SEQ. ID NO:1:

GCCGAGCTGA GCGGATCCTC ACATGACTGT GATCCGATTC TTTCCAGCGG 50

CTTCTGCAAC CAAGCGGGTC TTACCCCCGG TCCTCCGCGT CTCCAGTCCT 100

CGCACCTGGA ACCCCAACGT CCCCGAGAGT CCCCGAATCC CCGCTCCCAG 150

GCTACCTAAG AGGATGAGCG GTGCTCCGAC GGCCGGGGCA GCCCTGATGC 200

TCTGCGCCGC CACCGCCGTG CTACTGAGCG CTCAGGGCGG ACCCGTGCAG 250

TCCAAGTCGC CGCGCTTTGC GTCCTGGGAC GAGATGAATG TCCTGGCGCA 300

CGGACTCCTG CAGCTCGGCC AGGGGCTGCG CGAACACGCG GAGCGCACCC 350

GCAGTCAGCT GAGCGCGCTG GAGCGGCGCC TGAGCGCGTG CGGGTCCGCC 400

TGTCAGGGAA CCGAGGGGTC CACCGACCTC CCGTTAGCCC CTGAGAGCCG 450

GGTGGACCCT GAGGTCCTTC ACAGCCTGCA GACACAACTC AAGGCTCAGA 500

ACAGCAGGAT CCAGCAACTC TTCCACAAGG TGGCCCAGCA GCAGCGGCAC 550

CTGGAGAAGC AGCACCTGCG AATTCAGCAT CTGCAAAGCC AGTTTGGCCT 600

CCTGGACCAC AAGCACCTAG ACCATGAGGT GGCCAAGCCT GCCCGAAGAA 650

AGAGGCTGCC CGAGATGGCC CAGCCAGTTG ACCCGGCTCA CAATGTCAGC 700

CGCCTGCACC GGCTGCCCAG GGATTGCCAG GAGCTGTTCC AGGTTGGGGA 750

GAGGCAGAGT GGACTATTTG AAATCCAGCC TCAGGGGTCT CCGCCATTTT 800

TGGTGAACTG CAAGATGACC TCAGATGGAG GCTGGACAGT AATTCAGAGG 850

CGCCACGATG GCTCAGTGGA CTTCAACCGG CCCTGGGAAG CCTACAAGGC 900

GGGGTTTGGG GATCCCCACG GCGAGTTCTG GCTGGGTCTG GAGAAGGTGC 950

ATAGCATCAC GGGGGACCGC AACAGCCGCC TGGCCGTGCA GCTGCGGGAC 1000

TGGGATGGCA ACGCCGAGTT GCTGCAGTTC TCCGTGCACC TGGGTGGCGA 1050

GGACACGGCC TATAGCCTGC AGCTCACTGC ACCCGTGGCC GGCCAGCTGG 1100

GCGCCACCAC CGTCCCACCC AGCGGCCTCT CCGTACCCTT CTCCACTTGG 1150

GACCAGGATC ACGACCTCCG CAGGGACAAG AACTGCGCCA AGAGCCTCTC 1200

FIG._1A

TGGAGGCTGG TGGTTTGGCA CCTGCAGCCA TTCCAACCTC AACGGCCAGT 1250

ACTTCCGCTC CATCCCACAG CAGCGGCAGA AGCTTAAGAA GGGAATCTTC 1300

TGGAAGACCT GGCGGGGCCG CTACTACCCG CTGCAGGCCA CCACCATGTT 1350

GATCCAGCCC ATGGCAGCAG AGGCAGCCTC CTAGCGTCCT GGCTGGGCCT 1400

GGTCCCAGGC CCACGAAAGA CGGTGACTCT TGGCTCTGCC CGAGGATGTG 1450

GCCGTTCCCT GCCTGGGCAG GGGCTCCAAG GAGGGGCCAT CTGGAAACTT 1500

GTGGACAGAG AAGAAGACCA CGACTGGAGA AGCCCCCTTT CTGAGTGCAG 1550

GGGGGCTGCA TGCGTTGCCT CCTGAGATCG AGGCTGCAGG ATATGCTCAG 1600

ACTCTAGAGG CGTGGACCAA GGGGCATGGA GCTTCACTCC TTGCTGGCCA 1650

GGGAGTTGGG GACTCAGAGG GACCACTTGG GGCCAGCCAG ACTGGCCTCA 1700

ATGGCGGACT CAGTCACATT GACTGACGGG GACCAGGGCT TGTGTGGGTC 1750

GAGAGCGCCC TCATGGTGCT GGTGCTGTTG TGTGTAGGTC CCCTGGGGAC 1800

ACAAGCAGGC GCCAATGGTA TCTGGGCGGA GCTCACAGAG TTCTTGGAAT 1850

AAAAGCAACC TCAGAACAC 1869

FIG._1B

SEQ. ID NO:2:

```
Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala
 1               5                  10                  15

Ala Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser
            20                  25                  30

Lys Ser Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala
        35                  40                  45

His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu
    50                  55                  60

Arg Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala
65                  70                  75

Cys Gly Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro
                80                  85                  90

Leu Ala Pro Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu
            95                  100                 105

Gln Thr Gln Leu Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe
        110                 115                 120

His Lys Val Ala Gln Gln Gln Arg His Leu Glu Lys Gln His Leu
    125                 130                 135

Arg Ile Gln His Leu Gln Ser Gln Phe Gly Leu Leu Asp His Lys
140                 145                 150

His Leu Asp His Glu Val Ala Lys Pro Ala Arg Arg Lys Arg Leu
155                 160                 165

Pro Glu Met Ala Gln Pro Val Asp Pro Ala His Asn Val Ser Arg
                170                 175                 180

Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly
            185                 190                 195

Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro
        200                 205                 210

Pro Phe Leu Val Asn Cys Lys Met Thr Ser Xaa Gly Gly Trp Thr
    215                 220                 225

Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro
230                 235                 240
```

FIG._2A

```
Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe
                245                 250                 255

Trp Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg Asn
                260                 265                 270

Ser Arg Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu
                275                 280                 285

Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr
                290                 295                 300

Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr
                305                 310                 315

Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr Trp Asp
                320                 325                 330

Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser Leu
                335                 340                 345

Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn
                350                 355                 360

Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys
                365                 370                 375

Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu
                380                 385                 390

Gln Ala Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala Ala
                395                 400                 405

Ser
406
```

FIG._2B

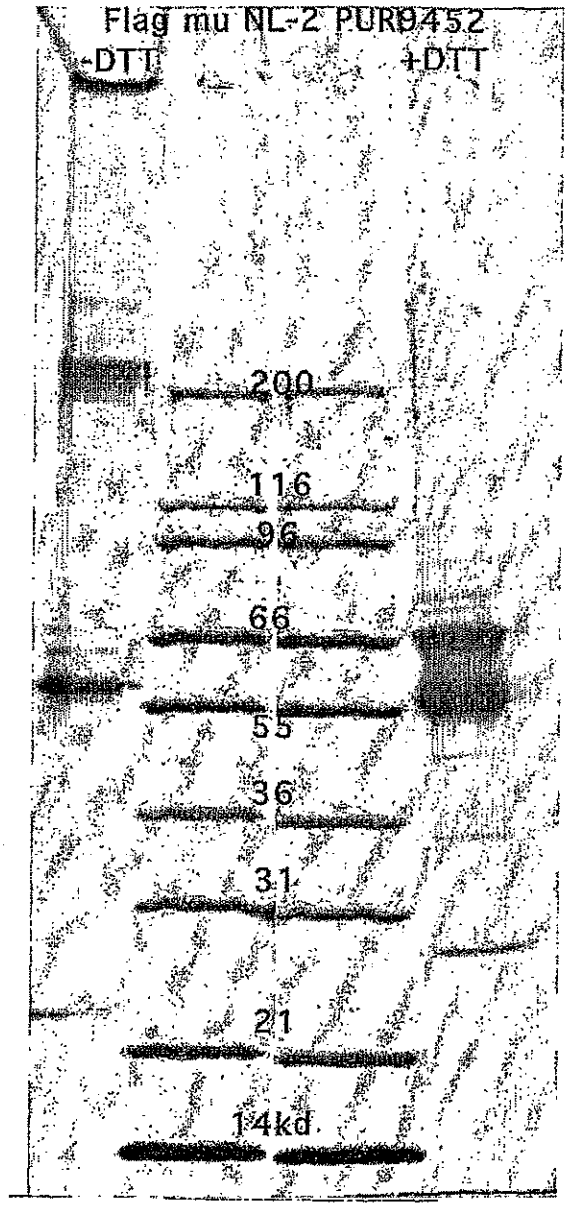

Flag mu NL-2 PUR0452
-DTT
+DTT
200
116
96
66
55
36
31
21
14kd

FIG._3A

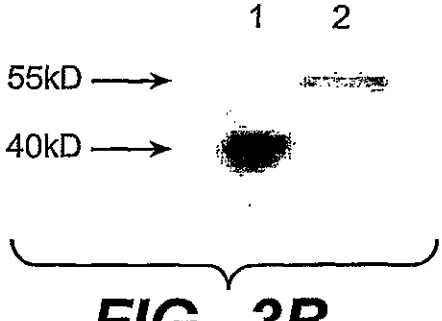

1
2
55kD
40kD

FIG._3B

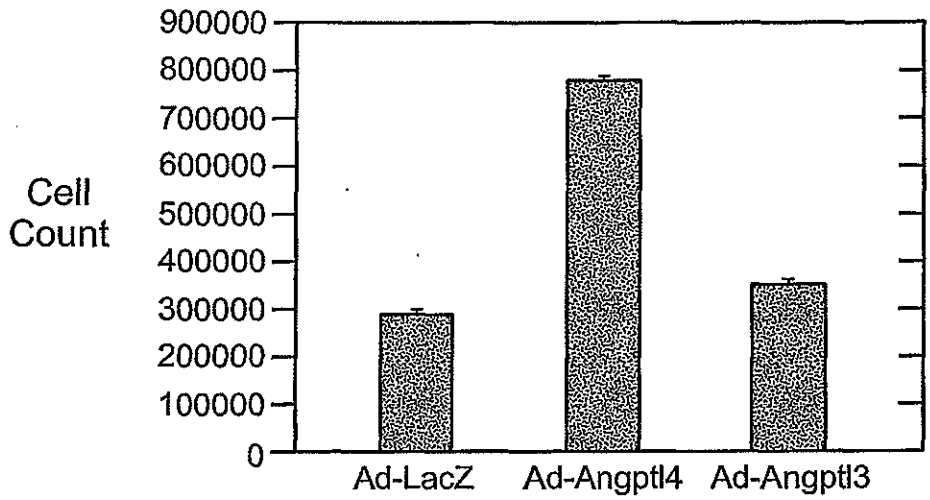

900000
800000
700000
600000
500000
400000
300000
200000
100000
0
Cell Count
Ad-LacZ
Ad-Angptl4
Ad-Angptl3

FIG._4A

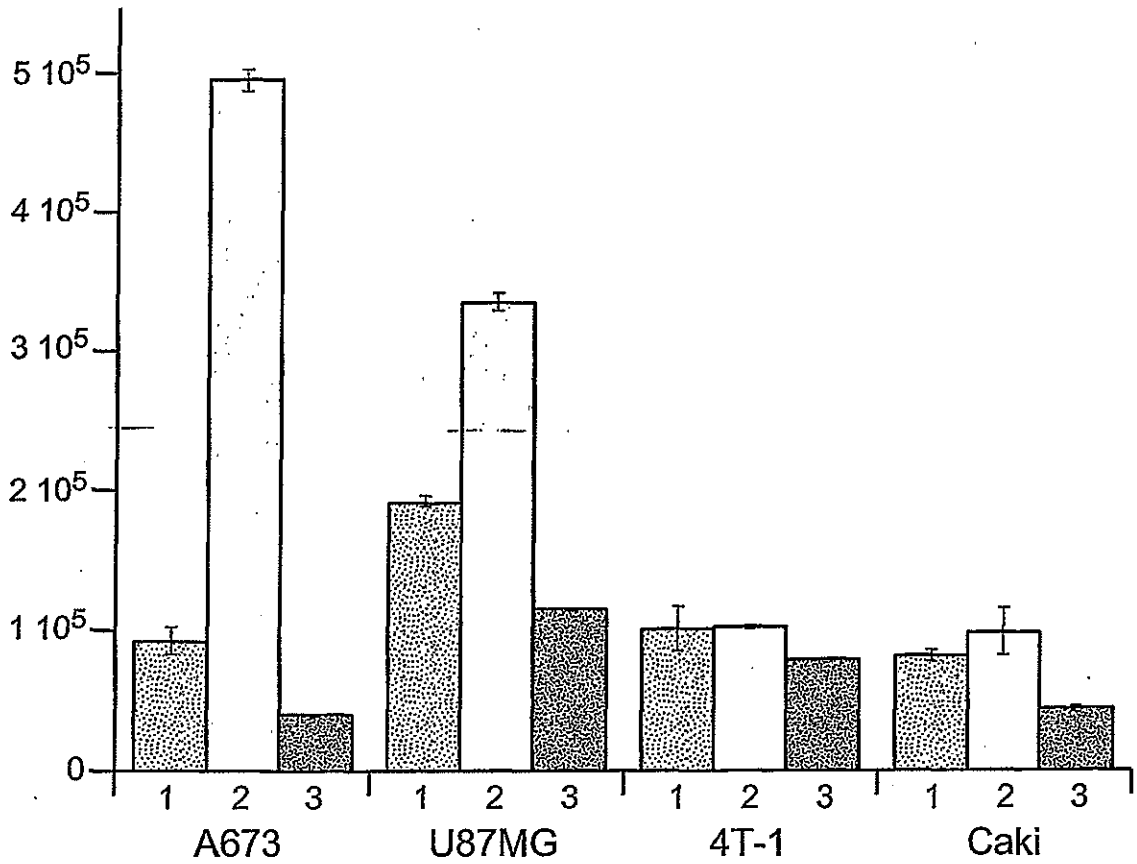

5 10^5
4 10^5
3 10^5
2 10^5
1 10^5
0
1 2 3
A673
U87MG
4T-1
Caki

FIG._4B

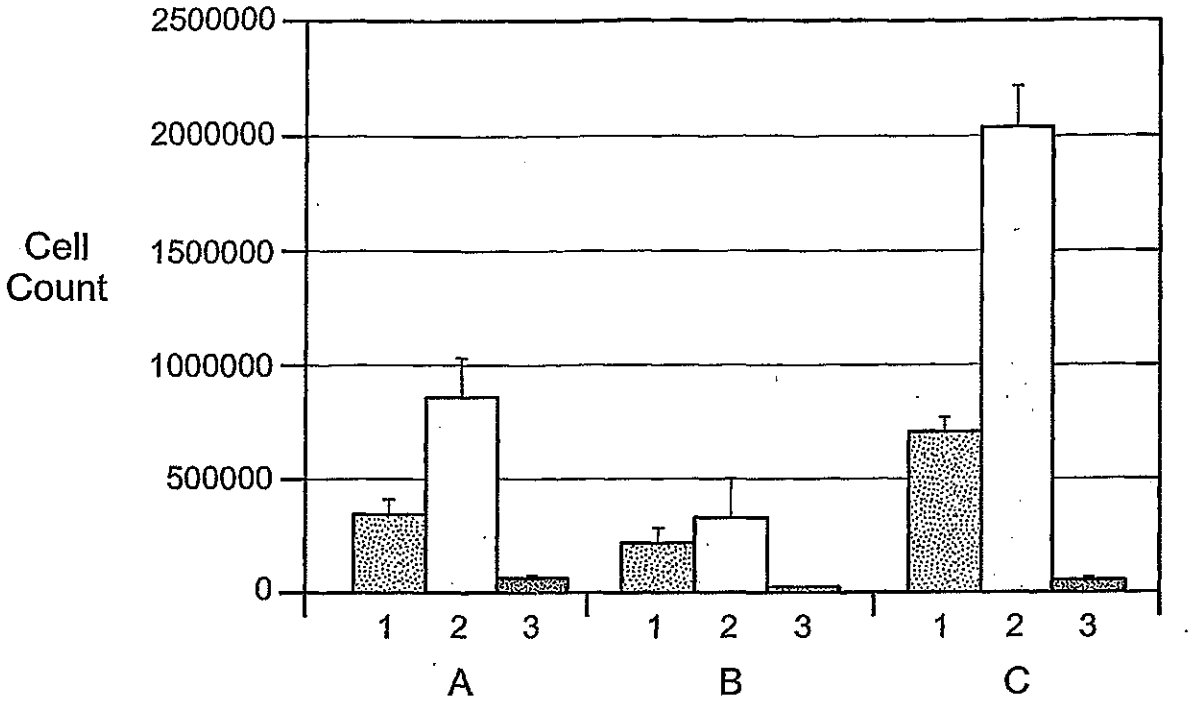

2500000
2000000
1500000
1000000
500000
0
Cell Count
1 2 3 1 2 3 1 2 3
A
B
C

FIG._4C

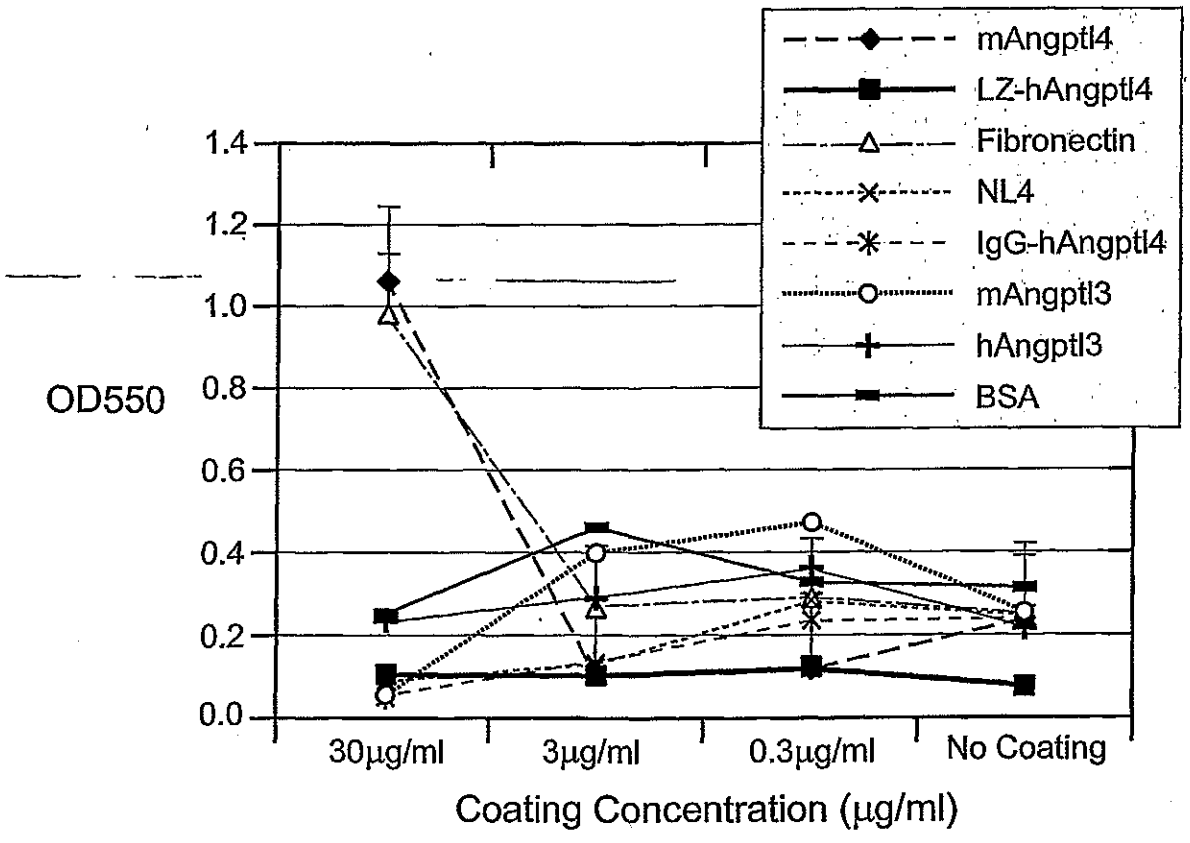

mAngptl4
LZ-hAngptl4
Fibronectin
NL4
IgG-hAngptl4
mAngptl3
hAngptl3
BSA
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
OD550
30µg/ml
3µg/ml
0.3µg/ml
No Coating
Coating Concentration (µg/ml)

FIG._5

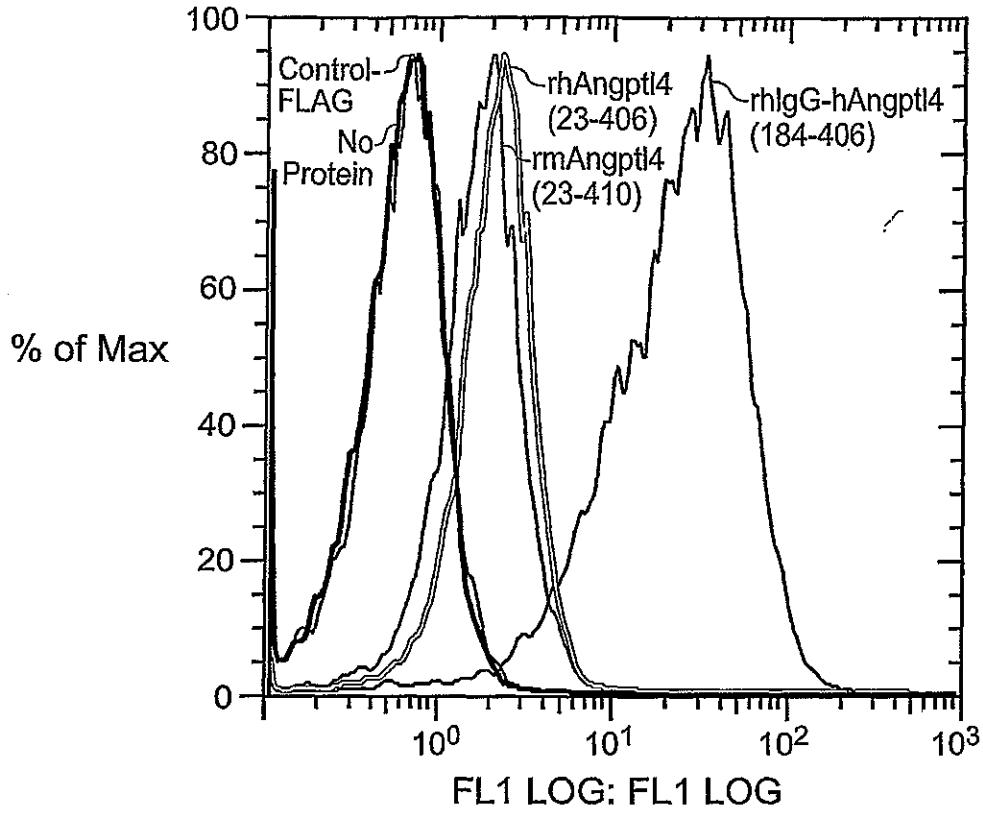

100
80
60
40
20
0
% of Max
Control-FLAG
No Protein
rhAngptl4 (23-406)
rmAngptl4 (23-410)
rhIgG-hAngptl4 (184-406)
10^0
10^1
10^2
10^3
FL1 LOG: FL1 LOG

FIG._6A

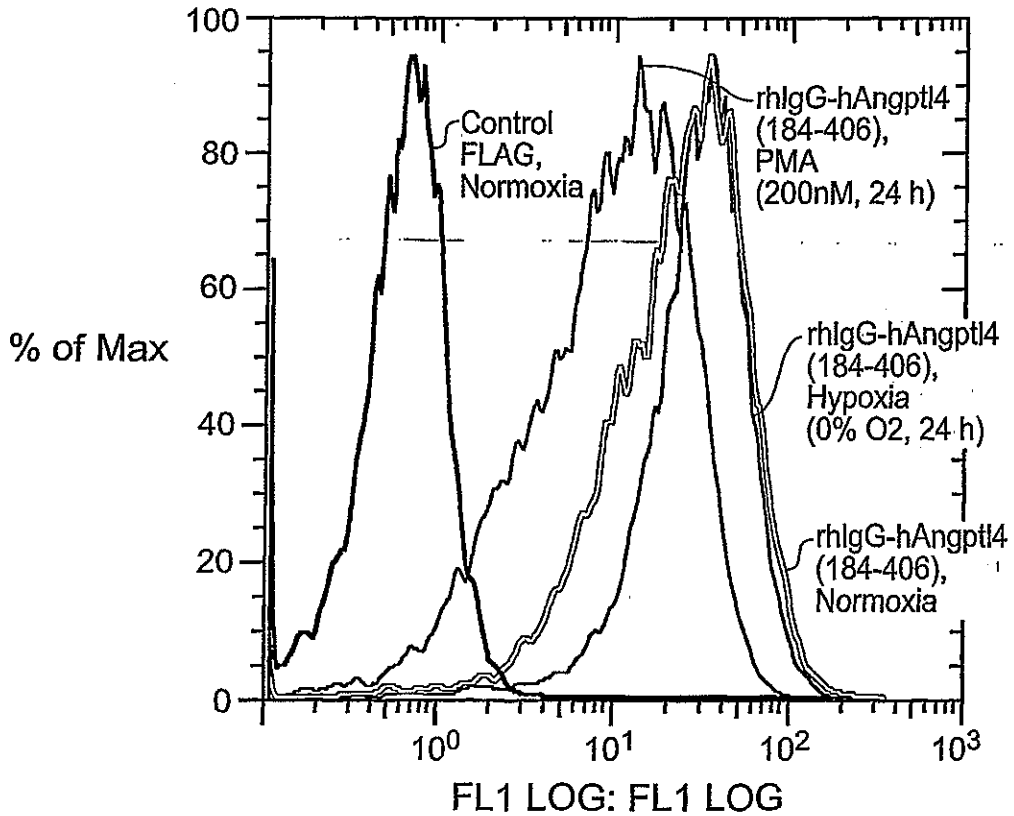

100
80
60
40
20
0
% of Max
Control FLAG, Normoxia
rhIgG-hAngptl4 (184-406), PMA (200nM, 24 h)
rhIgG-hAngptl4 (184-406), Hypoxia (0% O2, 24 h)
rhIgG-hAngptl4 (184-406), Normoxia
10^0
10^1
10^2
10^3
FL1 LOG: FL1 LOG

FIG._6B

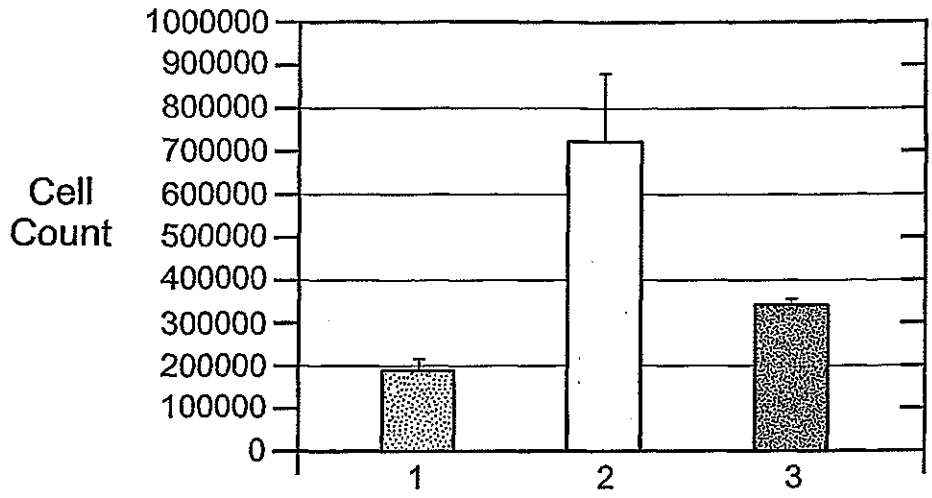

Cell Count
1000000
900000
800000
700000
600000
500000
400000
300000
200000
100000
0
1
2
3

FIG._7A

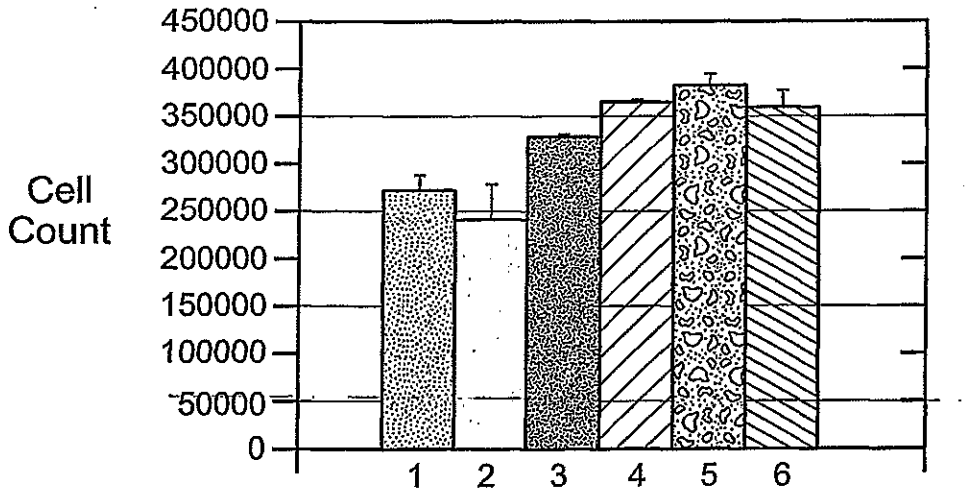

Cell Count
450000
400000
350000
300000
250000
200000
150000
100000
50000
0
1
2
3
4
5
6

FIG._7B

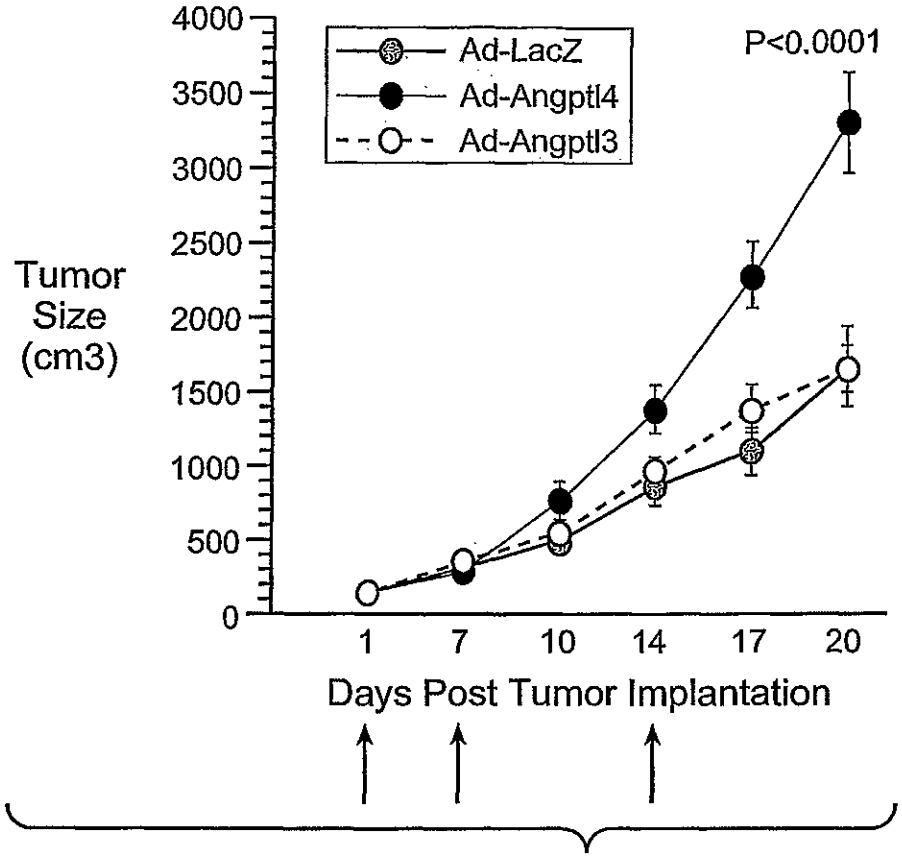

4000
3500
3000
2500
2000
1500
1000
500
0
Tumor Size (cm3)
Ad-LacZ
Ad-Angptl4
Ad-Angptl3
P<0.0001
1
7
10
14
17
20
Days Post Tumor Implantation

FIG._8A

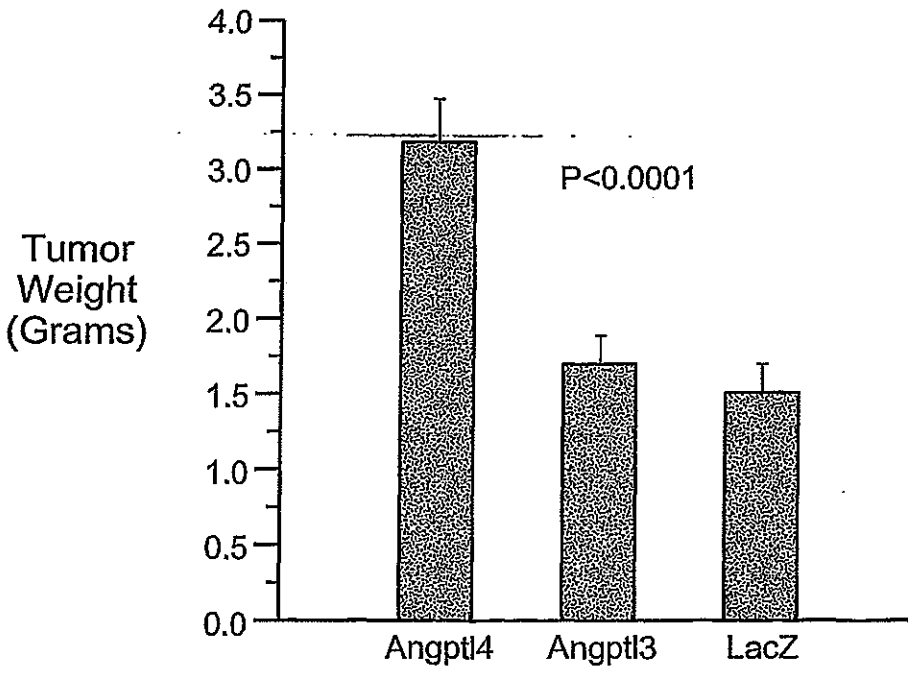

4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Tumor Weight (Grams)
P<0.0001
Angptl4
Angptl3
LacZ

FIG._8B

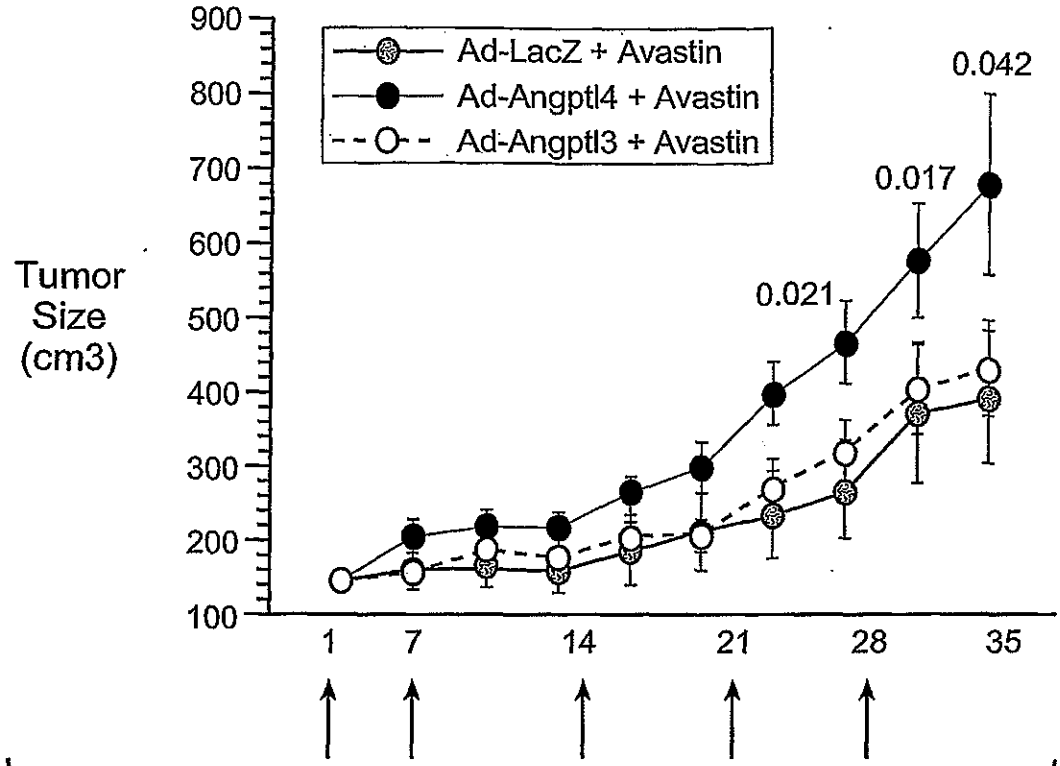

Ad-LacZ + Avastin
Ad-Angptl4 + Avastin
Ad-Angptl3 + Avastin
Tumor Size (cm3)
900
800
700
600
500
400
300
200
100
1
7
14
21
28
35
0.042
0.017
0.021

FIG._8C

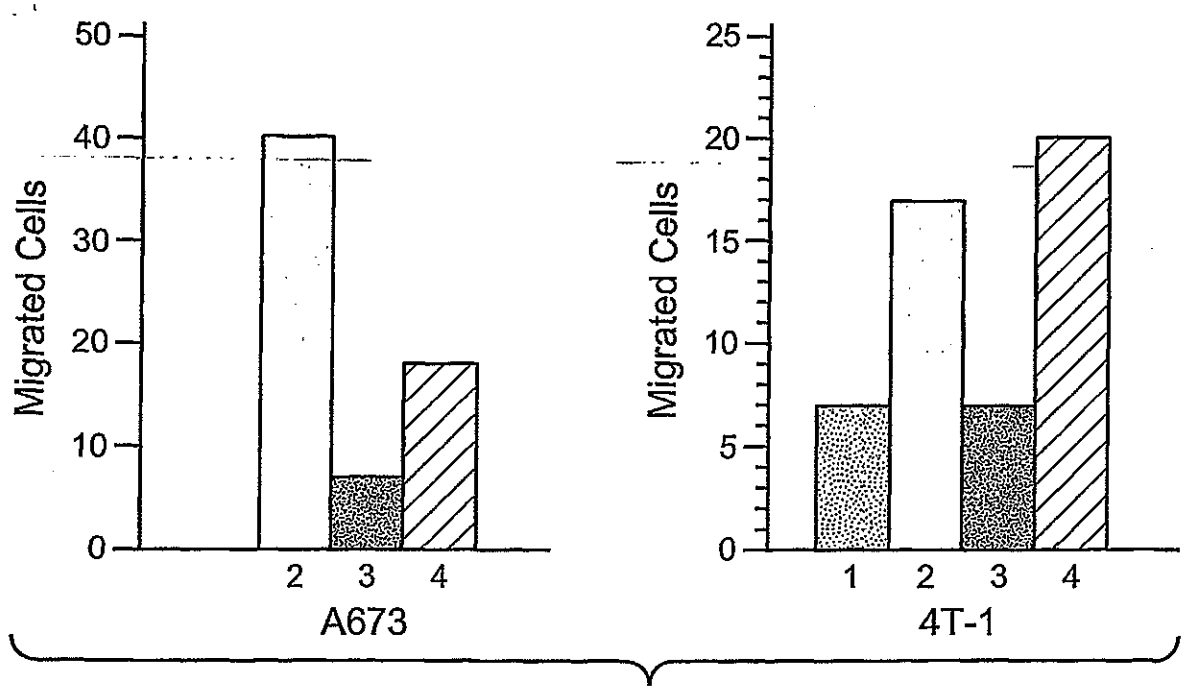

Migrated Cells
50
40
30
20
10
0
2
3
4
A673
Migrated Cells
25
20
15
10
5
0
1
2
3
4
4T-1

FIG._9

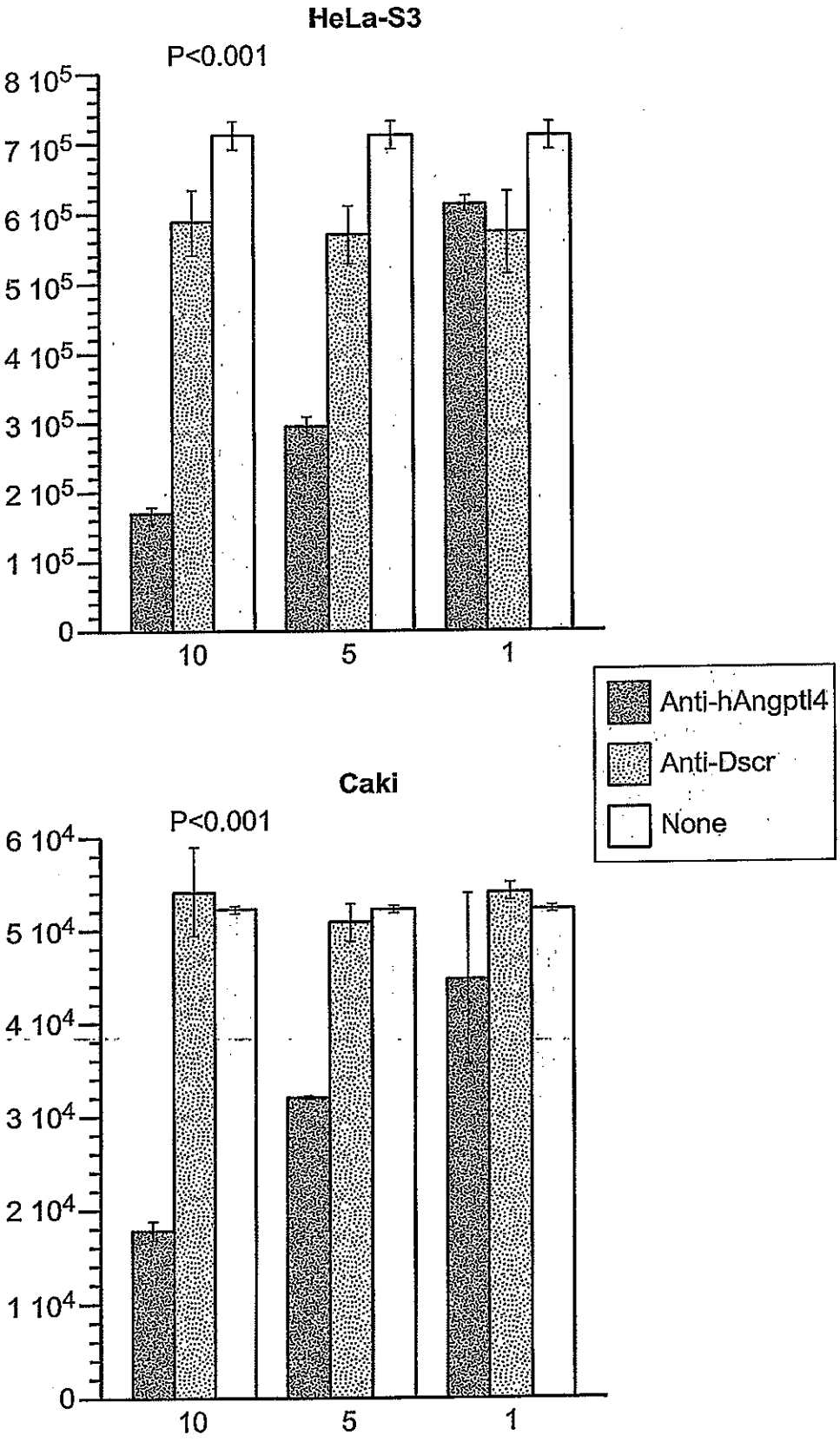

HeLa-S3
P<0.001
8 10^5
7 10^5
6 10^5
5 10^5
4 10^5
3 10^5
2 10^5
1 10^5
0
10
5
1
Anti-hAngptl4
Anti-Dscr
None
Caki
P<0.001
6 10^4
5 10^4
4 10^4
3 10^4
2 10^4
1 10^4
0
10
5
1

FIG._10A

P<0.0001

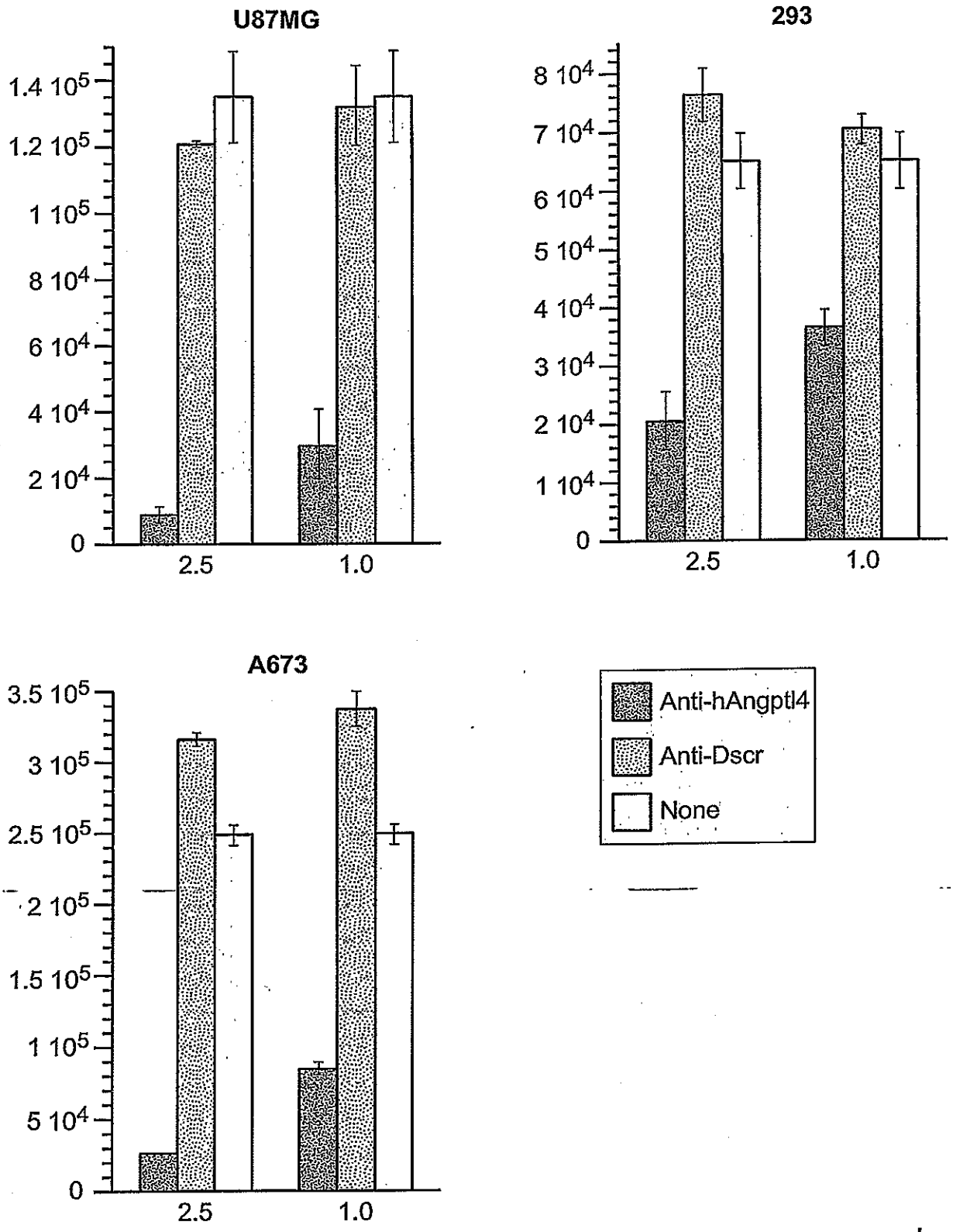


FIG._10B

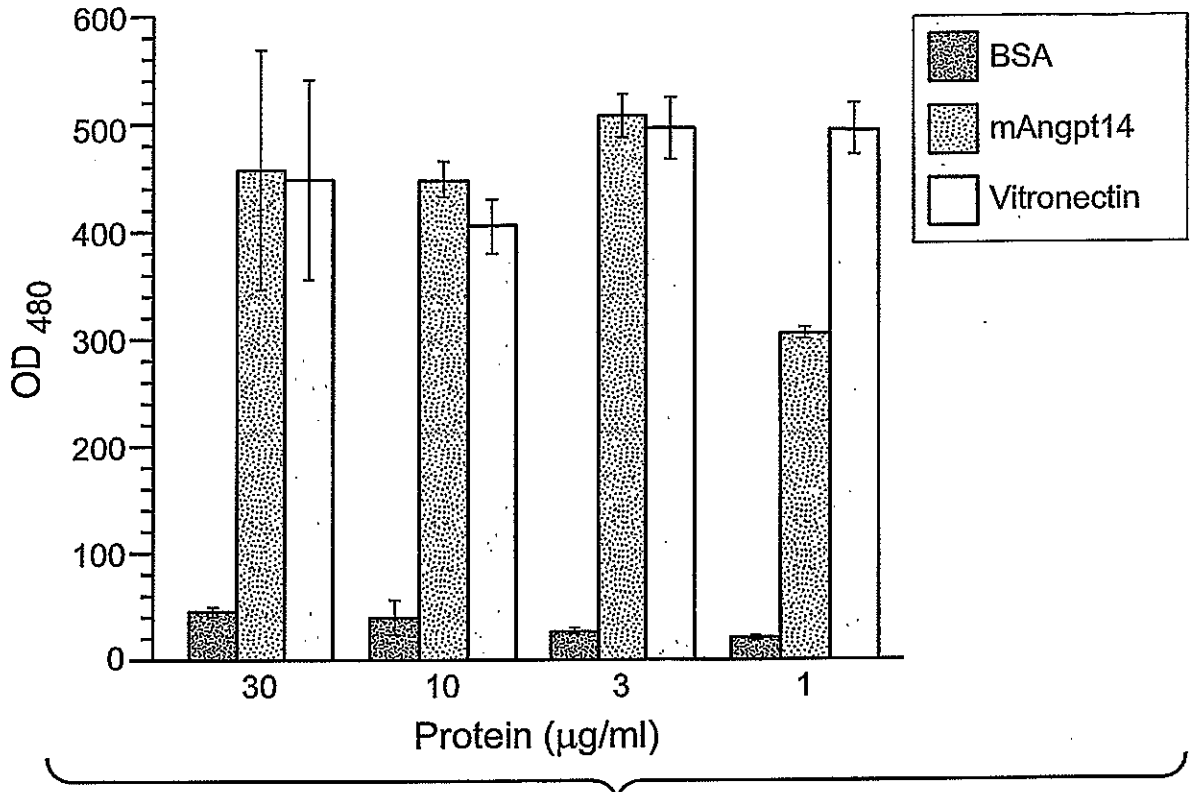

600
500
400
300
200
100
0
OD 480
BSA
mAngpt14
Vitronectin
30
10
3
1
Protein (μg/ml)

FIG._11

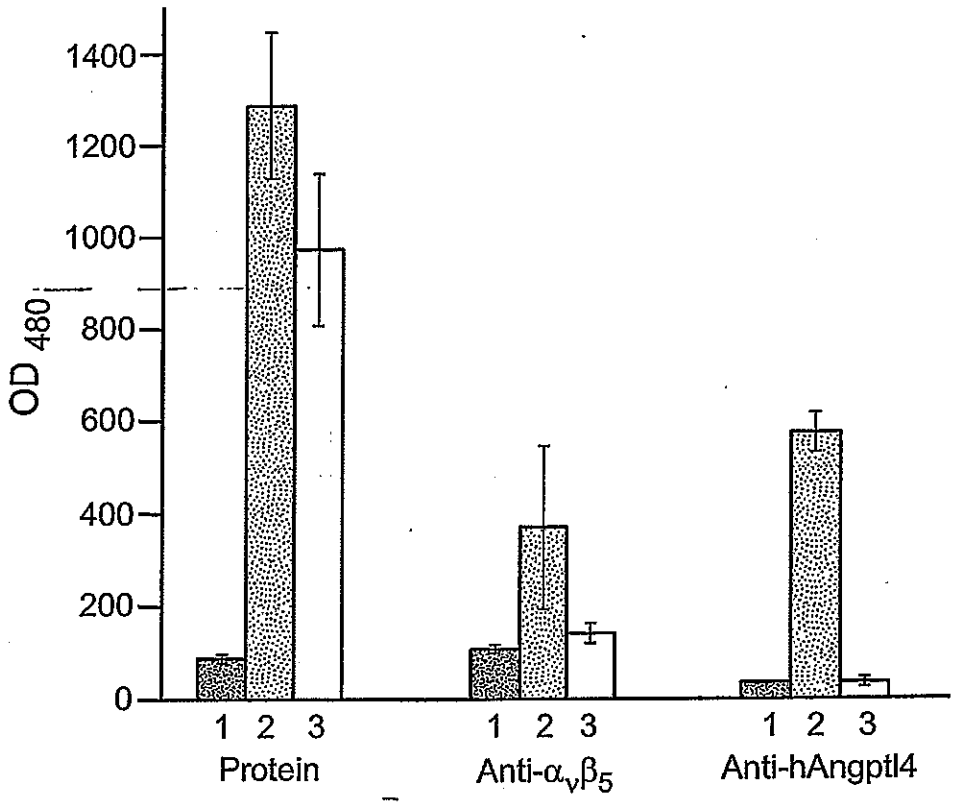

1400
1200
1000
800
600
400
200
0
OD 480
1 2 3
Protein
1 2 3
Anti-αvβ5
1 2 3
Anti-hAngptl4

FIG._12

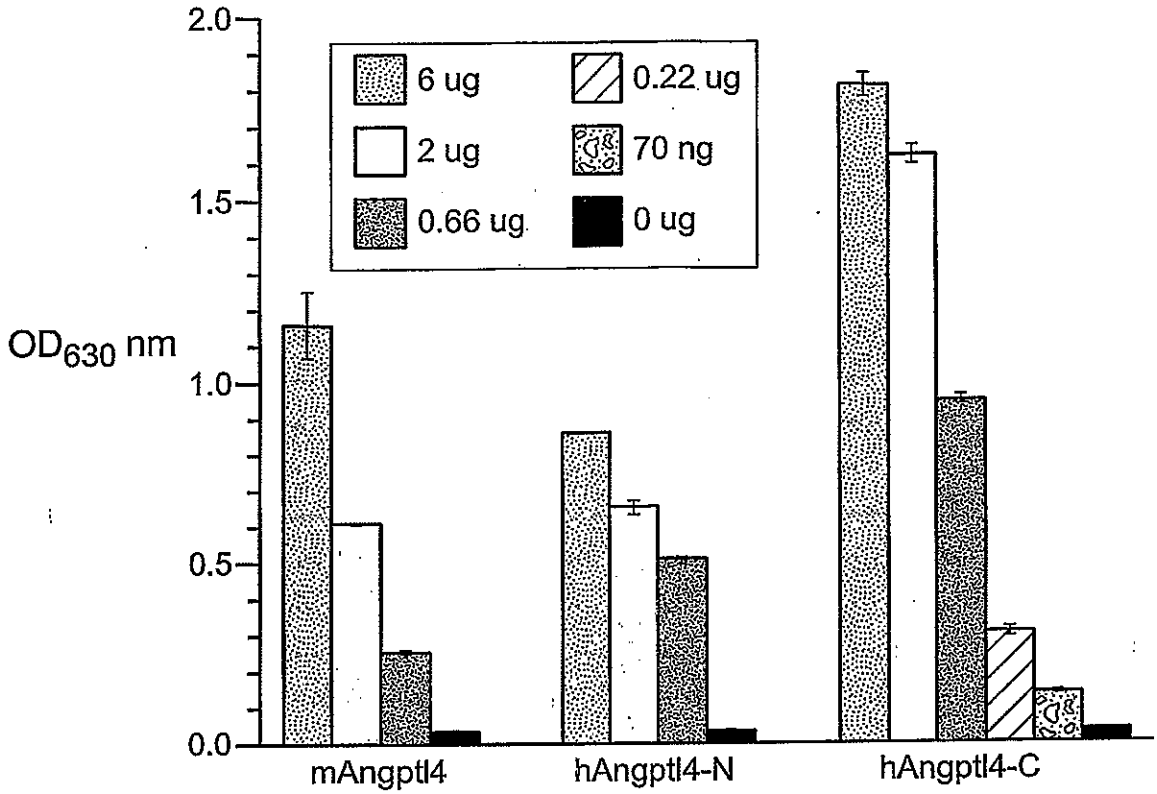


FIG._13A

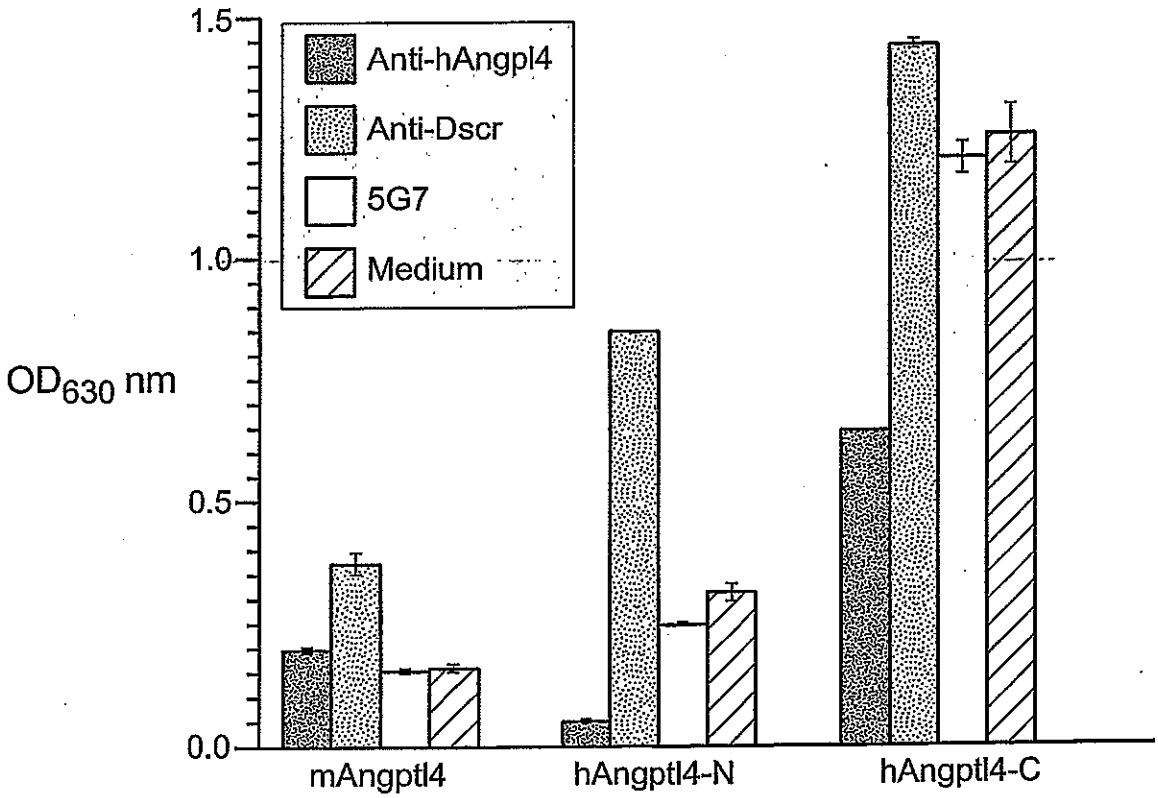


FIG._13B

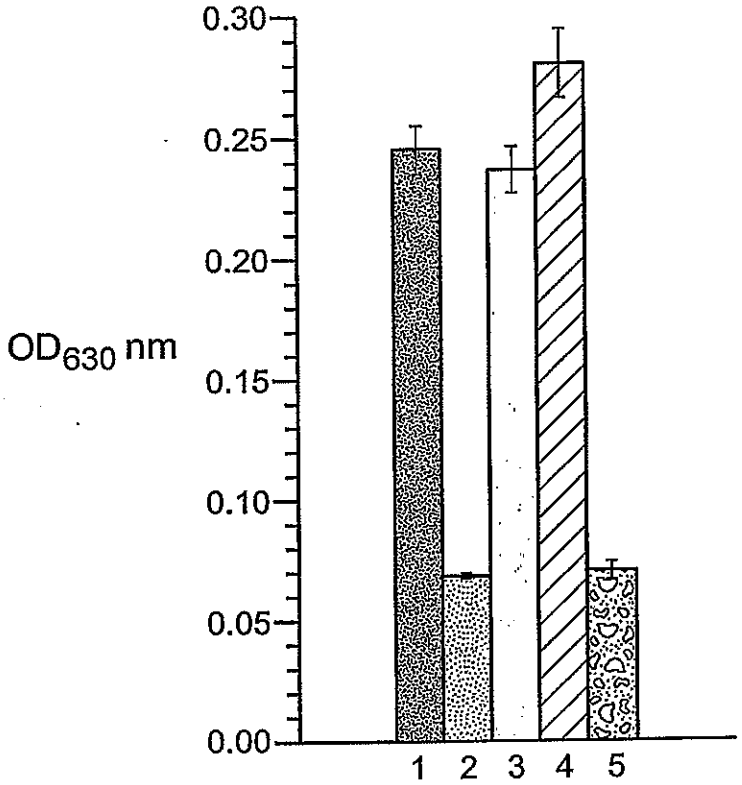


FIG._13C