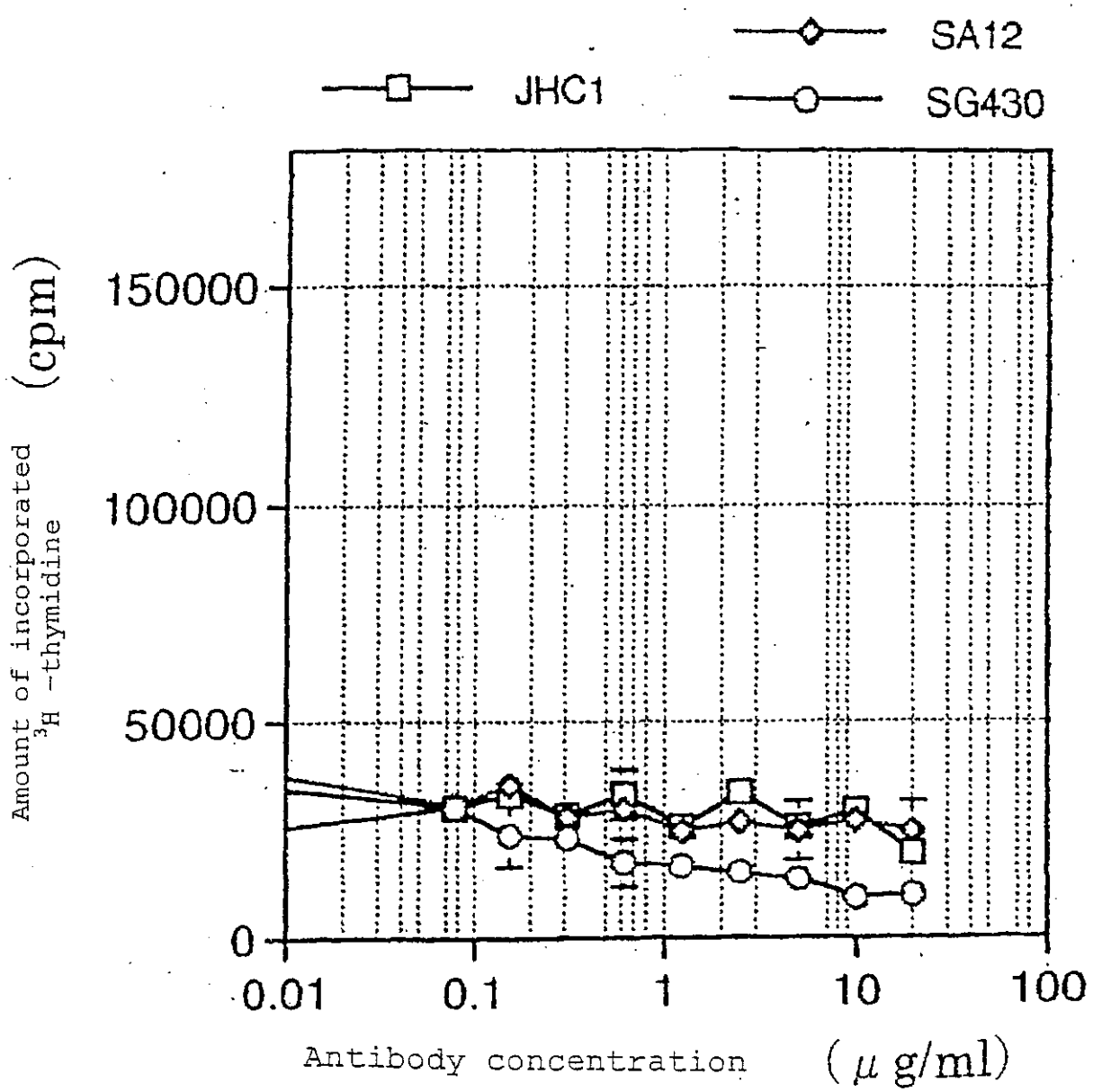

SA12
JHC1
SG430
150000
100000
50000
0
Amount of incorporated ^{3}H -thymidine (cpm)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 36

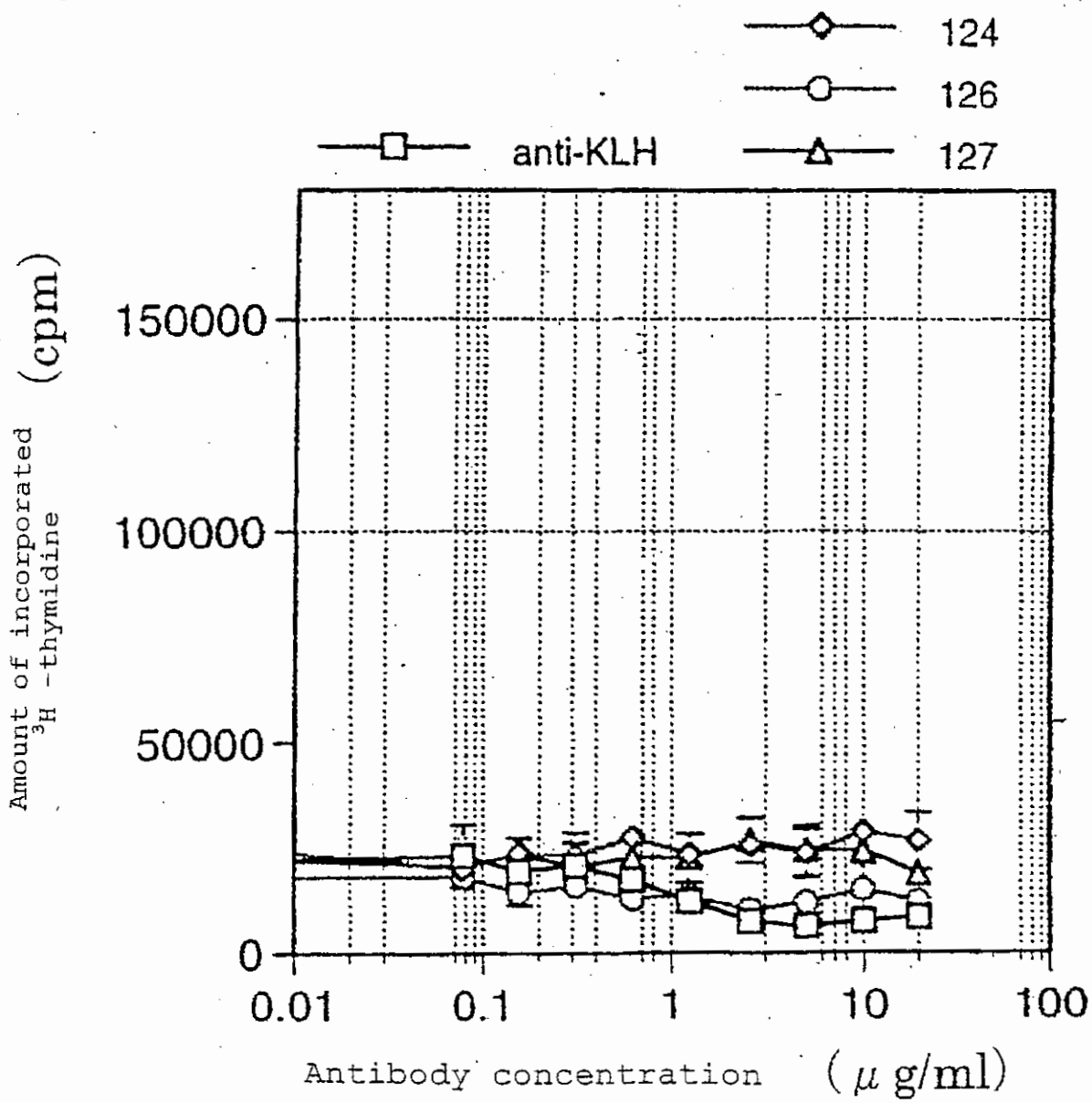

124
126
anti-KLH
127
Amount of incorporated ^{3}H -thymidine (cpm)
150000
100000
50000
0
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 37

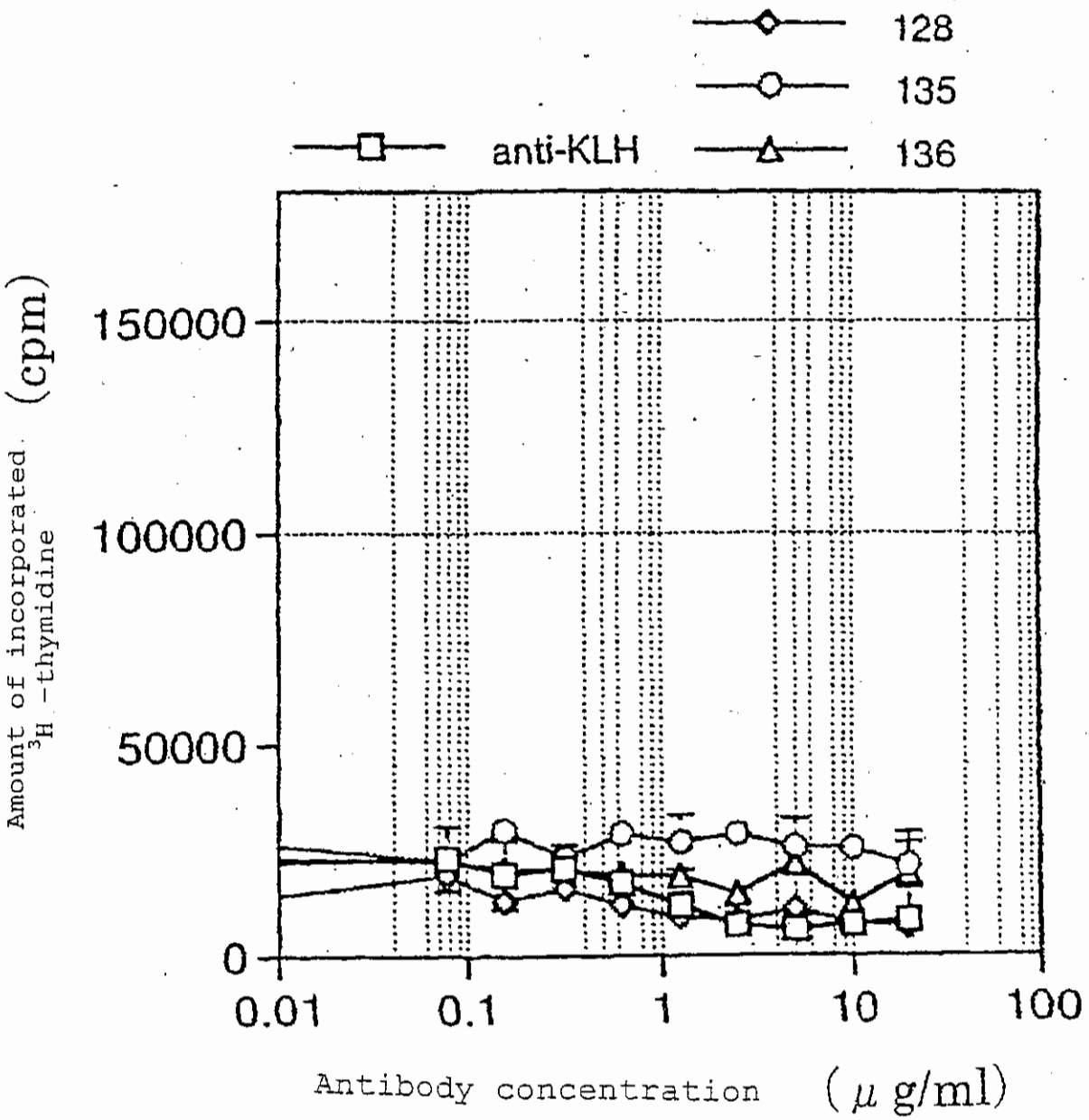

128
135
anti-KLH
136
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H -thymidine (cpm)
Antibody concentration (μg/ml)

Figure 38

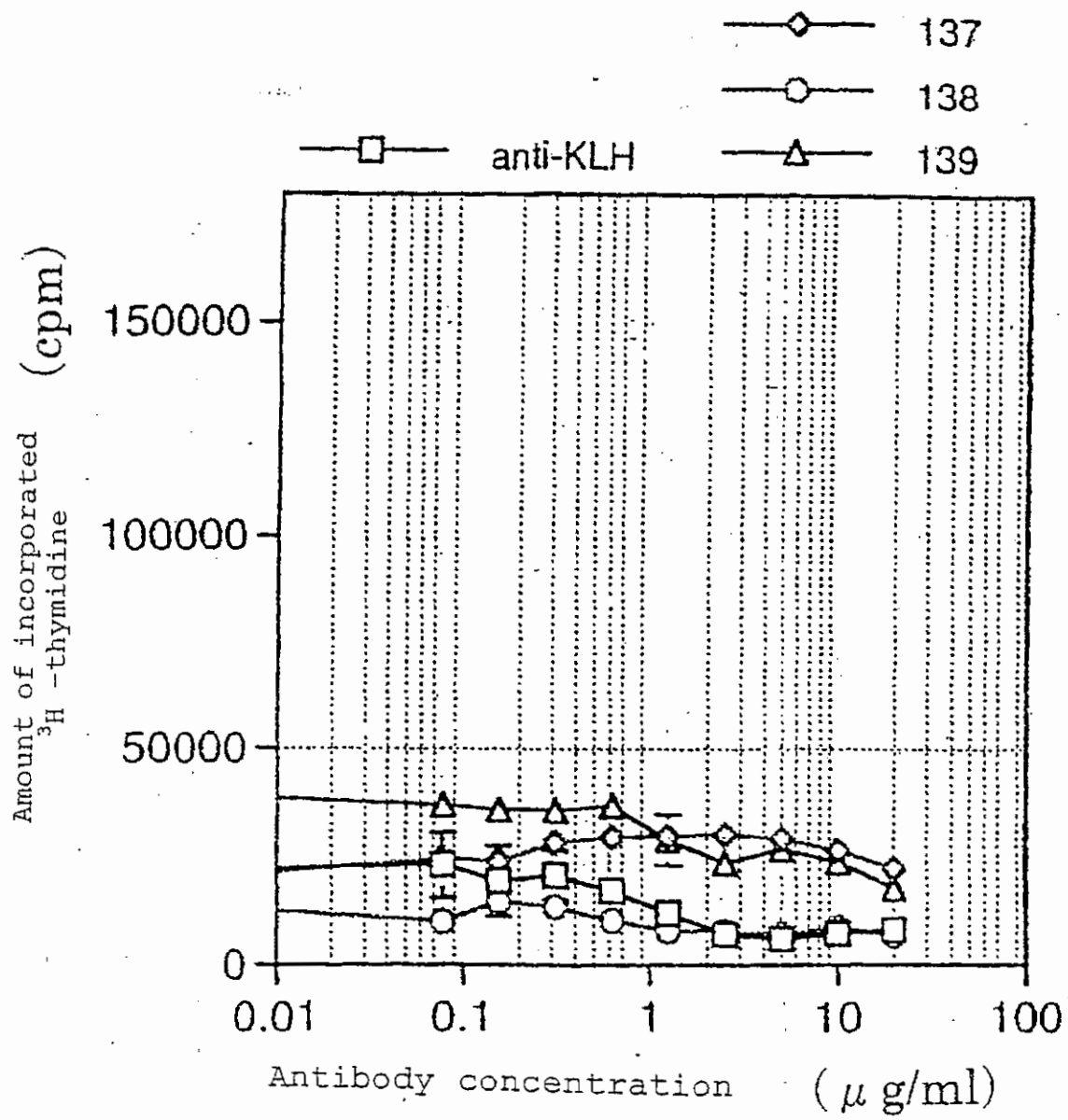

137
138
anti-KLH
139
150000
100000
50000
0
Amount of incorporated ^{3}H -thymidine (cpm)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 39

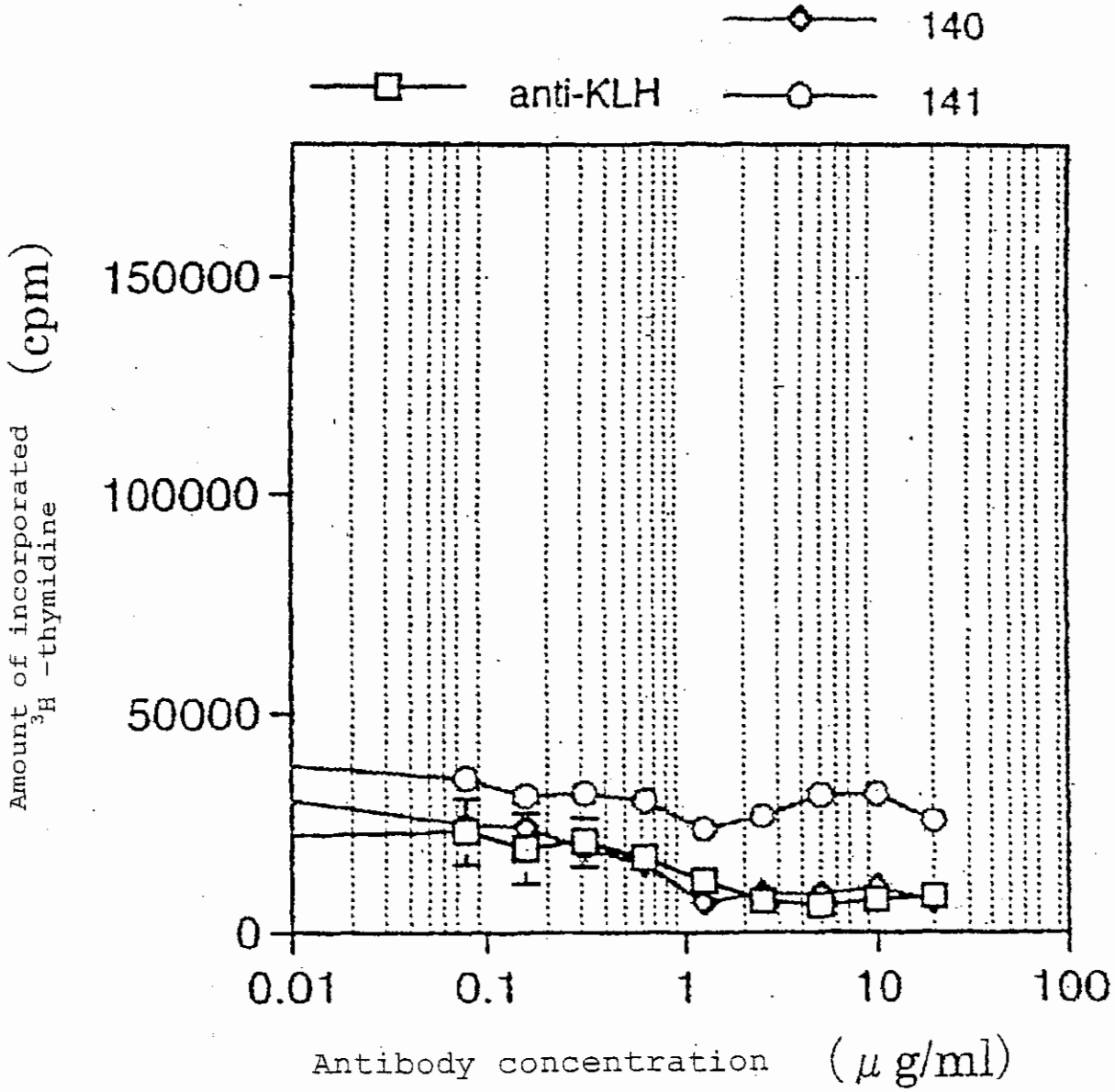

140
anti-KLH
141
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H -thymidine (cpm)
Antibody concentration (μg/ml)

Figure 40

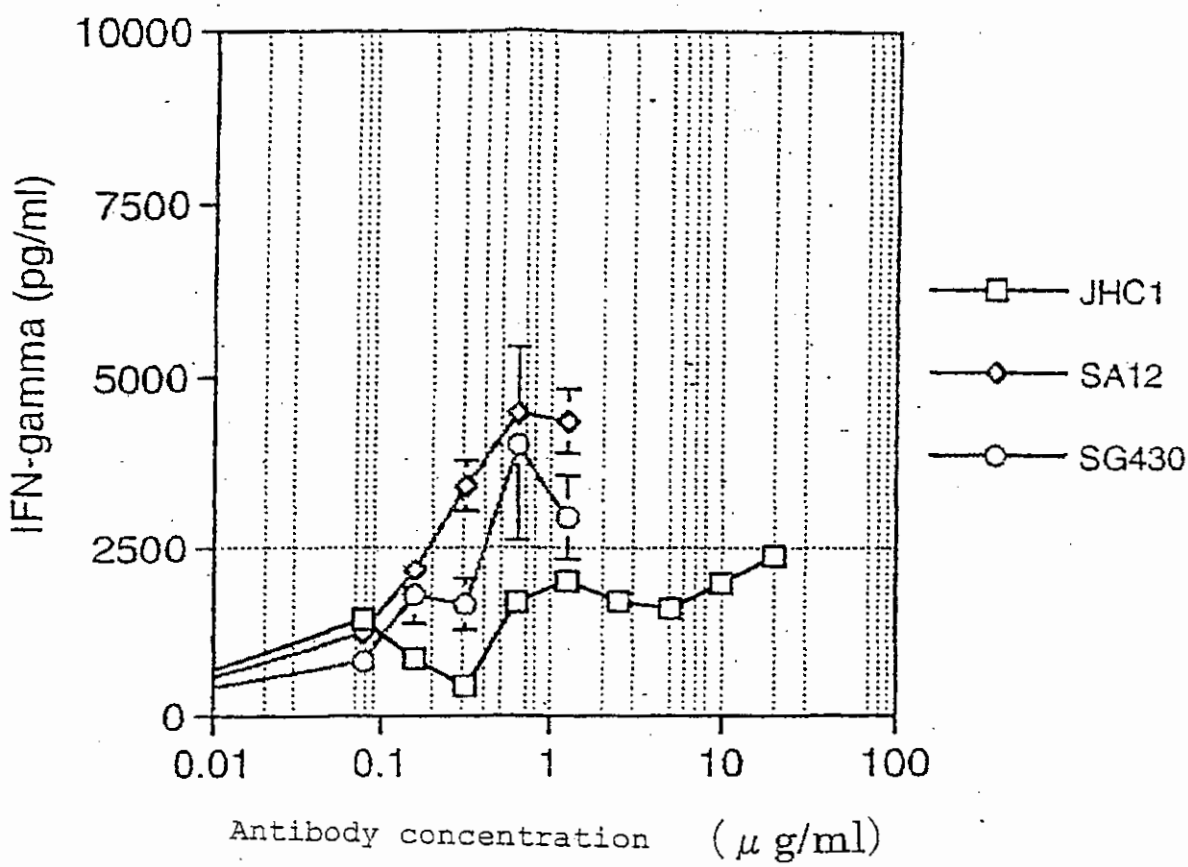

10000
7500
5000
2500
0
IFN-gamma (pg/ml)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)
JHC1
SA12
SG430

Figure 41

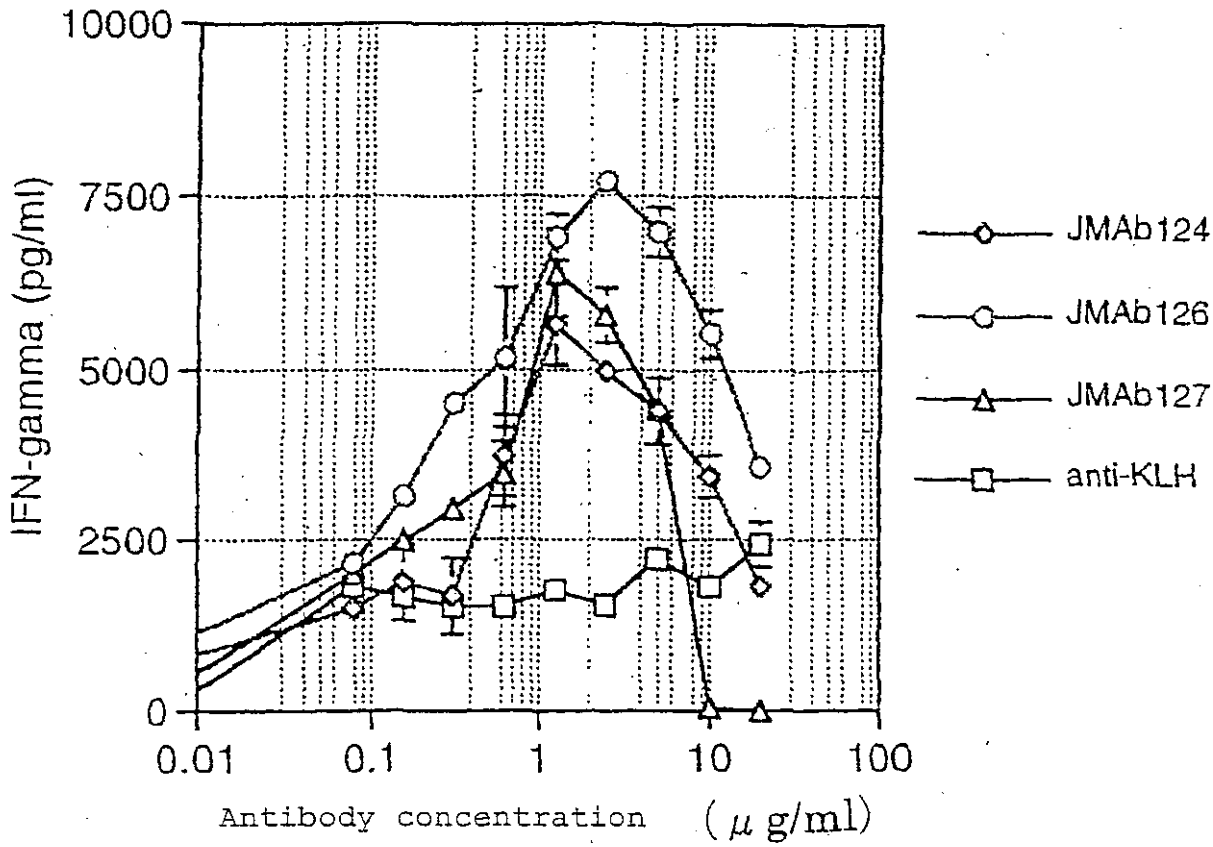

10000
7500
5000
2500
0
IFN-gamma (pg/ml)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)
JMAb124
JMAb126
JMAb127
anti-KLH

Figure 42

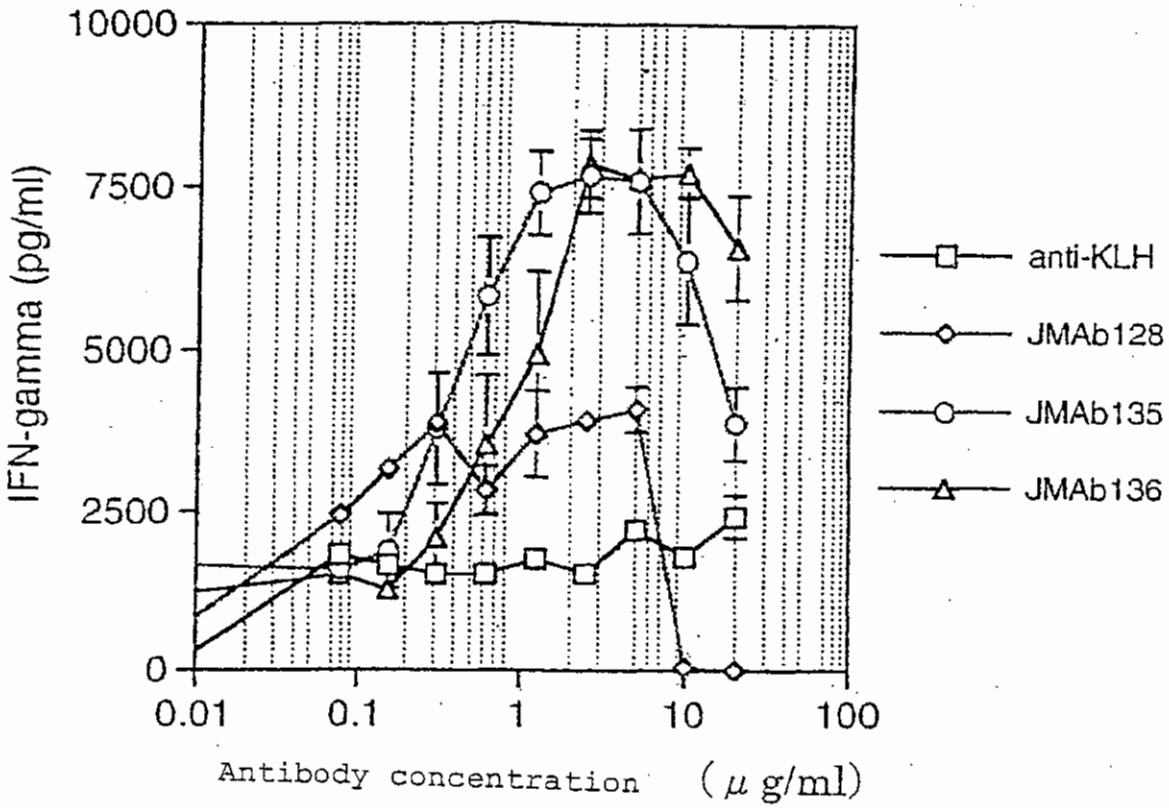

10000
7500
5000
2500
0
IFN-gamma (pg/ml)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)
anti-KLH
JMAb128
JMAb135
JMAb136

Figure 43

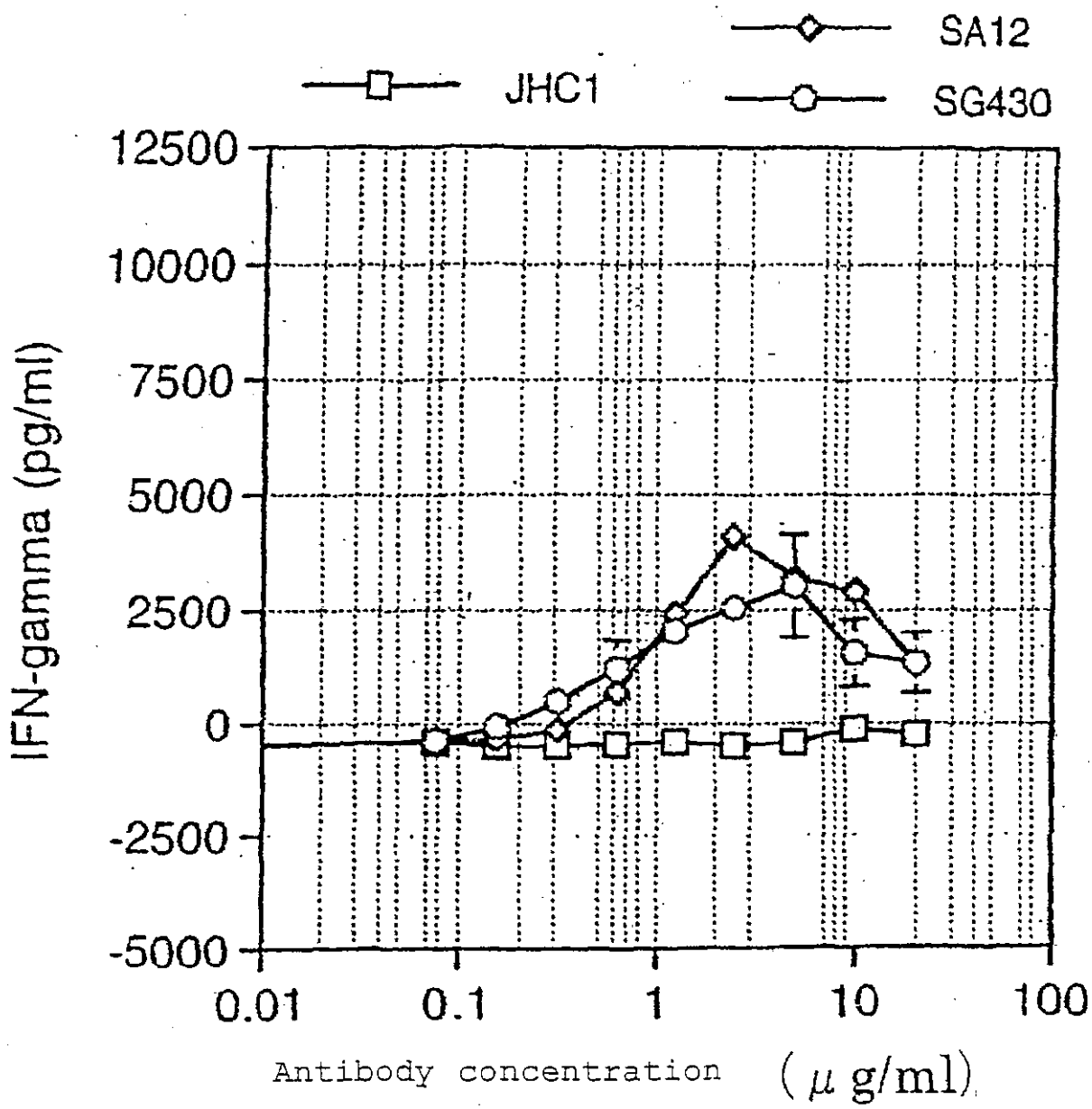

SA12
JHC1
SG430
12500
10000
7500
5000
2500
0
-2500
-5000
IFN-gamma (pg/ml)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 44

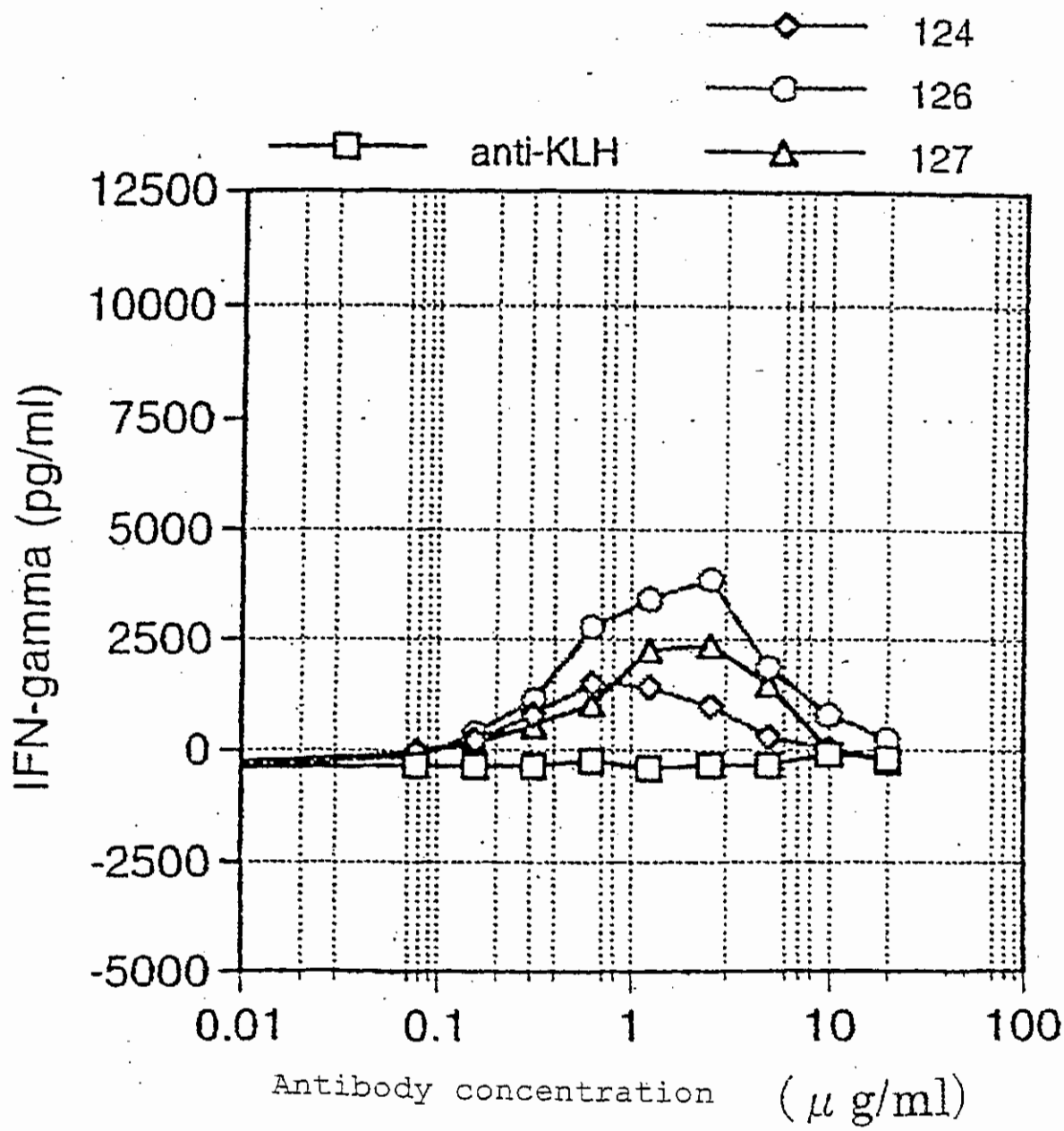

124
126
anti-KLH
127
12500
10000
7500
5000
2500
0
-2500
-5000
IFN-gamma (pg/ml)
0.01
0.1
1
10
100
Antibody concentration
(μg/ml)

Figure 45

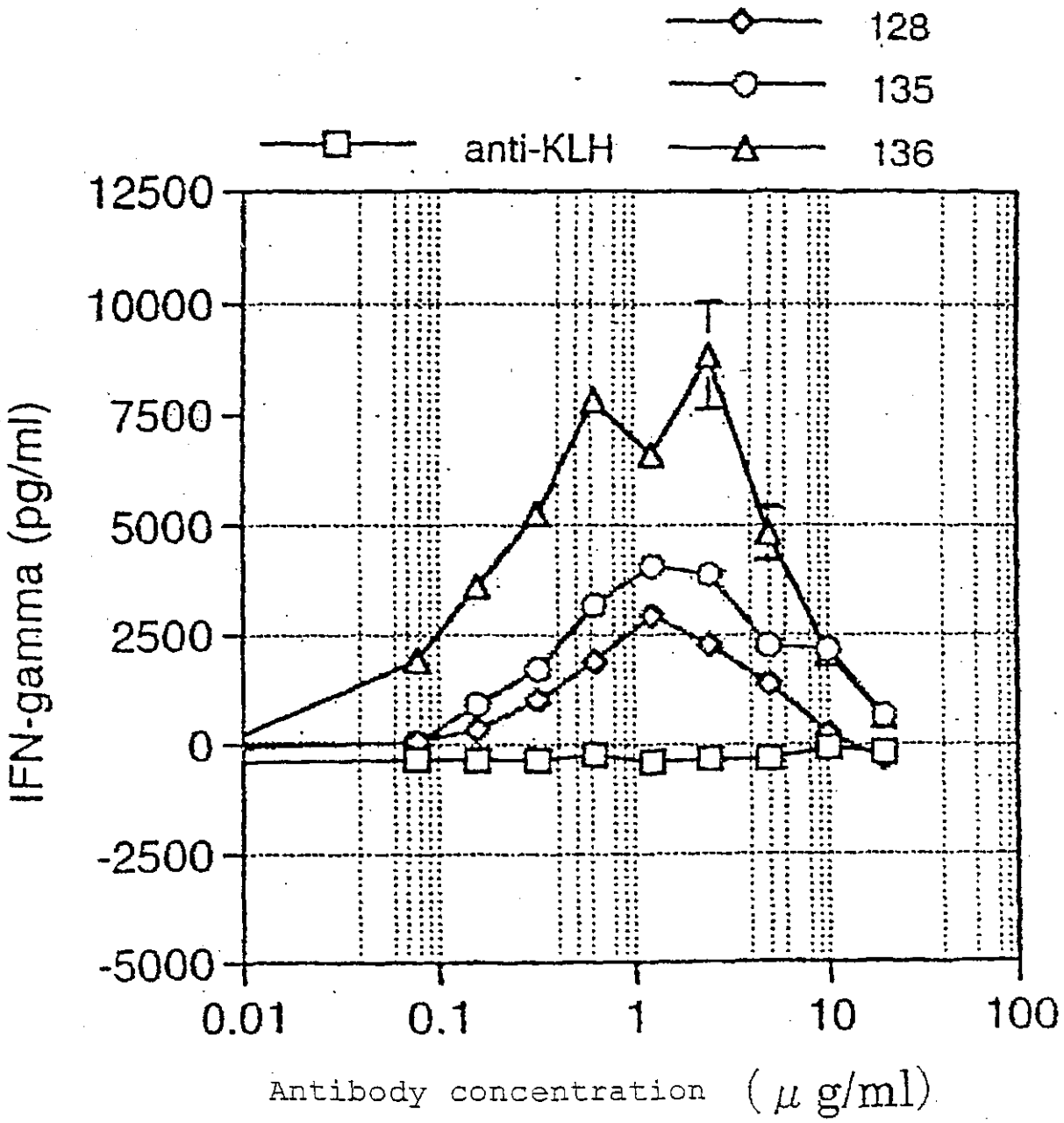

128
135
anti-KLH
136
12500
10000
7500
5000
2500
0
-2500
-5000
IFN-gamma (pg/ml)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 46

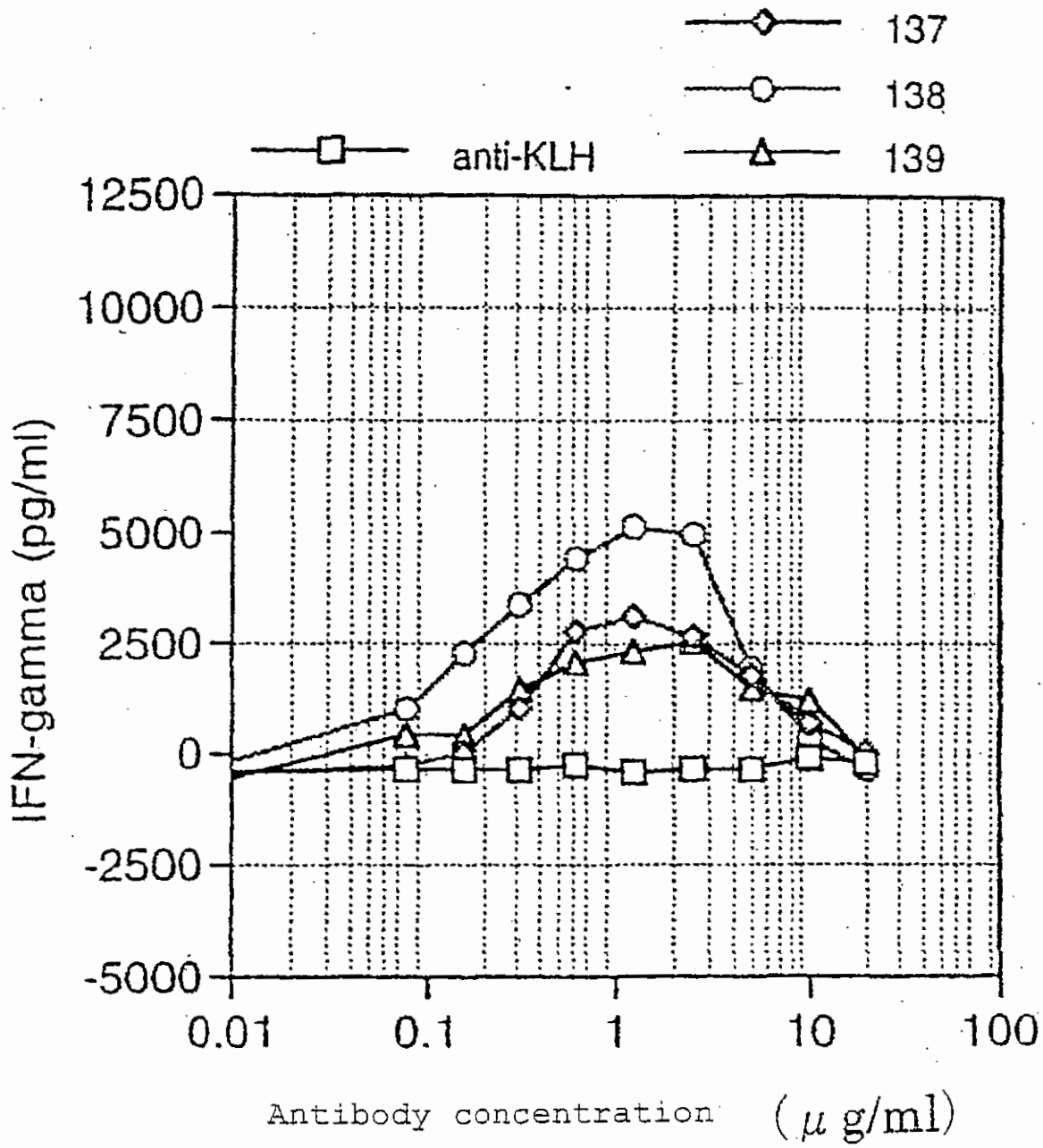

137
138
anti-KLH
139
12500
10000
7500
5000
2500
0
-2500
-5000
IFN-gamma (pg/ml)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 47

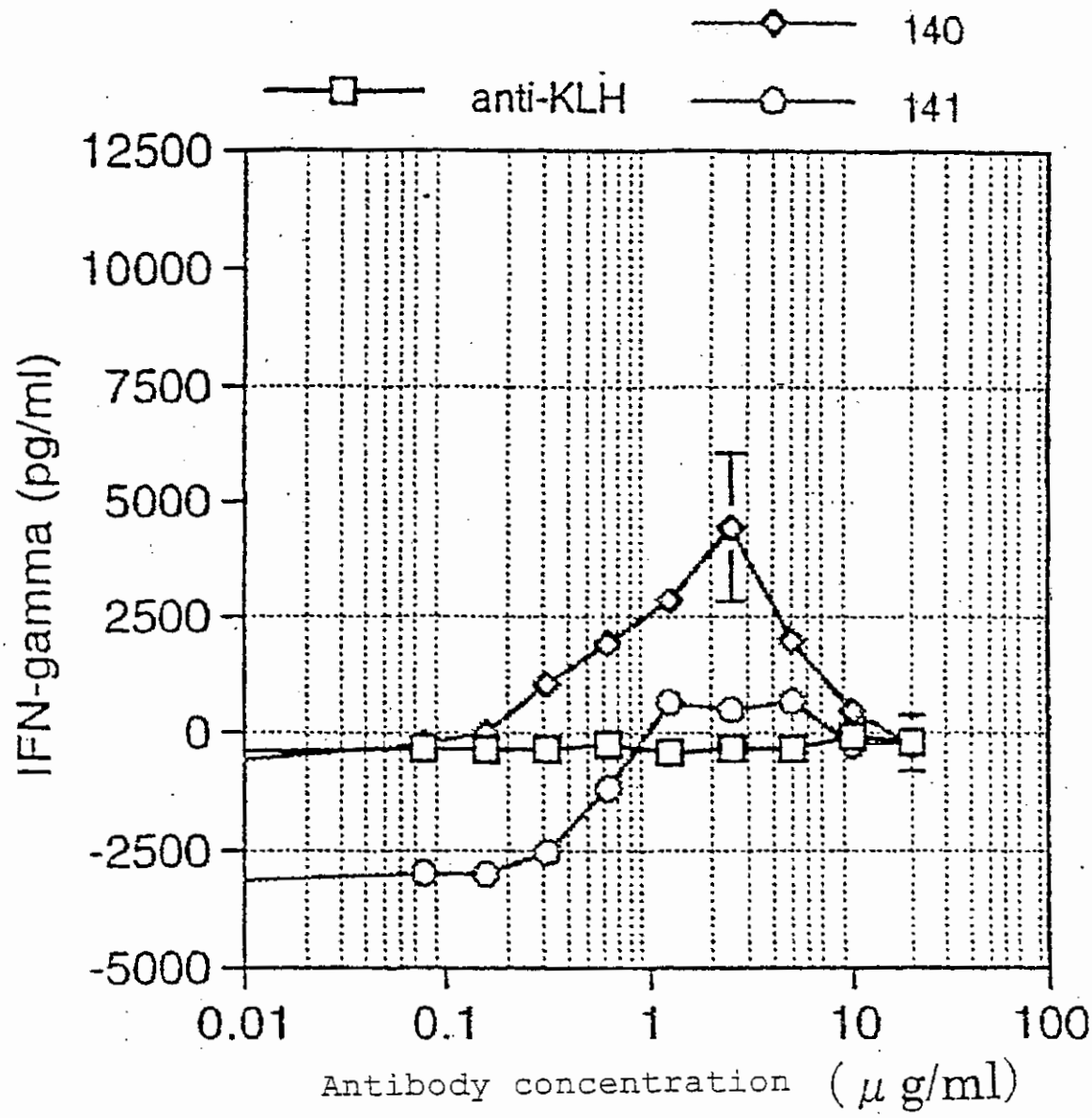

140
anti-KLH
141
12500
10000
7500
5000
2500
0
-2500
-5000
IFN-gamma (pg/ml)
0.01
0.1
1
10
100
Antibody concentration (μg/ml)

Figure 48

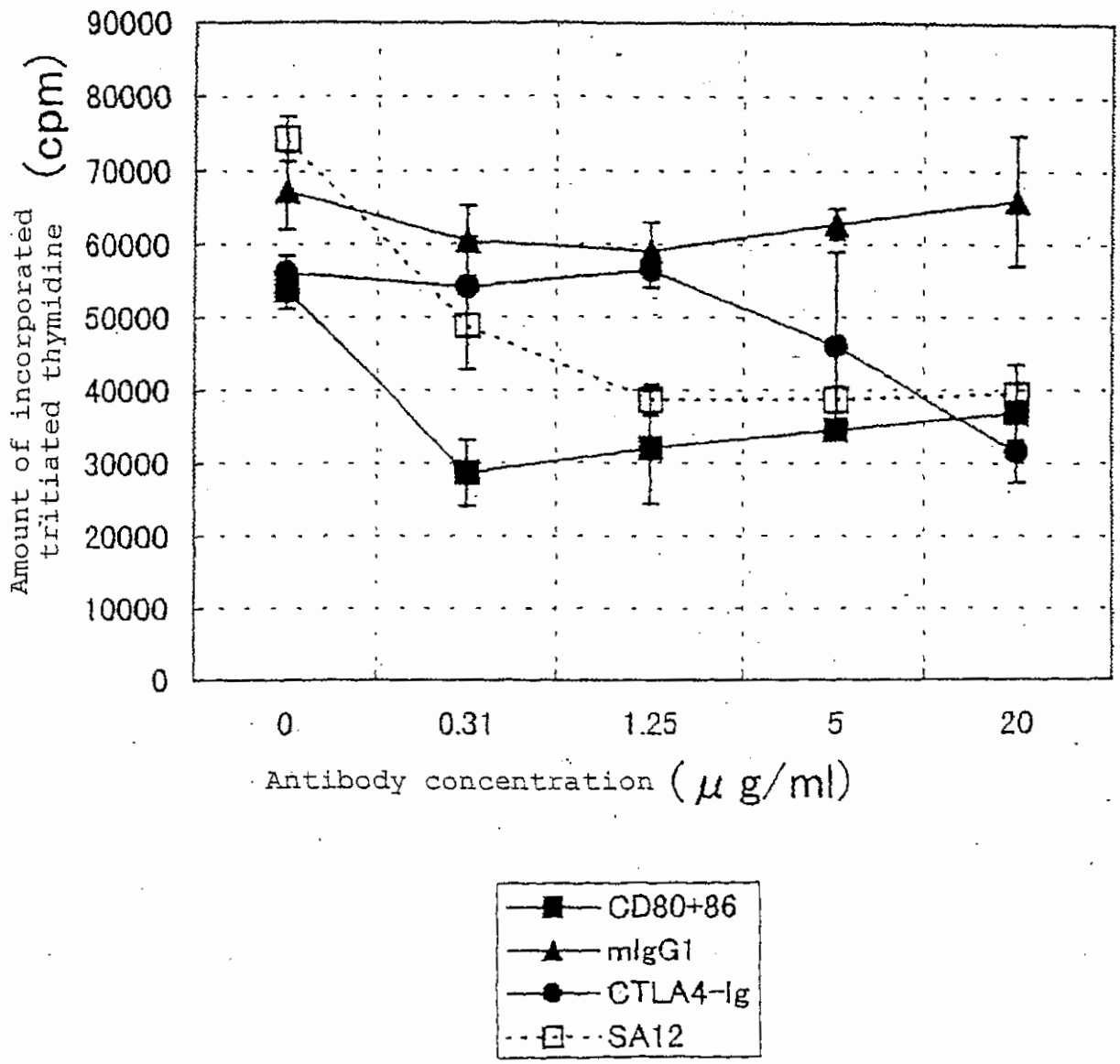

90000
80000
70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
CD80+86
mIgG1
CTLA4-Ig
SA12

Figure 49

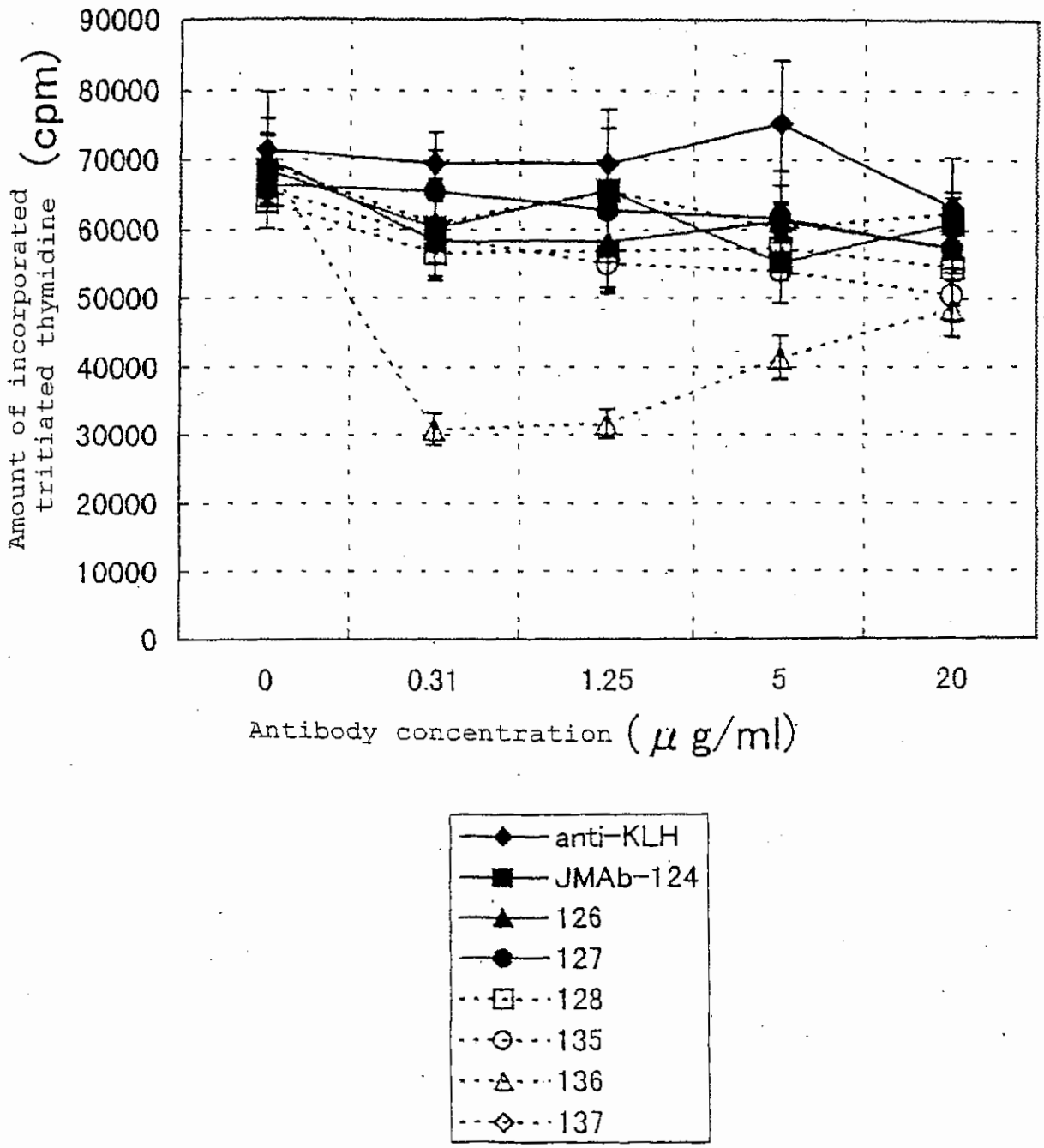

90000
80000
70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-124
126
127
128
135
136
137

Figure 50

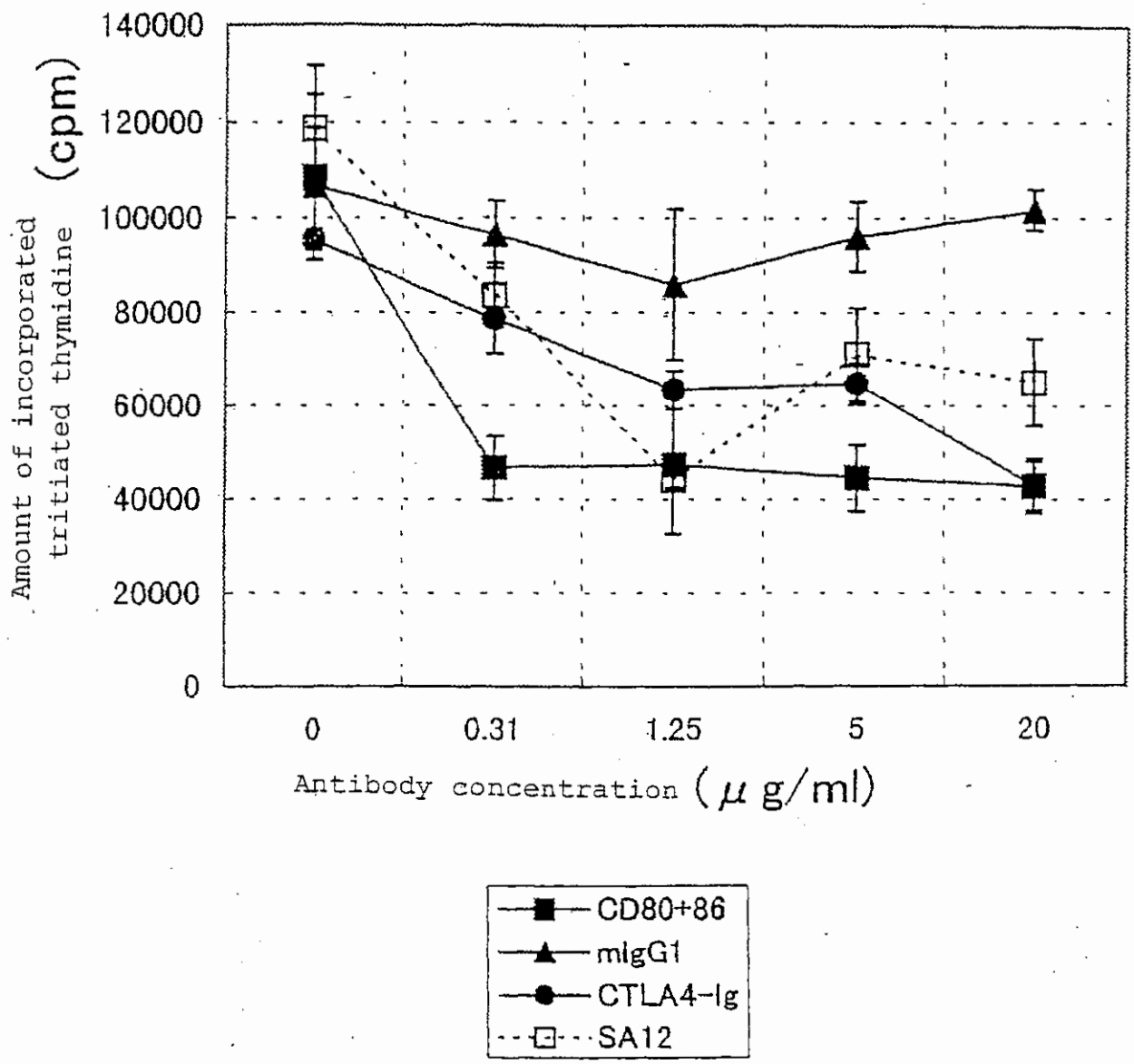

140000
120000
100000
80000
60000
40000
20000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
CD80+86
mIgG1
CTLA4-Ig
SA12

Figure 51

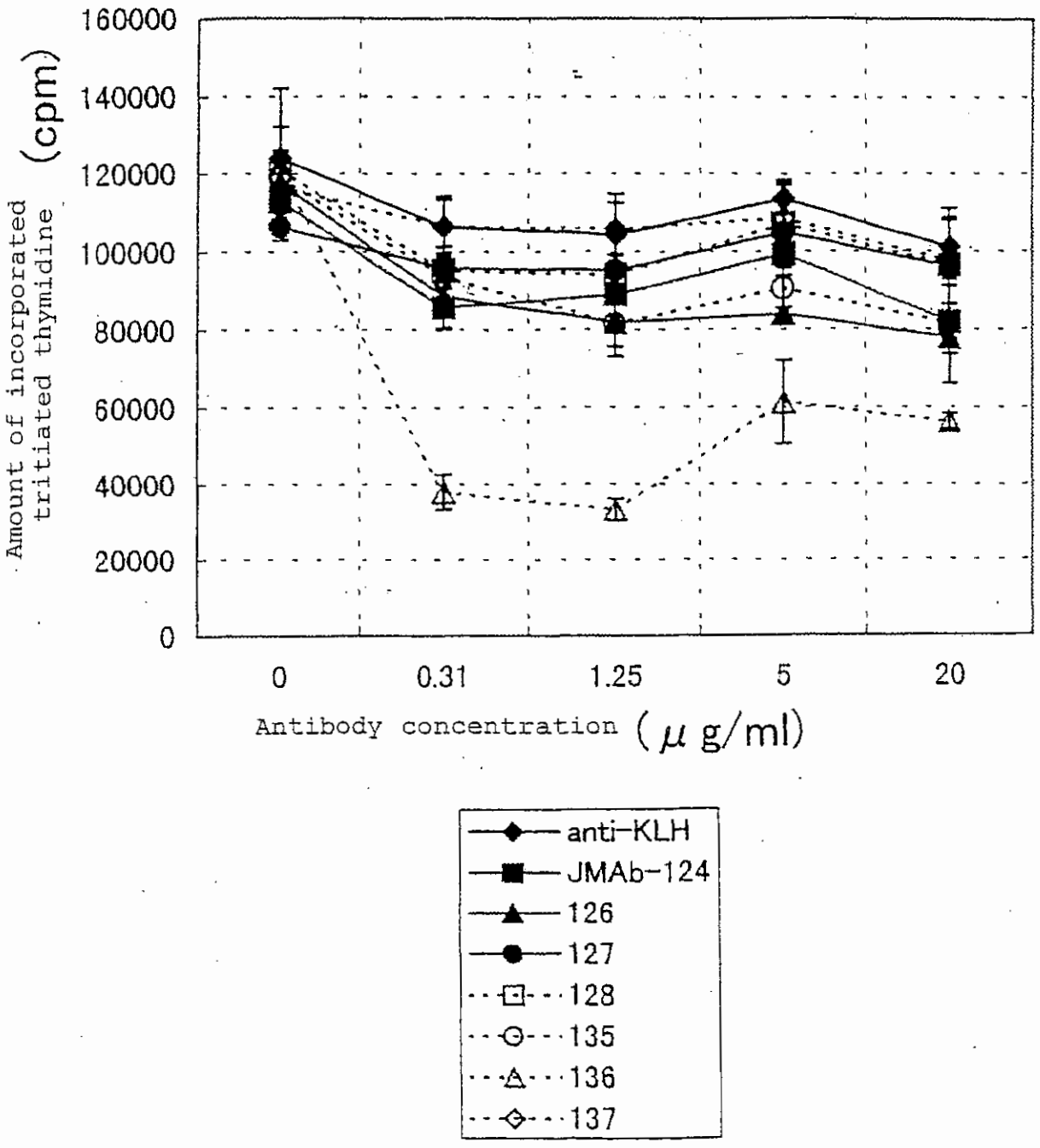

160000
140000
120000
100000
80000
60000
40000
20000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-124
126
127
128
135
136
137

Figure 52

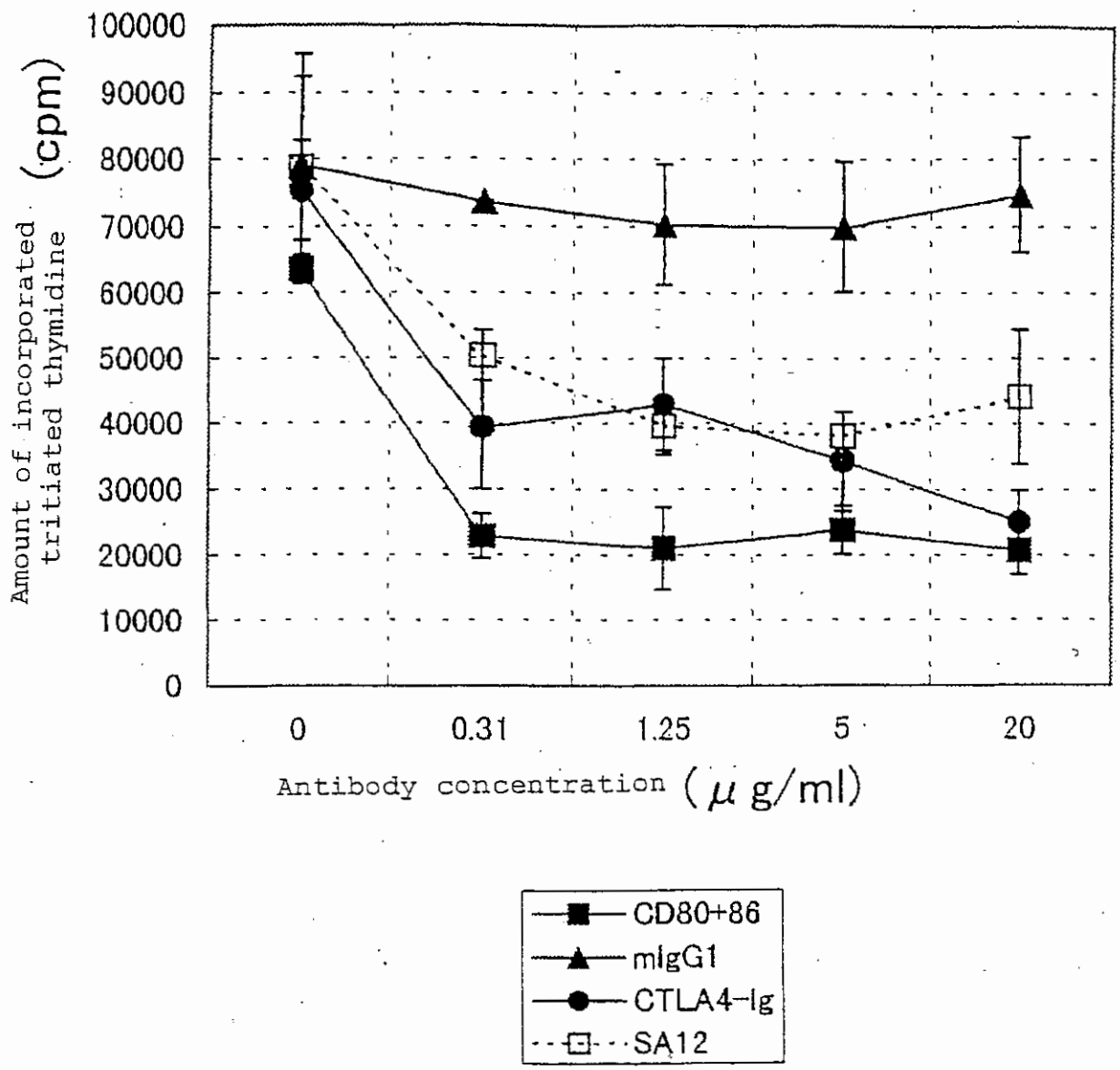

100000
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
CD80+86
mIgG1
CTLA4-Ig
SA12

Figure 53

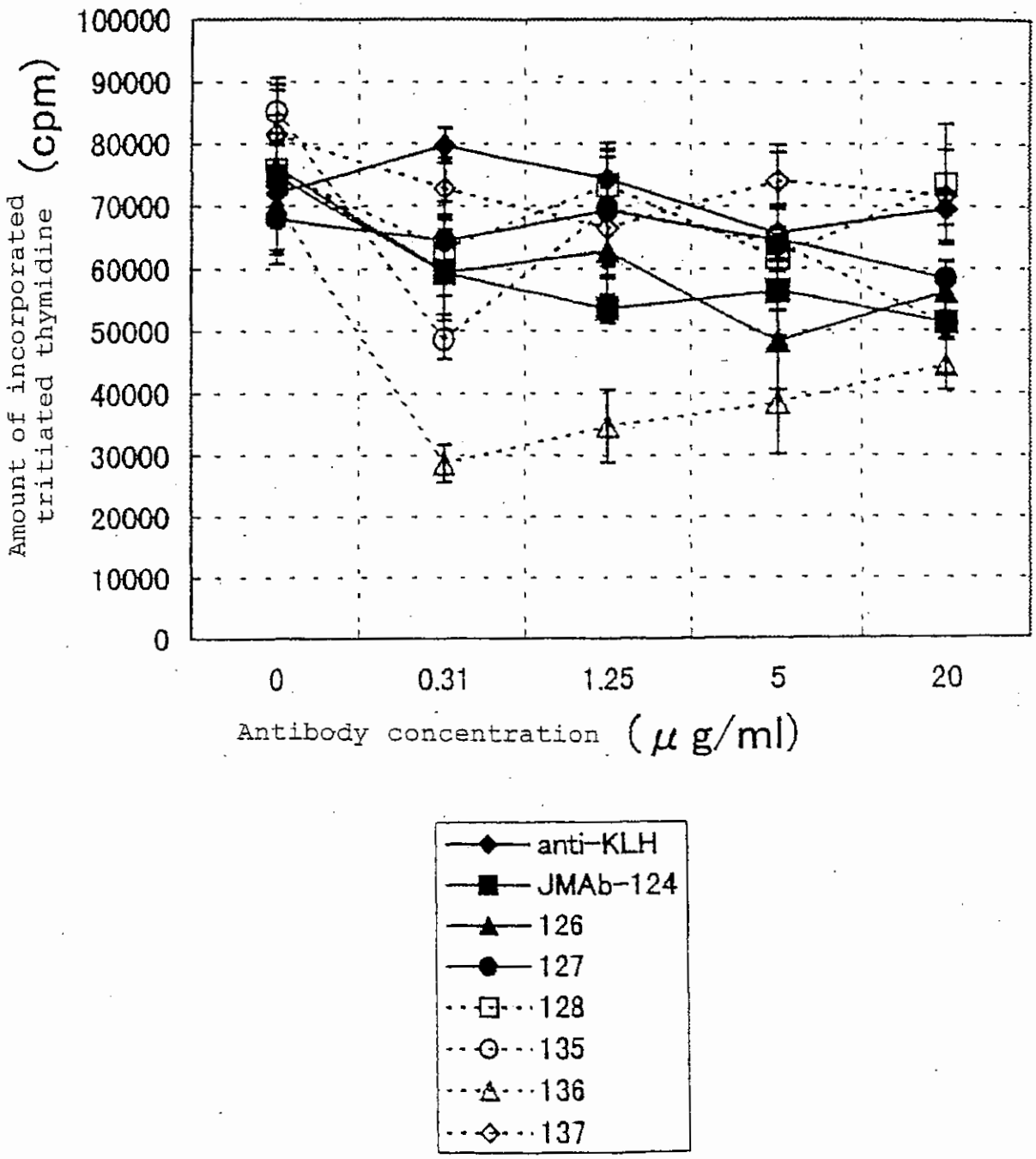

100000
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-124
126
127
128
135
136
137

Figure 54

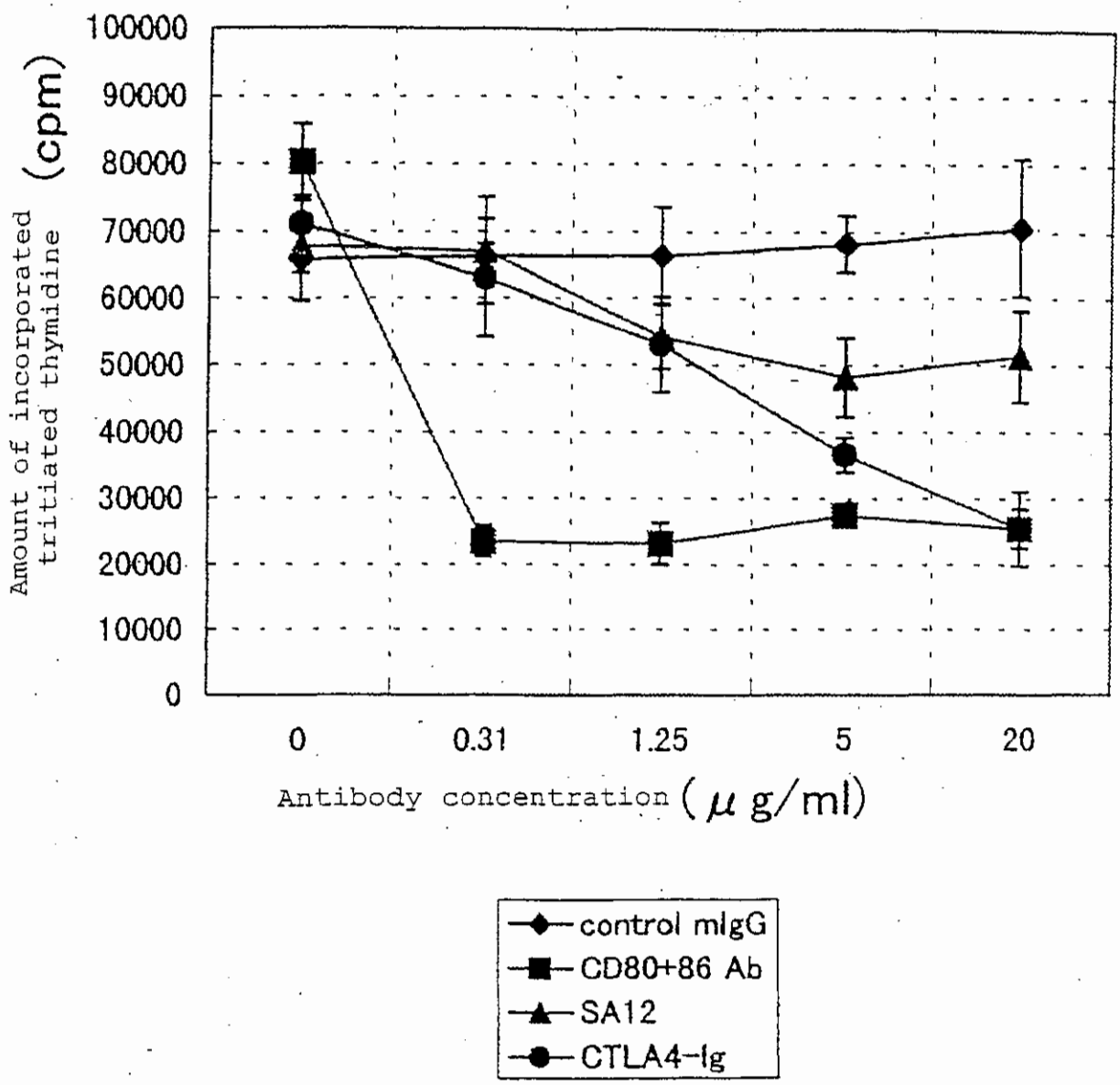

100000
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
control mIgG
CD80+86 Ab
SA12
CTLA4-Ig

Figure 55

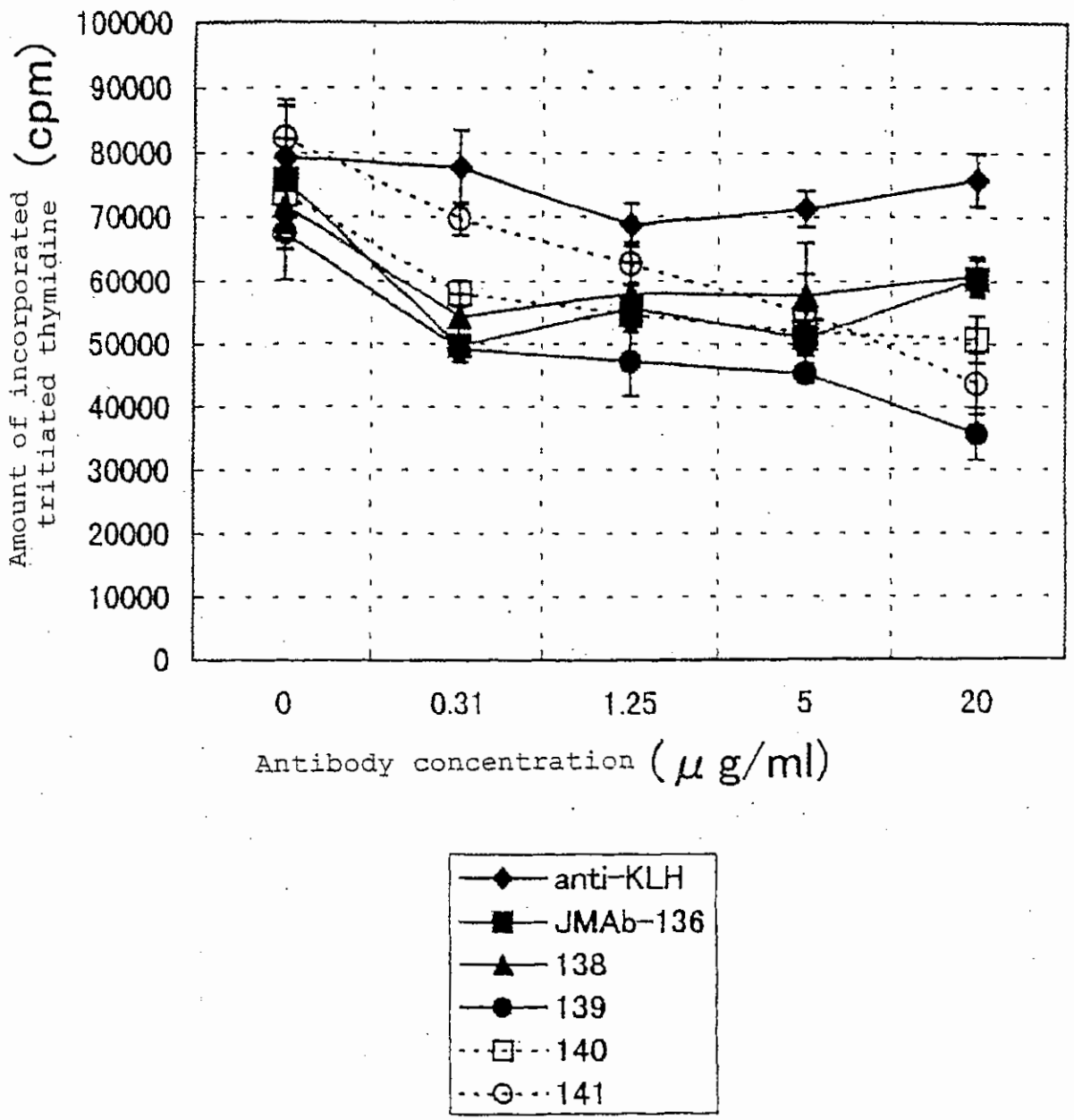

100000
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-136
138
139
140
141

Figure 56

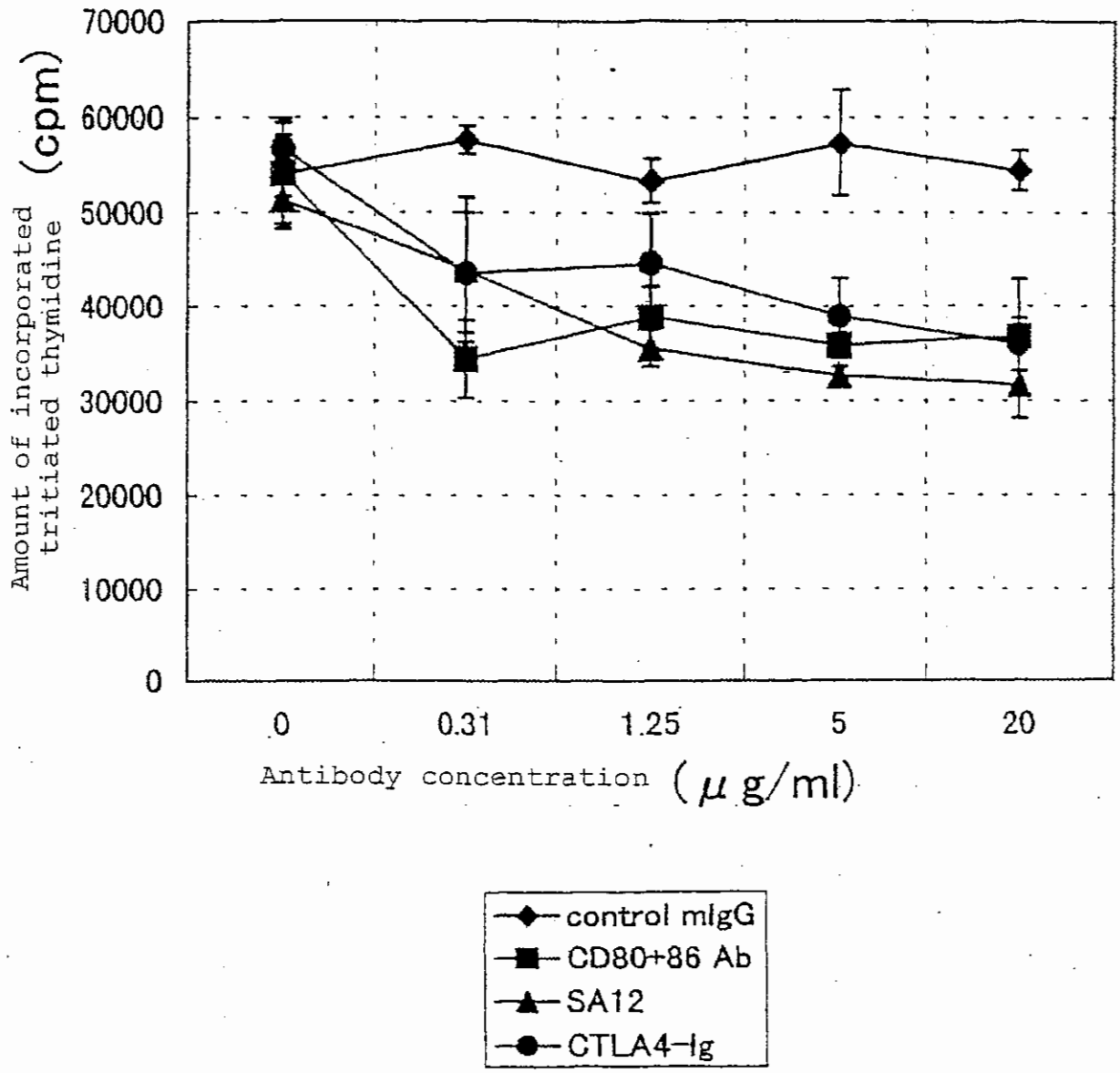

70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
control mIgG
CD80+86 Ab
SA12
CTLA4-Ig

Figure 57

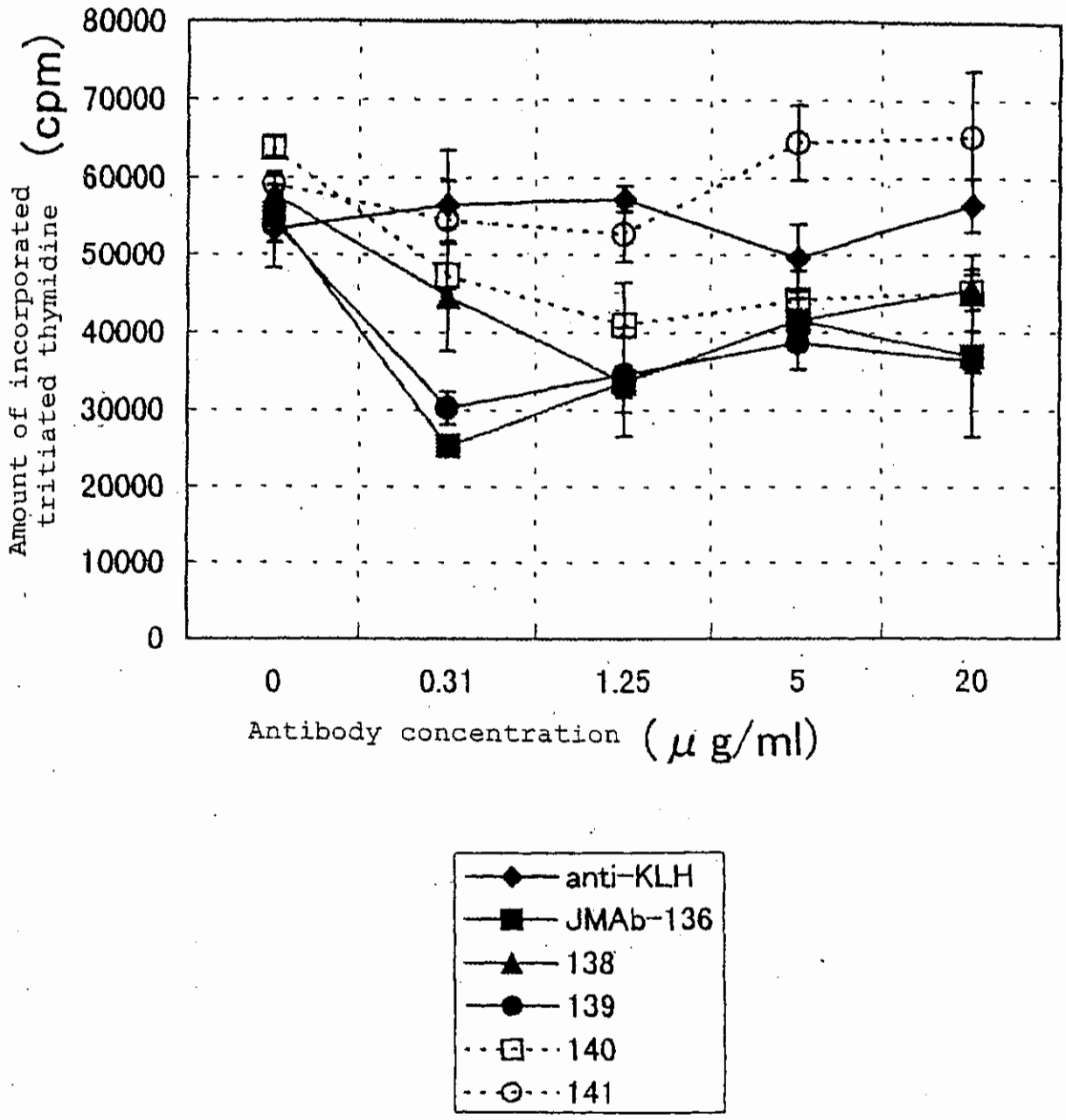

80000
70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-136
138
139
140
141

Figure 58

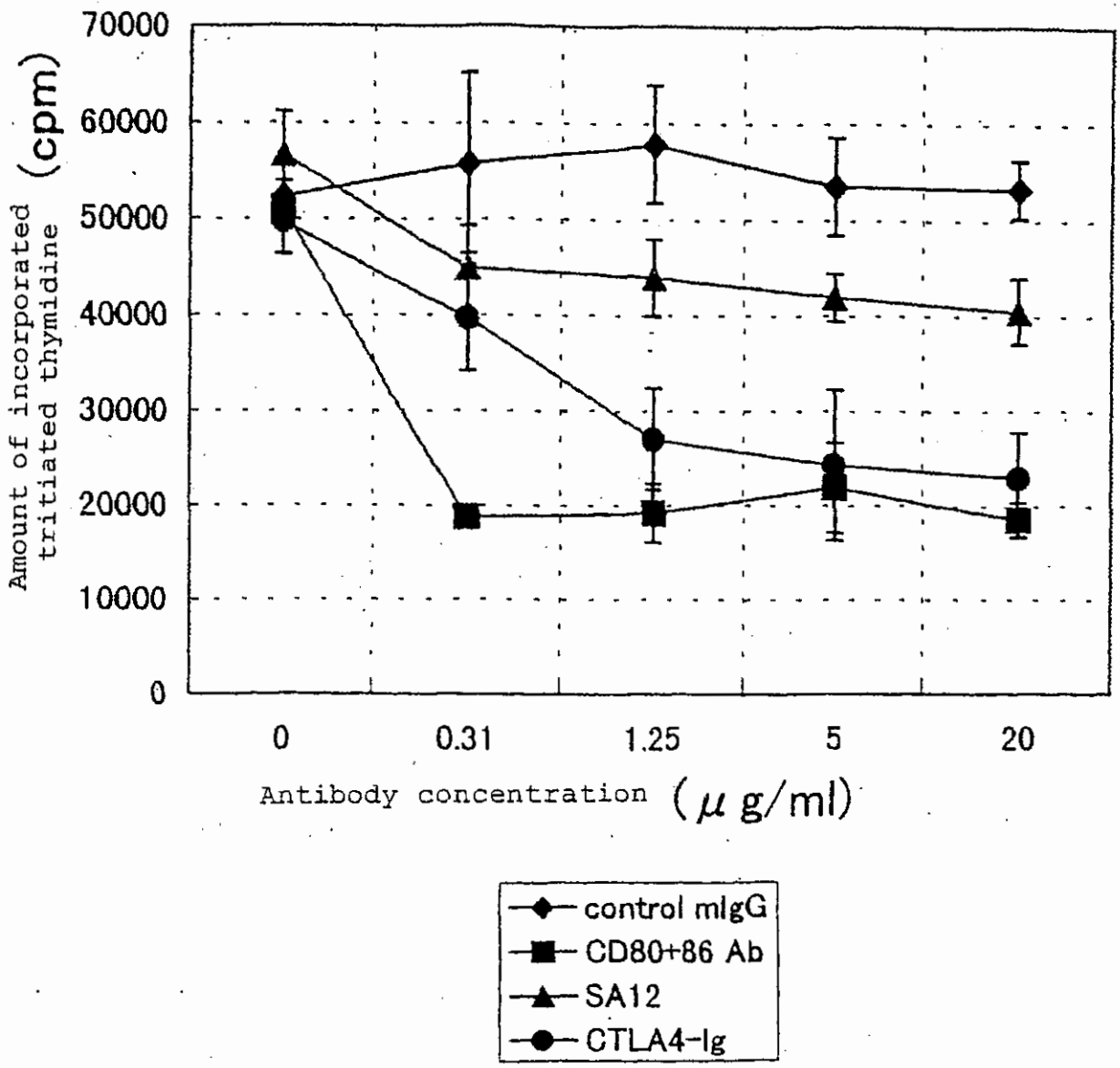

70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
control mIgG
CD80+86 Ab
SA12
CTLA4-Ig

Figure 59

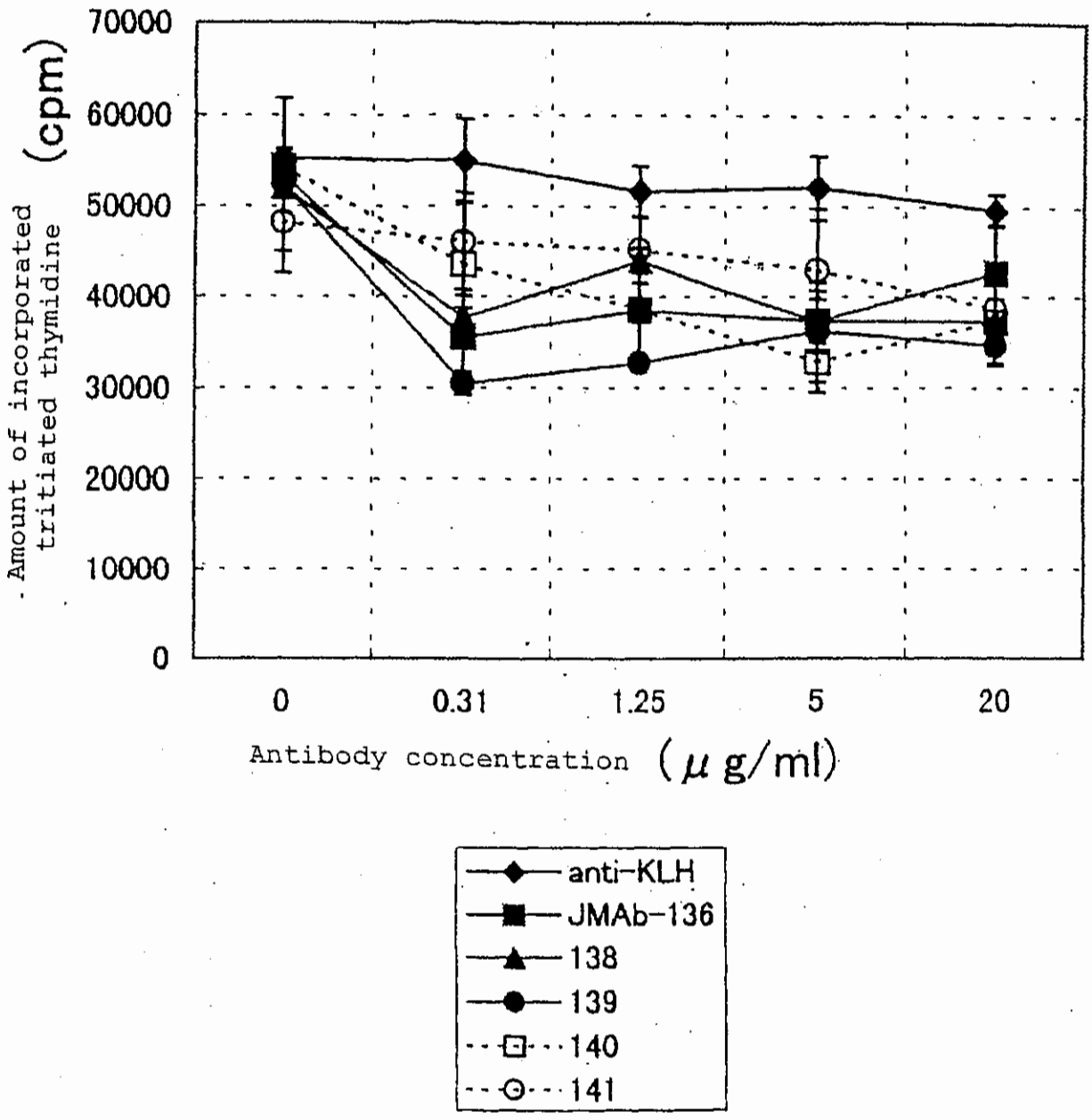

70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-136
138
139
140
141

Figure 60

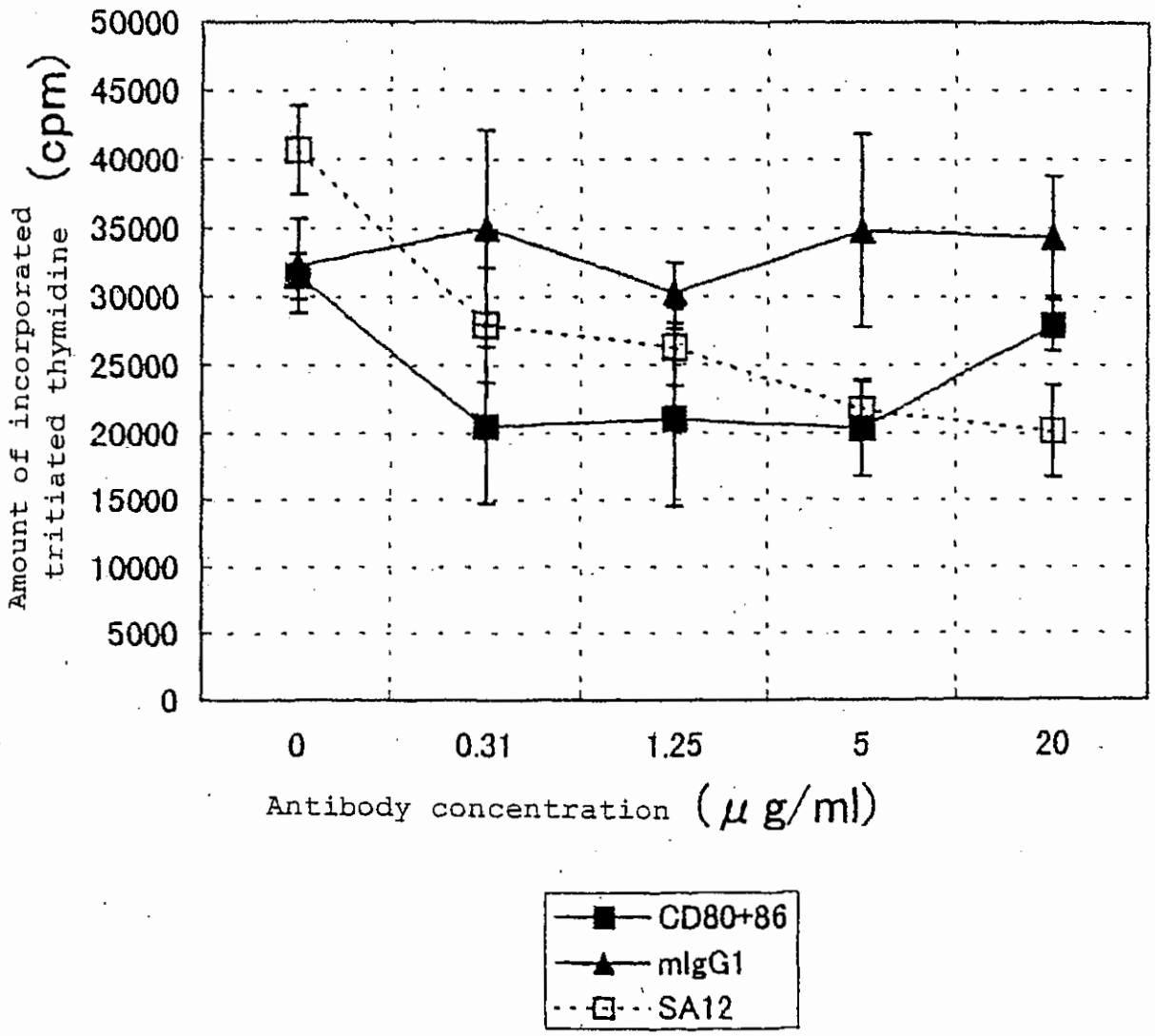

50000
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
CD80+86
mIgG1
SA12

Figure 61

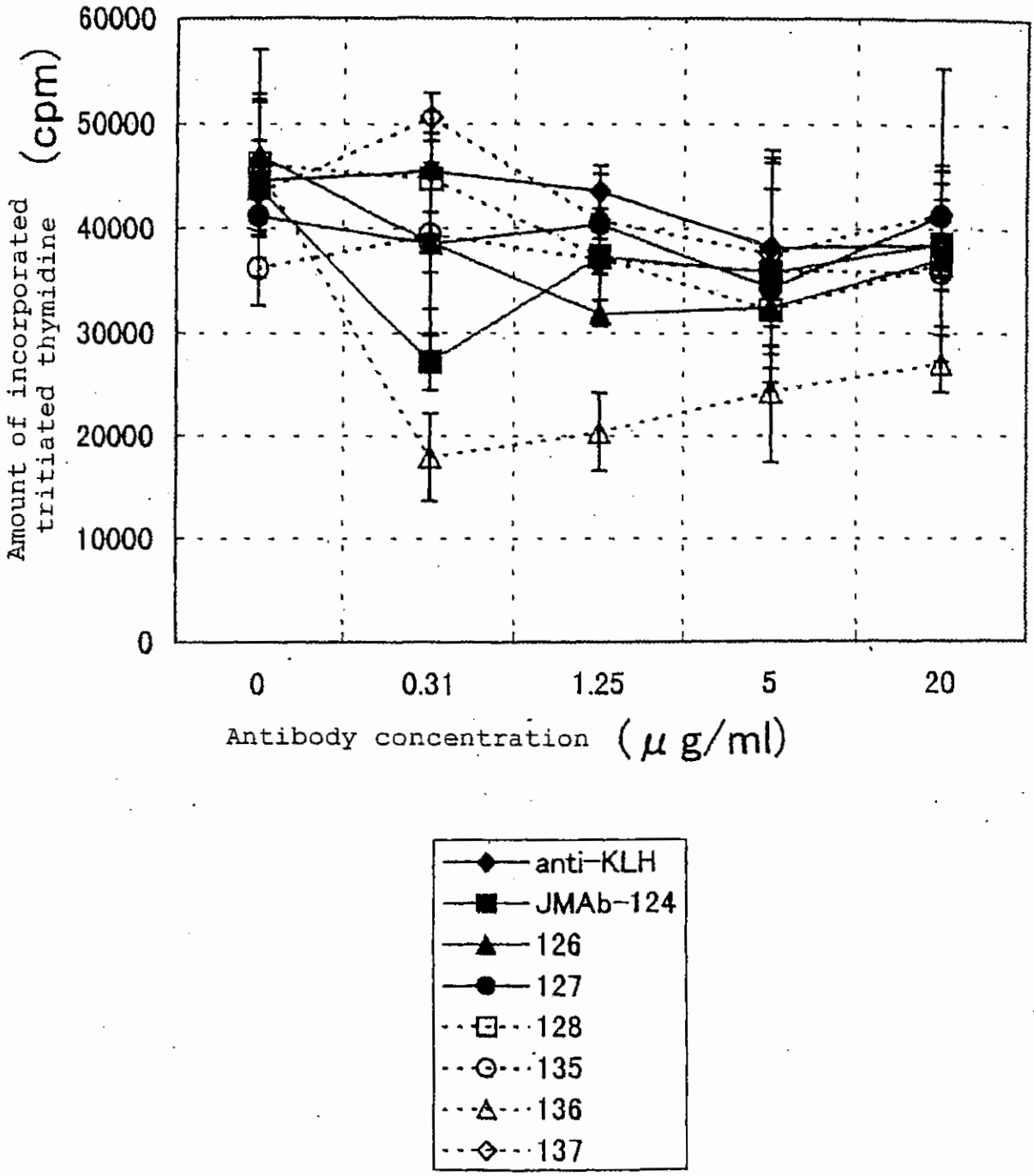

60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-124
126
127
128
135
136
137

Figure 62

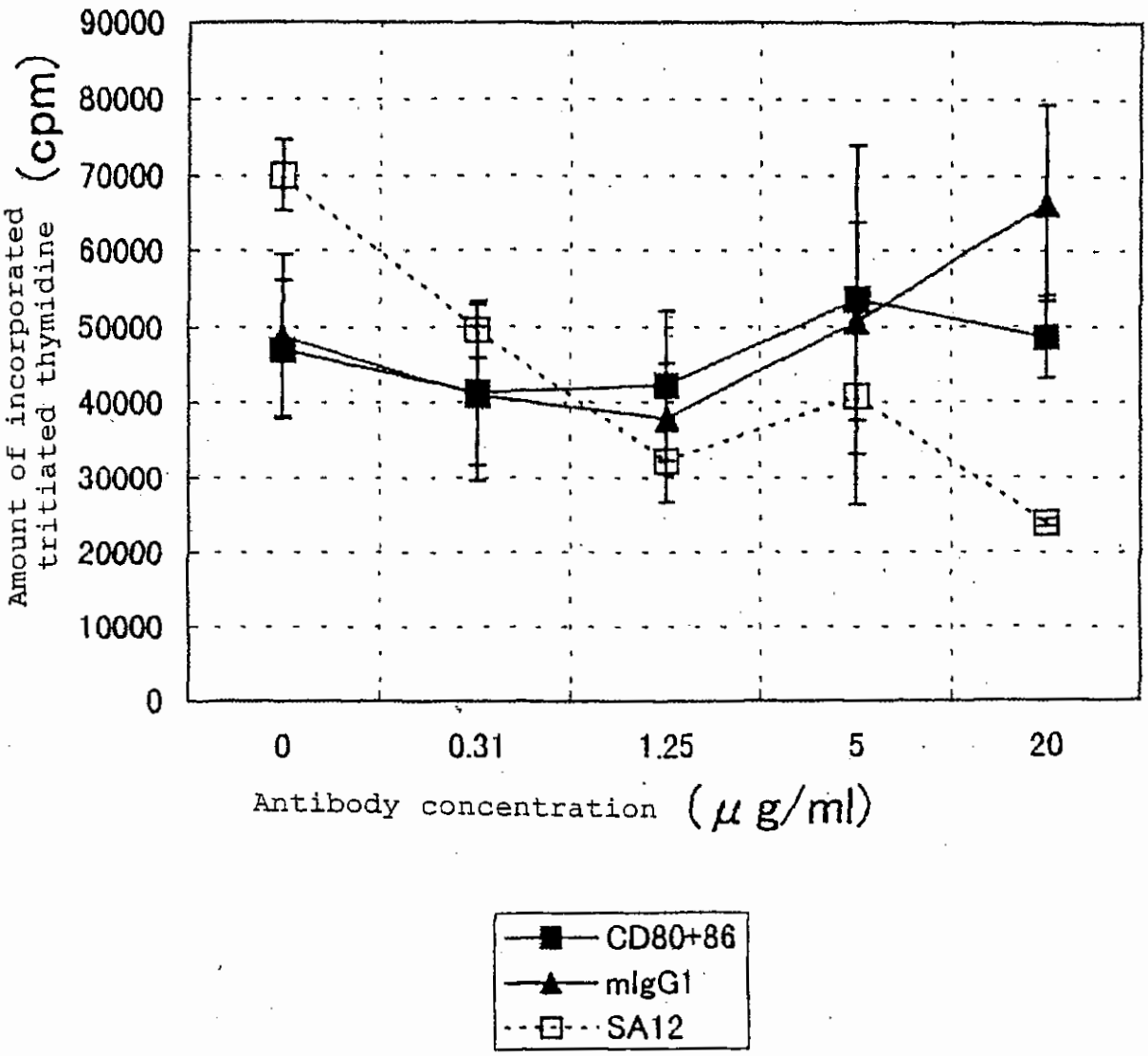

90000
80000
70000
60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
CD80+86
mIgG1
SA12

Figure 63

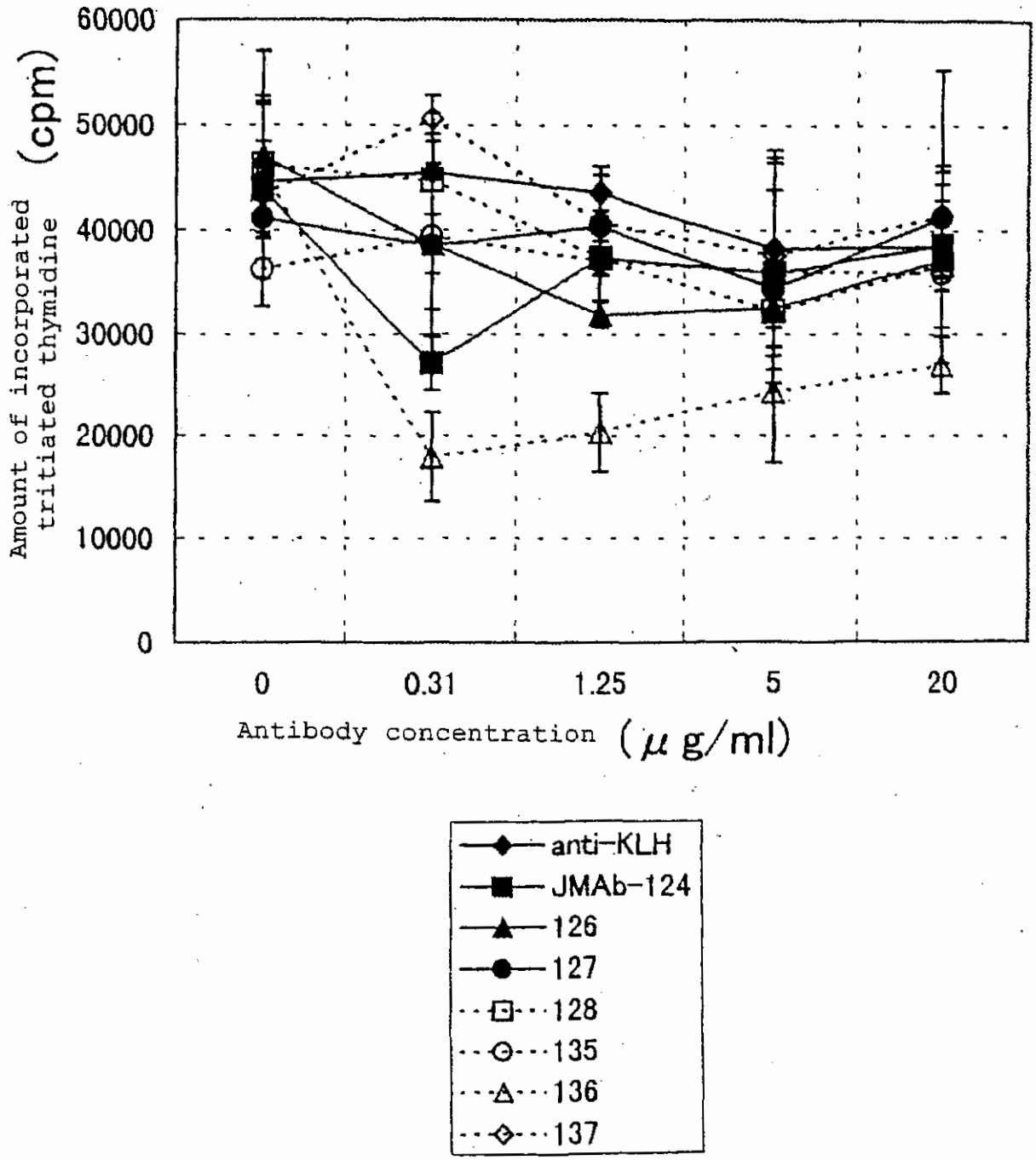

60000
50000
40000
30000
20000
10000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-124
126
127
128
135
136
137

Figure 64

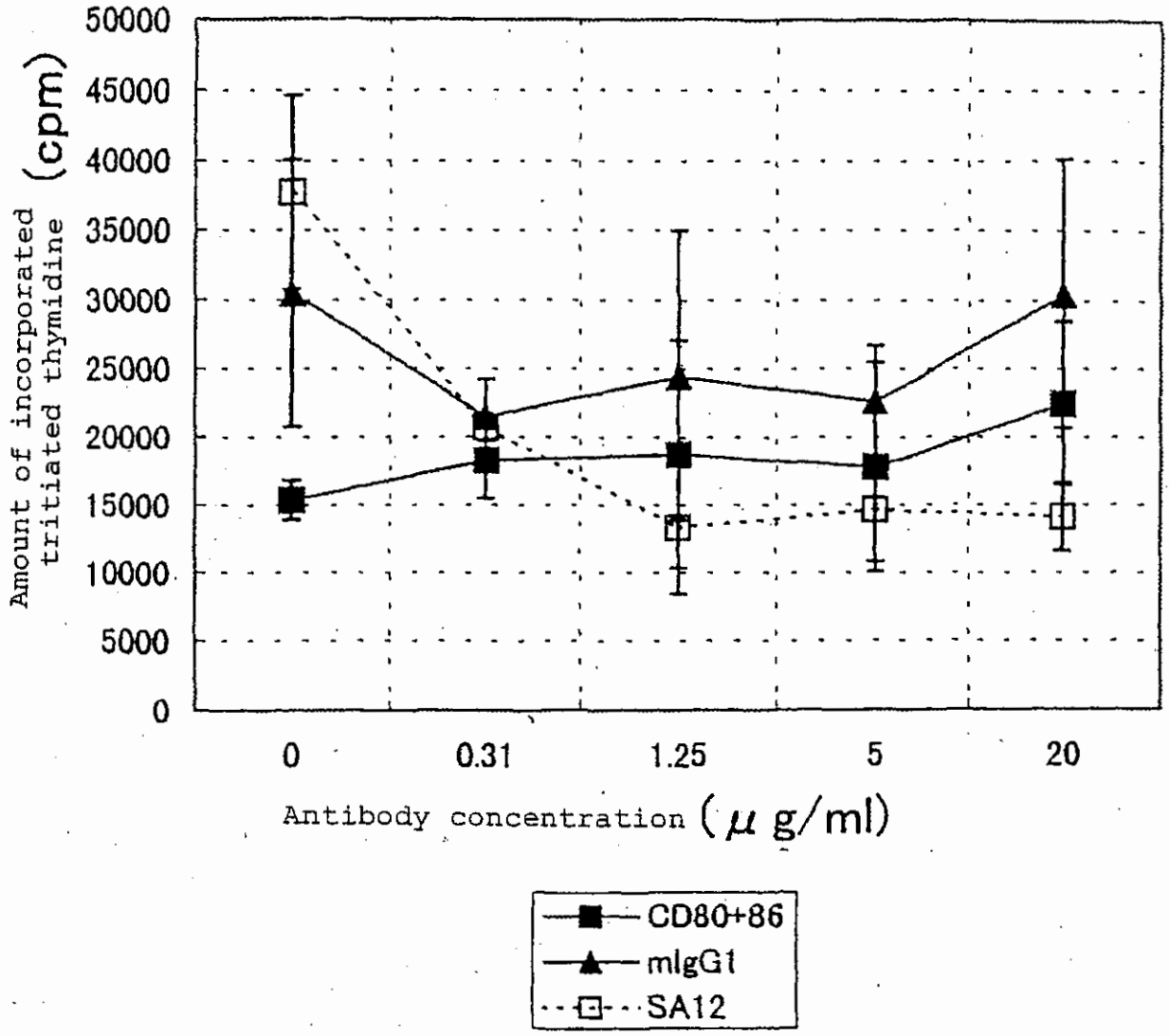

50000
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
CD80+86
mIgG1
SA12

Figure 65

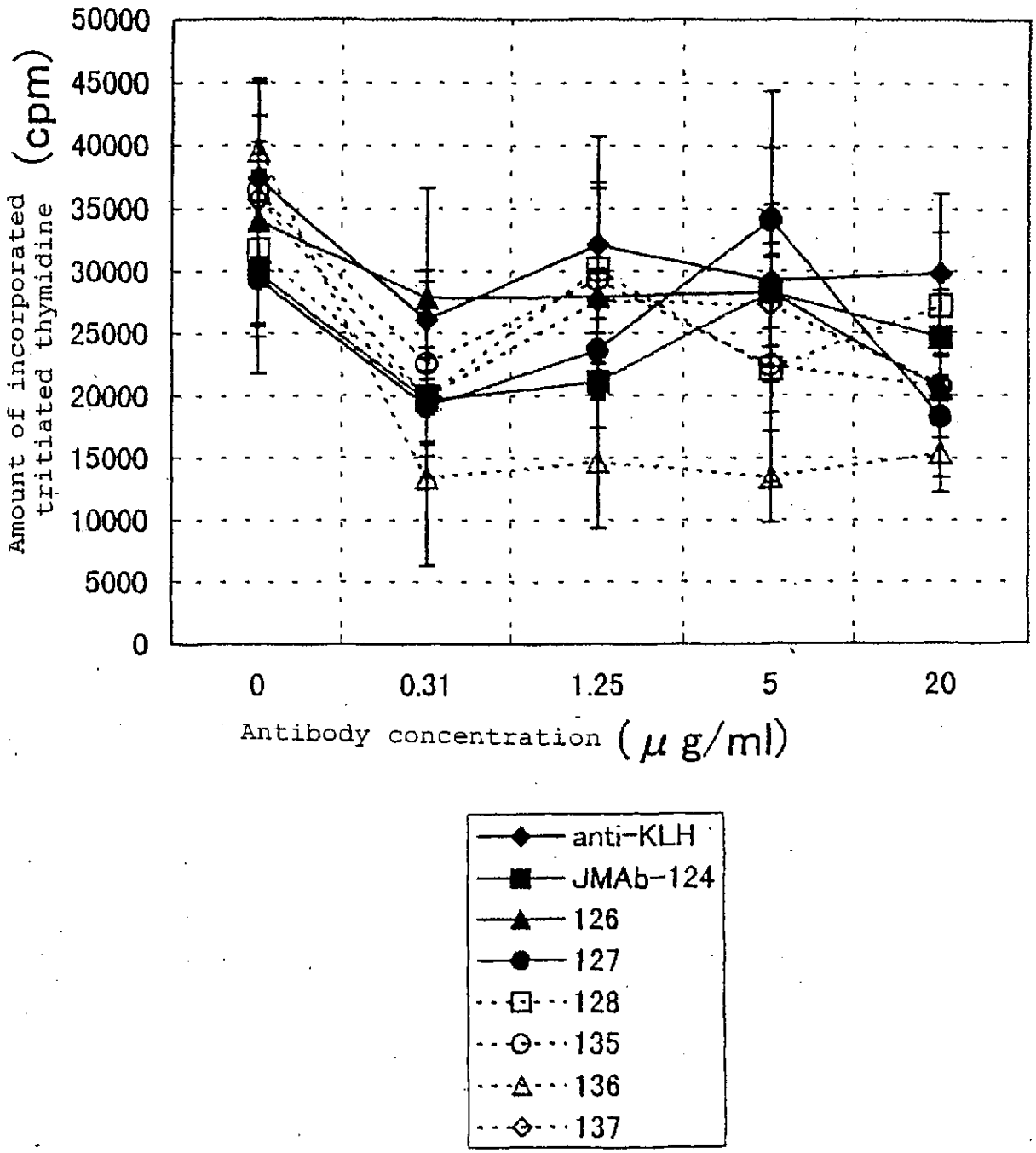

50000
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-124
126
127
128
135
136
137

Figure 66

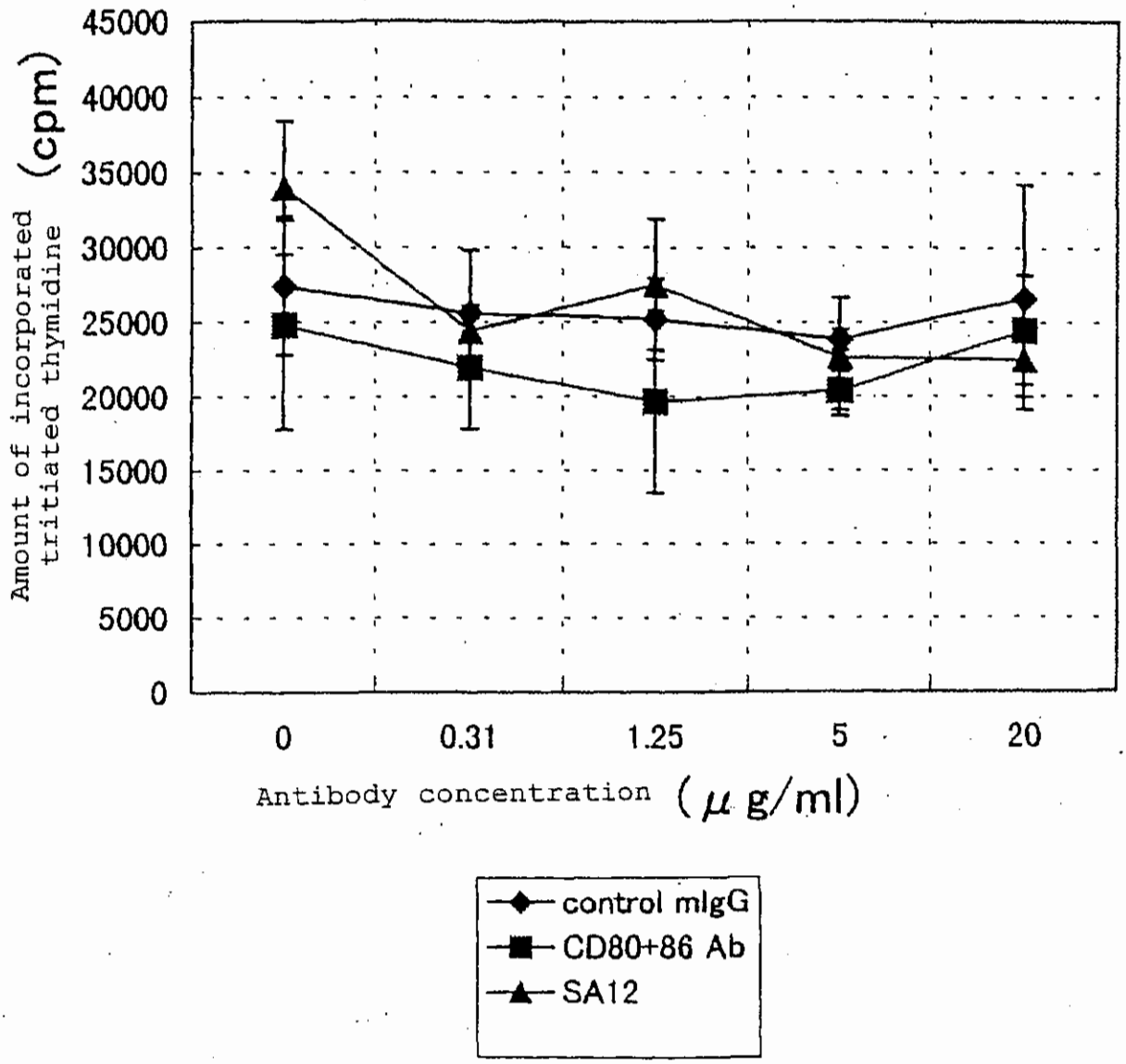

45000
40000
35000
30000
25000
20000
15000
10000
5000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
control mIgG
CD80+86 Ab
SA12

Figure 67

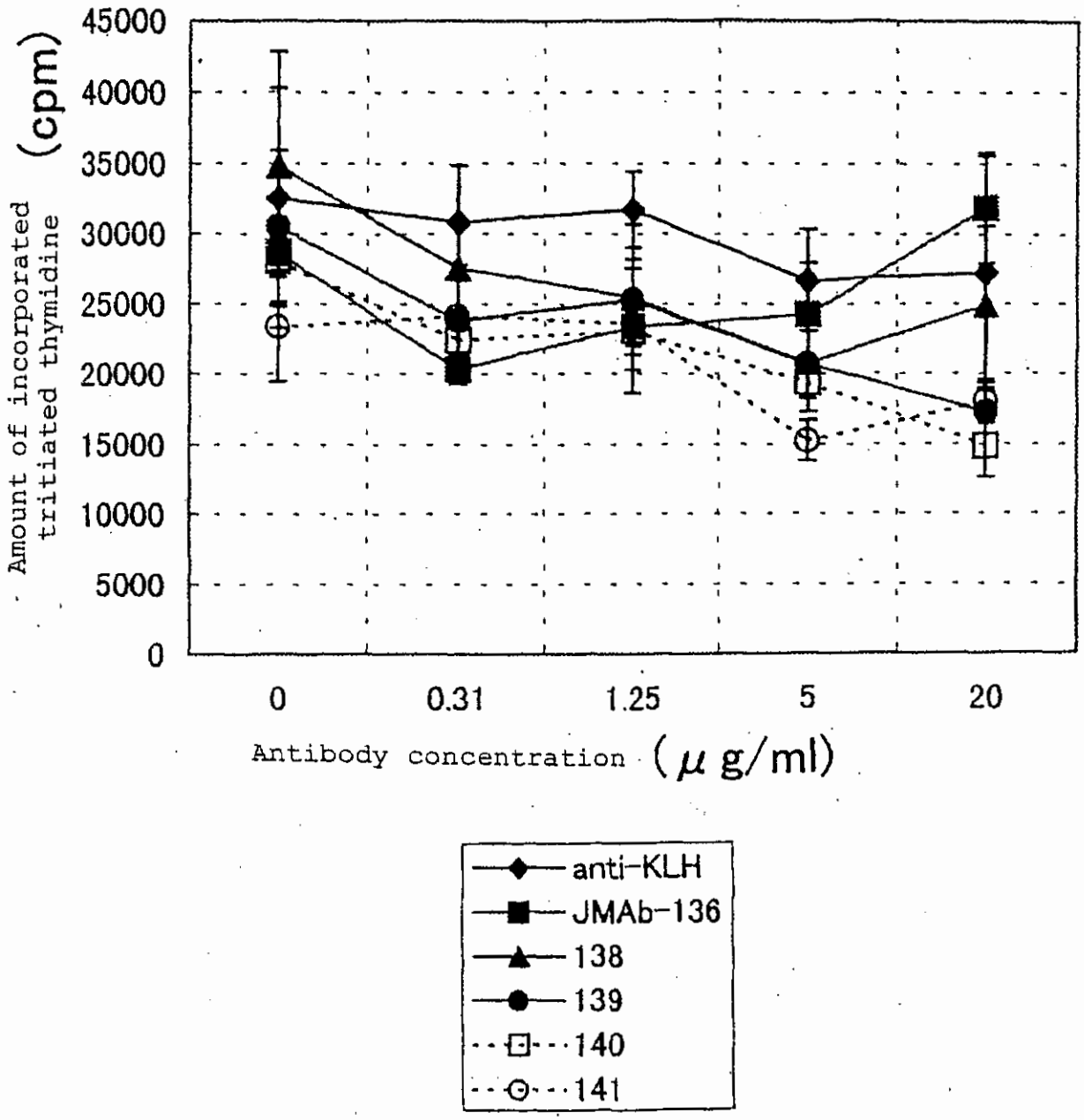

45000
40000
35000
30000
25000
20000
15000
10000
5000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-136
138
139
140
141

Figure 68

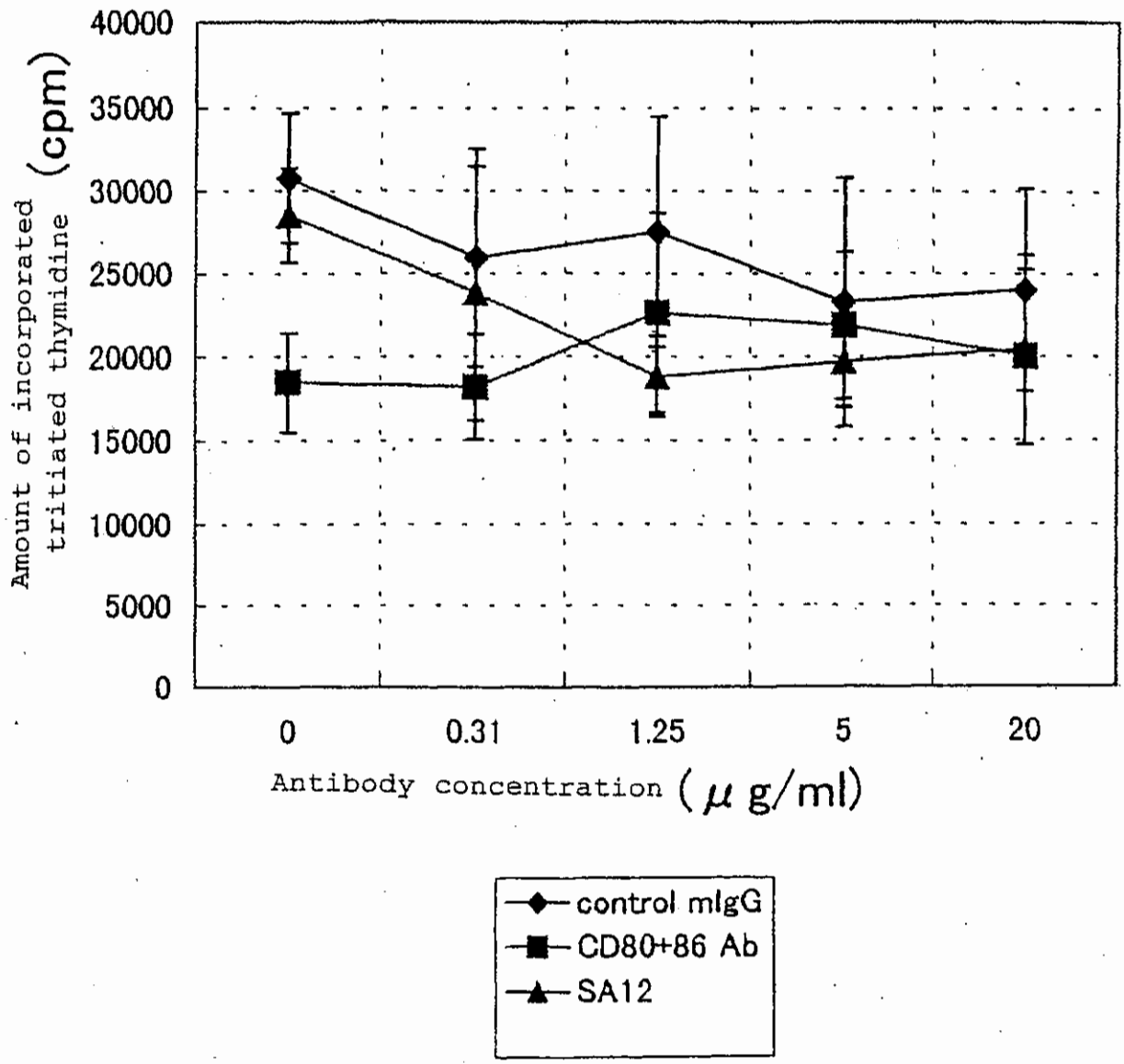

40000
35000
30000
25000
20000
15000
10000
5000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
control mIgG
CD80+86 Ab
SA12

Figure 69

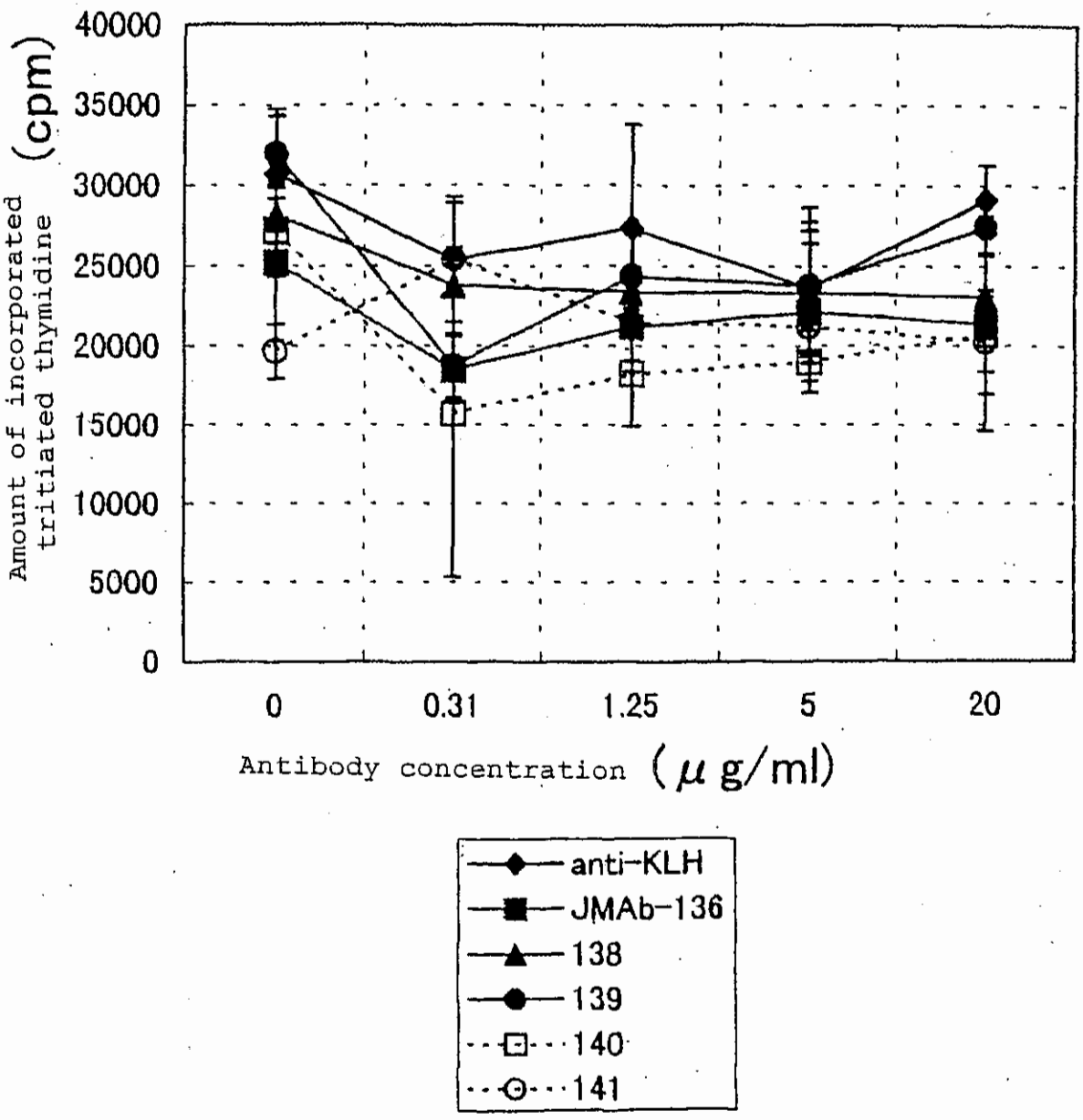

40000
35000
30000
25000
20000
15000
10000
5000
0
Amount of incorporated tritiated thymidine (cpm)
0
0.31
1.25
5
20
Antibody concentration (μg/ml)
anti-KLH
JMAb-136
138
139
140
141

Figure 70

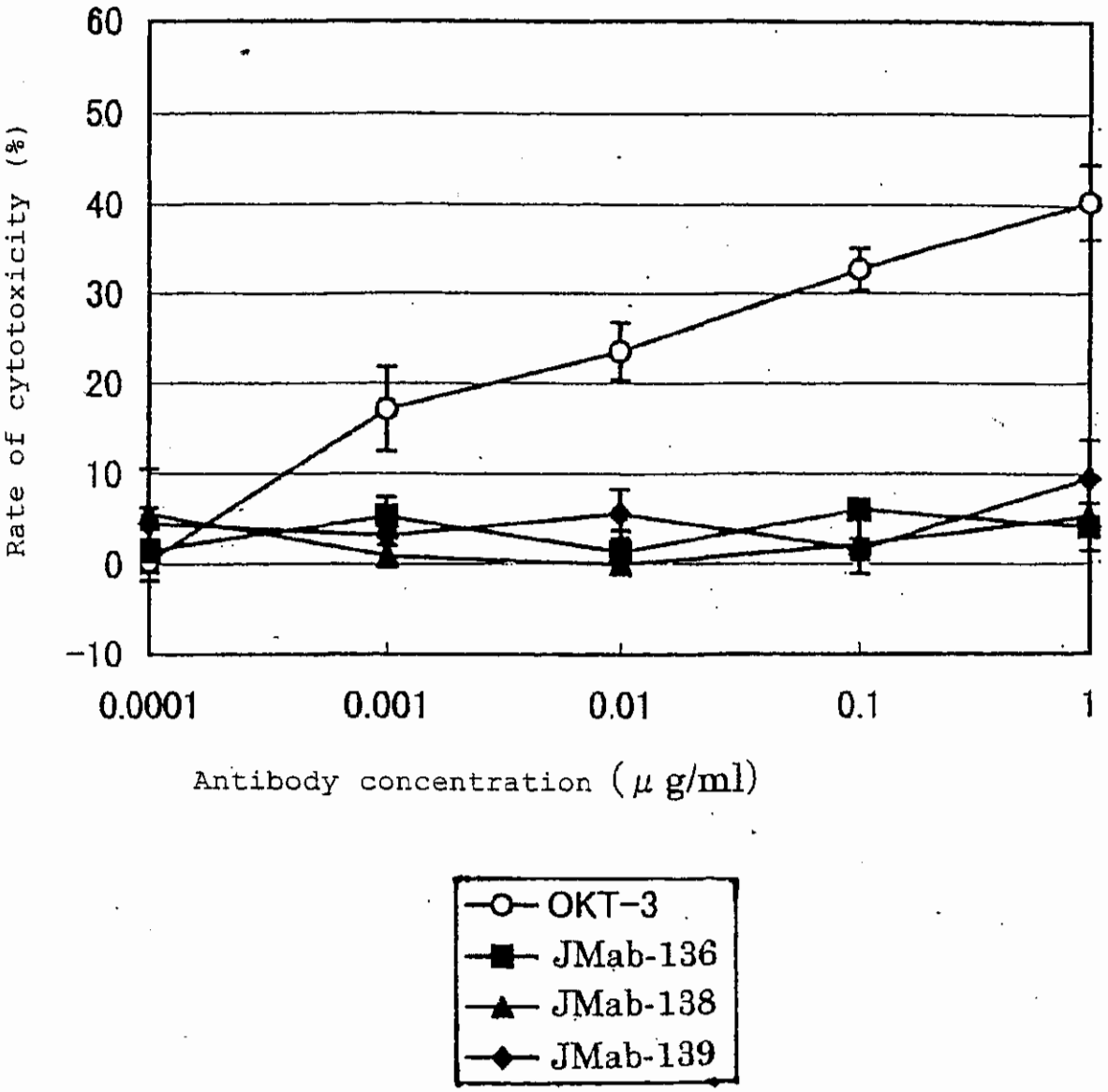

60
50
40
30
20
10
0
−10
Rate of cytotoxicity (%)
0.0001
0.001
0.01
0.1
1
Antibody concentration (μg/ml)
OKT-3
JMab-136
JMab-138
JMab-139

Figure 71

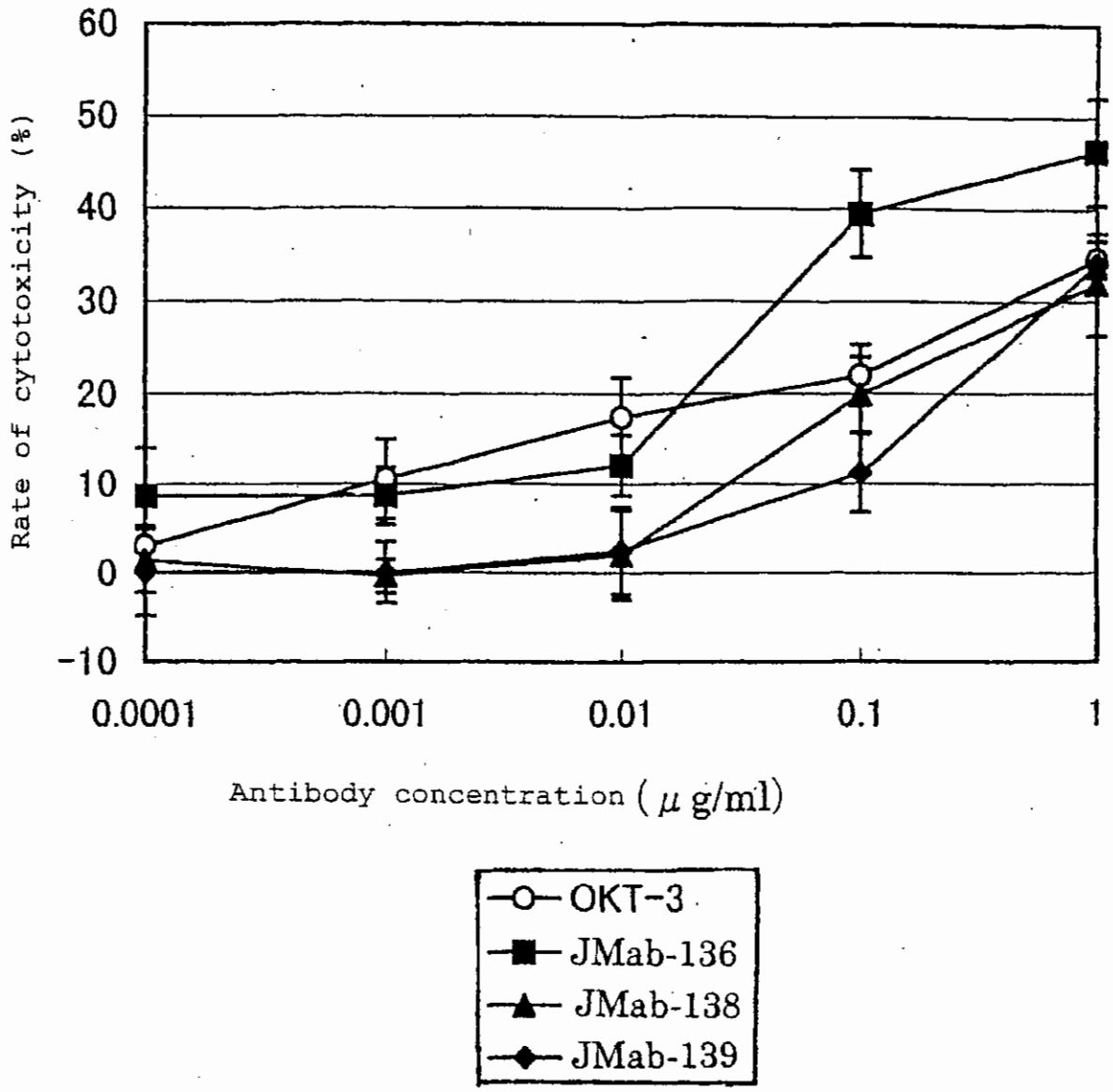

60
50
40
30
20
10
0
-10
Rate of cytotoxicity (%)
0.0001
0.001
0.01
0.1
1
Antibody concentration (μg/ml)
OKT-3
JMab-136
JMab-138
JMab-139

Figure 72

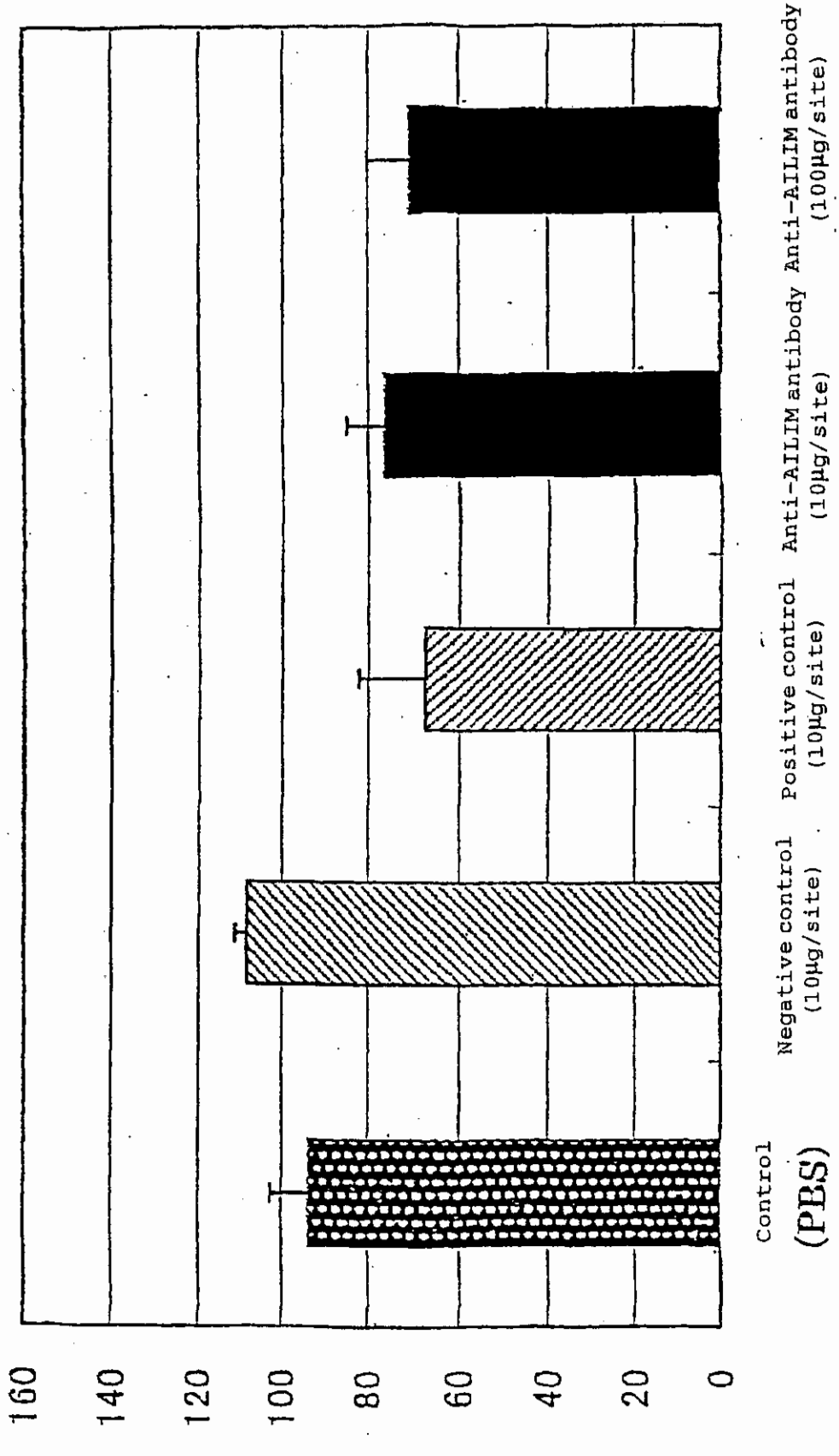

160
140
120
100
80
60
40
20
0
Control (PBS)
Negative control (10μg/site)
Positive control (10μg/site)
Anti-AILIM antibody (10μg/site)
Anti-AILIM antibody (100μg/site)

Figure 73

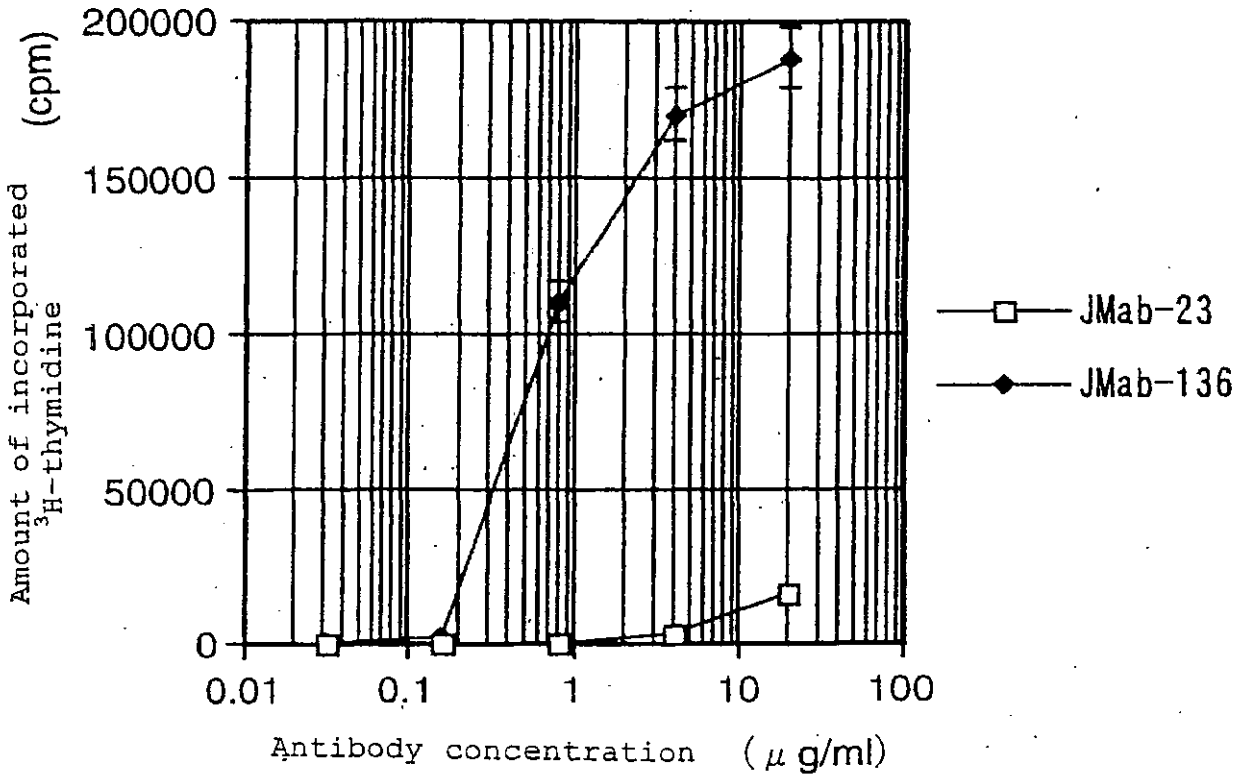

200000
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H-thymidine (cpm)
Antibody concentration (μg/ml)
JMab-23
JMab-136

Figure 74

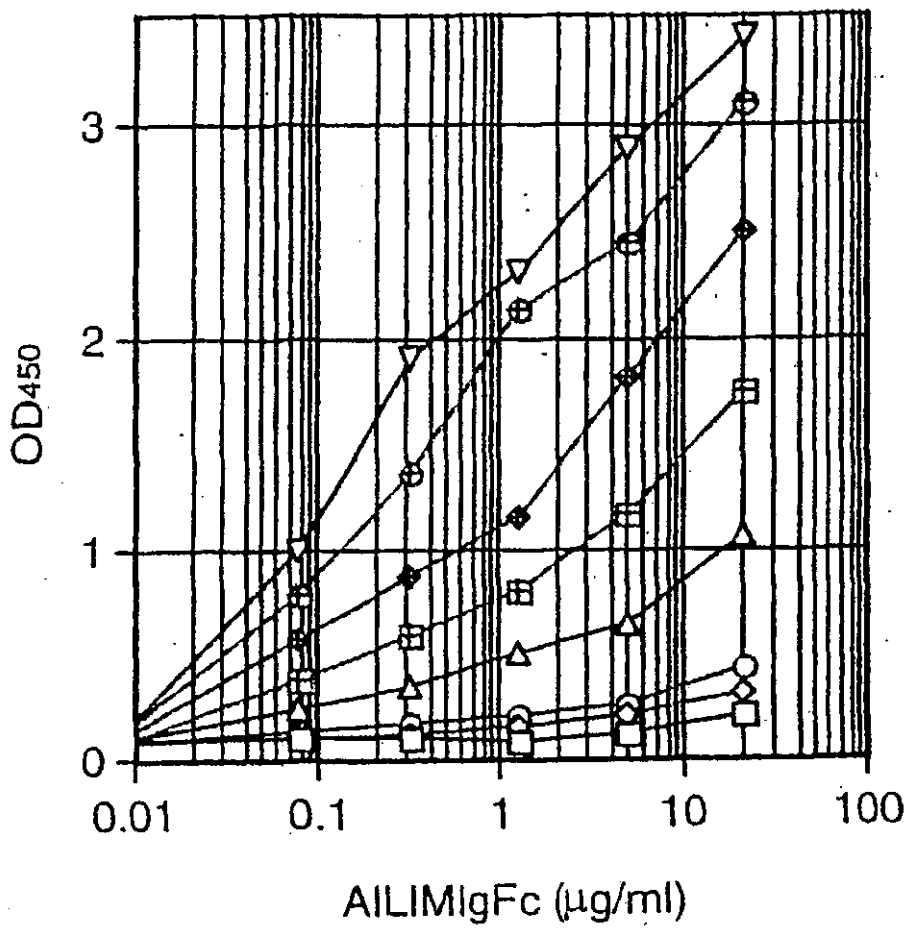
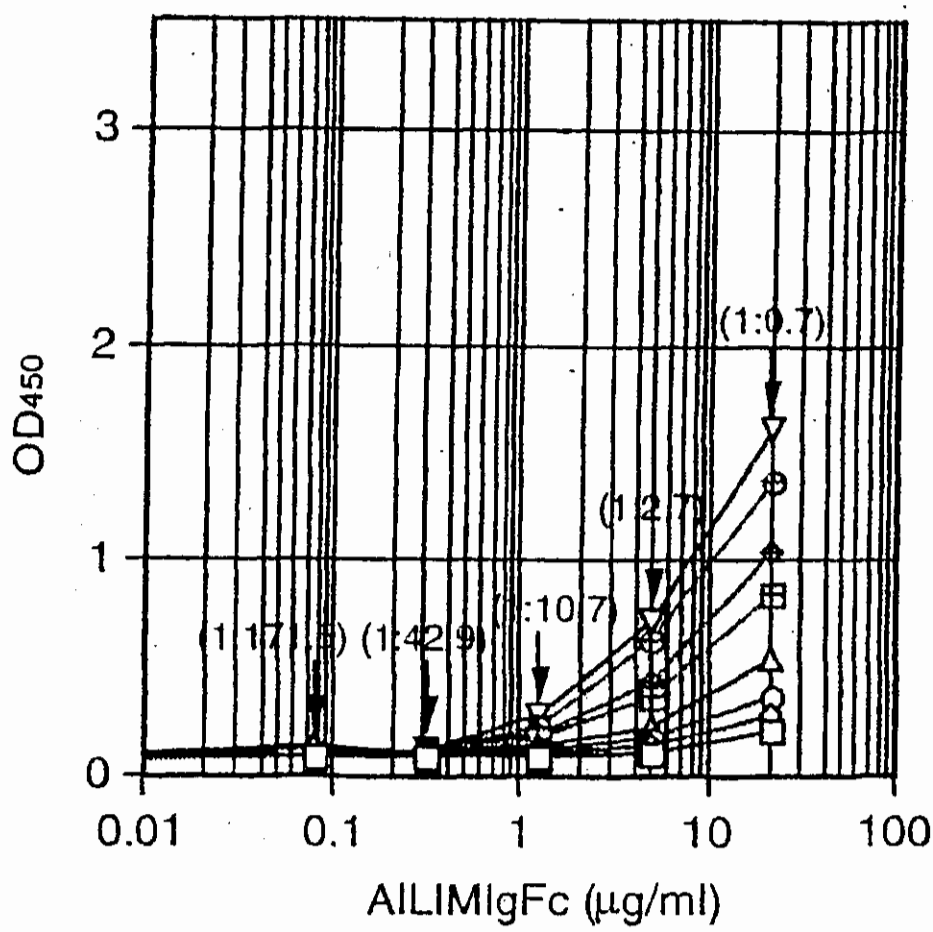

OD450
3
2
1
0
0.01
0.1
1
10
100
AILIMIgFc (μg/ml)
Coated amount of B7hIgFc
0 ng/well-B7hIgFc
25 ng/well -B7hIgFc
50 ng/well -B7hIgFc
100 ng/well -B7hIgFc
200 ng/well-B7hIgFc
400 ng/well -B7hIgFc
800 ng/well-B7hIgFc

Figure 75



Coated amount of B7hIgFc

0 ng/well-B7hIgFc

25 ng/well -B7hIgFc

50 ng/well -B7hIgFc

100 ng/well -B7hIgFc

200 ng/well-B7hIgFc

400 ng/well -B7hIgFc

800 ng/well-B7hIgFc

1600 ng/well-B7hIgFc

Figure 76

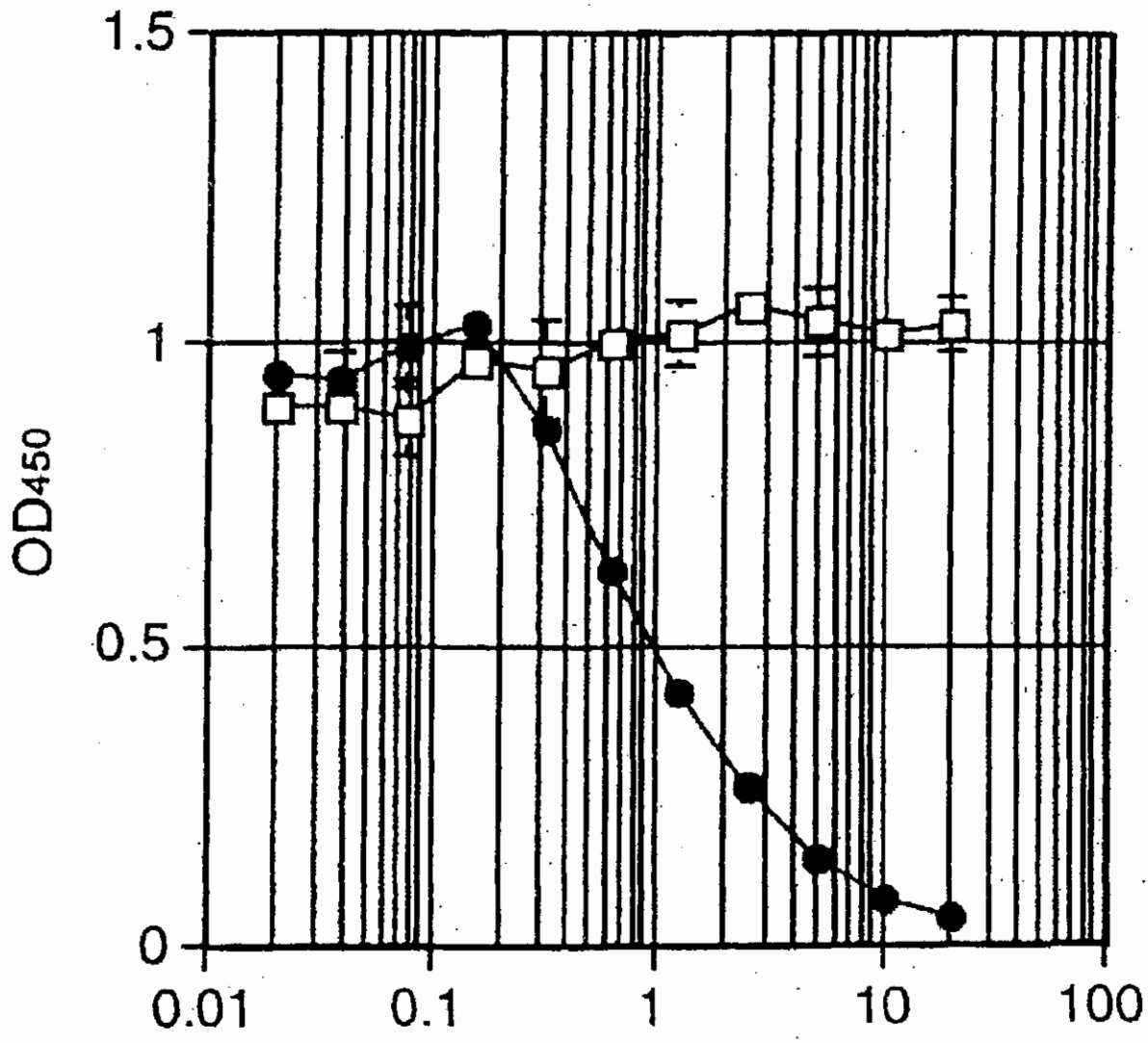


Figure 77

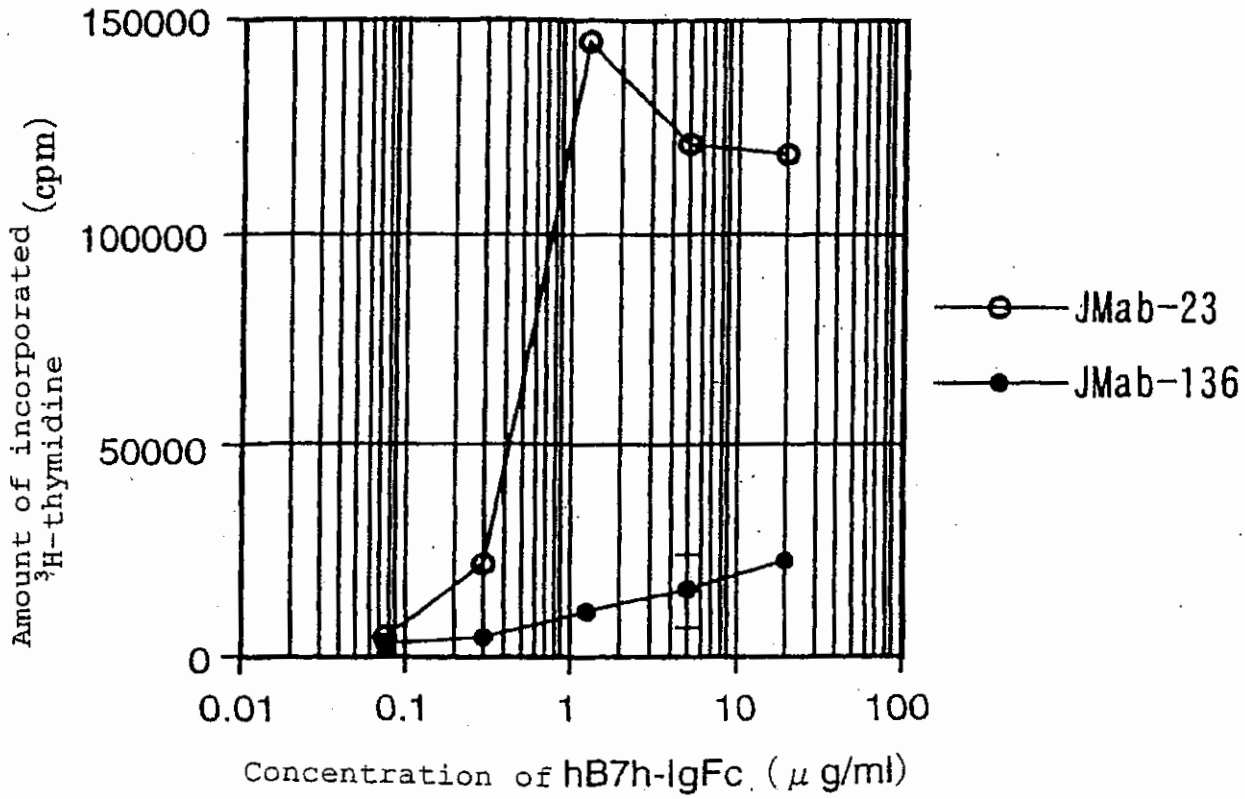
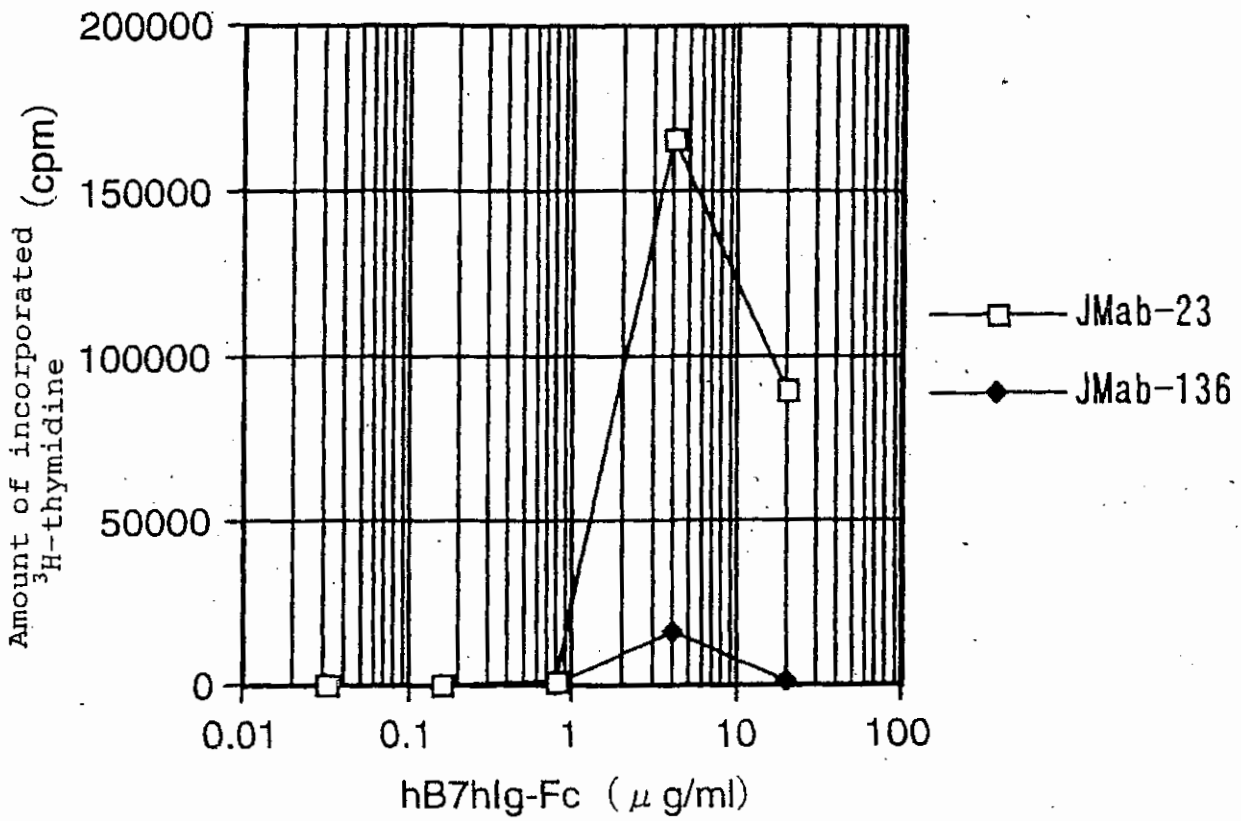

150000
100000
50000
0
Amount of incorporated ^{3}H-thymidine (cpm)
0.01
0.1
1
10
100
Concentration of hB7h-IgFc (μg/ml)
JMab-23
JMab-136

Figure 78


200000
150000
100000
50000
0
0.01
0.1
1
10
100
Amount of incorporated ^{3}H-thymidine (cpm)
hB7hIg-Fc (μg/ml)
JMab-23
JMab-136

SEQUENCE LISTING

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<120> Human Monoclonal Antibody Against A Costimulatory Signal Transduction Molecule AILIM And Pharmaceutical Use Thereof

<130> J1-A0101Y1P

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<151> 2000-05-18

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<212> DNA

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<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

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<210> 4

<211> 23

<212> DNA

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<400> 4

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<210> 5

<211> 21

<212> DNA

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<400> 6

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<211> 25

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<210> 10

<211> 21

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<210> 11

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<211> 21

<212> DNA

<213> Artificial Sequence

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<212> DNA

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<220>

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<210> 15

<211> 23

<212> DNA

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<223> Description of Artificial Sequence:Artificially synthesized primer sequence, HCc3.

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<400> 15

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<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized primer sequence, HCc4.

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<222> (1)..(23)

<400> 16

tgcacttgta ctccttgccg ttc 23

<210> 17

<211> 23

<212> DNA

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<220>

<223> Description of Artificial Sequence:Artificially synthesized primer sequence, HCc6.

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<210> 18

<211> 22

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<210> 19

<211> 22

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<210> 20

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized primer sequence, HCc5.

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<210> 21

<211> 21

<212> DNA

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<221> primer_bind

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<211> 21

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<223> Description of Artificial Sequence:Artificially synthesized primer sequence, AILIMLC1.

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<211> 22

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially synthesized primer sequence, LCc1.

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<211> 21

<212> DNA

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<220>

<223> Description of Artificial Sequence:Artificially synthesized primer sequence, LCc2.

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<400> 25

caaagagctt caacagggga g 21

<210> 26

<211> 20

<213> Artificial Sequence

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<220>

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<210> 27

<211> 1616

<212> DNA

<213> Homo sapiens

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<220>

<221> CDS

<222> (69)..(1481)

<220>

<221> 3'UTR

<222> (1482)..(1616)

<220>

<221> sig_peptide

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Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala
1 5 10

aca gga gcc cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg 158
Thr Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
15 20 25 30

aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gct tct gga tac 206
Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

acc ttc acc ggc tac tat atg cac tgg gtg cga cag gcc cct gga caa 254
Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln

50 55 60

ggg ctt gag tgg atg gga tgg atc aac cct cac agt ggt ggc aca aac 302
Gly Leu Glu Trp Met Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn
65 70 75

tat gca cag aag ttt cag ggc agg gtc acc atg acc agg gac acg tcc 350
Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
80 85 90

atc agc aca gcc tac atg gag ctg agc agg ctg aga tcc gac gac acg 398
Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
95 100 105 110

gcc gtg tat tac tgt gcg agg acg tat tac tat gat agt agt ggt tat 446
Ala Val Tyr Tyr Cys Ala Arg Thr Tyr Tyr Tyr Asp Ser Ser Gly Tyr
115 120 125

tac cat gat gct ttt gat atc tgg ggc caa ggg aca atg gtc acc gtc 494
Tyr His Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val
130 135 140

tct tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gcg ccc tgc 542
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
145 150 155

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tcc agg agc acc tcc gag agc aca gcg gcc ctg ggc tgc ctg gtc aag   590
Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
    160                 165                 170

gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gct ctg   638
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
175                 180                 185                 190

acc agc ggc gtg cac acc ttc cca gct gtc cta cag tcc tca gga ctc   686
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                195                 200                 205

tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc aac ttc ggc acc   734
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr
            210                 215                 220

cag acc tac acc tgc aac gta gat cac aag ccc agc aac acc aag gtg   782
Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
        225                 230                 235

gac aag aca gtt gag cgc aaa tgt tgt gtc gag tgc cca ccg tgc cca   830
Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
    240                 245                 250

gca cca cct gtg gca gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc   878
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255 260 265 270

aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg gtg 926
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
275 280 285

gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg tac gtg 974
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
290 295 300

gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag gag cag 1022
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305 310 315

ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg cac cag 1070
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
320 325 330

gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac aaa ggc 1118
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
335 340 345 350

ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggg cag ccc 1166
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
355 360 365

cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc 1214
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
370 375 380

aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc 1262
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385 390 395

gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac 1310
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
400 405 410

aag acc aca cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc tac 1358
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
415 420 425 430

agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc 1406
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
435 440 445

tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag 1454
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
450 455 460

agc ctc tcc ctg tct ccg ggt aaa tga gtgccacggc cggcaagccc 1501
Ser Leu Ser Leu Ser Pro Gly Lys

465 470

ccgctcccca ggctctcggg gtcgcgtgag gatgcttggc acgtaccccg tgtacatact 1561

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<212> PRT

<213> Homo sapiens

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20 25 30

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35 40 45

Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn Tyr Ala
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val

100 105 110

Tyr Tyr Cys Ala Arg Thr Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr His

115 120 125

Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

130 135 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg

145 150 155 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr

165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr

210 215 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys

225 230 235 240

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro

245 250 255

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

275 280 285

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

290 295 300

305 310 315 320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp

325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro

340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu

355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

450 455 460

Ser Leu Ser Pro Gly Lys

465 470

<210> 29

<211> 974

<212> DNA

<213> Homo sapiens

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Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Phe Pro Gly Ser Arg Cys

10 15 20

gac atc cag atg acc cag tct cca tct tcc gtg tct gca tct gta gga 152
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
25 30 35

gac aga gtc acc atc act tgt cgg gcg agt cag ggt att agc agg ttg 200
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Arg Leu
40 45 50

tta gcc tgg tat cag cag aaa cca ggg aaa gcc cct aaa ctc ctg atc 248
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
55 60 65 70

tat gtt gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc 296
Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
75 80 85

agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 344
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
90 95 100

gaa gat ttt gca act tac tat tgt caa cag gct aac agt ttc ccg tgg 392
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Trp
105 110 115

acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca 440
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
120 125 130

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 488
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
135 140 145 150

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
155 160 165

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 584
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
170 175 180

gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 632
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
185 190 195

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 680
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
200 205 210

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 728
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser

215 220 225 230

ttc aac agg gga gag tgt tag agggagaagt gcccccacct gctcctcagt 779
Phe Asn Arg Gly Glu Cys
235

tccagcctga ccccctccca tcctttggcc tctgaccctt tttccacagg ggacctaccc 839

ctattgcggt cctccagctc atctttcacc tcacccccct cctcctcctt ggctttaatt 899

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20 25 30
Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser

35 40 45

Gln Gly Ile Ser Arg Leu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys

50 55 60

Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val

65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln

100 105 110

Ala Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu

165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp

180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr

195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser

210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

225 230 235

<210> 31

<211> 1708

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)..(93)

<220>

<221> CDS

<222> (94)..(1506)

<220>

<221> 3'UTR

<222> (1507)..(1708)

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tcagtgatca ggactgagca cacaggactc acc atg gag ttg ggg ctg agc tgg 114
Met Glu Leu Gly Leu Ser Trp
1 5

gtt ttc ctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag ctg 162
Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln Leu
10 15 20

gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga ctc 210
Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
25 30 35

tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac tgg 258
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His Trp
40 45 50 55

gtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att ggt 306
Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Gly
60 65 70

act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc acc 354
Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe Thr
75 80 85

atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac agc 402
Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser

90 95 100

ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aat agg 450
Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Asn Arg
105 110 115

aag gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg ggc 498
Lys Val Thr His Glu His Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly
120 125 130 135

caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg 546
Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
140 145 150

gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca gcg 594
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
155 160 165

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 642
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
170 175 180

tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca gct 690
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
185 190 195

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 738
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
200 205 210 215

ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat cac 786
Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
220 225 230

aag ccc agc aac acc aag gtg gac aag aca gtt gag cgc aaa tgt tgt 834
Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
235 240 245

gtc gag tgc cca ccg tgc cca gca cca cct gtg gca gga ccg tca gtc 882
Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
250 255 260

ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc 930
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
265 270 275

cct gag gtc acg tgc gtg gtg gtg gac gtg agc cac gaa gac ccc gag 978
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
280 285 290 295

gtc cag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag 1026
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

300 305 310

aca aag cca cgg gag gag cag ttc aac agc acg ttc cgt gtg gtc agc 1074
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
315 320 325

gtc ctc acc gtt gtg cac cag gac tgg ctg aac ggc aag gag tac aag 1122
Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
330 335 340

tgc aag gtc tcc aac aaa ggc ctc cca gcc ccc atc gag aaa acc atc 1170
Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
345 350 355

tcc aaa acc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc 1218
Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
360 365 370 375

cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg 1266
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
380 385 390

gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aat 1314
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
395 400 405

ggg cag ccg gag aac aac tac aag acc aca cct ccc atg ctg gac tcc 1362
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
410 415 420

gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg 1410
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
425 430 435

tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg 1458
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
440 445 450 455

cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1506
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
460 465 470

gtgccacggc cggcaagccc ccgctcccca ggctctcggg gtcgcgtgag gatgcttggc 1566

acgtaccccg tgtacatact tcccaggcac ccagcatgga aataaagcac ccagcgctgc 1626

cctgggcccc tgcnaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1686

aaaaaaaaat ctctgcggcc gc 1708

<211> 470

<212> PRT

<213> Homo sapiens

<400> 32

Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Glu Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly
65 70 75 80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr
100 105 110

Tyr Cys Val Arg Asp Asn Arg Lys Val Thr His Glu His Tyr Tyr Tyr
115 120 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
130 135 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
145 150 155 160

165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr

210 215 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys

225 230 235 240

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro

245 250 255

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

275 280 285

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn

305 310 315 320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp

325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro

340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu

355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

450 455 460

Ser Leu Ser Pro Gly Lys

465 470

<210> 33

<211> 948

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)..(27)

<220>

<221> CDS

<222> (28)..(738)

<220>

<221> 3'UTR

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<220>

<221> sig_peptide

<222> (28)..(87)

<400> 33

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Met Glu Thr Pro Ala Gln Leu Leu Phe
1 5

ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg ttg acg 102
Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val Leu Thr
10 15 20 25

cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc 150
Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
30 35 40

tcc tgc agg gcc agt cag aat att aga agc agc tac tta gcc tgg tac 198
Ser Cys Arg Ala Ser Gln Asn Ile Arg Ser Ser Tyr Leu Ala Trp Tyr

45 50 55

cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc tat ggt gca tcc 246
Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Tyr Gly Ala Ser
60 65 70

agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg tct ggg 294
Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
75 80 85

aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat ttt gca 342
Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
90 95 100 105

gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt ttt ggc 390
Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser Phe Gly
110 115 120

cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca tct gtc 438
Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
125 130 135

ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct 486
Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
140 145 150

gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag 534
Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
155 160 165

tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc 582
Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
170 175 180 185

aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg 630
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
190 195 200

acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa 678
Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
205 210 215

gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg 726
Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
220 225 230

gga gag tgt tag agggagaant gcccccacct gctcctcagt tccagcctga 778
Gly Glu Cys
235

ccccctccca tcctttggcc tctgaccctt tttccacagg ggacctaccc ctattgcggt 838

cctccagctc atctttcacc tcacccccct cctcctcctt ggctttaatt atgctaatgt 898

tggaggagaa tgaataaata aagtgaatct ttgcacctgt gaaaaaaaaa 948

<210> 34

<211> 236

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn
35 40 45

Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Gly Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
100 105 110

Gly Ser Ser Pro Met Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile

115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu

165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp

180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr

195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser

210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

225 230 235

<210> 35

<211> 1673

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)..(95)

<220>

<221> CDS

<222> (96)..(1508)

<220>

<221> 3'UTR

<222> (1509)..(1673)

<220>

<221> sig_peptide

<222> (96)..(152)

<400> 35

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attcagtgat caggactgaa cacacaggac tcacc atg gag ttg ggg ctg agc 113
Met Glu Leu Gly Leu Ser
1 5

tgg gtt ttc ctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag 161
Trp Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln
10 15 20

ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga 209
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg

25 30 35

ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac 257
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His
40 45 50

tgg gtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att 305
Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile
55 60 65 70

ggt act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc 353
Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe
75 80 85

acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac 401
Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
90 95 100

agc ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aag 449
Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Lys
105 110 115

agg acg gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg 497
Arg Thr Val Thr His Glu His Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
120 125 130

ggc caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca 545
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
135 140 145 150

tcg gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca 593
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
155 160 165

gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acc 641
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
170 175 180

gtg tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca 689
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
185 190 195

gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc 737
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
200 205 210

gtg ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat 785
Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
215 220 225 230

cac aag ccc agc aac acc aag gtg gac aag aca gtt gag cgc aaa tgt 833
His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys

235 240 245

tgt gtc gag tgc cca ccg tgc cca gca cca cct gtg gca gga ccg tca 881
Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
250 255 260

gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg 929
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
265 270 275

acc cct gag gtc acg tgc gtg gtg gtg gac gtg agc cac gaa gac ccc 977
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
280 285 290

gag gtc cag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc 1025
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
295 300 305 310

aag aca aag cca cgg gag gag cag ttc aac agc acg ttc cgt gtg gtc 1073
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
315 320 325

agc gtc ctc acc gtt gtg cac cag gac tgg ctg aac ggc aag gag tac 1121
Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
330 335 340

aag tgc aag gtc tcc aac aaa ggc ctc cca gcc ccc atc gag aaa acc 1169
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
345 350 355

atc tcc aaa acc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg 1217
Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
360 365 370

ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc 1265
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
375 380 385 390

ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc 1313
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
395 400 405

aat ggg cag ccg gag aac aac tac aag acc aca cct ccc atg ctg gac 1361
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
410 415 420

tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc 1409
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
425 430 435

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct 1457
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

440 445 450

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 1505
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
455 460 465 470

tga gtgccacggc cggcaagccc ccgctcccca ggctctcggg gtcgcgtgag 1558

gatgcttggc acgtaccccg tgtacatact tcccaggcac ccagcatgga aataaagcac 1618

ccagcgctgc cctgggcccc tgcgaaaaaa aaaaaaaaaa aatctctgcg gccgc 1673

<210> 36
<211> 470
<212> PRT
<213> Homo sapiens

<400> 36
Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Glu Gly
1 5 10 15
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

50 55 60

Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly

65 70 75 80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser

85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr

100 105 110

Tyr Cys Val Arg Asp Lys Arg Thr Val Thr His Glu His Tyr Tyr Tyr

115 120 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

130 135 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg

145 150 155 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr

165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr

210 215 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys

225 230 235 240

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro

245 250 255

260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

275 280 285

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn

305 310 315 320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp

325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro

340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu

355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

450 455 460

Ser Leu Ser Pro Gly Lys

465 470

<210> 37

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> 5' UTR

<222> (1)..(32)

<220>

<221> CDS

<222> (33)..(743)

<220>

<221> 3' UTR

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<220>

<221> sig_peptide

<222> (33)..(92)

<400> 37

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1 5

ctc ttc ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg 101
Leu Phe Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val
10 15 20

ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc 149
Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
25 30 35

acc ctc tcc tgc agg gcc agt cag agt att agc agc agc tcc tta gcc 197
Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Ser Ser Leu Ala
40 45 50 55

tgg tac cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc ttt ggt 245
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Phe Gly
60 65 70

gca tcc agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg 293
Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
75 80 85

tct ggg aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat 341
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp

90 95 100

ttt gca gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt 389
Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser
105 110 115

ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca 437
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
120 125 130 135

tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act 485
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
140 145 150

gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa 533
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
155 160 165

gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag 581
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
170 175 180

agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc agc 629
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
185 190 195

acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc 677
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
200 205 210 215

tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc 725
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
220 225 230

aac agg gga gag tgt tag agggagaagt gcccccacct gctcctcagt 773
Asn Arg Gly Glu Cys
235

tccagcctga ccccctccca tcctttggcc tctgaccctt tttccacagg ggacctaccc 833

ctattgcggt cctccagctc atctttcacc tcacccccct cctcctcctt ggctttaatt 893

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<212> PRT

<213> Homo sapiens

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Ile Ser Ser Ser Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Gly Leu Leu Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
100 105 110

Gly Ser Ser Pro Met Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr

195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser

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Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

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