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SEQ. ID NO:1:

GCCGAGCTGA GCGGATCCTC ACATGACTGT GATCCGATTC TTTCCAGCGG 50
CTTCTGCAAC CAAGCGGGTC TTACCCCCGG TCCTCCGCGT CTCCAGTCCT 100
CGCACCTGGA ACCCCAACGT CCCCAGAGAT 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 GACACAATC AAGGCTCAGA 500
ACAGCAGGAT CCAGCAATC 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
TGGTGAAGT 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

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TGGAGGCTGG TGGTTTGGCA CCTGCAGCCA TTCCAACCTC AACGGCCAGT 1250
ACTTCCGCTC CATCCCACAG CAGCGGCAGA AGCTTAAGAA GGAATCTTC 1300
TGGAAGACCT GGC GGGGCCG 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 TGC GTTGCCT CCTGAGATCG AGGCTGCAGG ATATGCTCAG 1600
ACTCTAGAGG CGTGGACCAA GGGGCATGGA GCTTCACTCC TTGCTGGCCA 1650
GGGAGTTGGG GACTCAGAGG GACCACTTGG GGCCAGCCAG ACTGGCCTCA 1700
ATGGCGGACT CAGTCACATT GACTGACGGG GACCAGGGCT TGTGTGGGTC 1750
GAGAGCGCCC TCATGGTGCT GTGCTGTTG TGTGTAGGTC CCCTGGGGAC 1800
ACAAGCAGGC GCCAATGGTA TCTGGGCGGA GCTCACAGAG TTCTTGGAAT 1850
AAAAGCAACC TCAGAACAC 1869

FIG. 1B

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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	

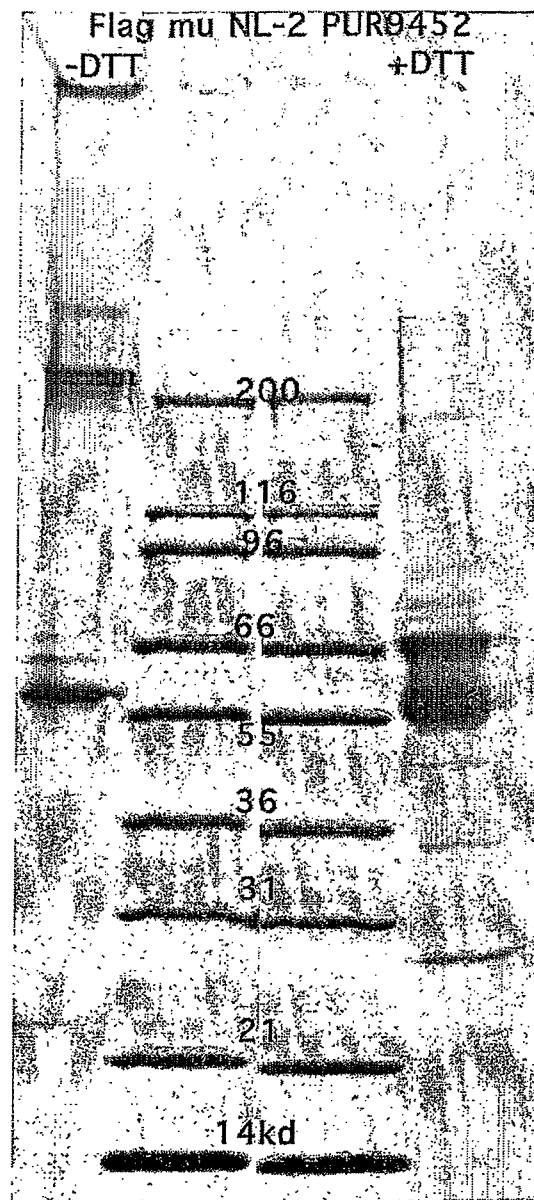
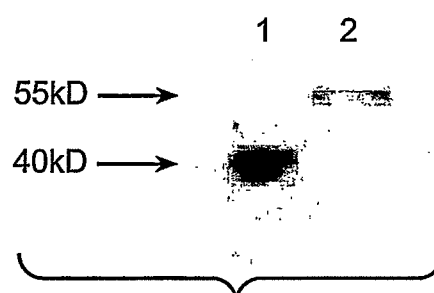
FIG. 2A

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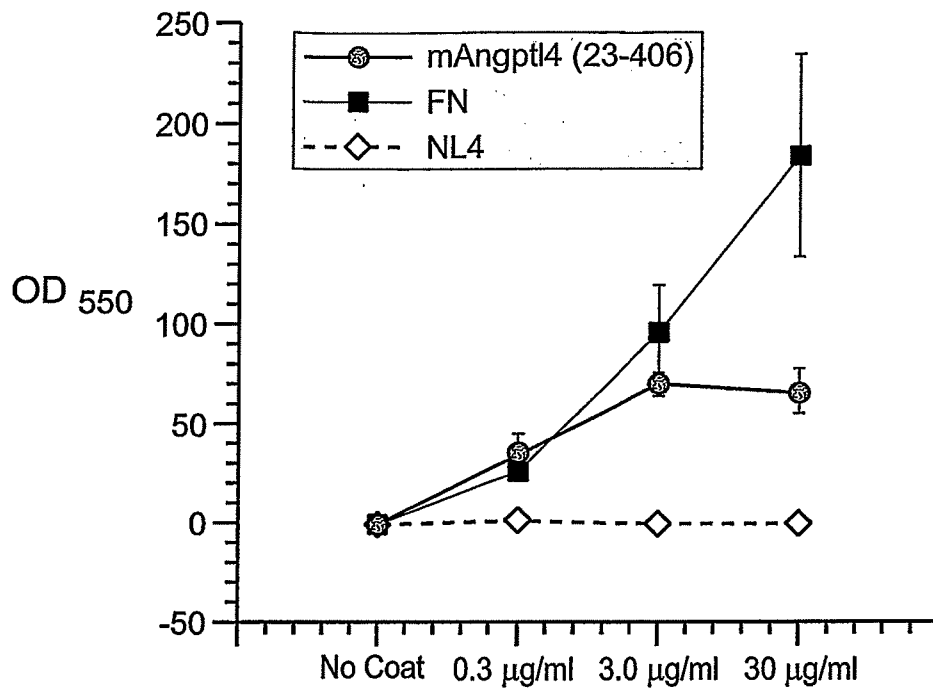
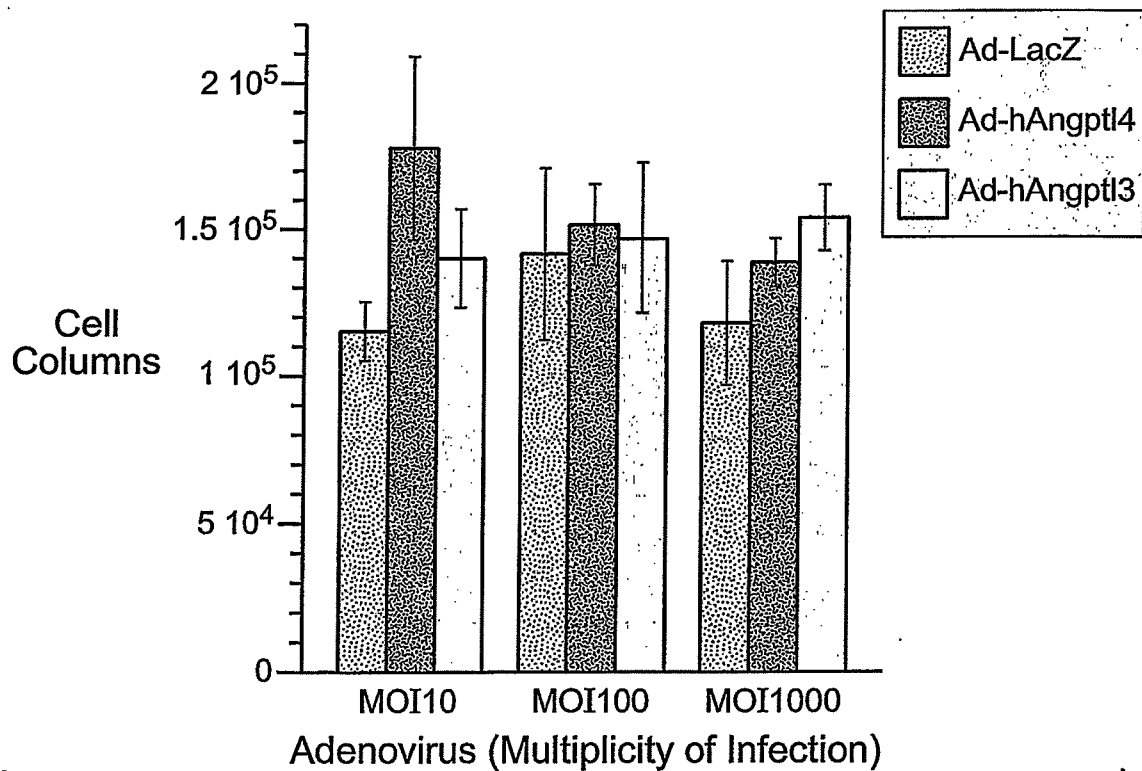
Trp	Glu	Ala	Tyr	Lys	Ala	Gly	Phe	Gly	Asp	Pro	His	Gly	Glu	Phe	245	250	255
Trp	Leu	Gly	Leu	Glu	Lys	Val	His	Ser	Ile	Thr	Gly	Asp	Arg	Asn	260	265	270
Ser	Arg	Leu	Ala	Val	Gln	Leu	Arg	Asp	Trp	Asp	Gly	Asn	Ala	Glu	275	280	285
Leu	Leu	Gln	Phe	Ser	Val	His	Leu	Gly	Gly	Glu	Asp	Thr	Ala	Tyr	290	295	300
Ser	Leu	Gln	Leu	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

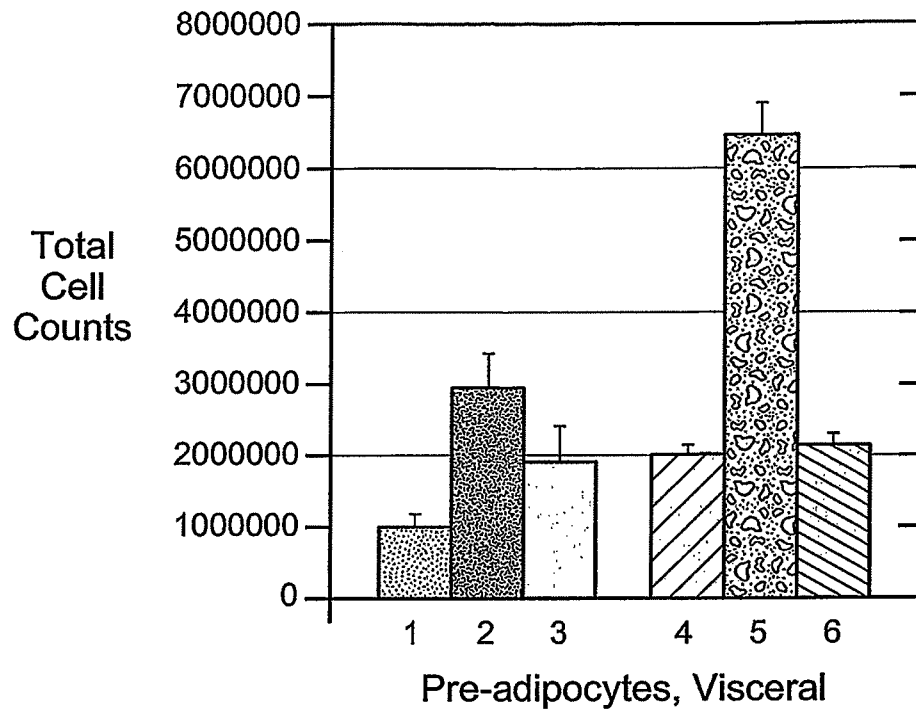
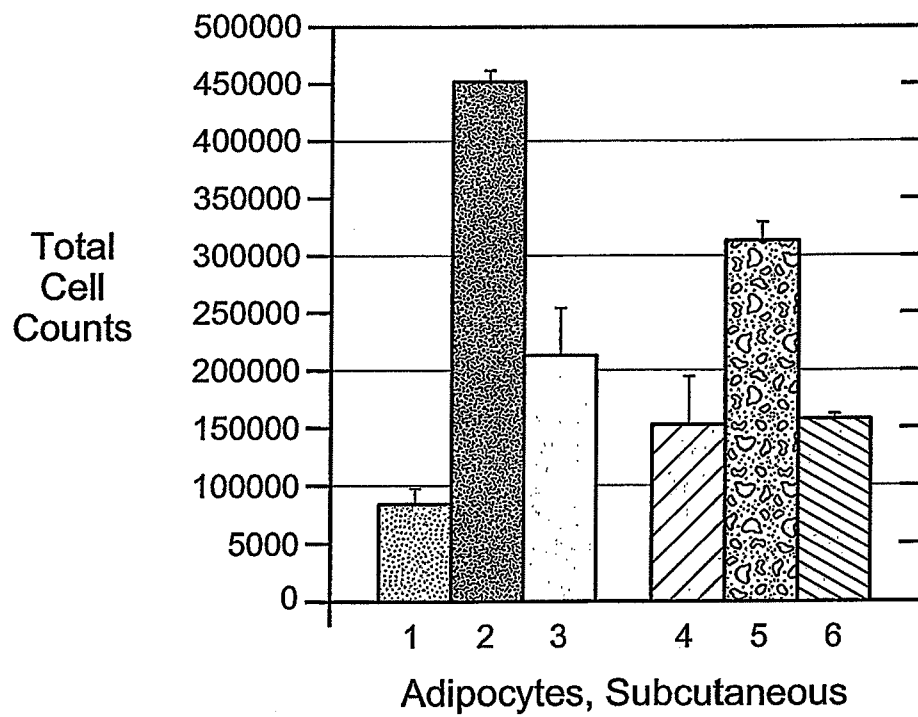
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**FIG._3A****FIG._3B**

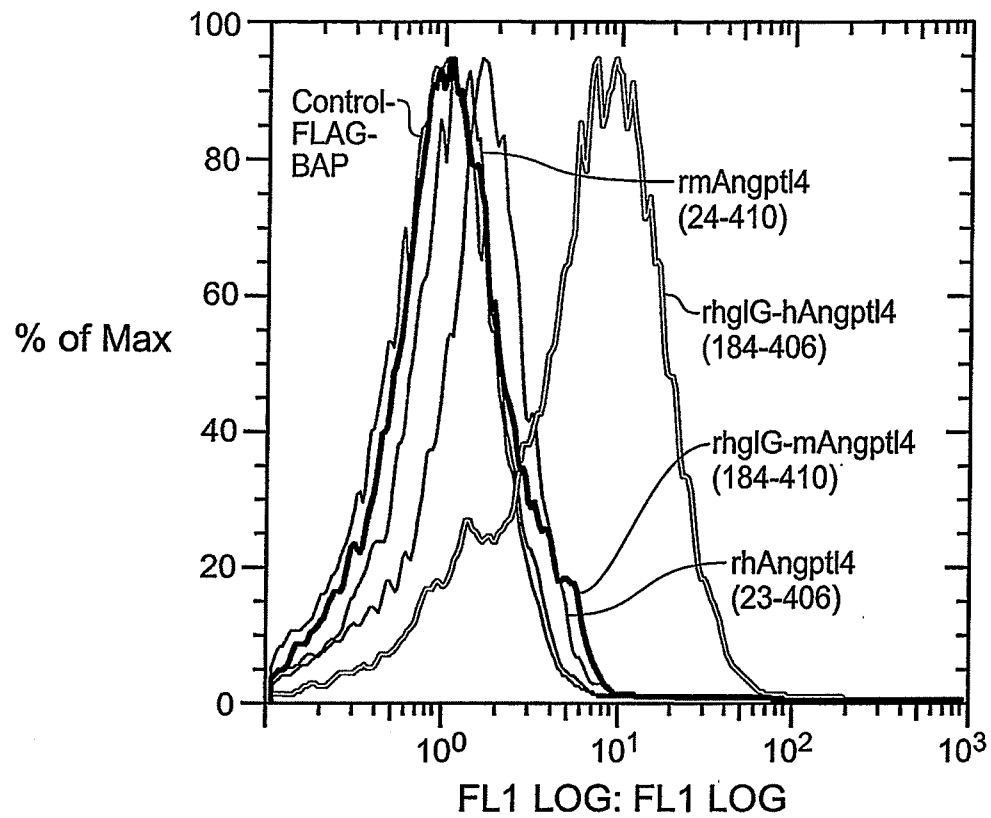
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**FIG. 4****FIG. 5**

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**FIG._6A****FIG._6B**

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**FIG. 7**

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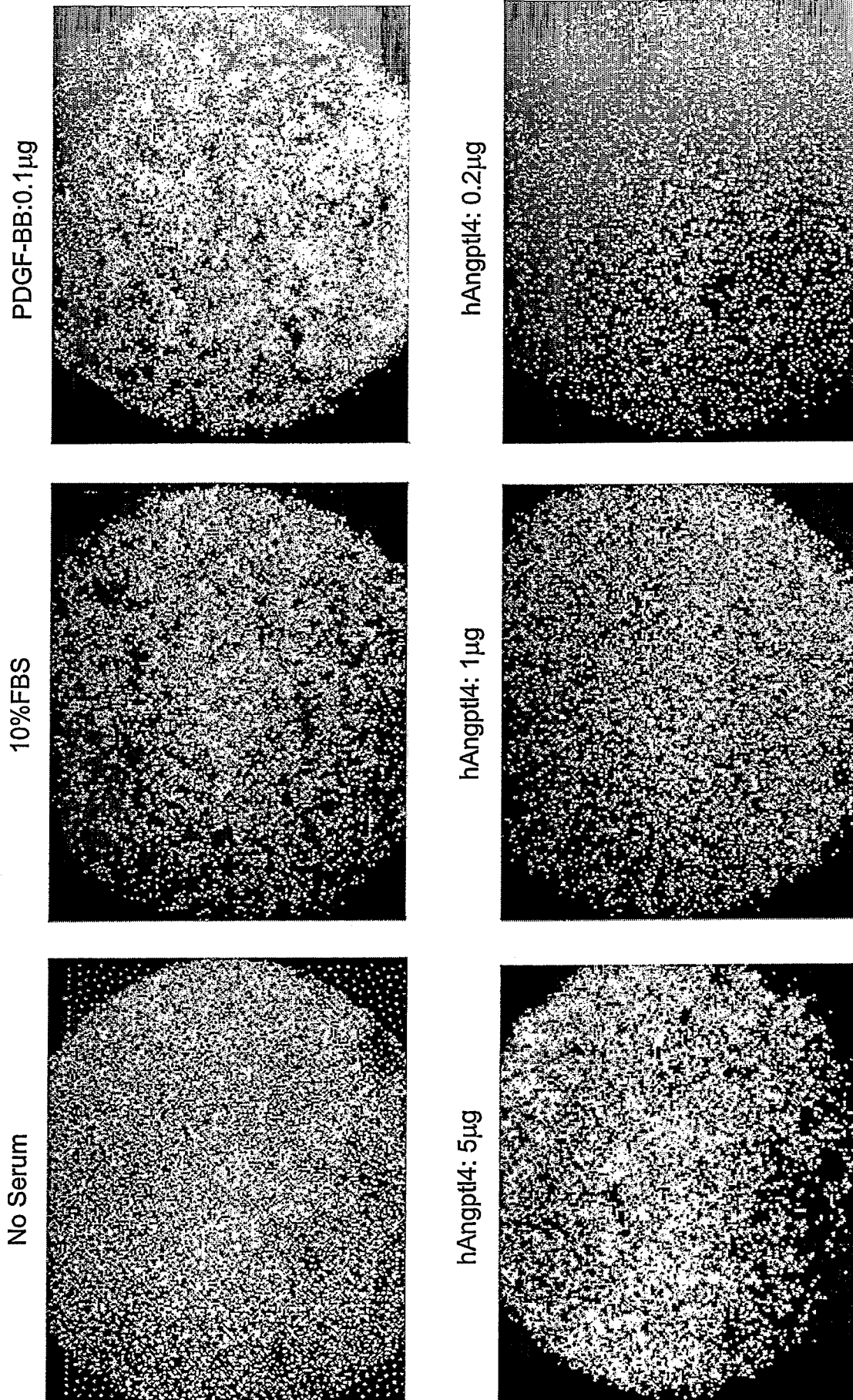


FIG._8A

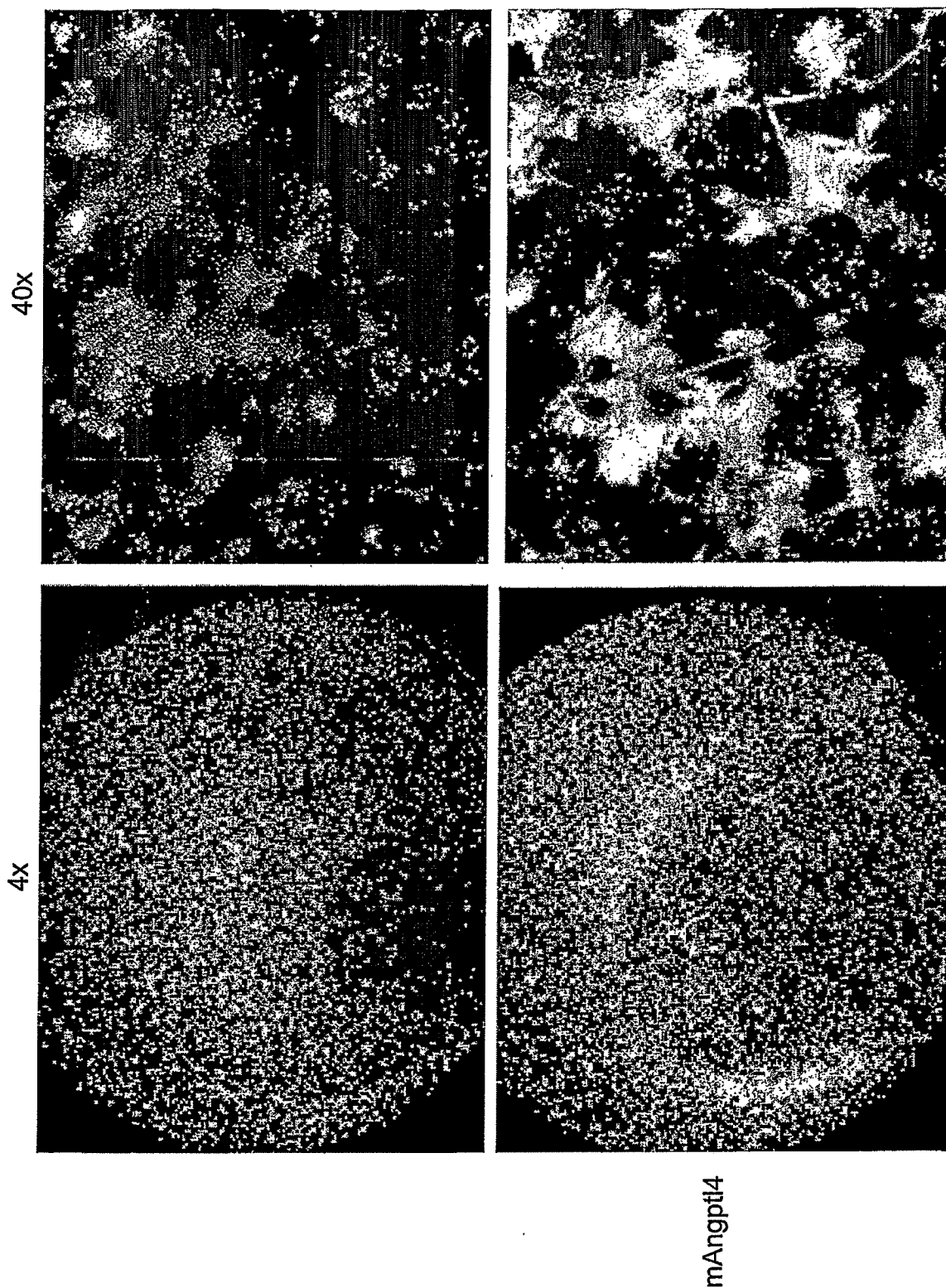
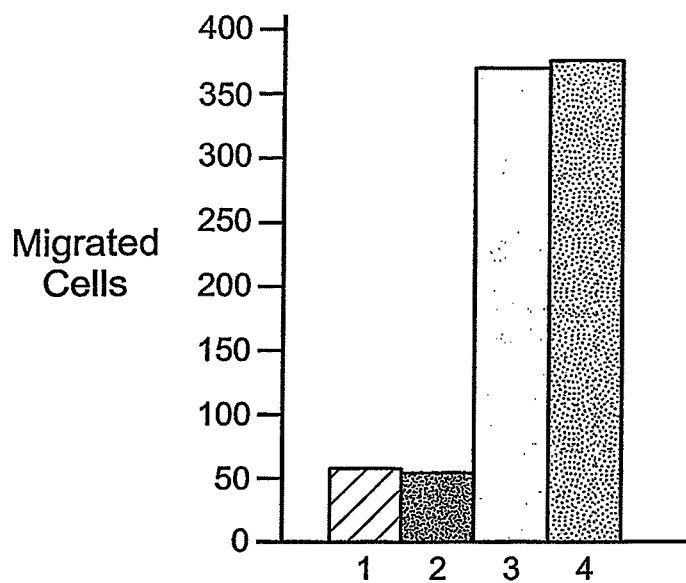
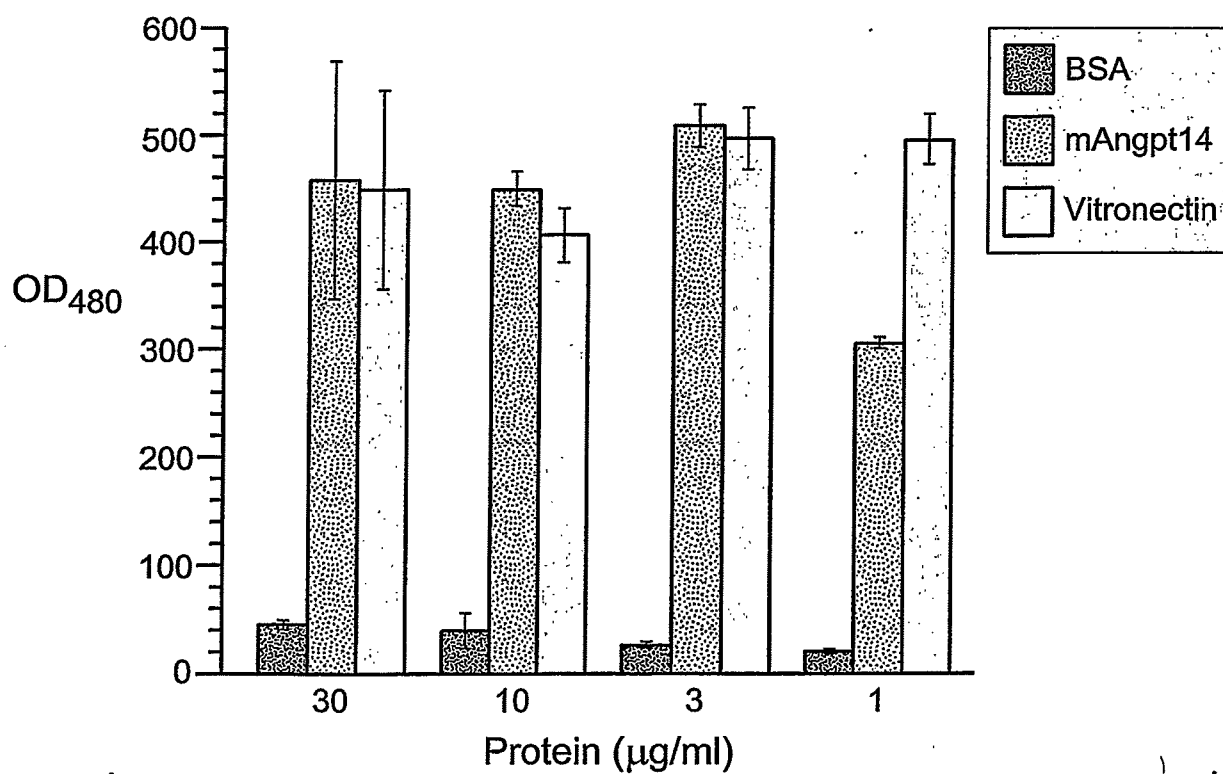
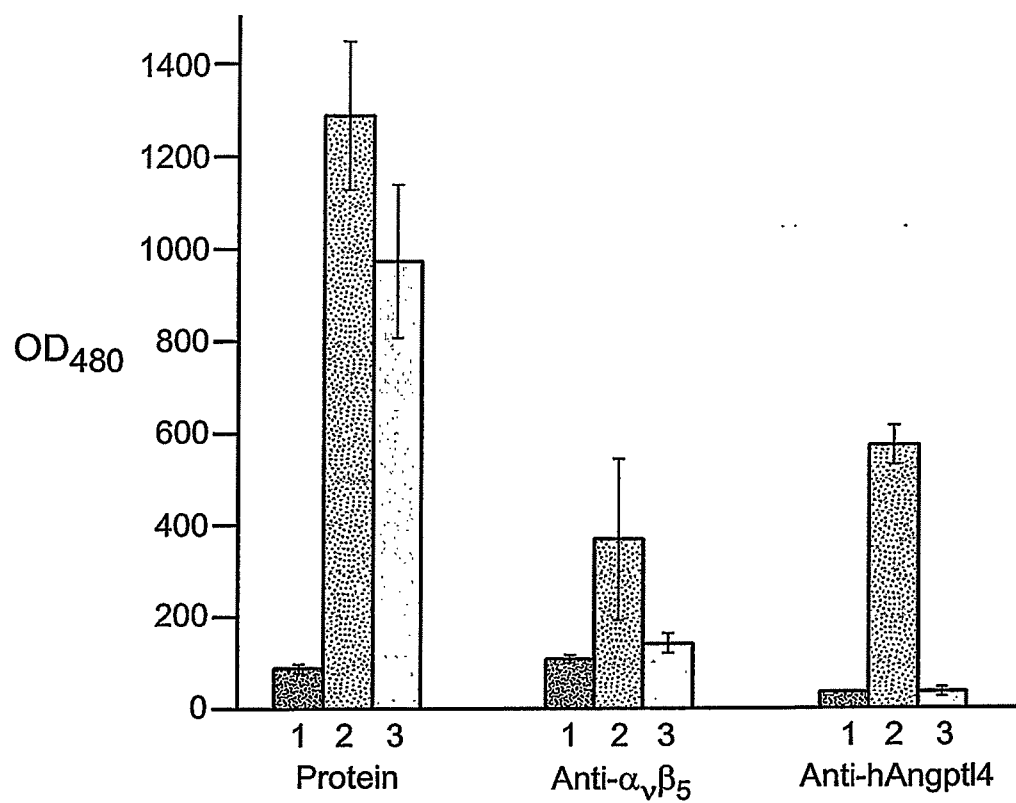
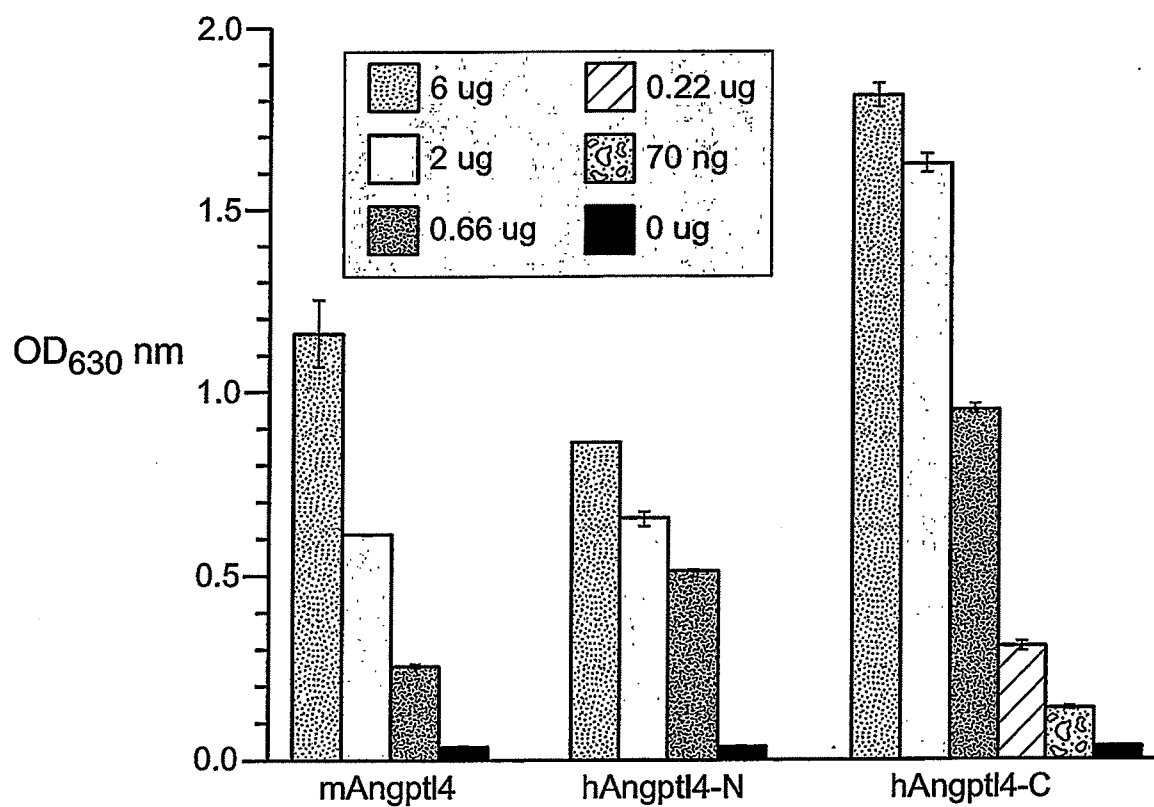


FIG. 8B

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**FIG._8C****FIG._9A**

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**FIG. 9B****FIG. 9C**

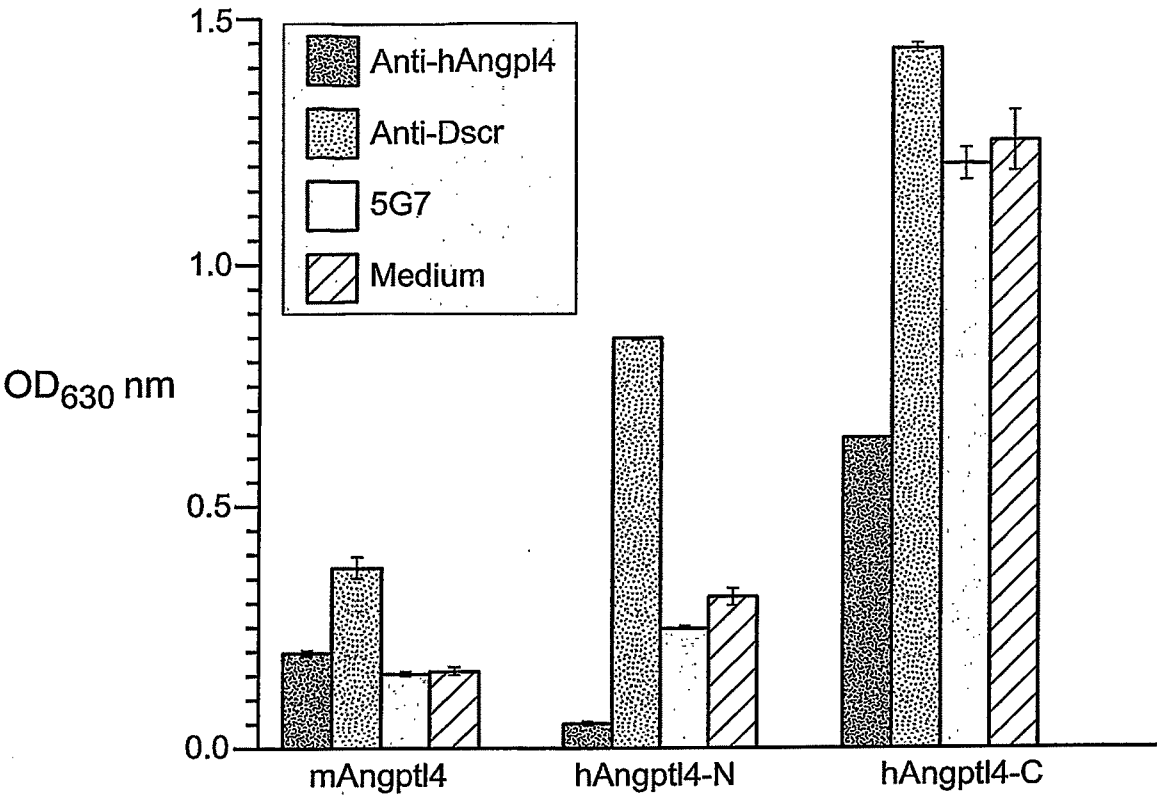


FIG. 9D

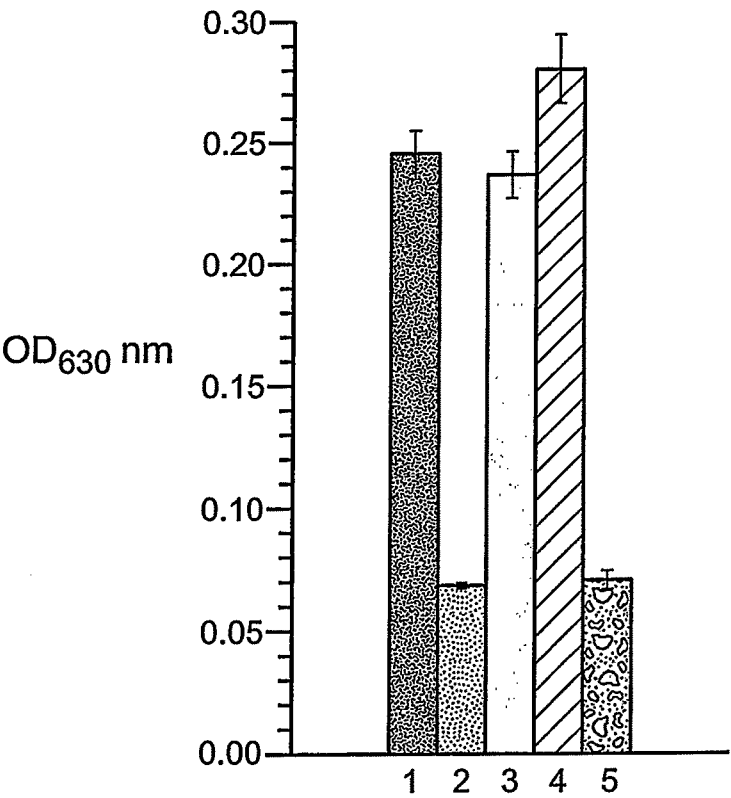
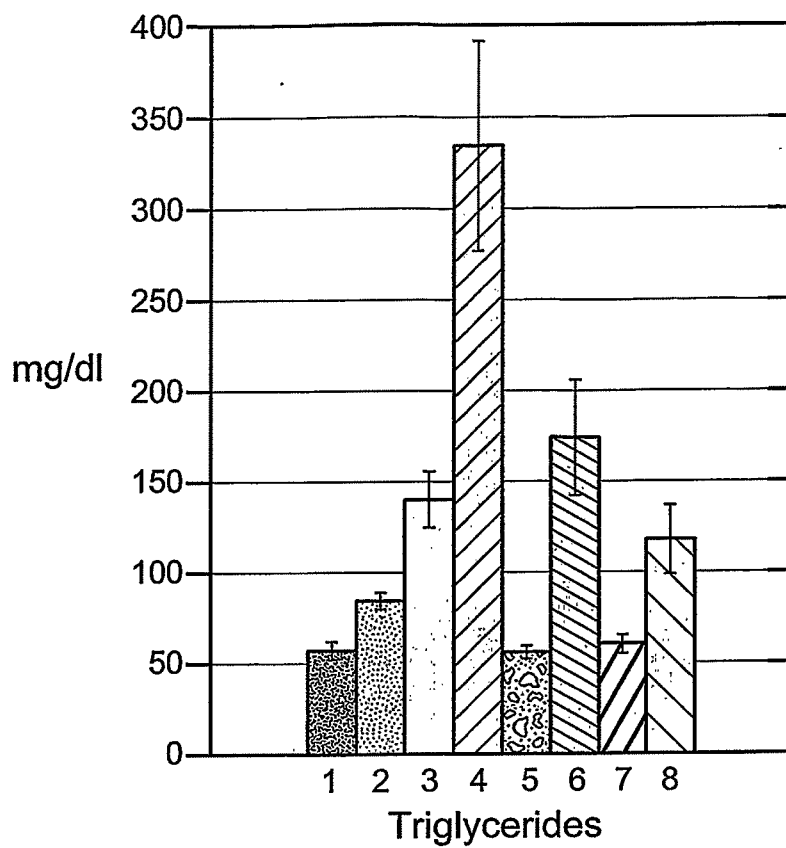


FIG. 9E

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**FIG. 10**