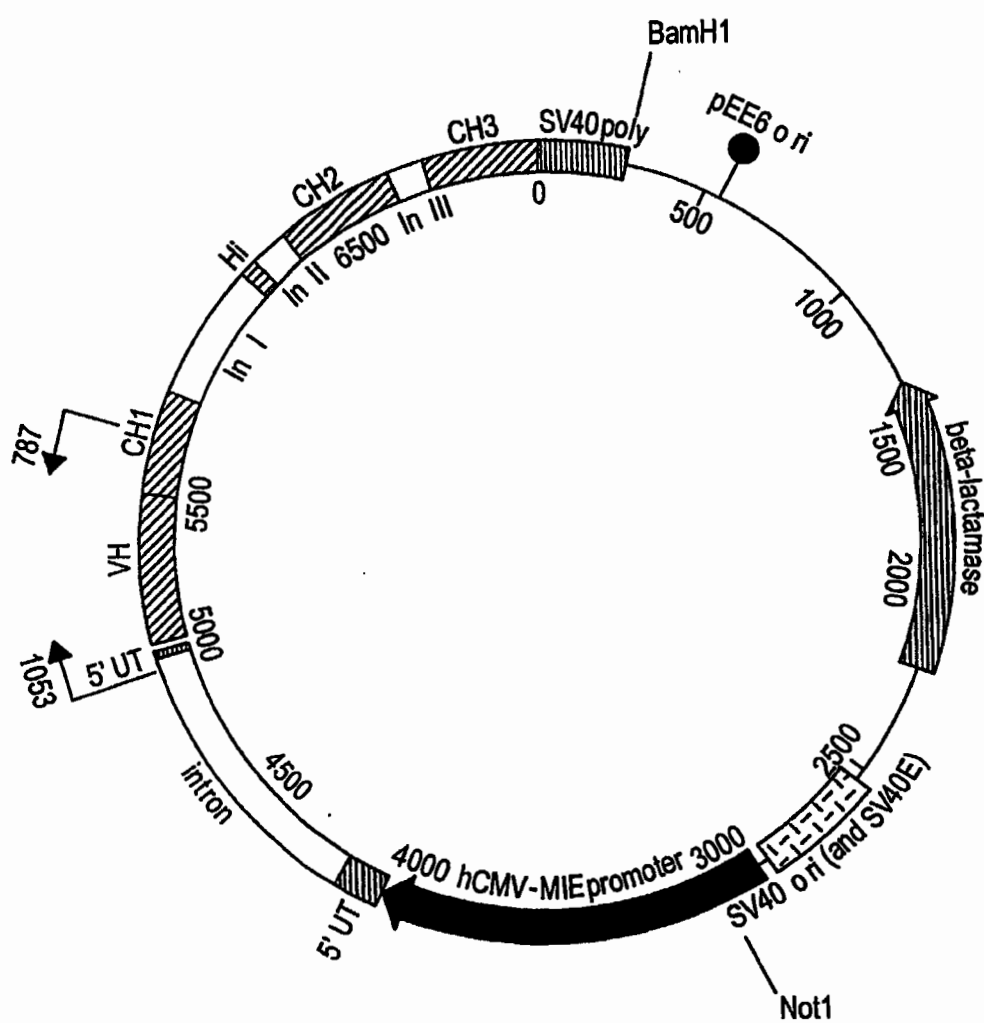
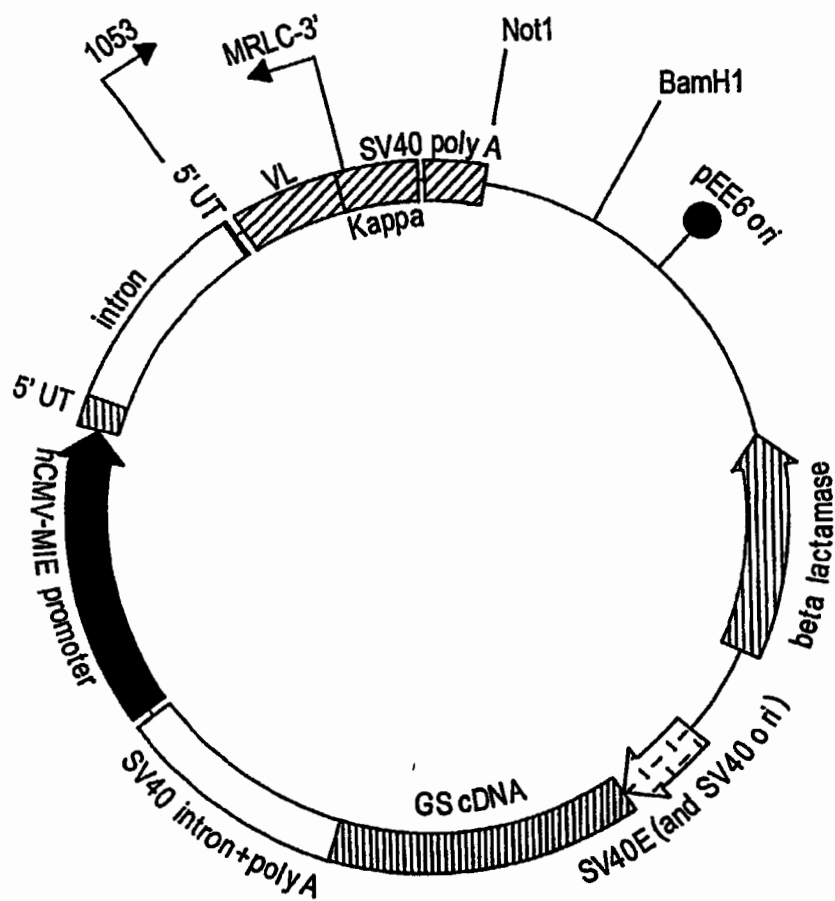


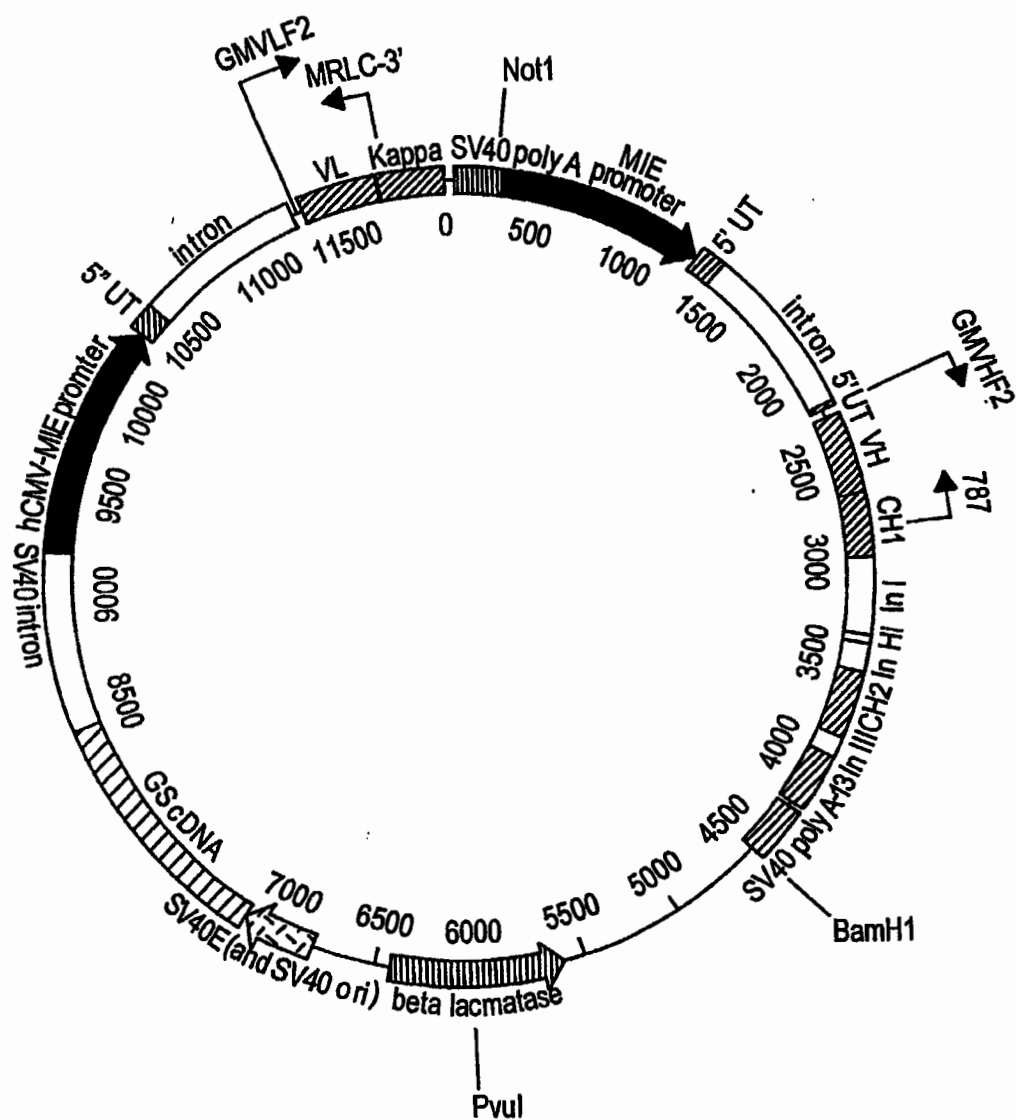
1/65

*Fig. 1*

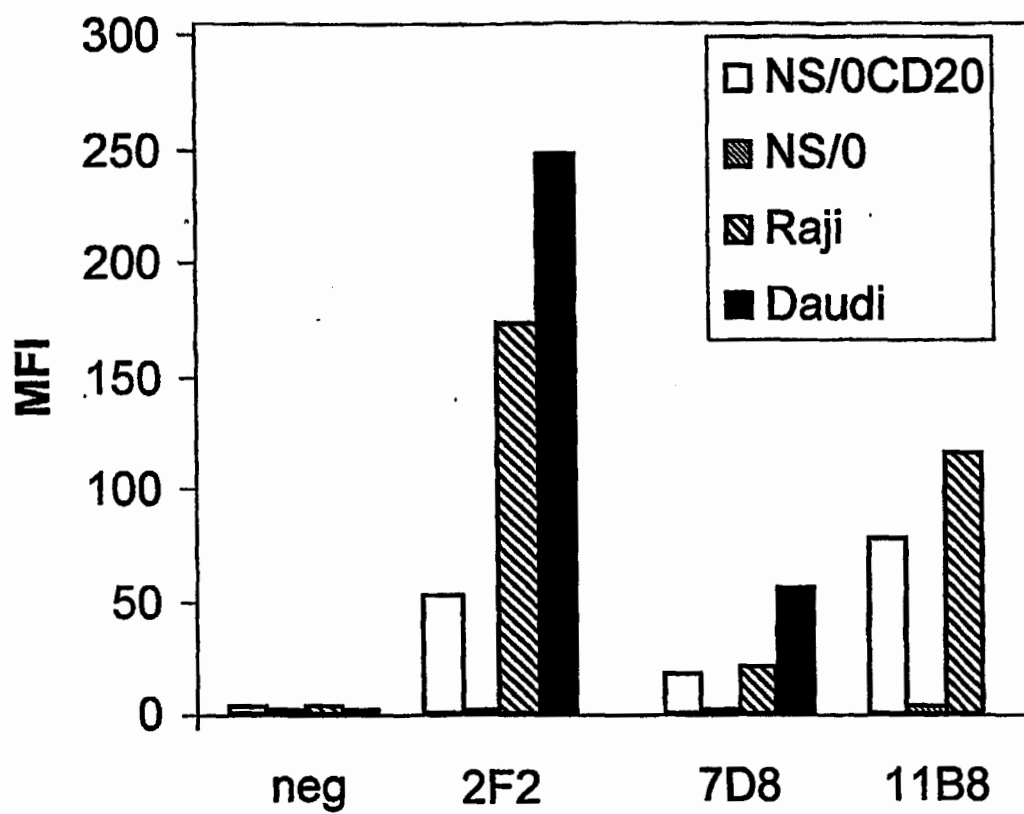
2/65

*Fig. 2*

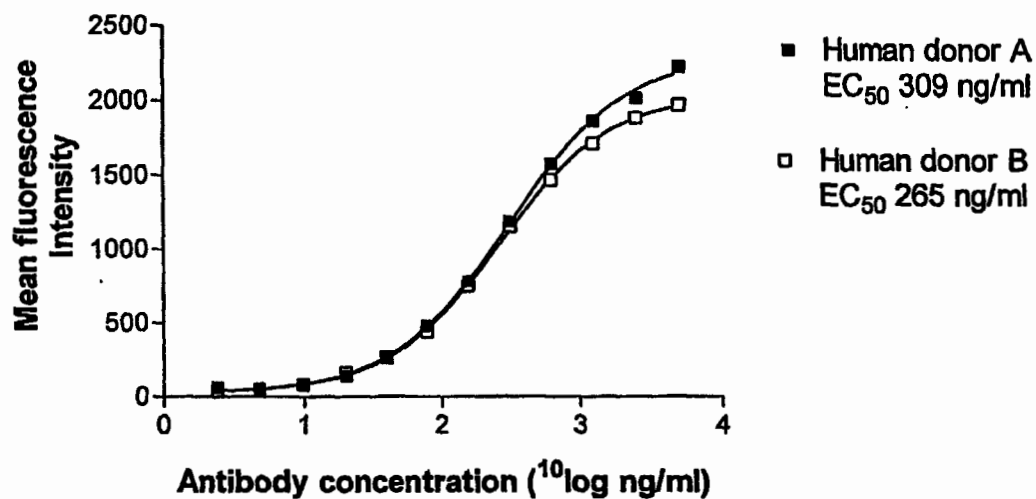
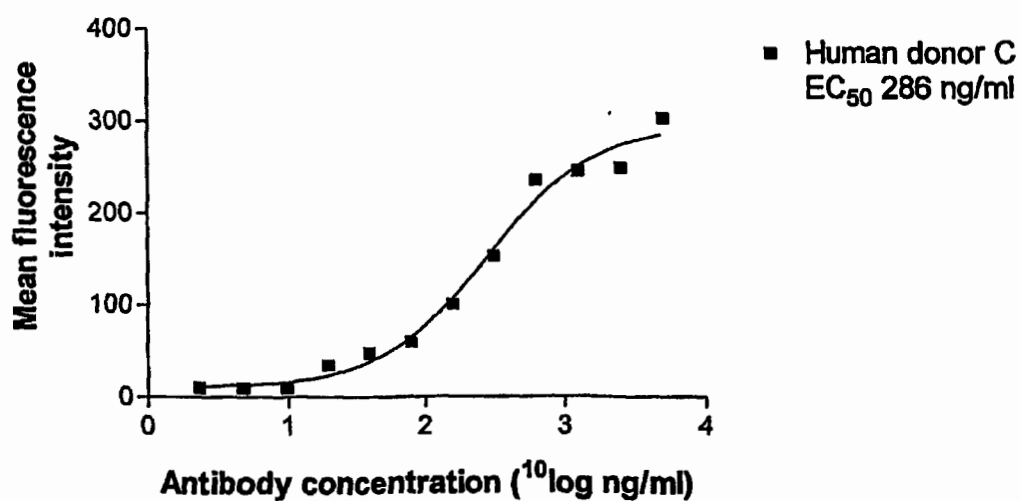
3/65

*Fig. 3*

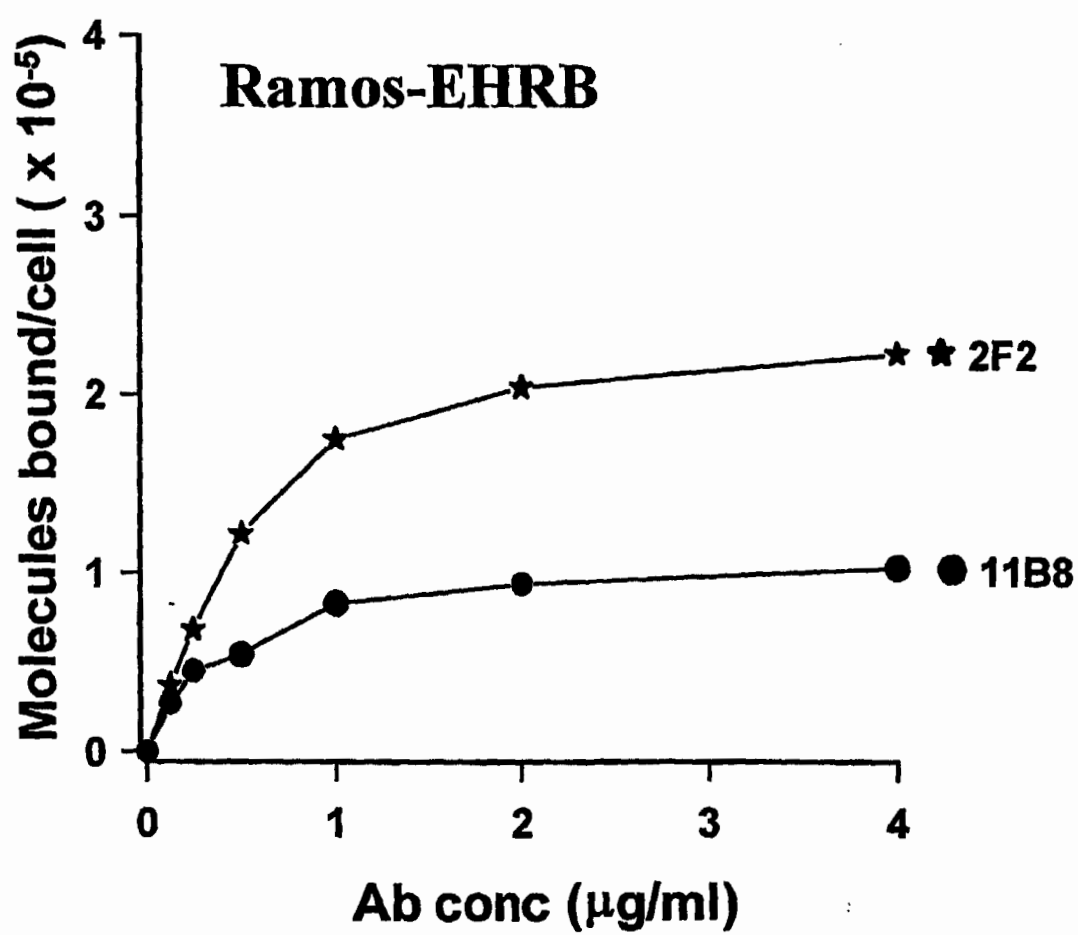
4/65

*Fig. 4*

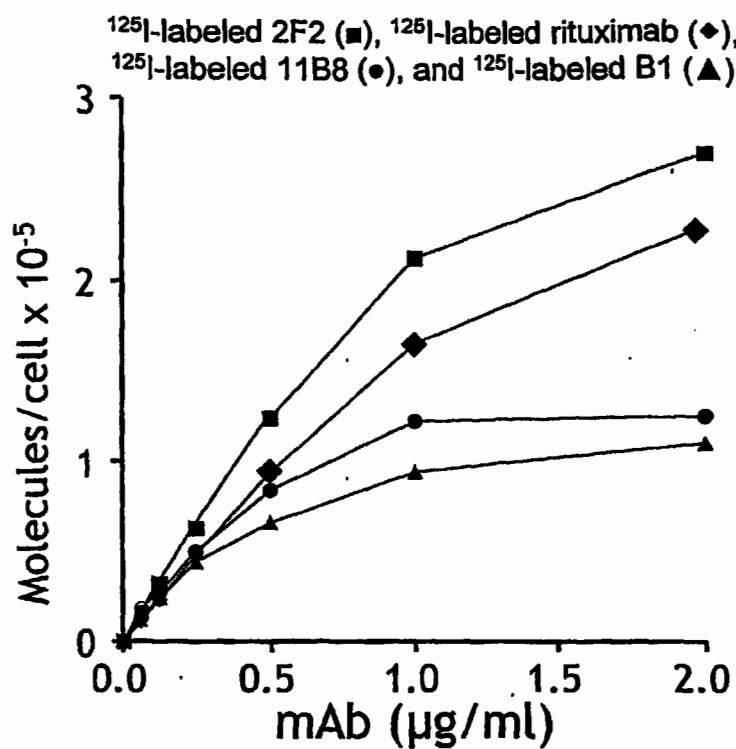
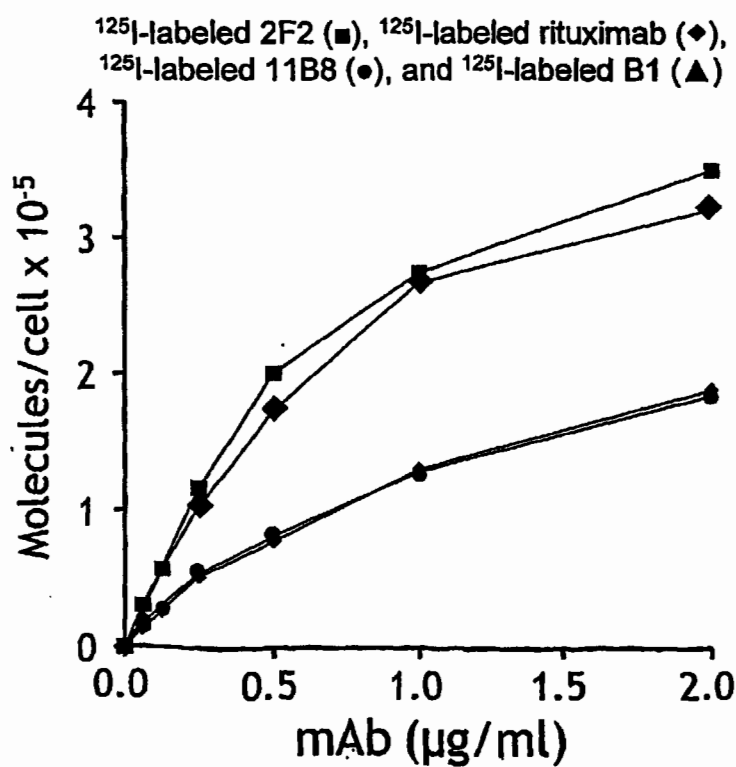
5/65

*Fig. 5A**Fig. 5B*

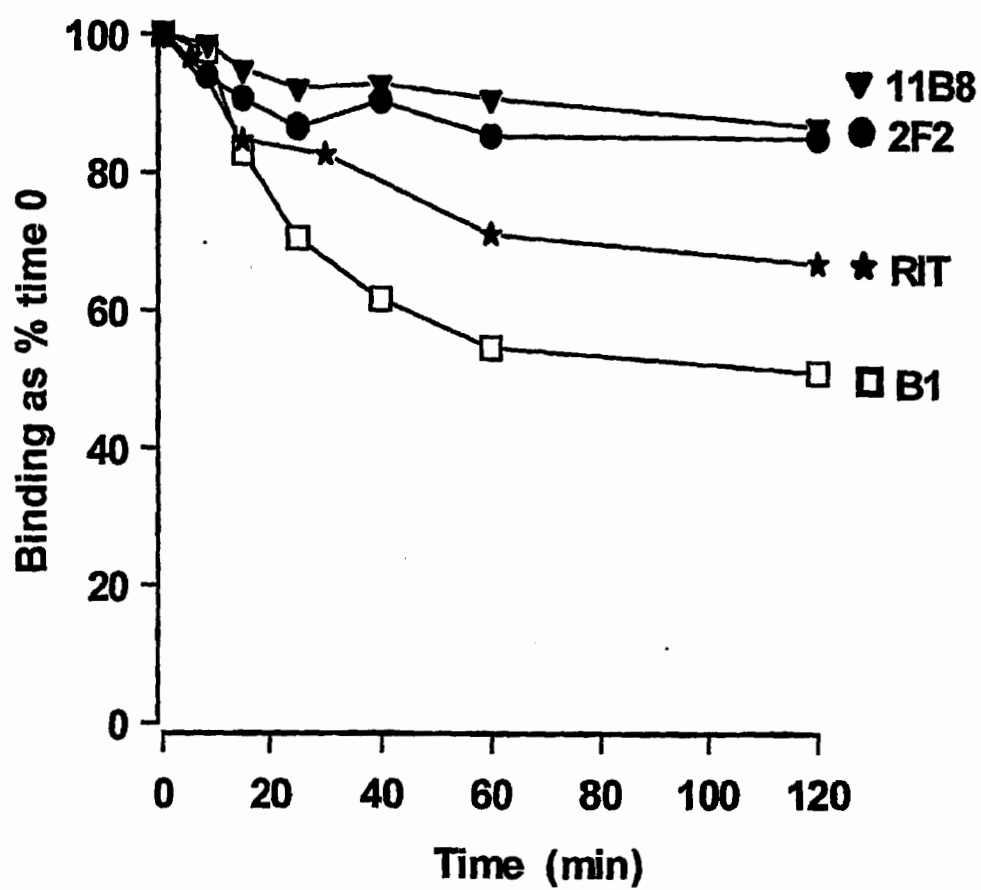
6/65

*Fig 6*

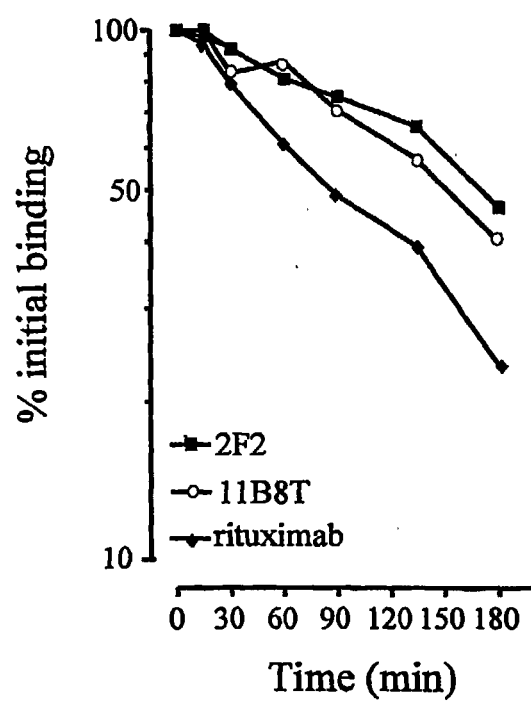
7/65

*Fig. 7A**Fig. 7B*

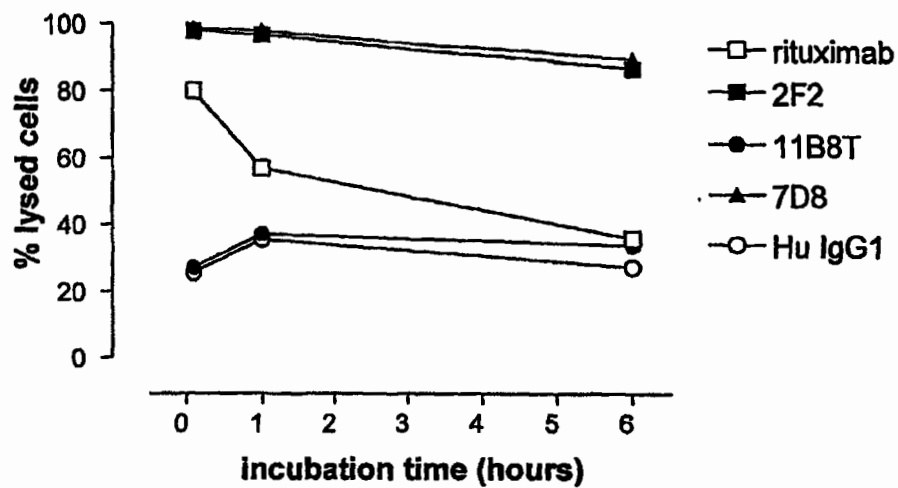
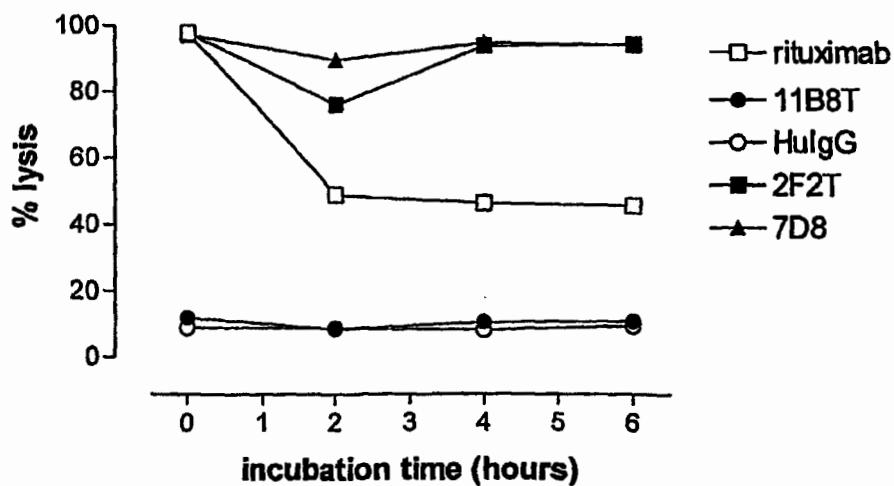
8/65

*Fig. 8*

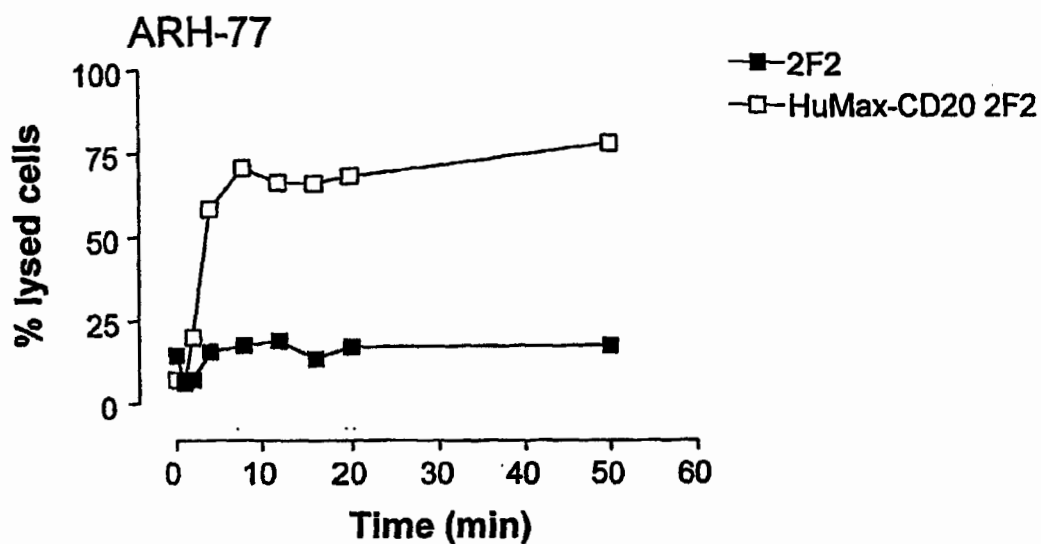
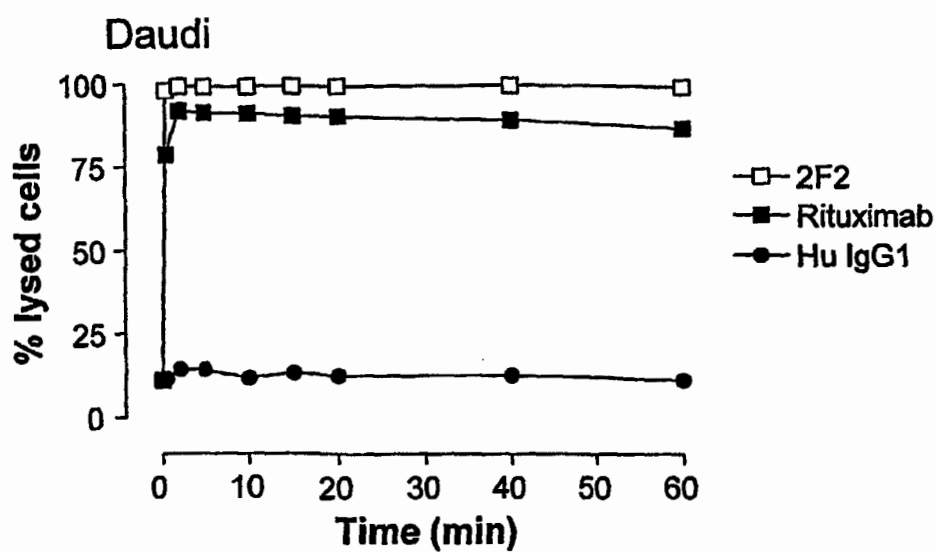
9/65

*Fig. 9*

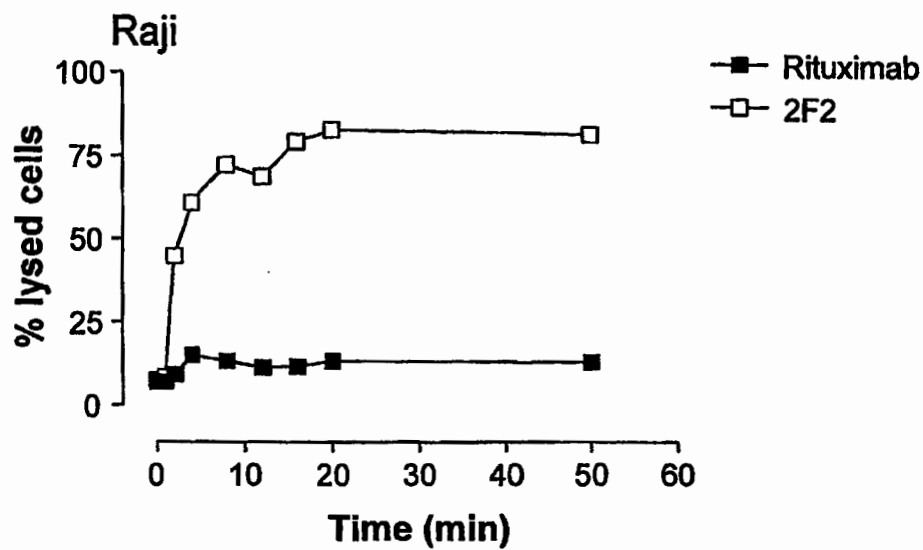
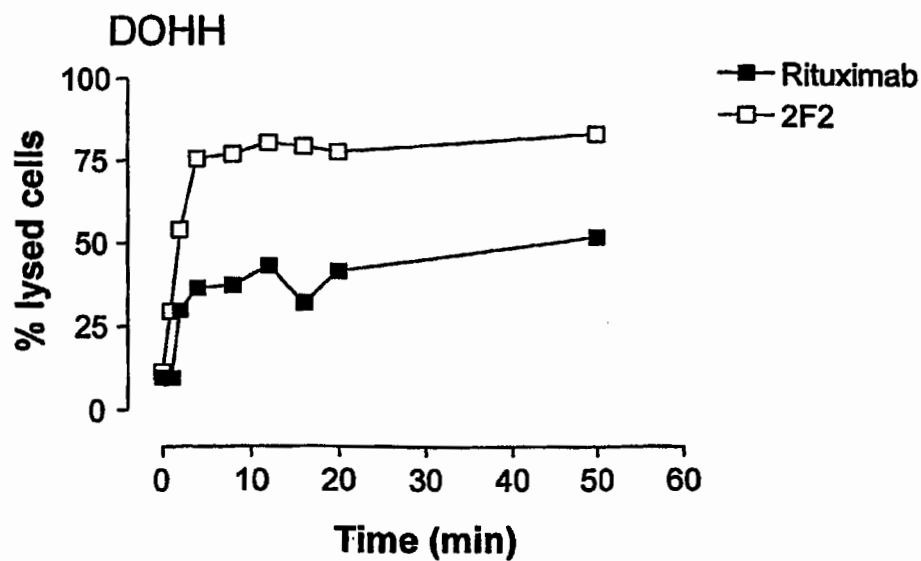
10/65

*Fig. 10A**Fig. 10B*

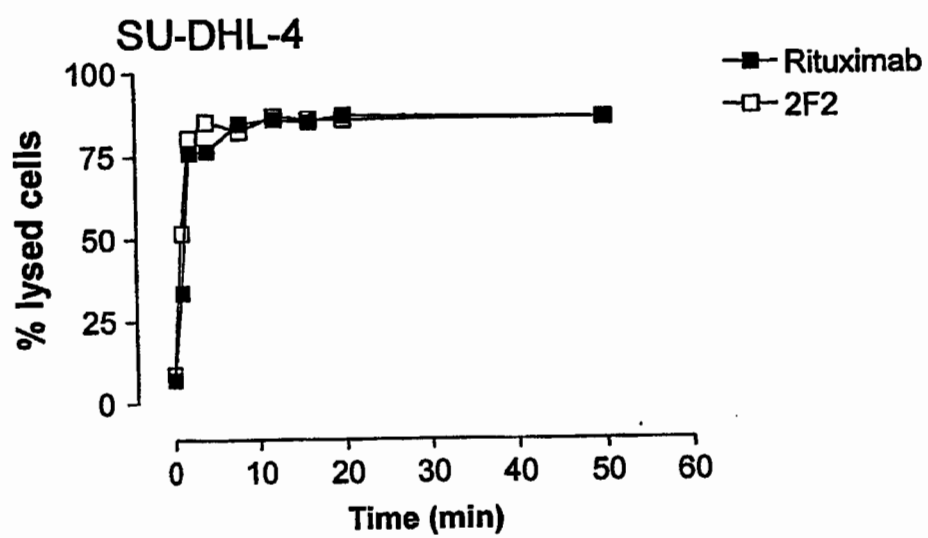
11/65

*Fig. 11A**Fig. 11A*

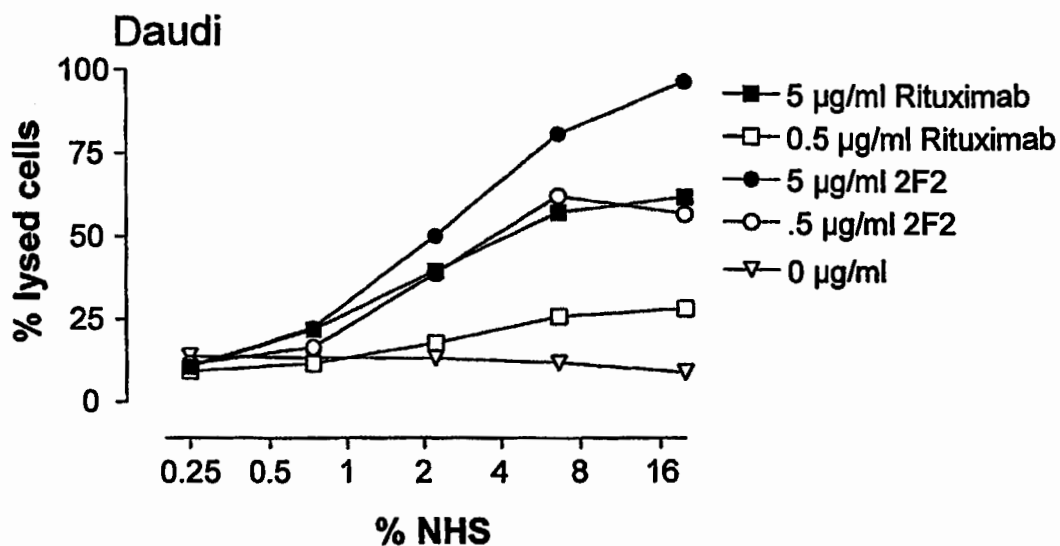
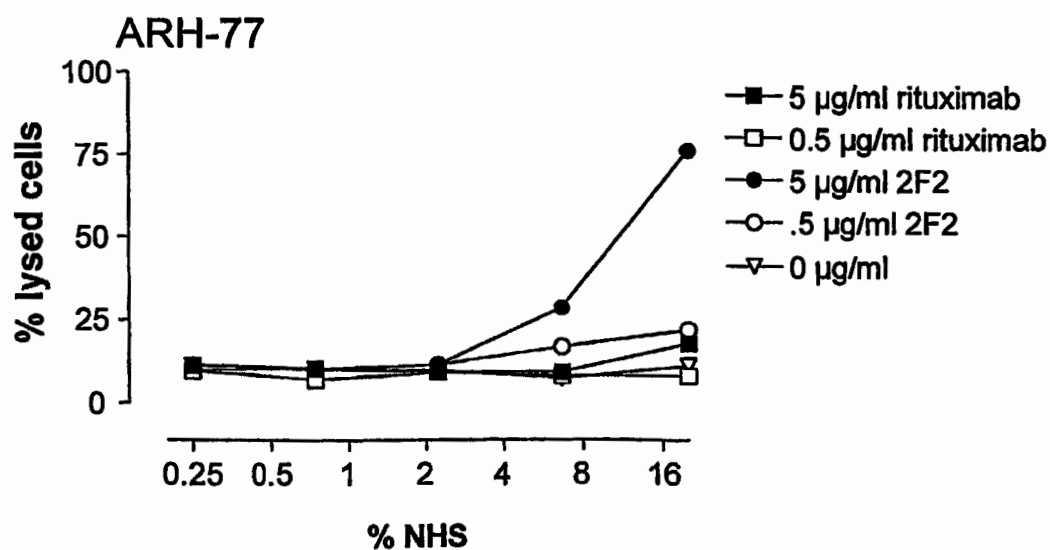
12/65

*Fig. 11C**Fig. 11D*

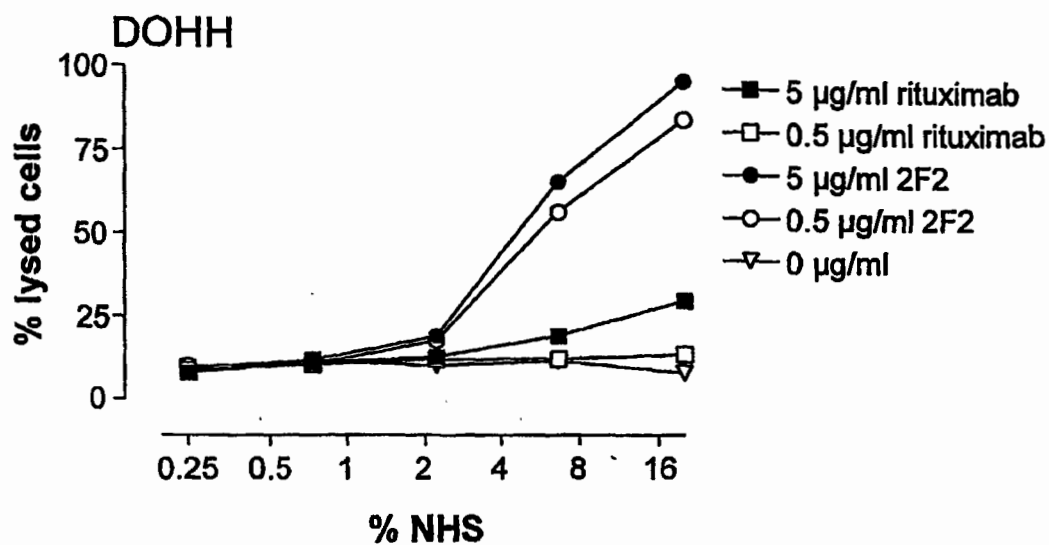
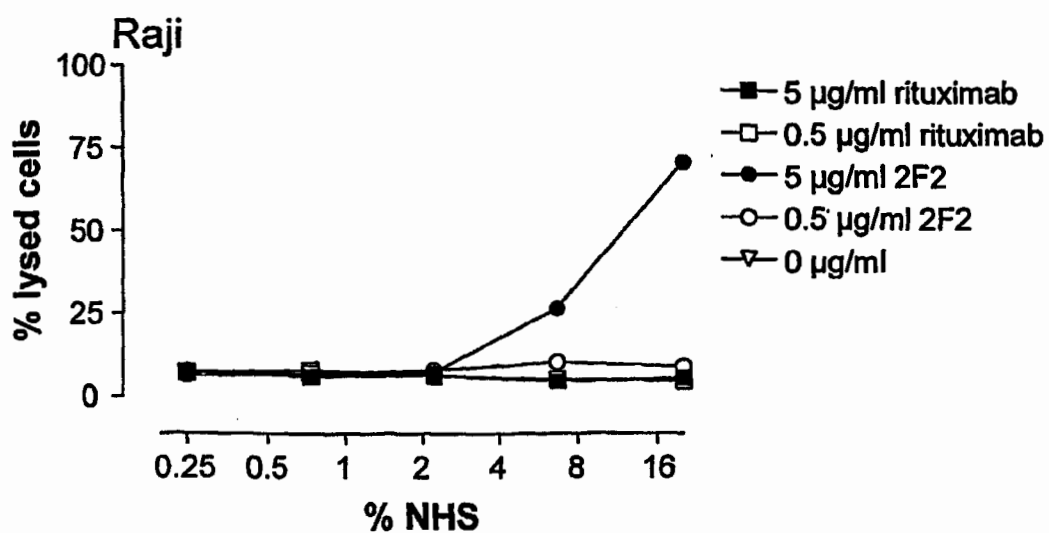
13/65

*Fig. 11E*

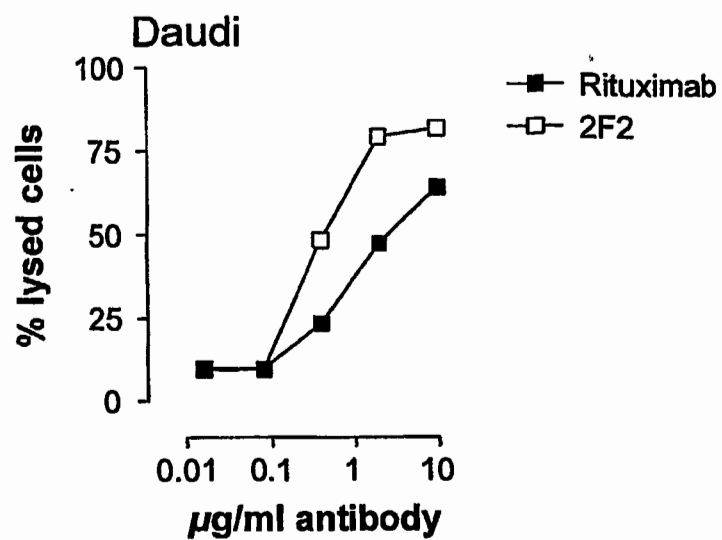
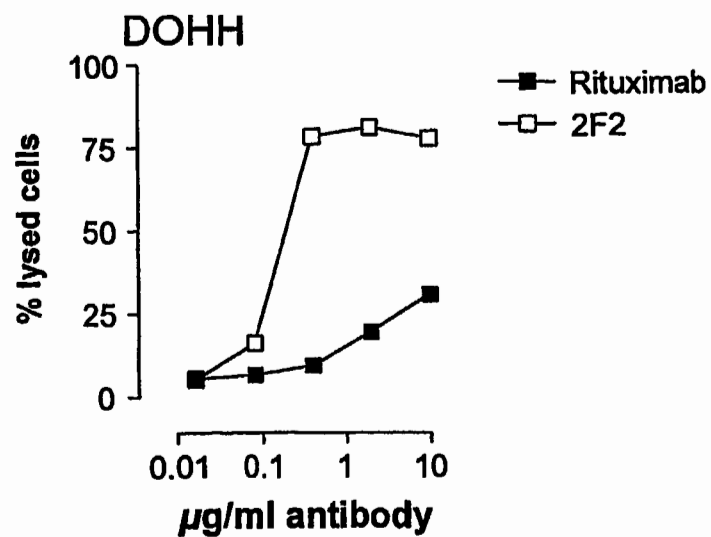
14/65

*Fig. 12A**Fig. 12B*

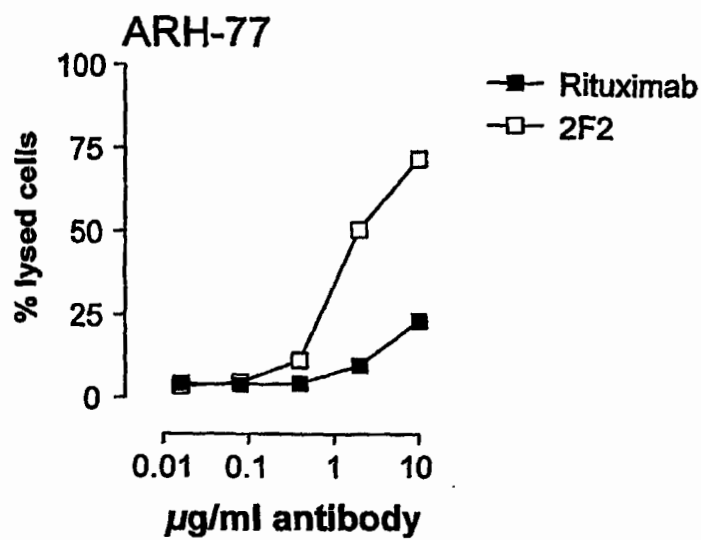
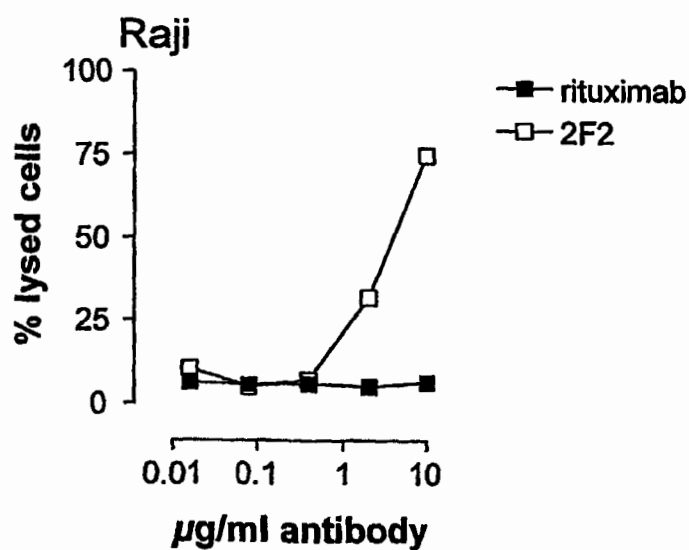
15/65

*Fig. 12C**Fig. 12D*

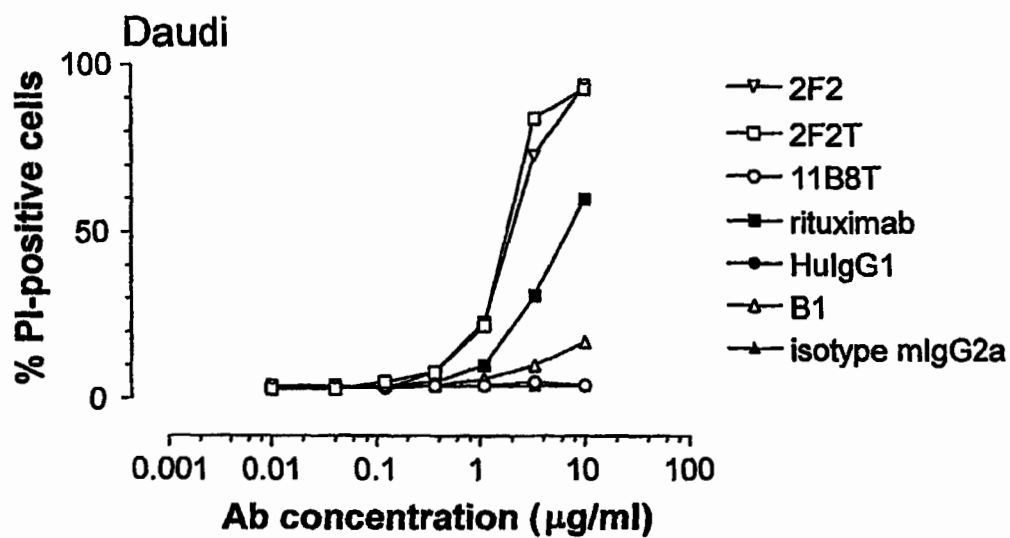
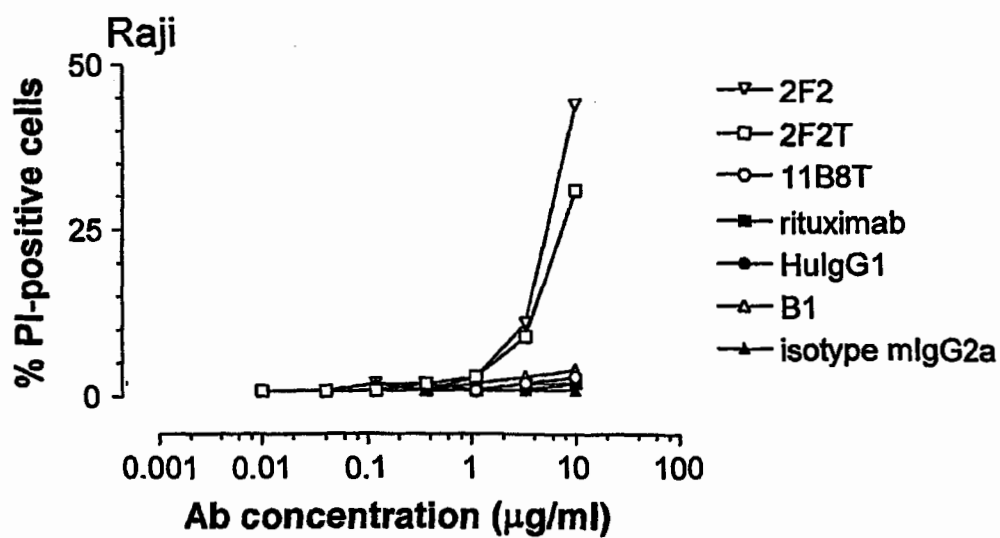
16/65

*Fig. 13A**Fig. 13B*

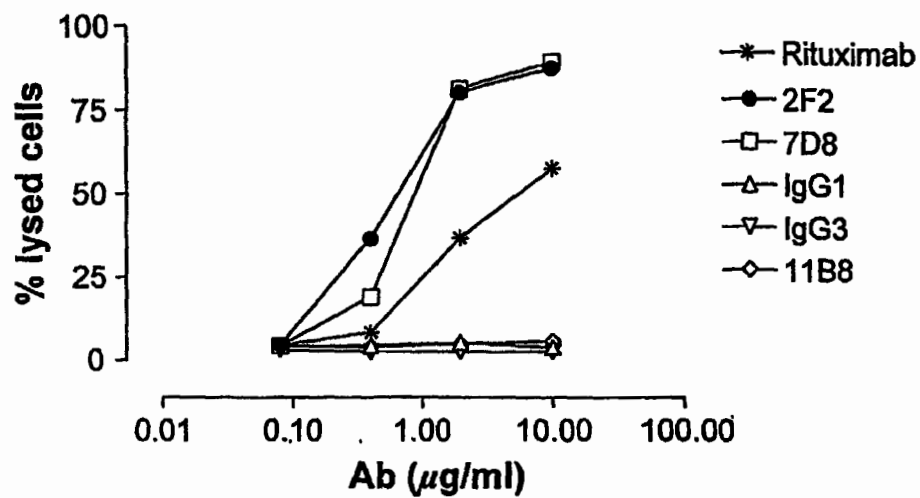
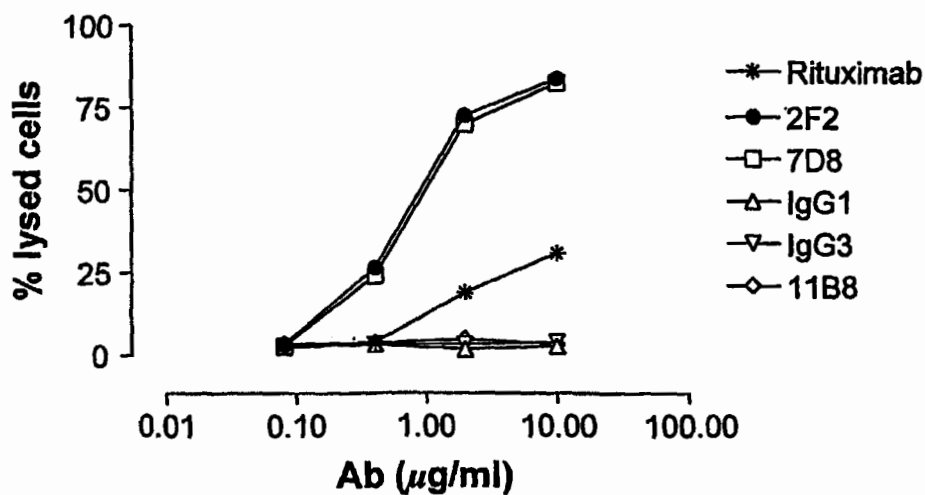
17/65

*Fig. 13C**Fig. 13D*

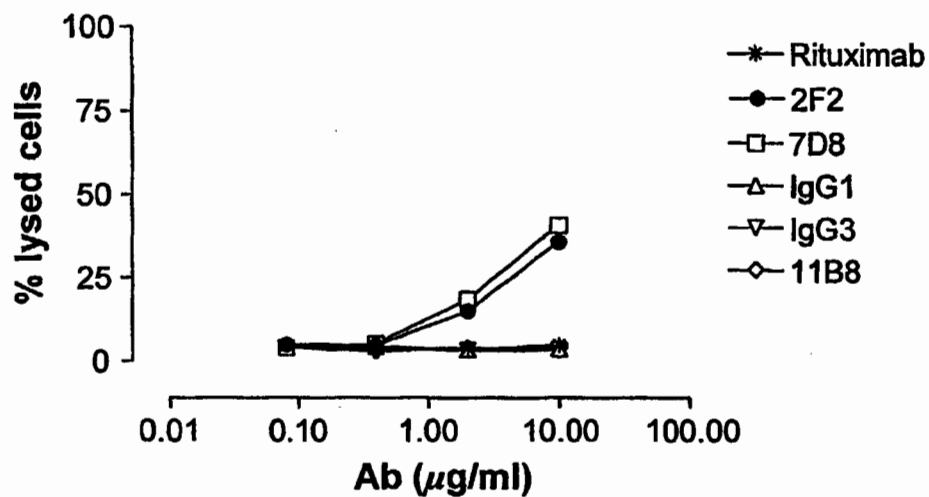
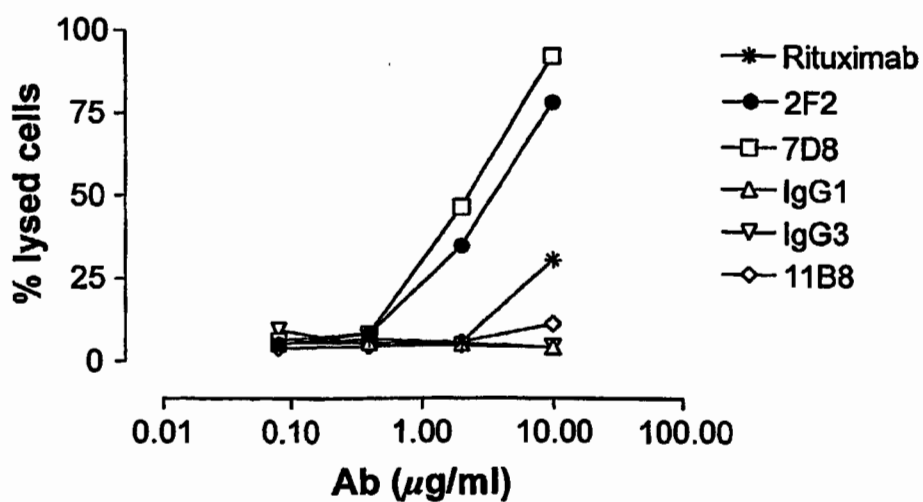
18/65

*Fig. 14A**Fig. 14B*

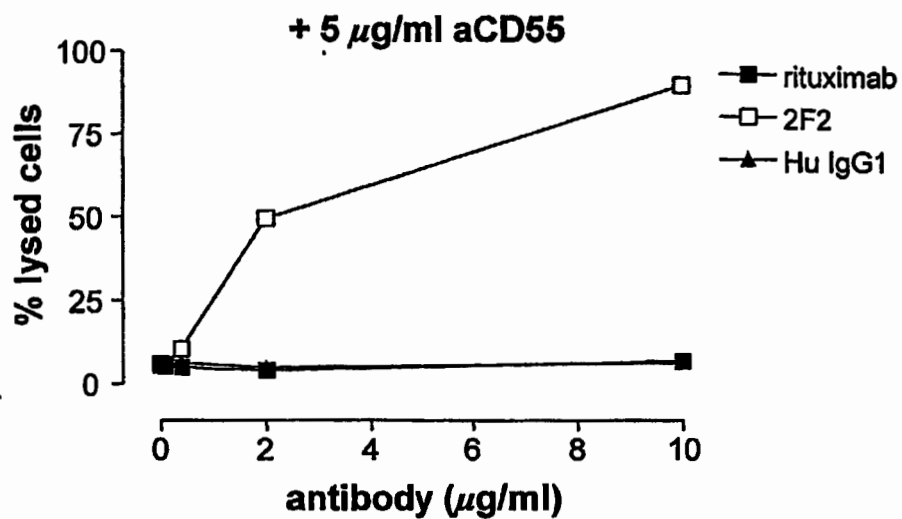
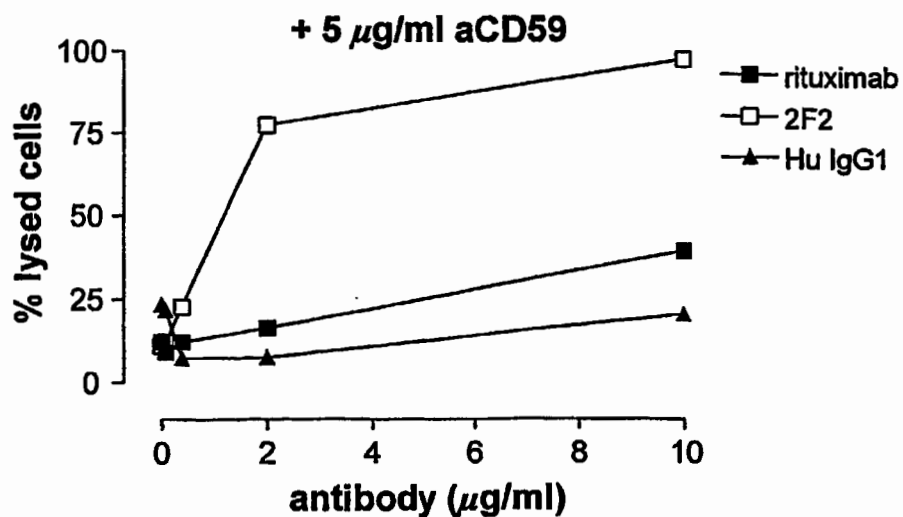
19/65

*Fig. 15A**Fig. 15B*

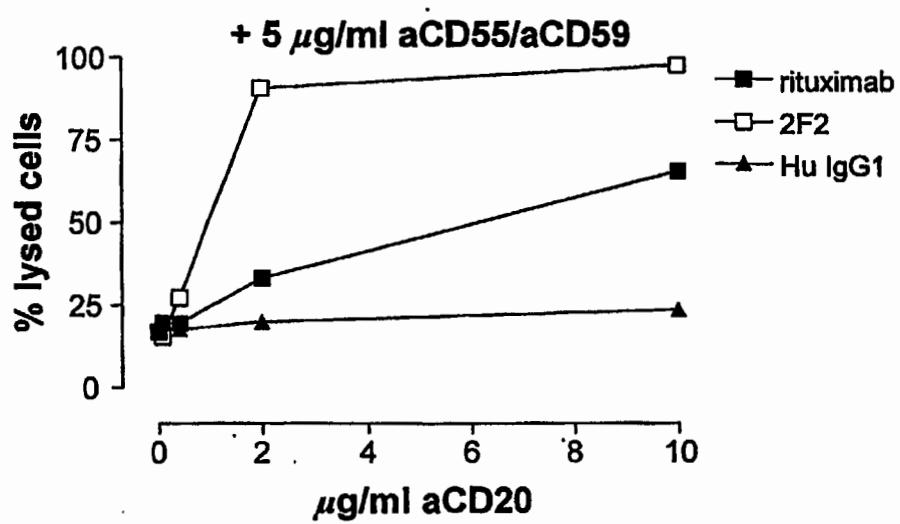
20/65

*Fig. 16A**Fig. 16B*

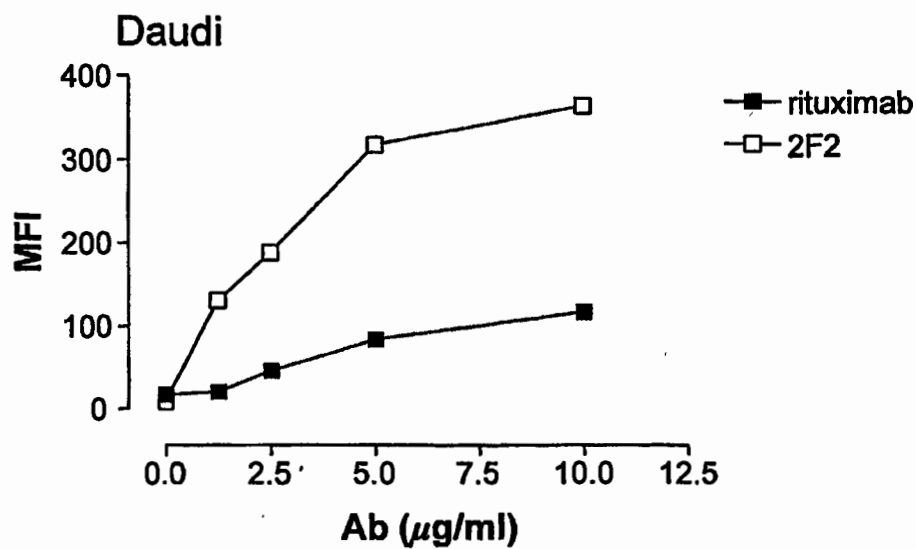
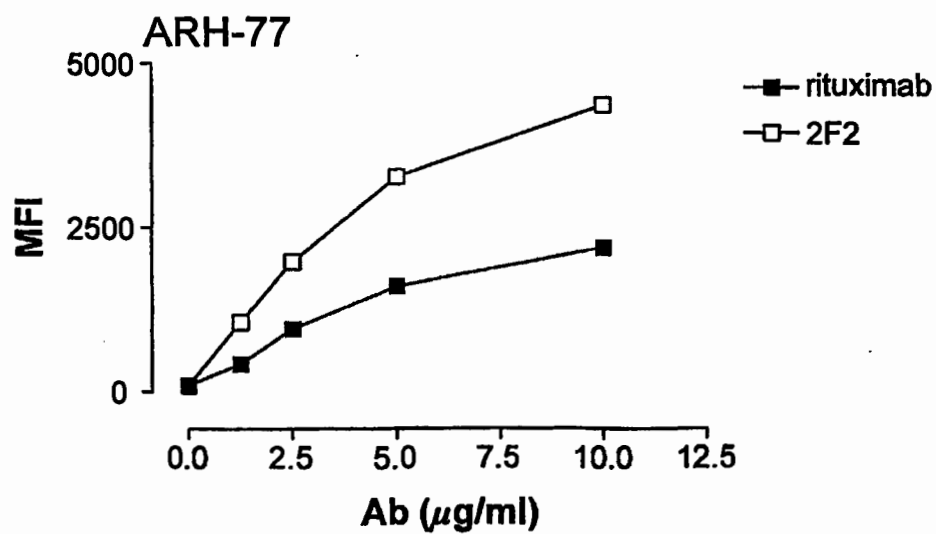
21/65

*Fig. 17A**Fig. 17B*

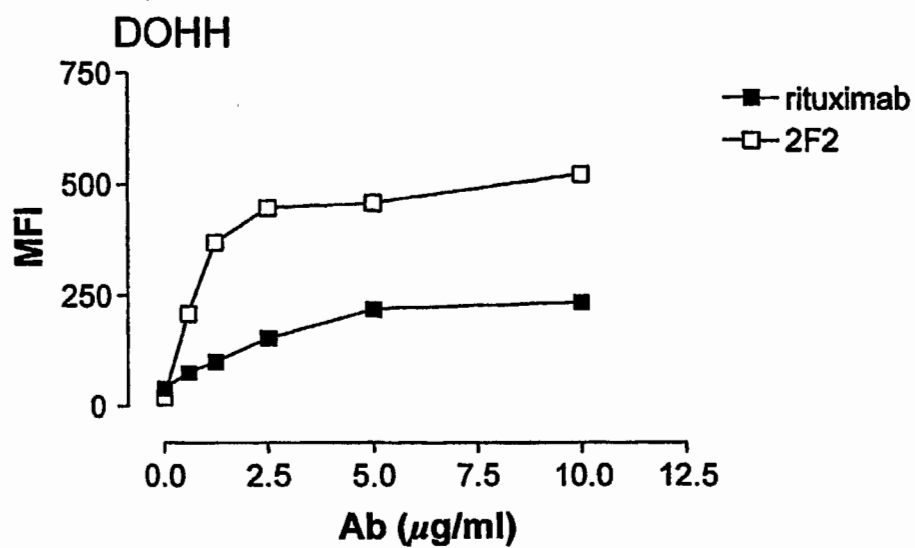
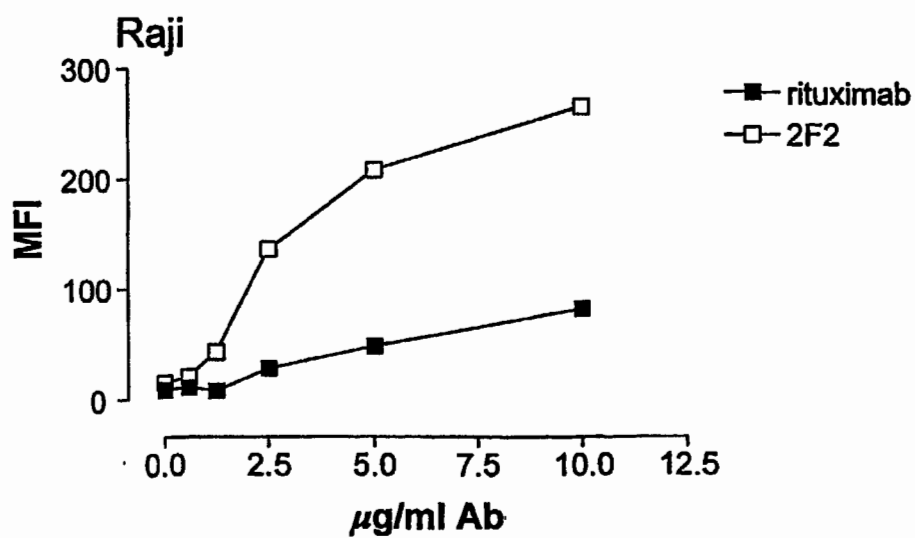
22/65

*Fig. 17C*

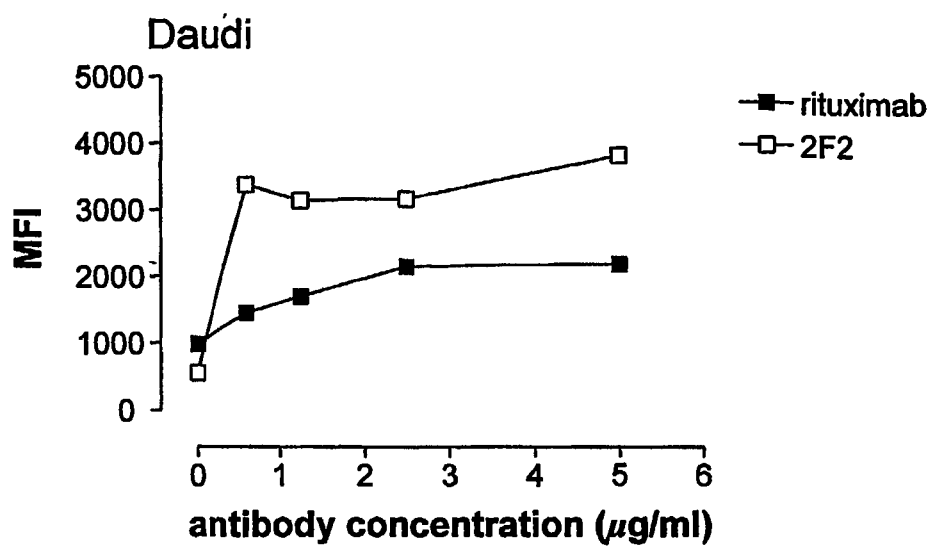
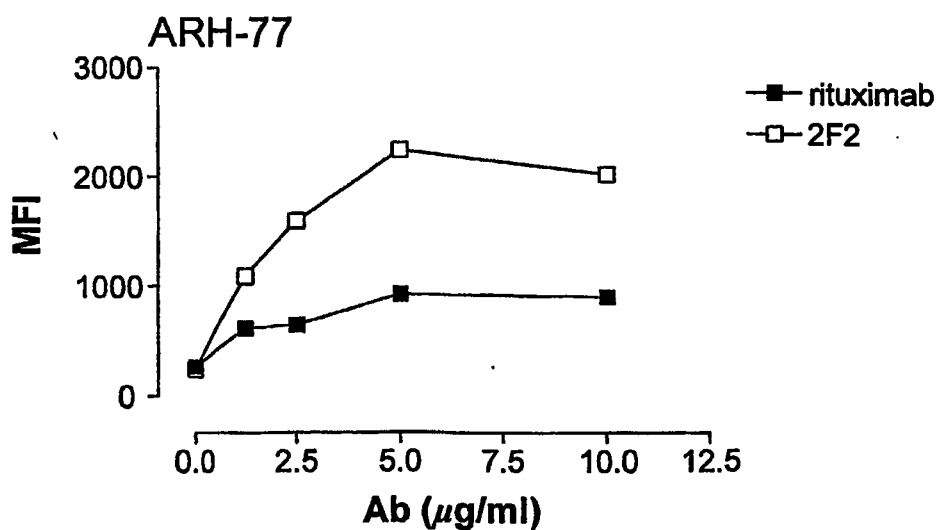
23/65

*Fig. 18A**Fig. 18B*

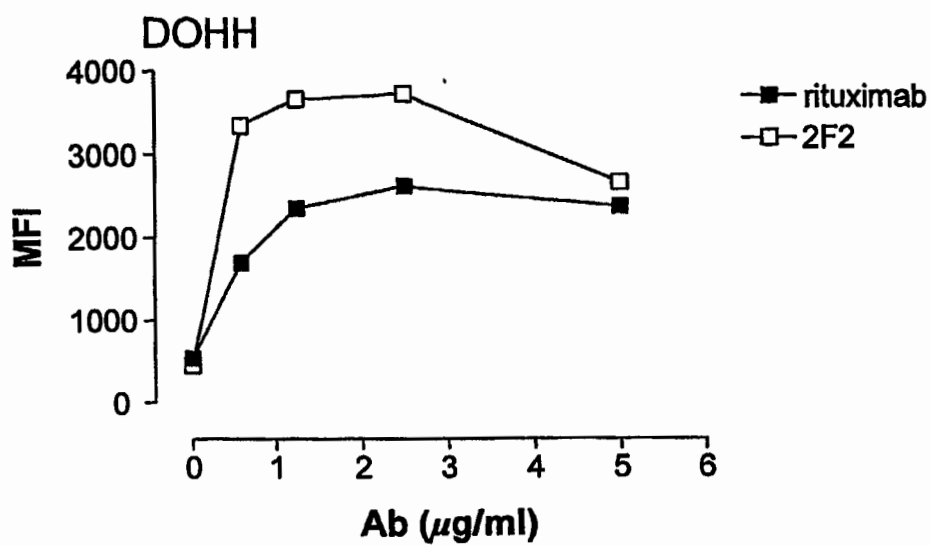
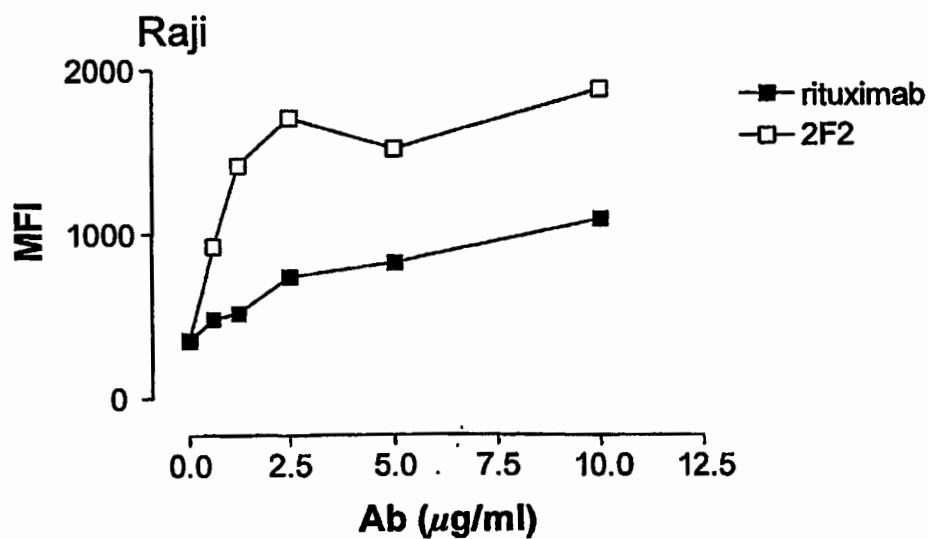
24/65

*Fig. 18C**Fig. 18D*

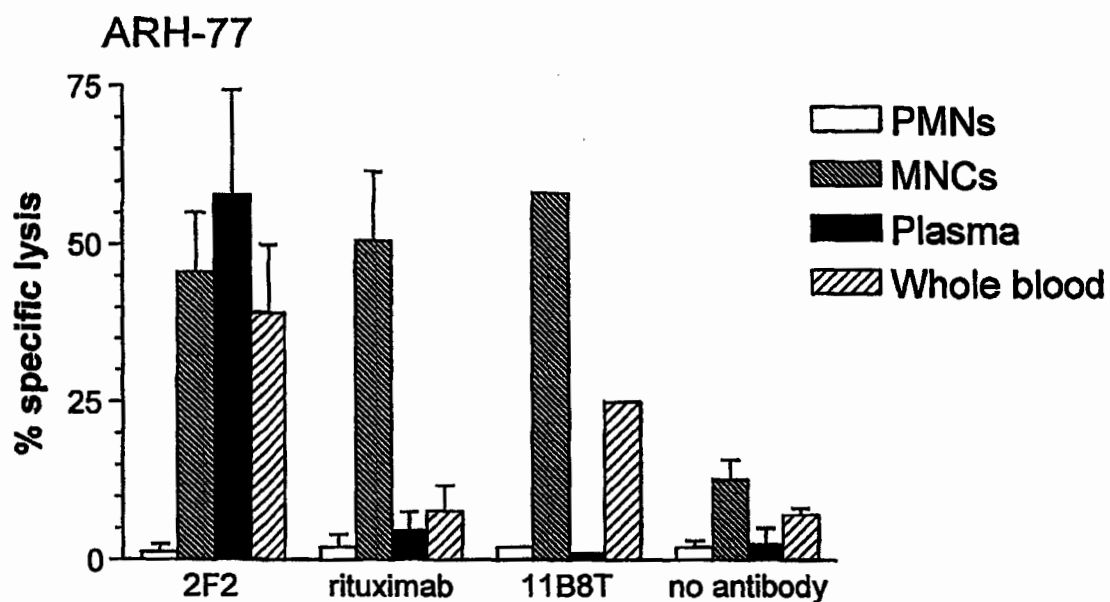
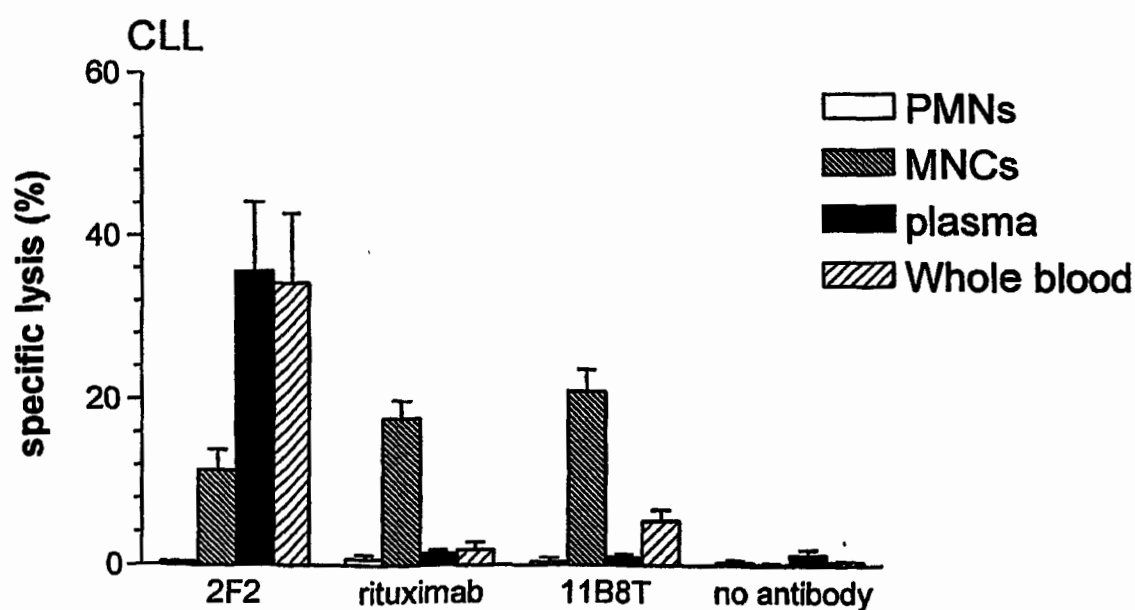
25/65

*Fig. 19A**Fig. 19B*

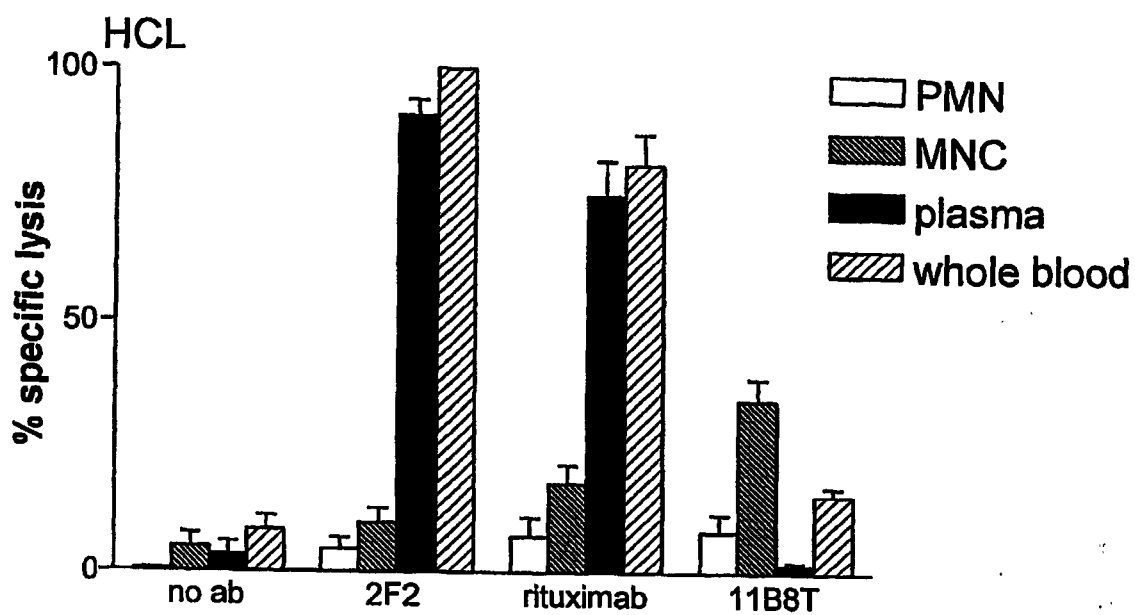
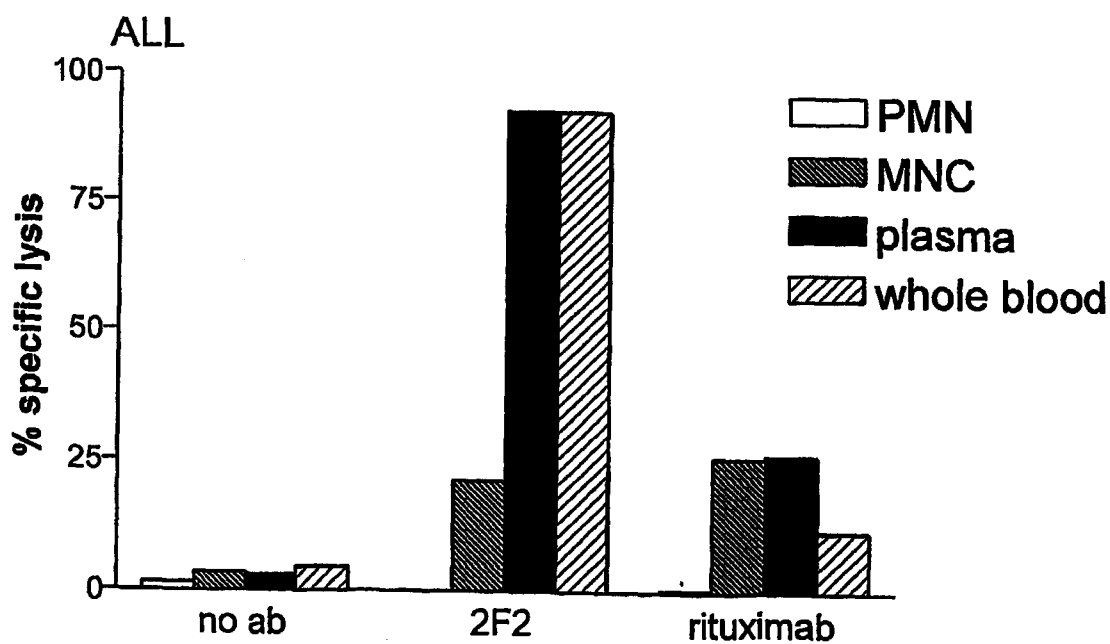
26/65

*Fig. 19C**Fig. 19D*

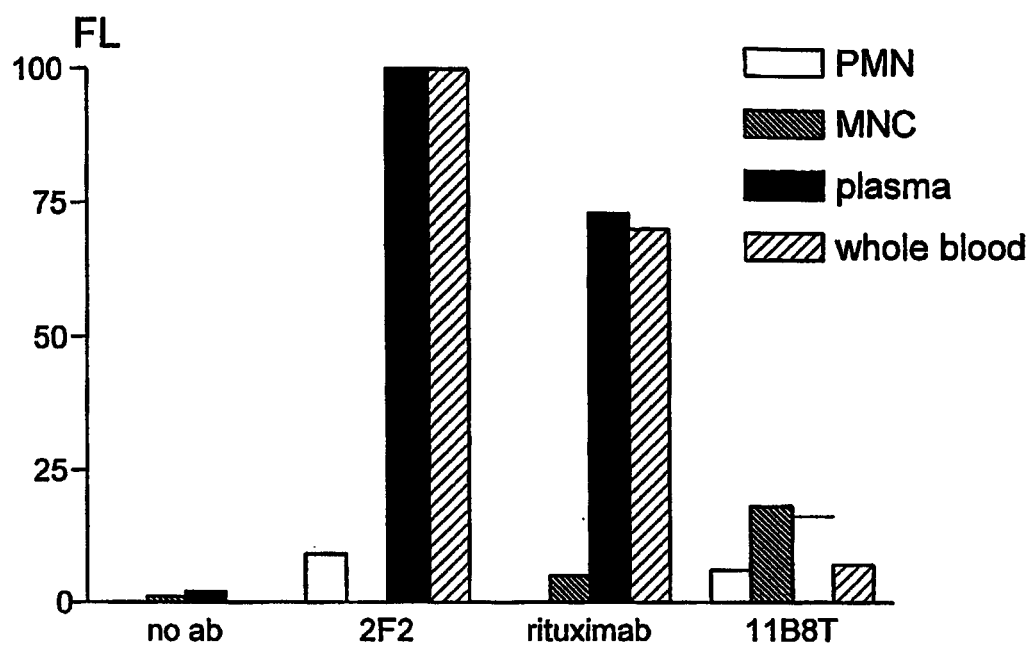
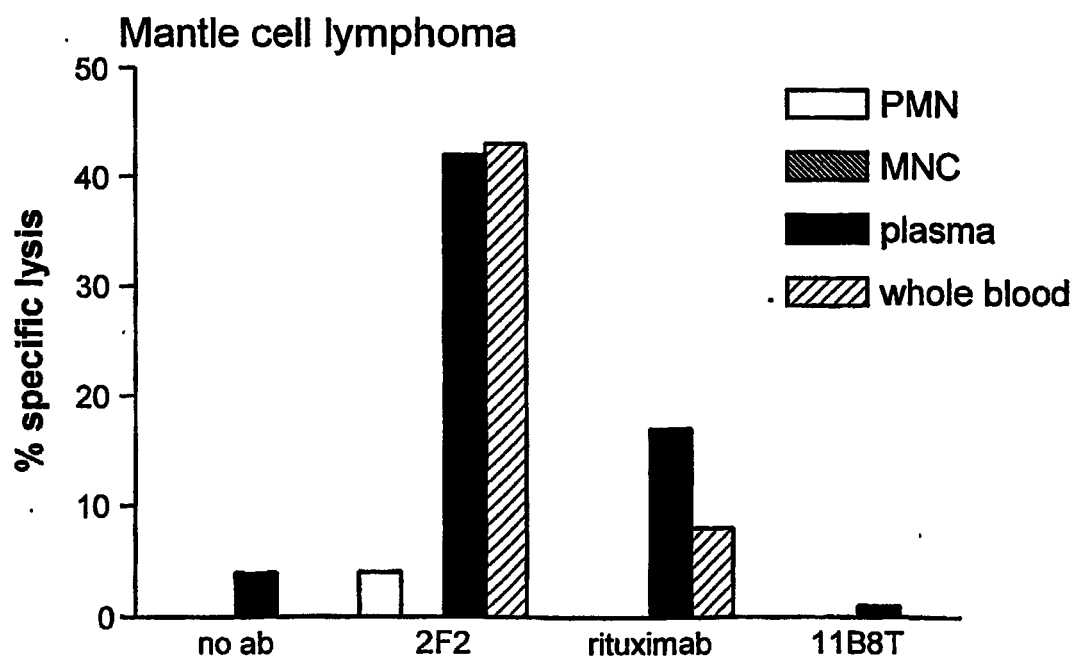
27/65

*Fig. 20**Fig. 21*

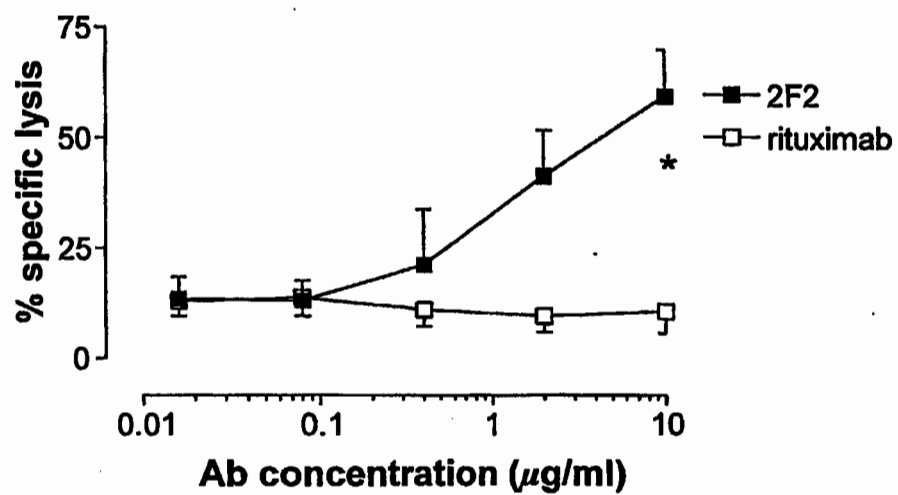
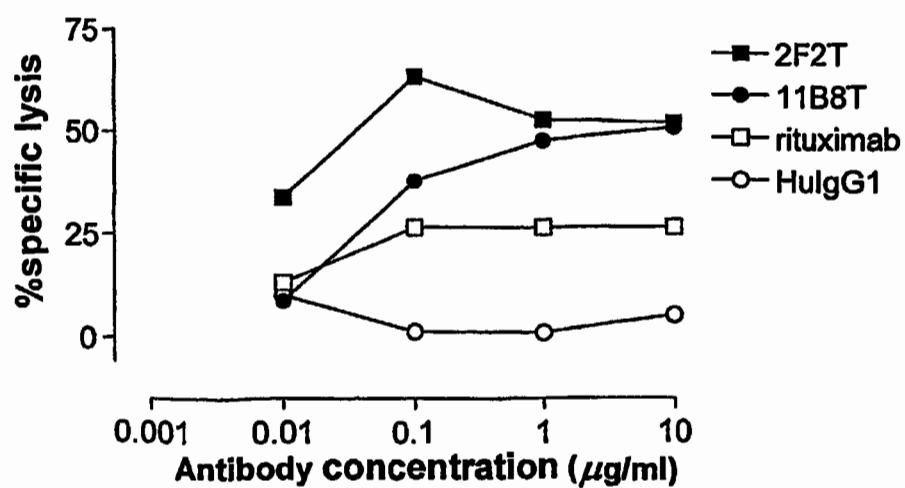
28/65

*Fig. 22**Fig. 23*

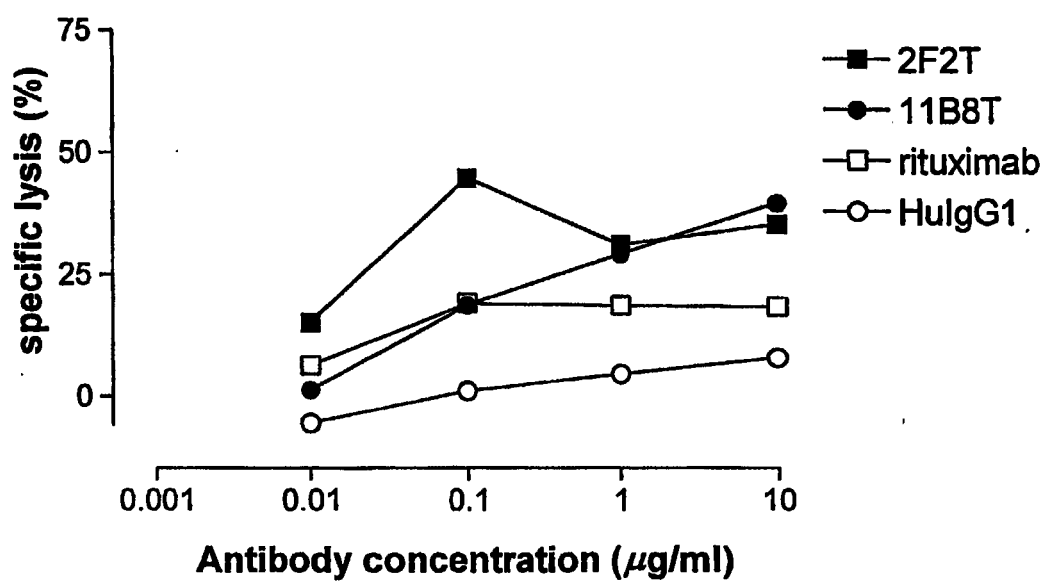
29/65

*Fig. 24**Fig. 25*

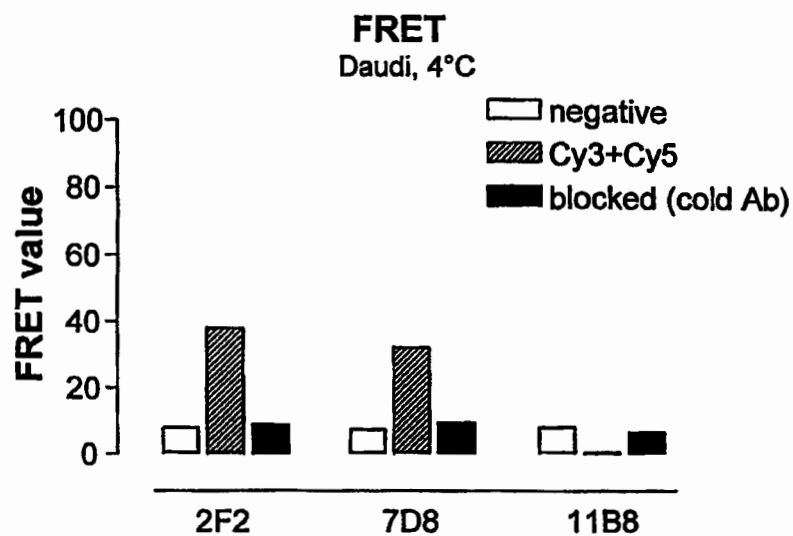
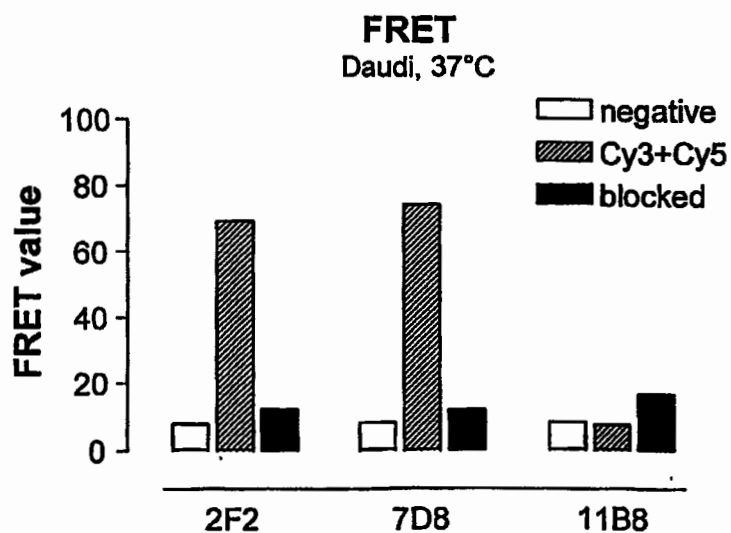
30/65

*Fig. 26**Fig. 27*

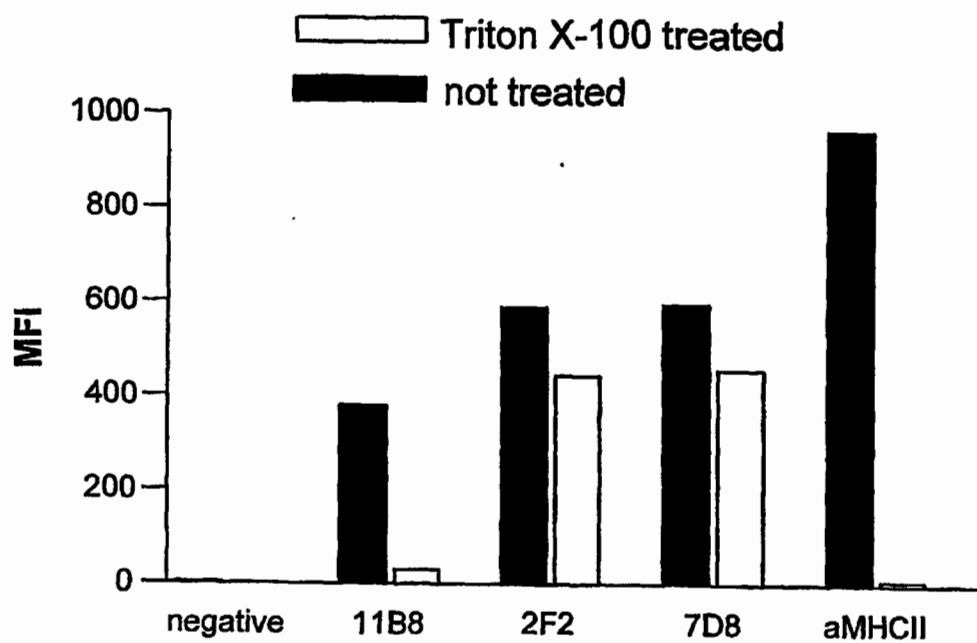
31/65

*Fig. 28*

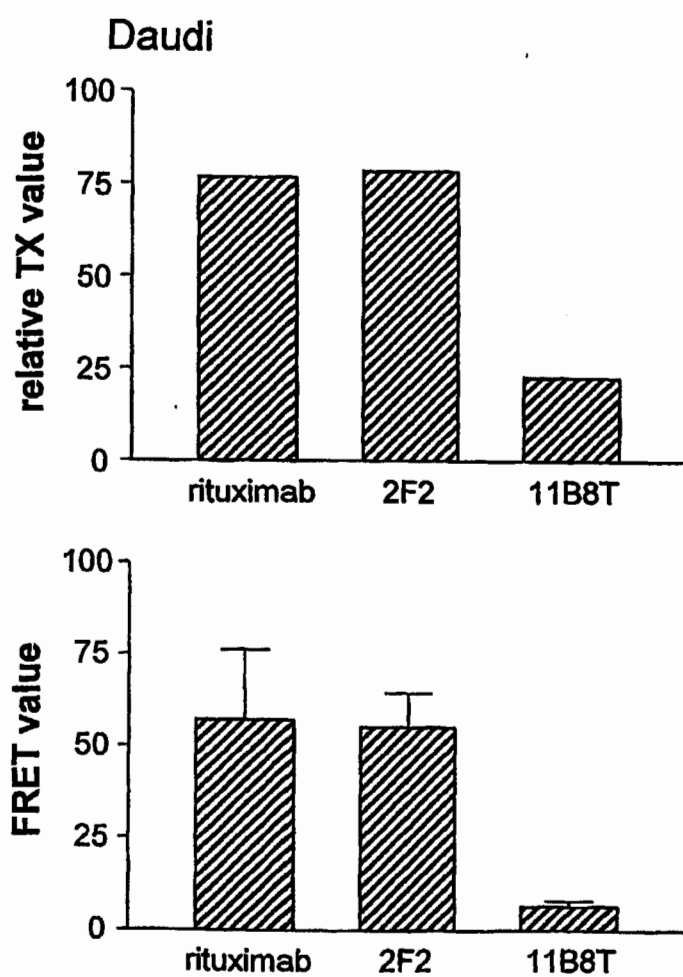
32/65

*Fig. 29A**Fig. 29B*

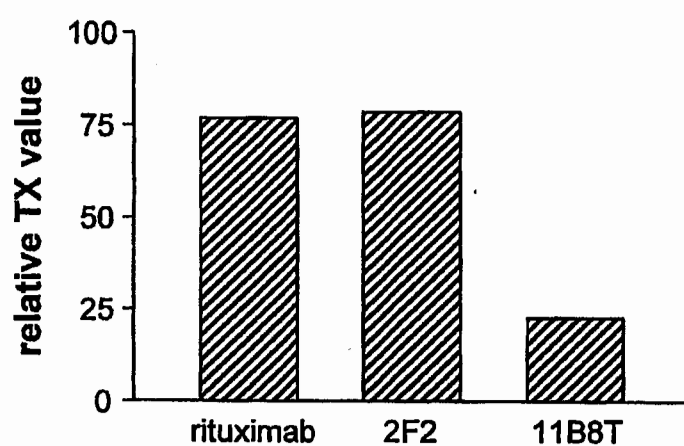
33/65

*Fig. 29C*

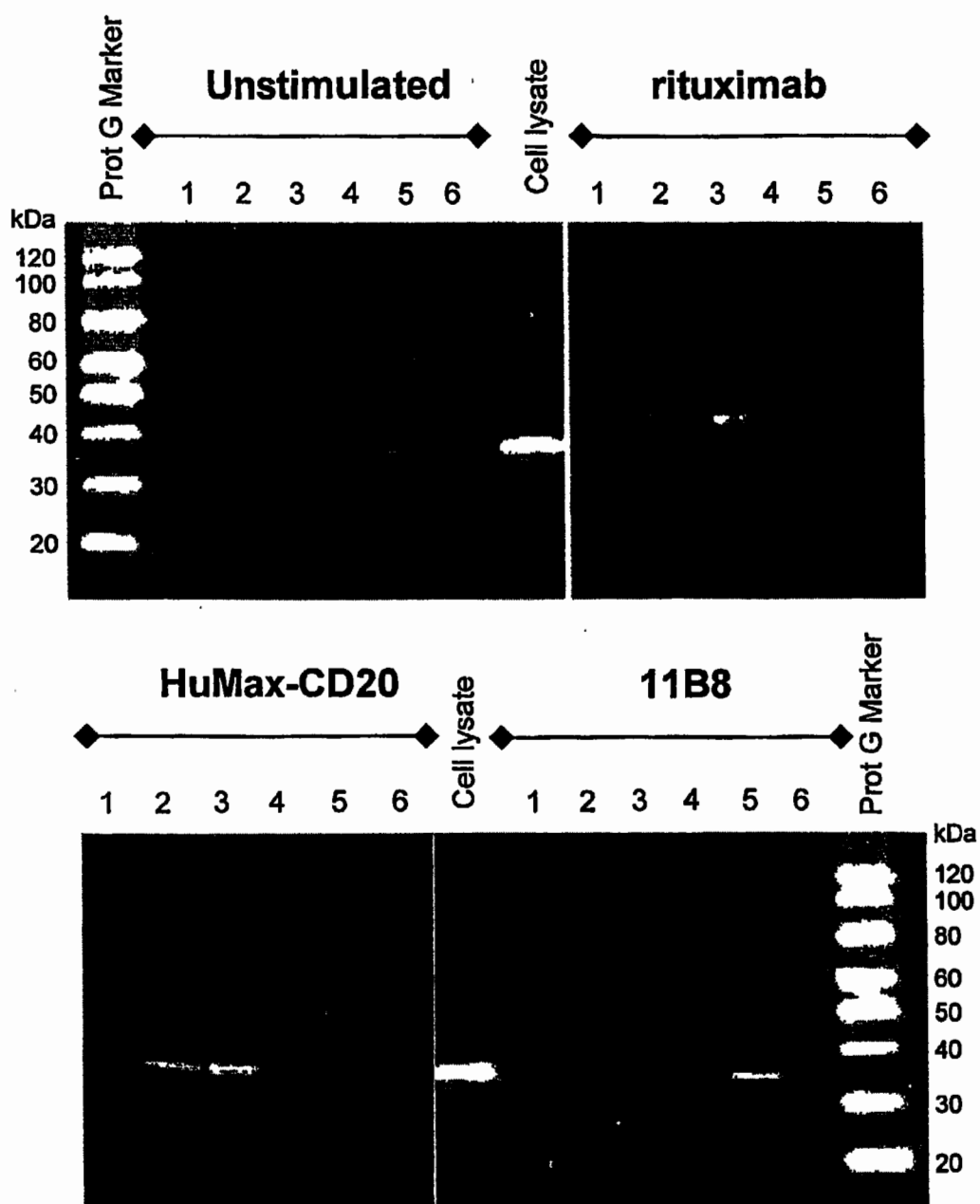
34/65

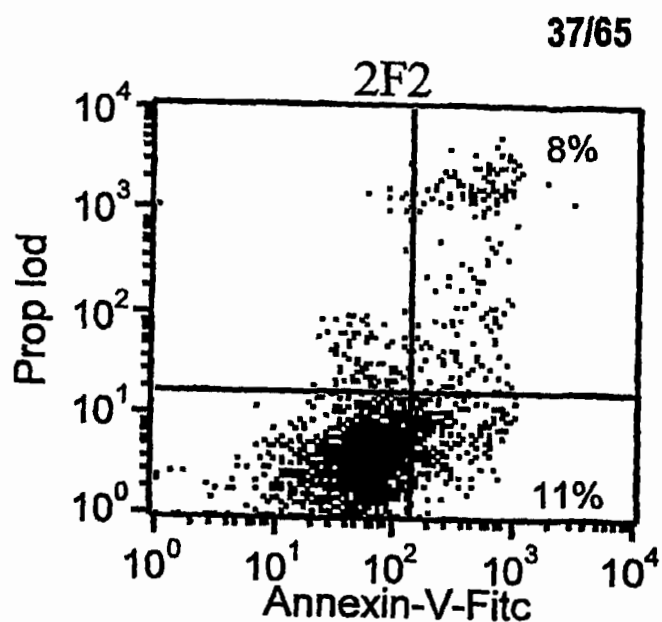
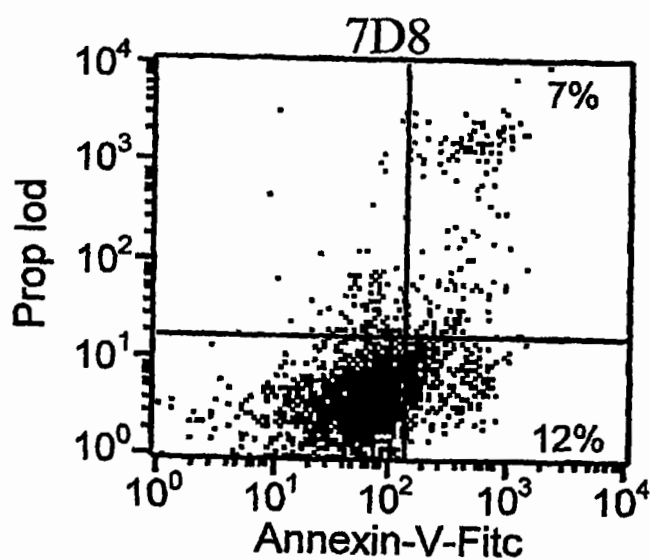
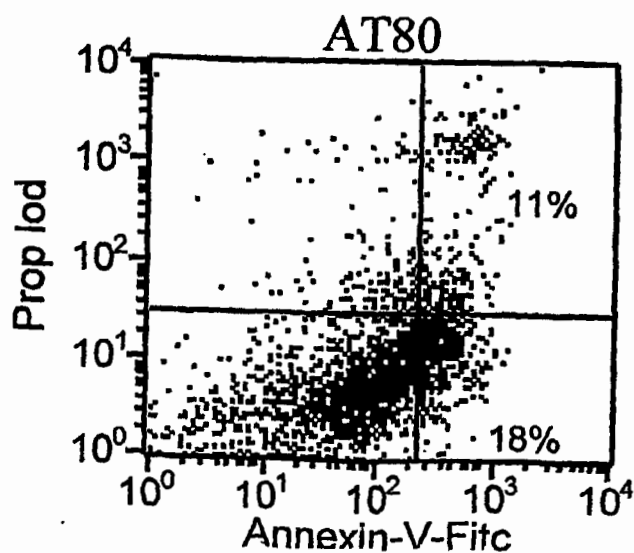
*Fig. 30*

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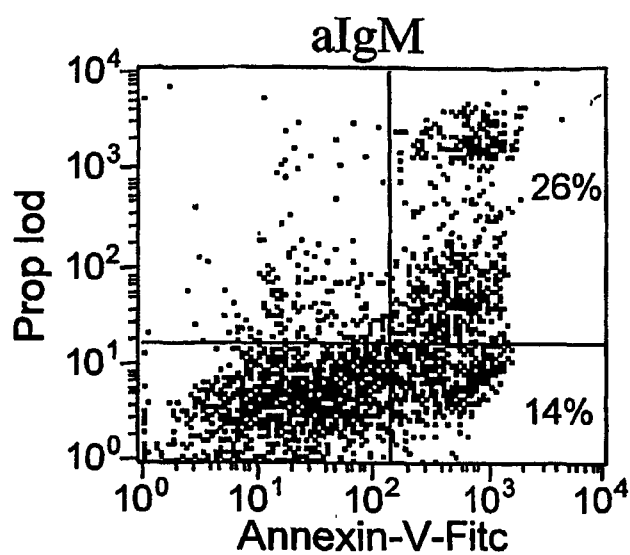
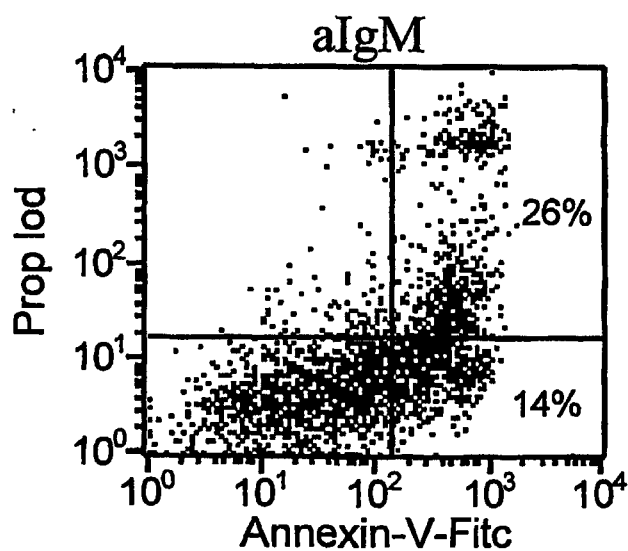
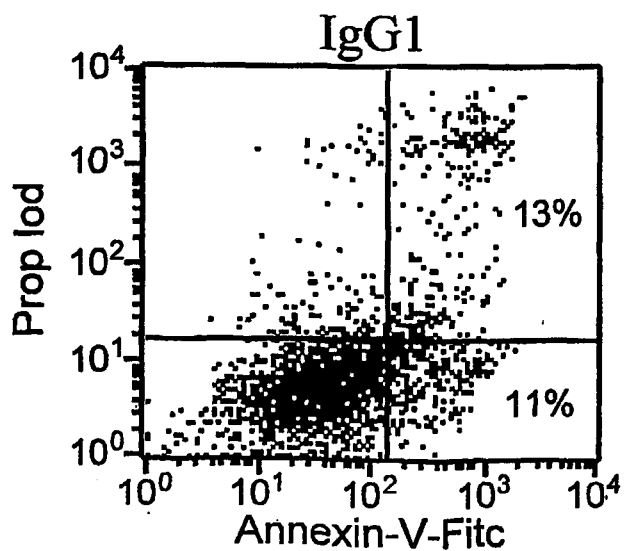
*Fig. 31*

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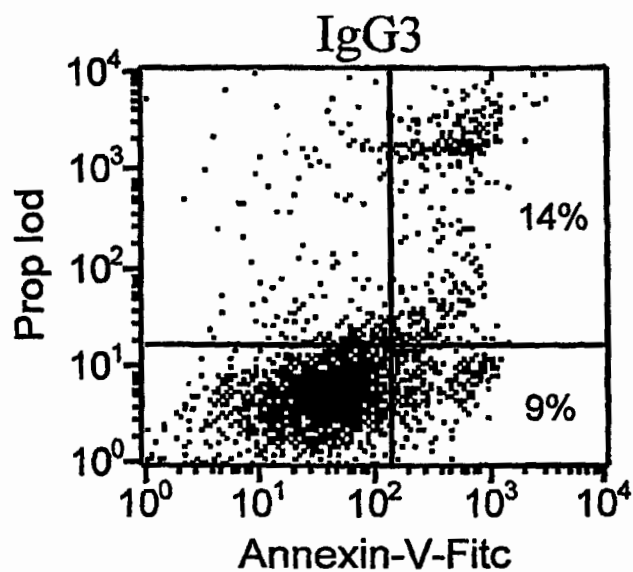
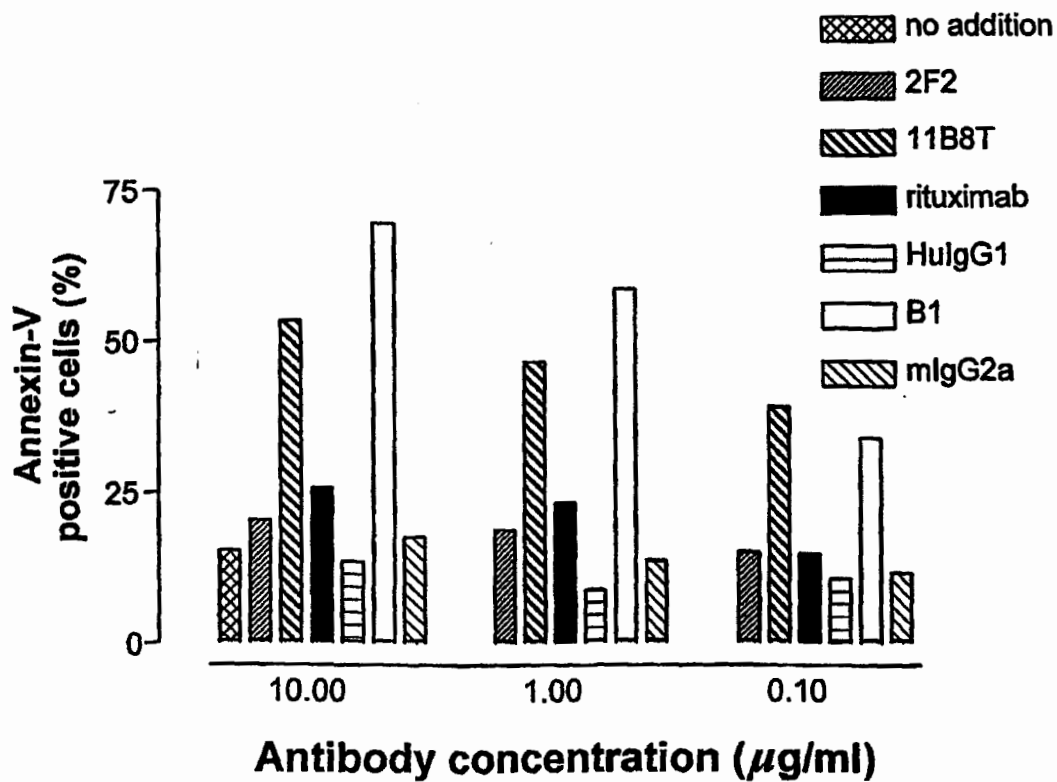
*Fig. 32*

*Fig. 33A**Fig. 33B**Fig. 33C*

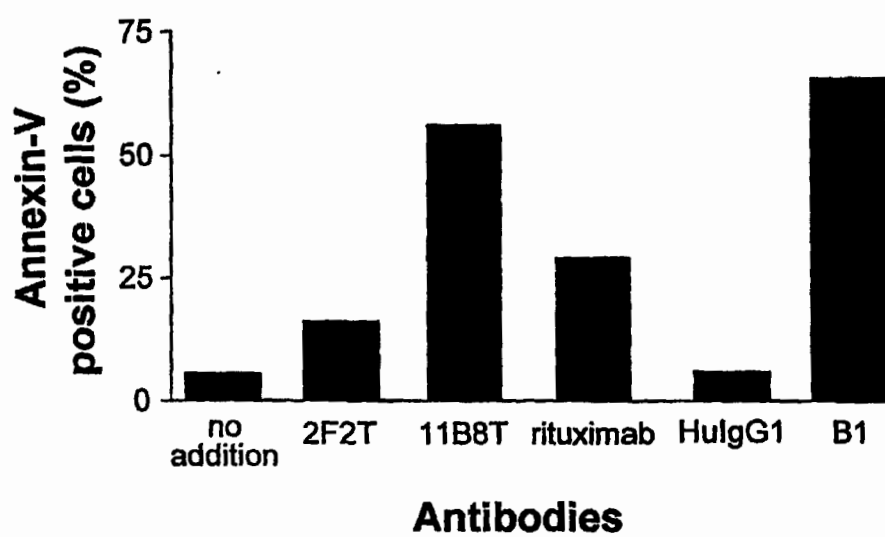
38/65

*Fig. 33D**Fig. 33E**Fig. 33F*

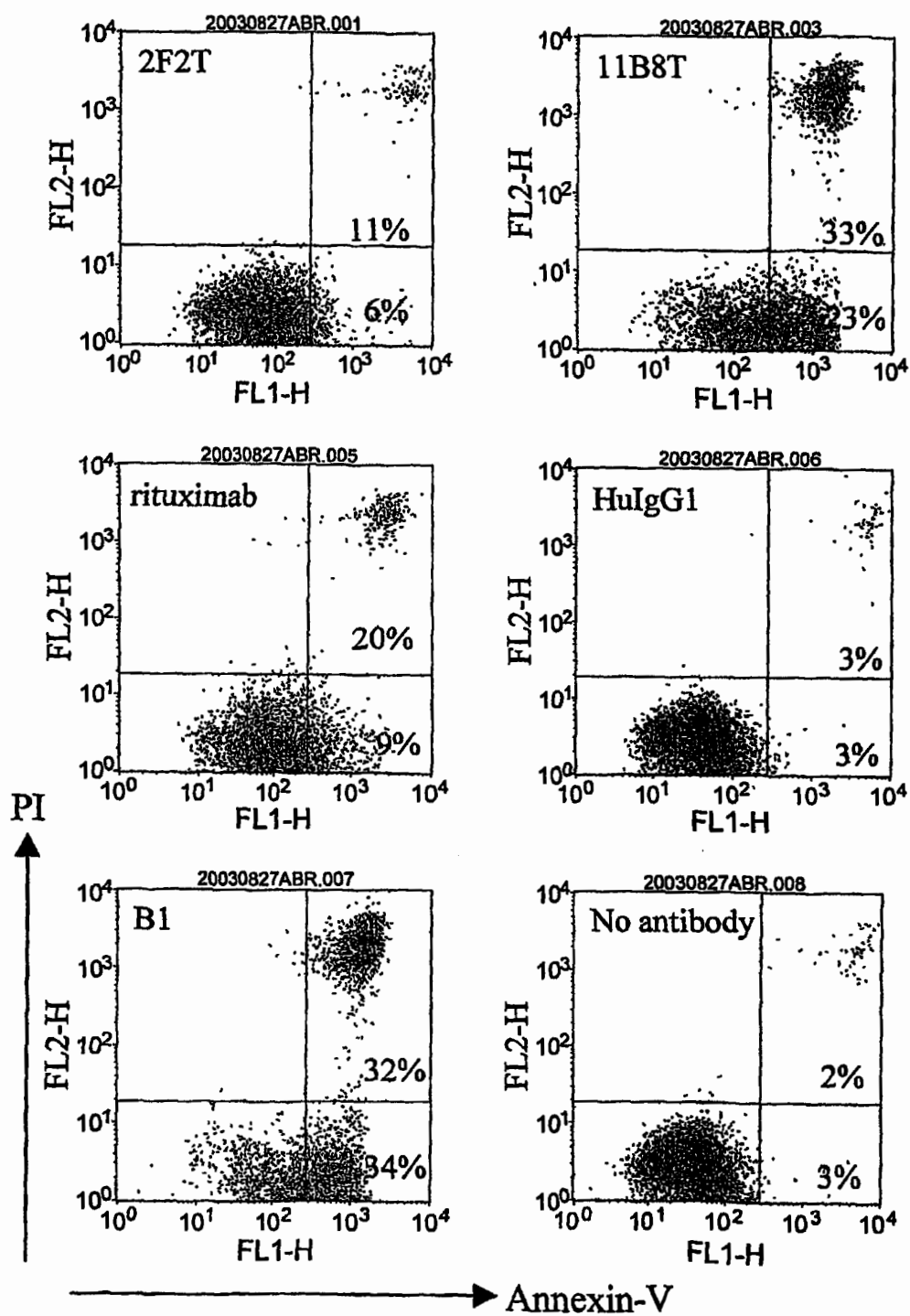
39/65

*Fig. 33G**Fig. 34*

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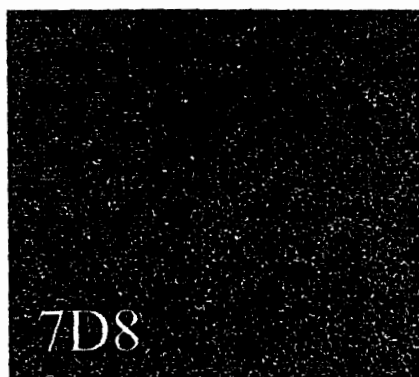
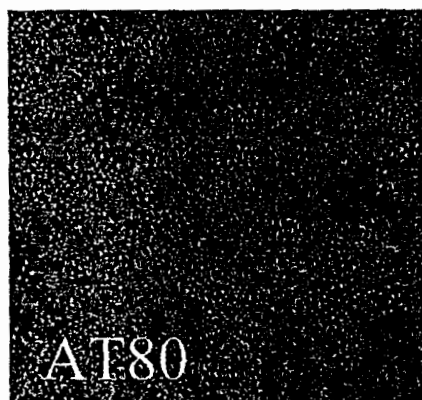
*Fig. 35A*

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*Fig. 35B*

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Homotypic adhesion of Ramos cells.

*Fig. 36A**Fig. 36B**Fig. 36C**Fig. 36D**Fig. 36E*

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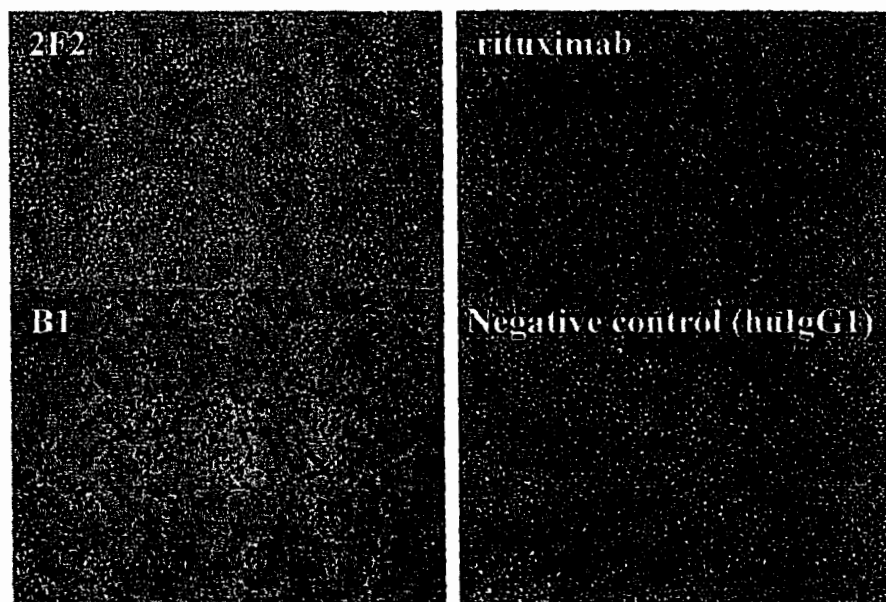
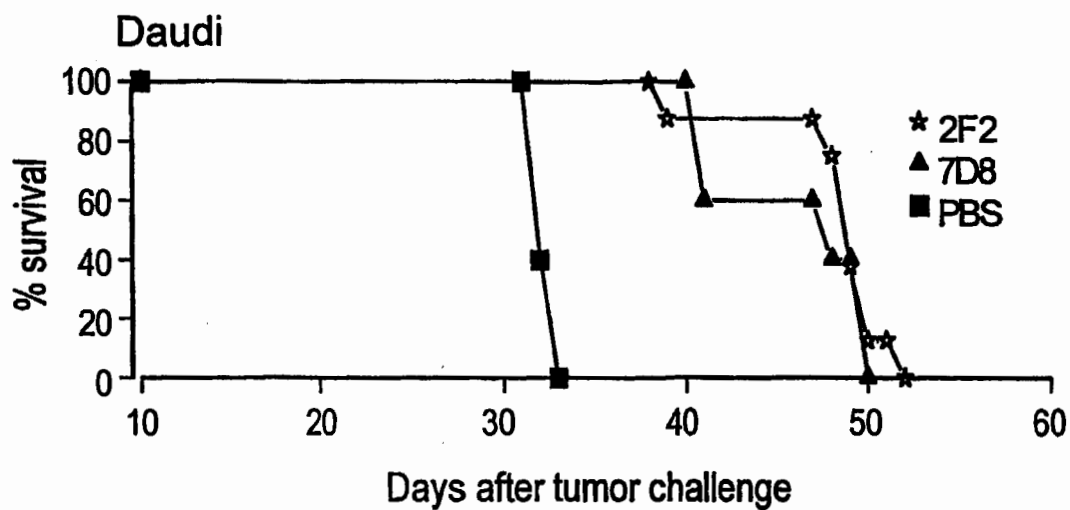
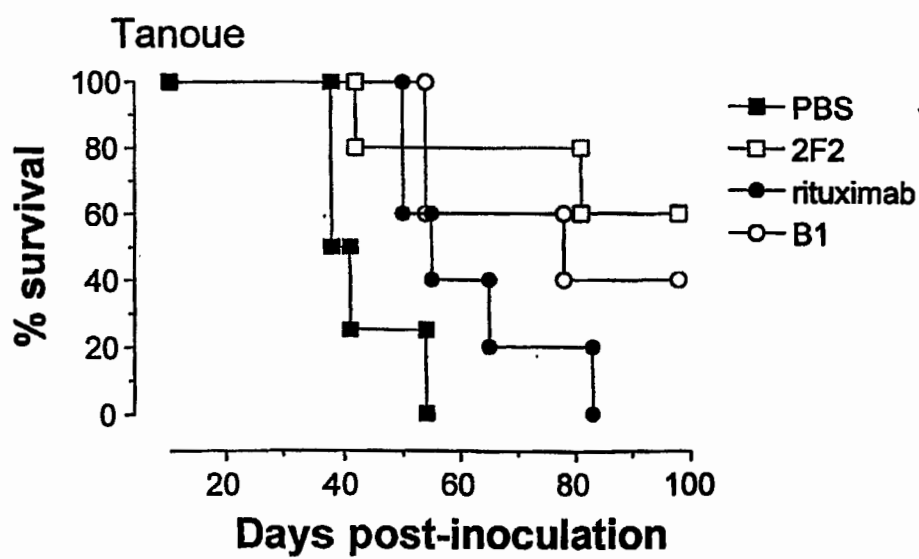
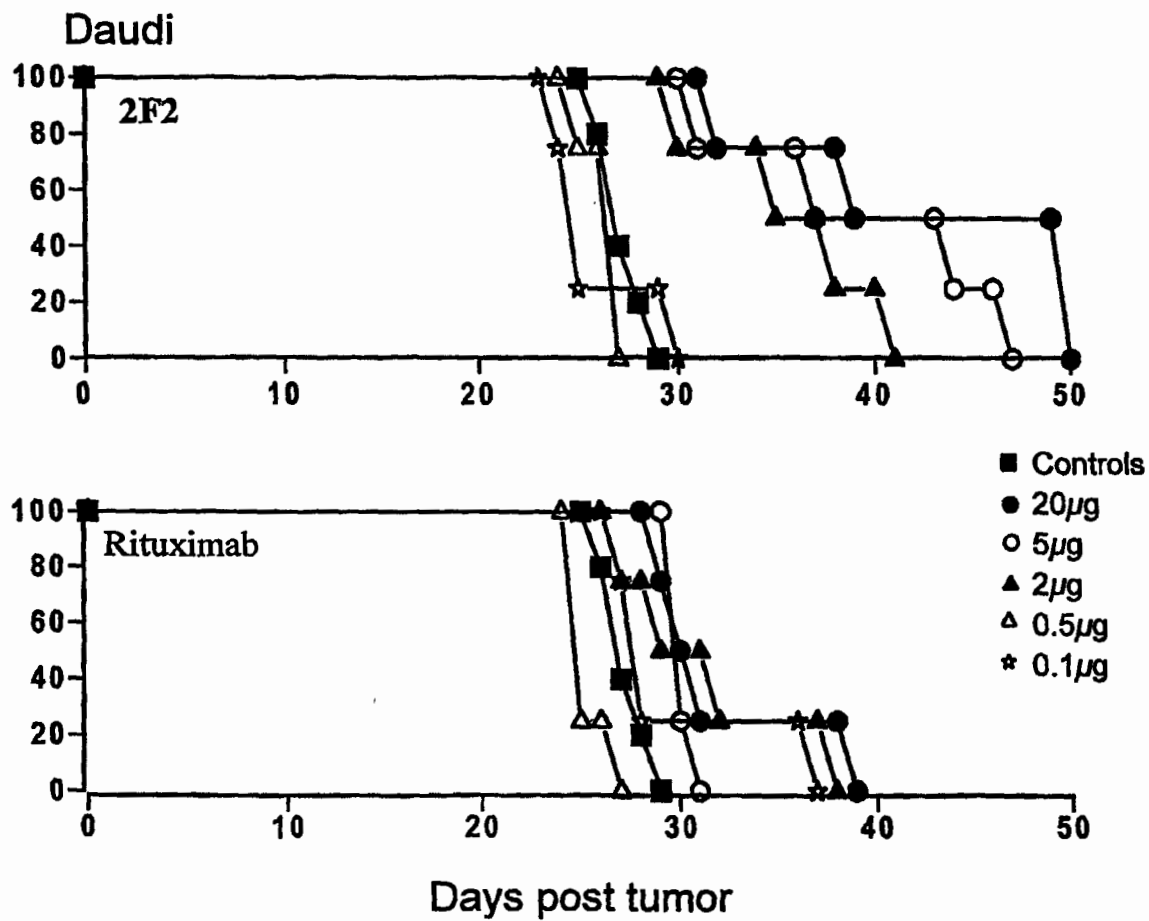


Fig. 37

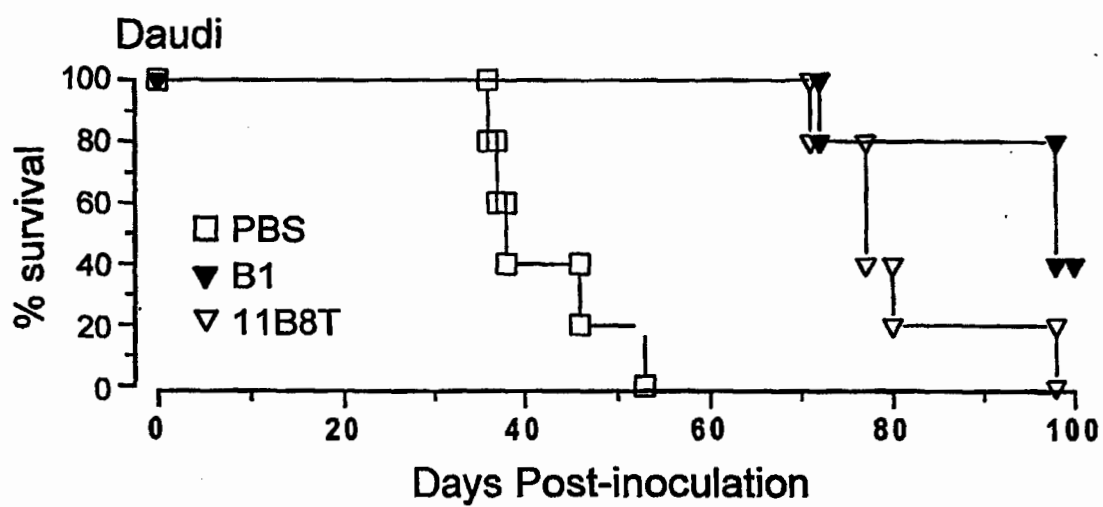
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*Fig. 38**Fig. 39*

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*Fig. 40*

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*Fig. 41*

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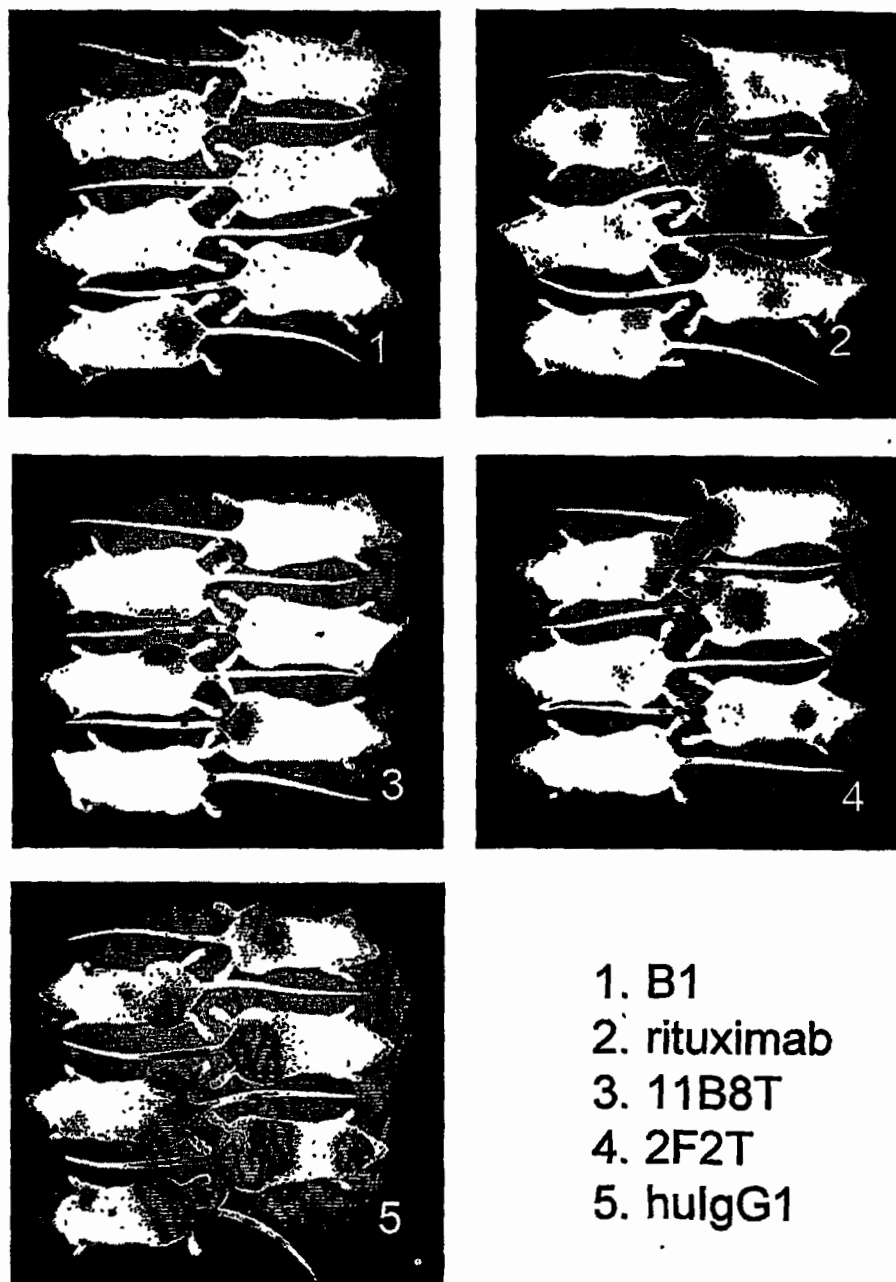
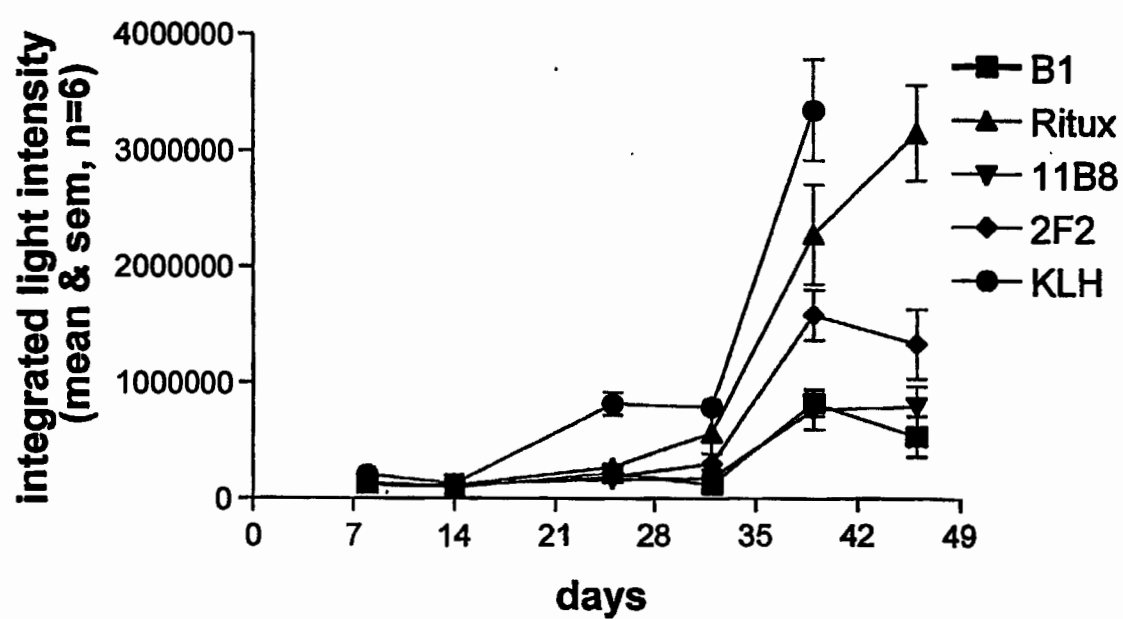
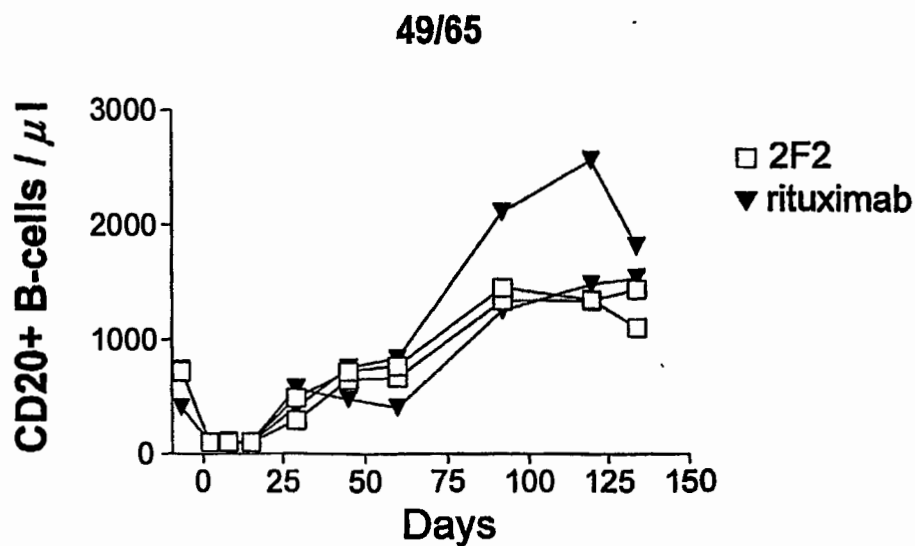
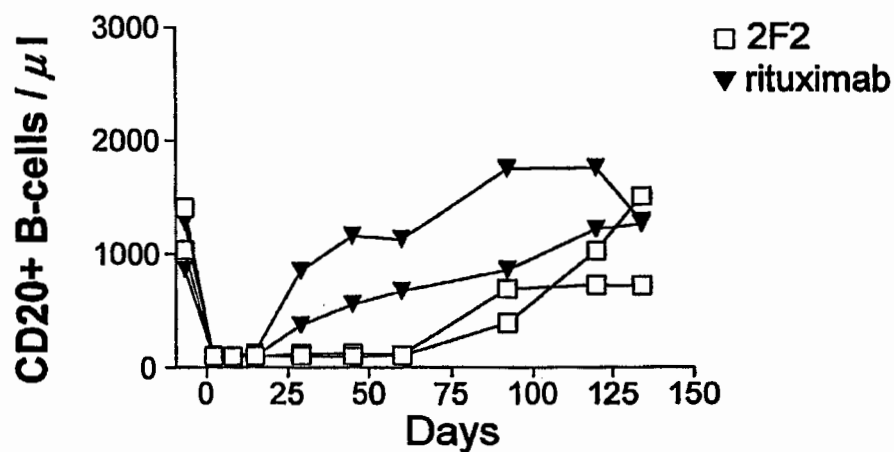
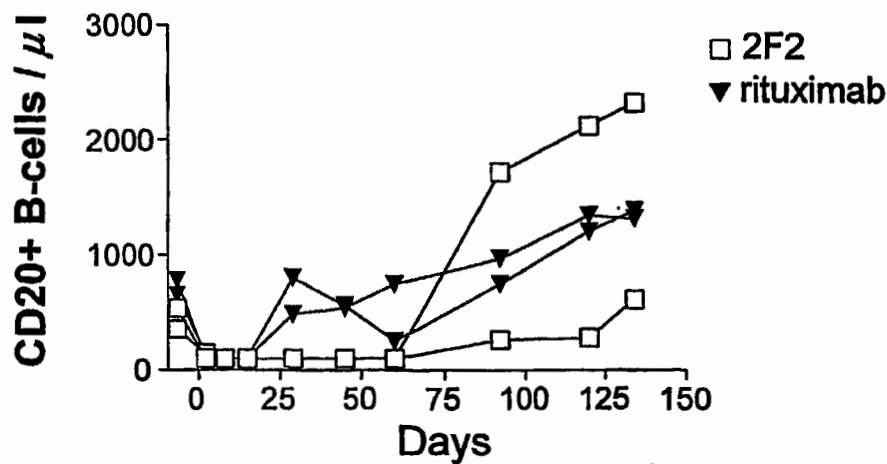
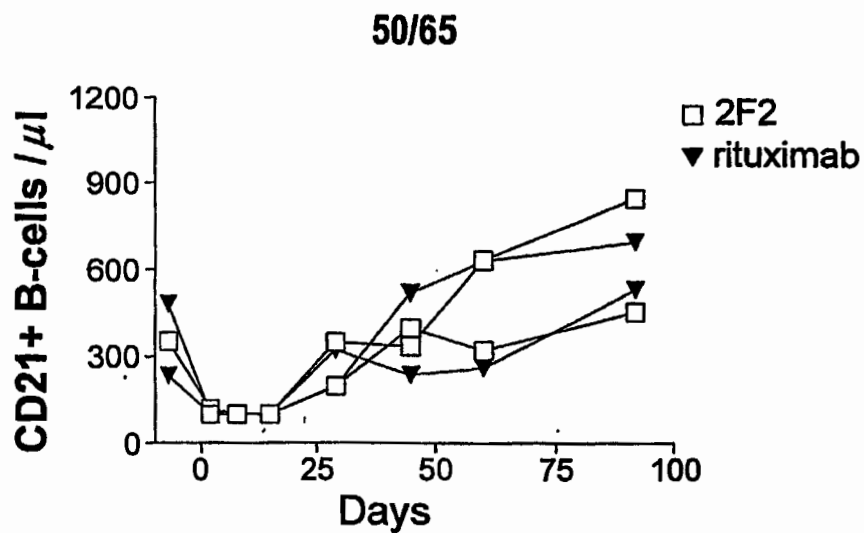
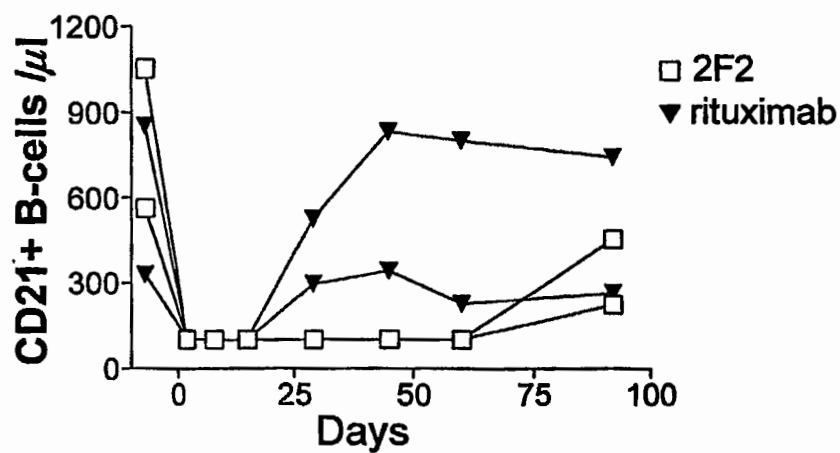
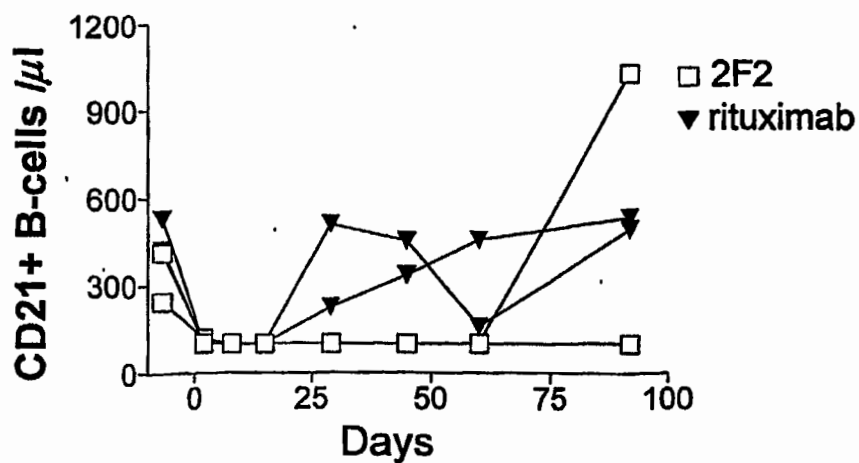


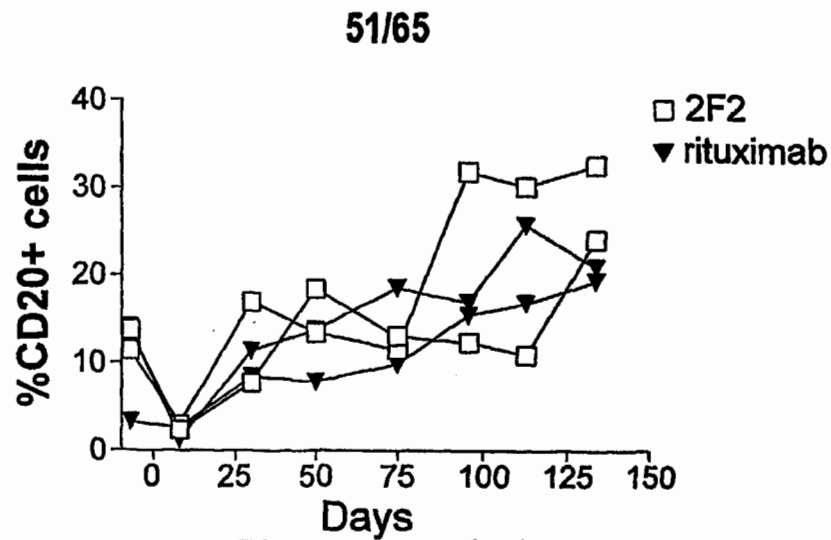
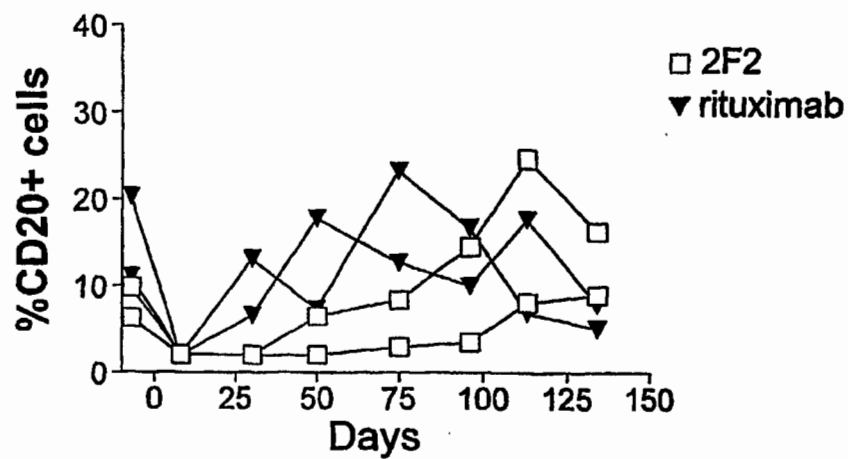
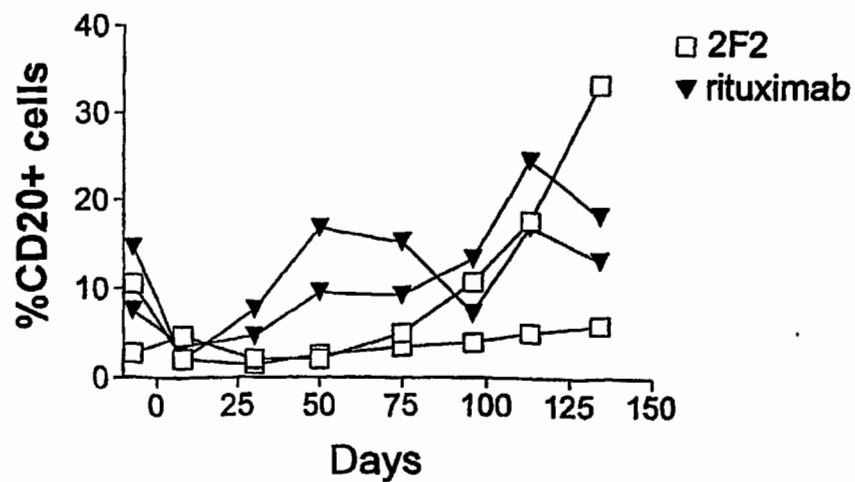
Fig. 42

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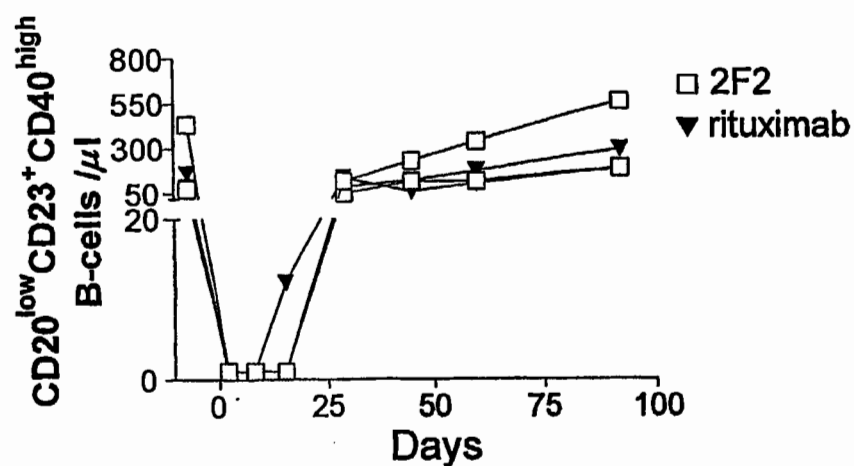
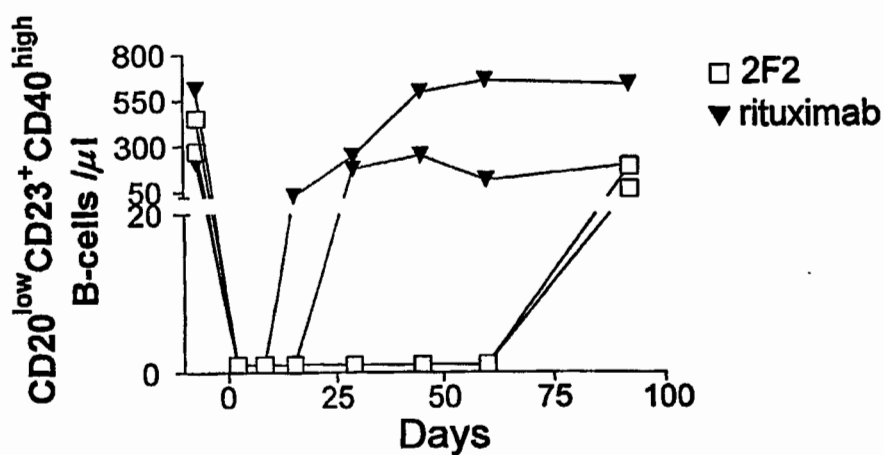
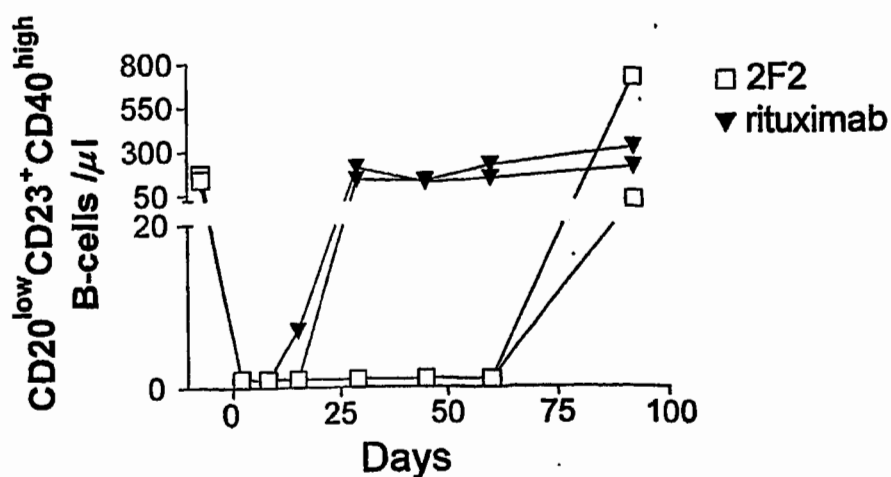
*Fig. 43*

*Fig. 44A**Fig. 44B**Fig. 44C*

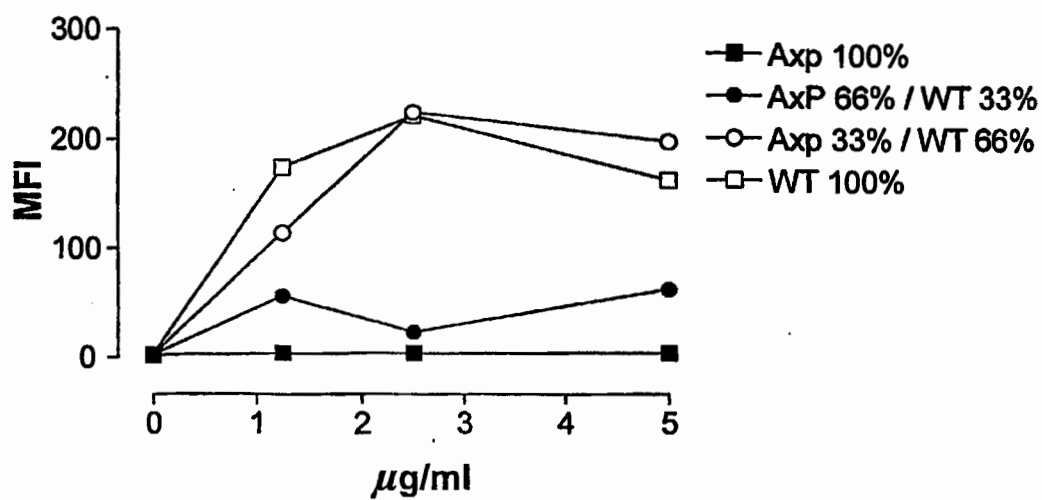
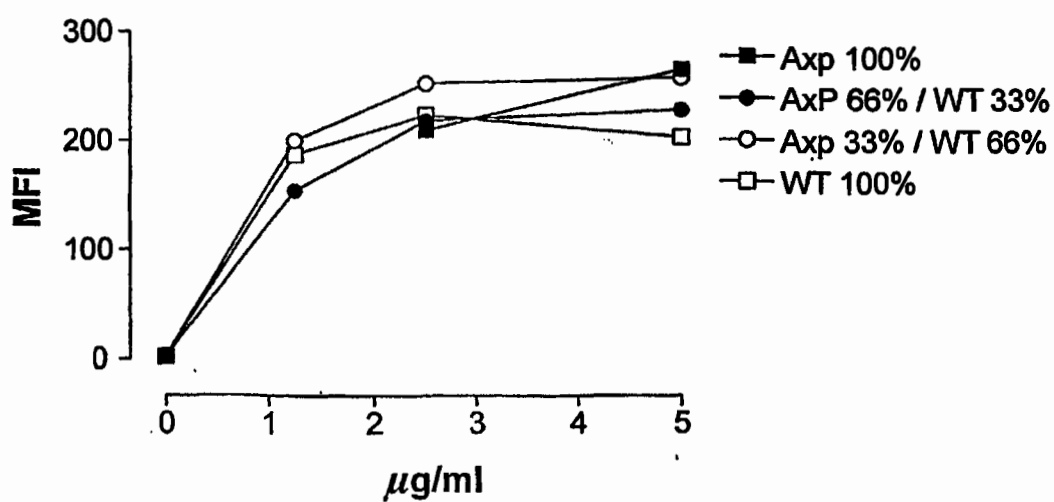
*Fig. 45A**Fig. 45B**Fig. 45C*

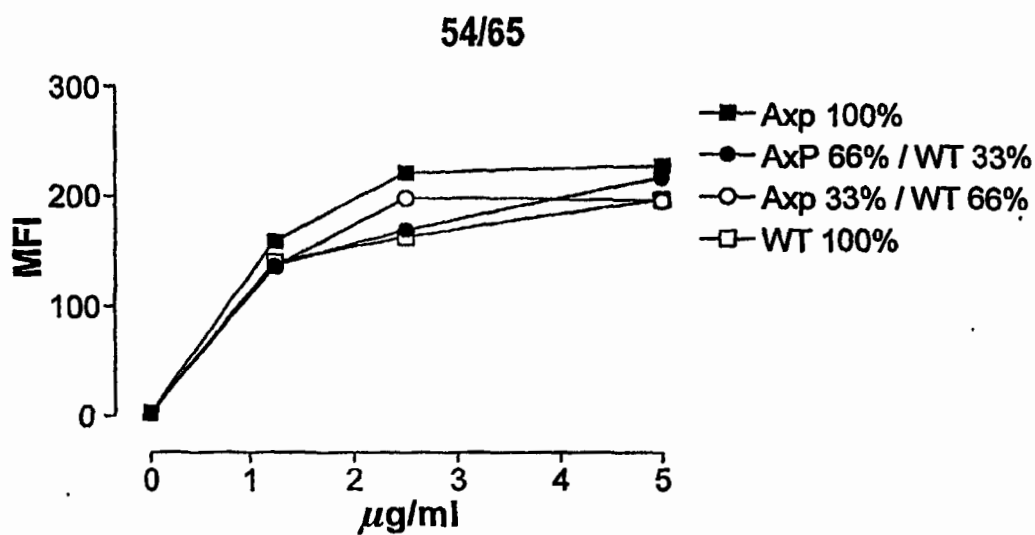
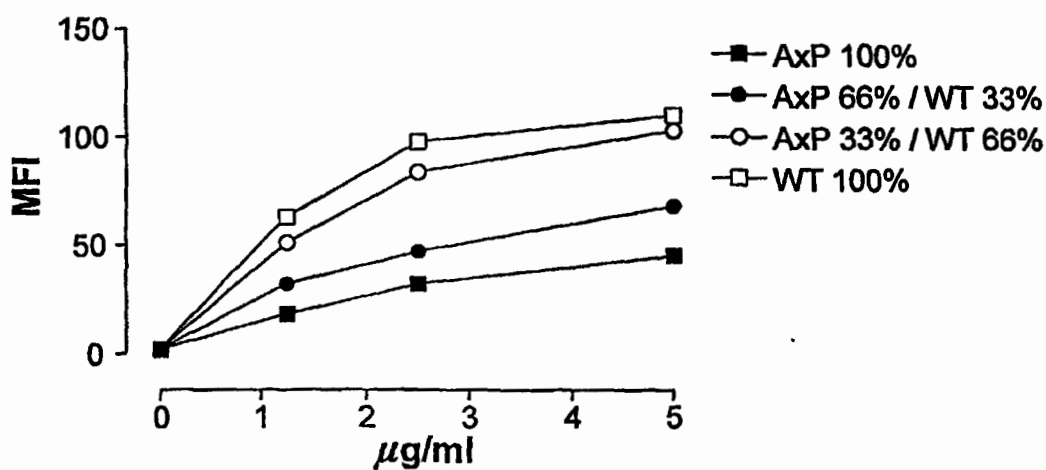
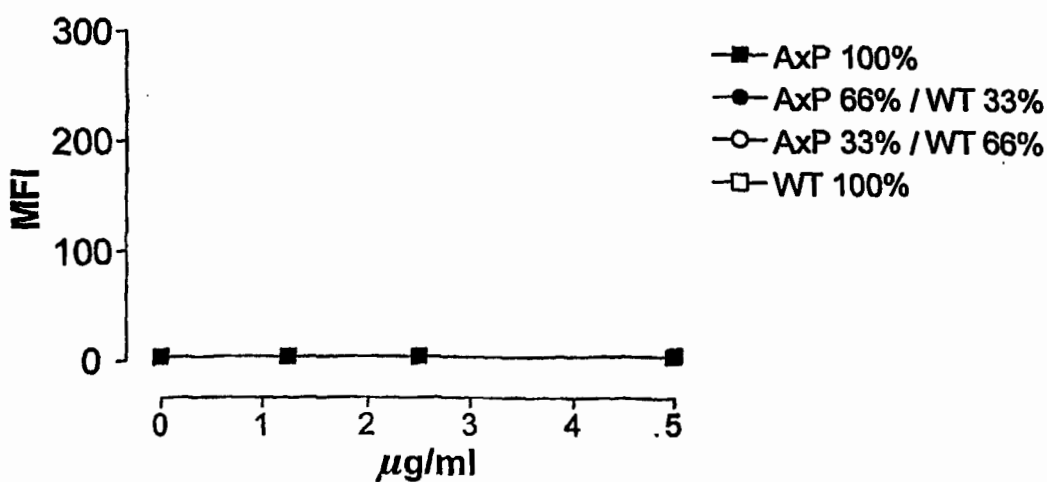
*Fig. 46A**Fig. 46B**Fig. 46C*

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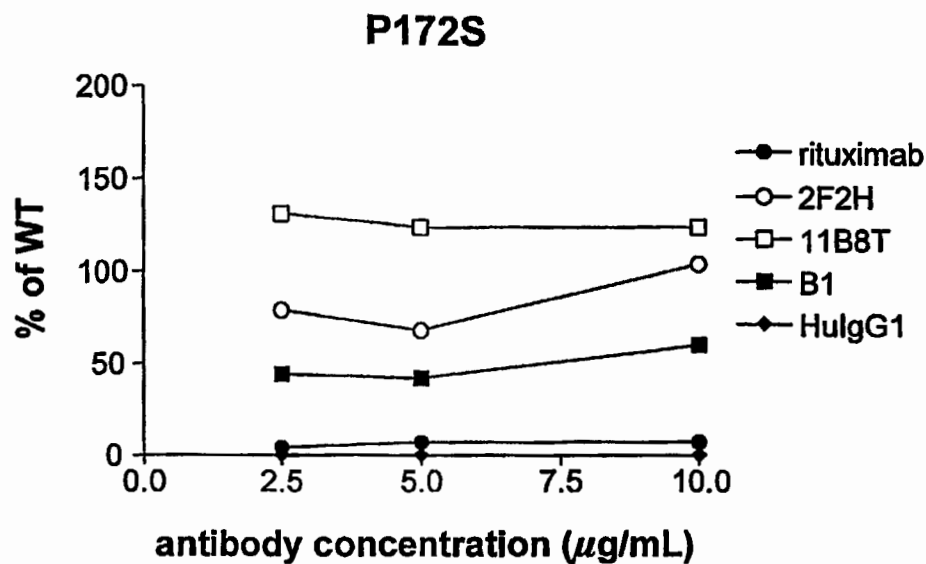
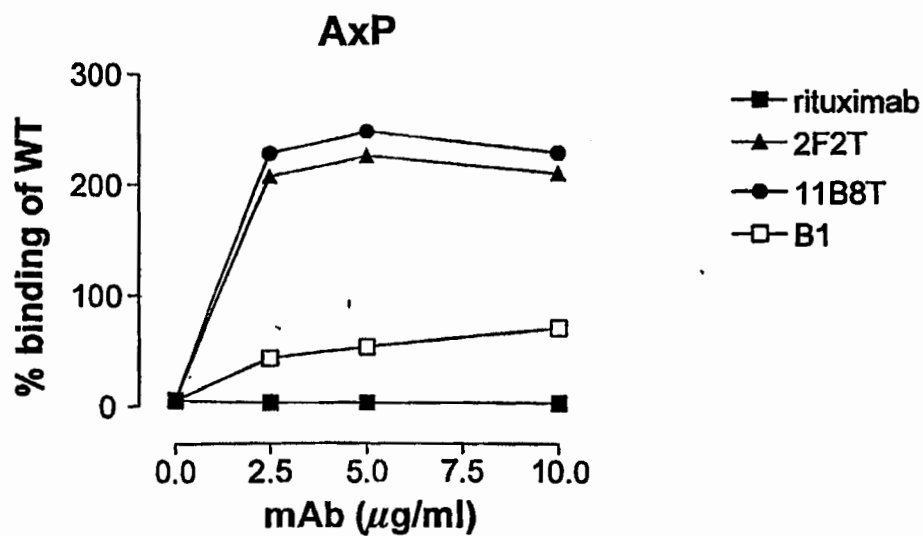
*Fig. 47B**Fig. 47B**Fig. 47C*

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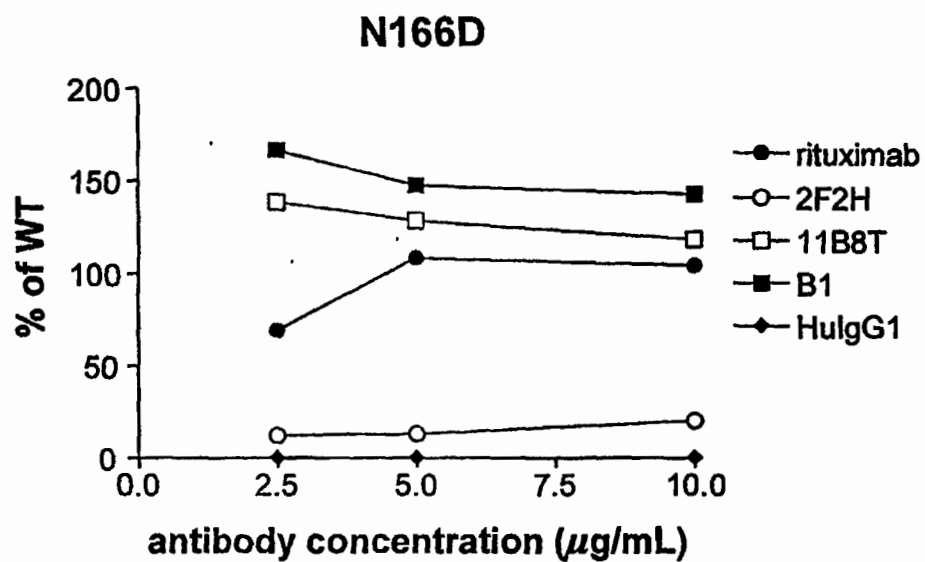
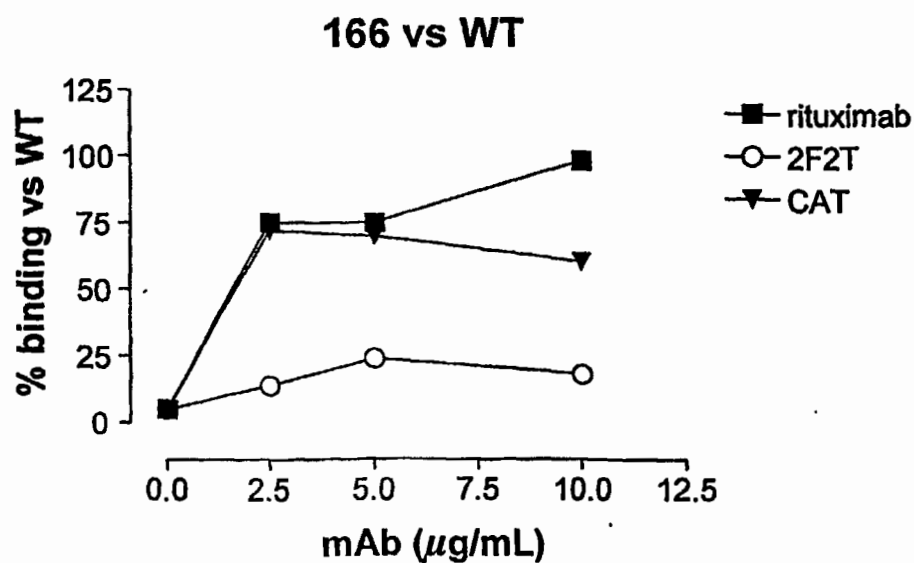
*Fig. 48A**Fig. 48B*

*Fig. 48C**Fig. 48D**Fig. 48E*

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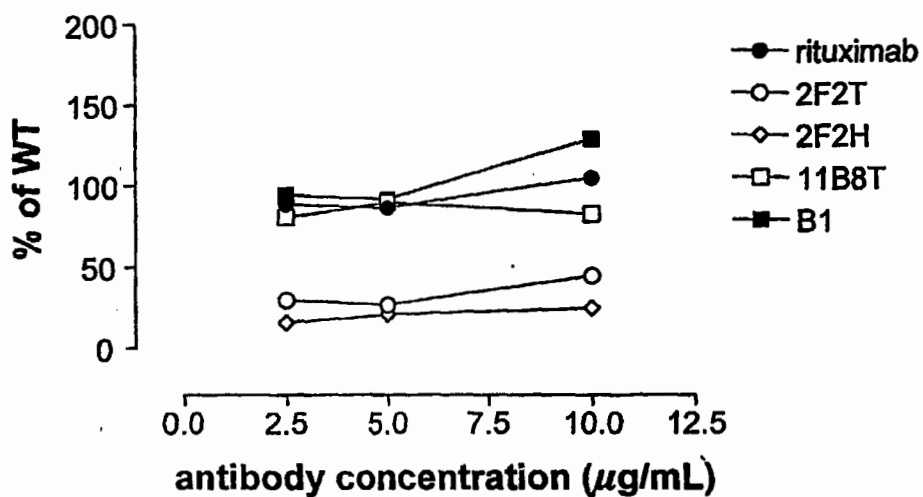
*Fig. 49A**Fig. 49B*

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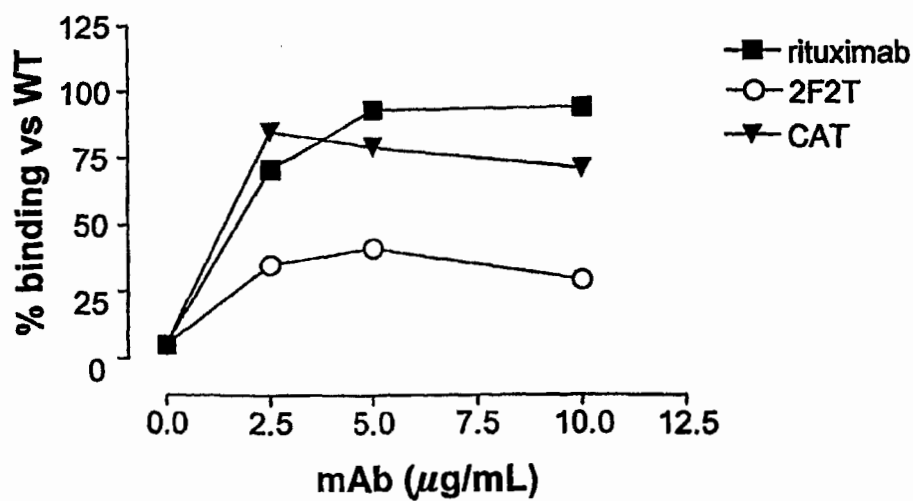
*Fig. 49C**Fig. 49D*

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N163D

*Fig. 49E*

163 vs WT

*Fig. 49F*

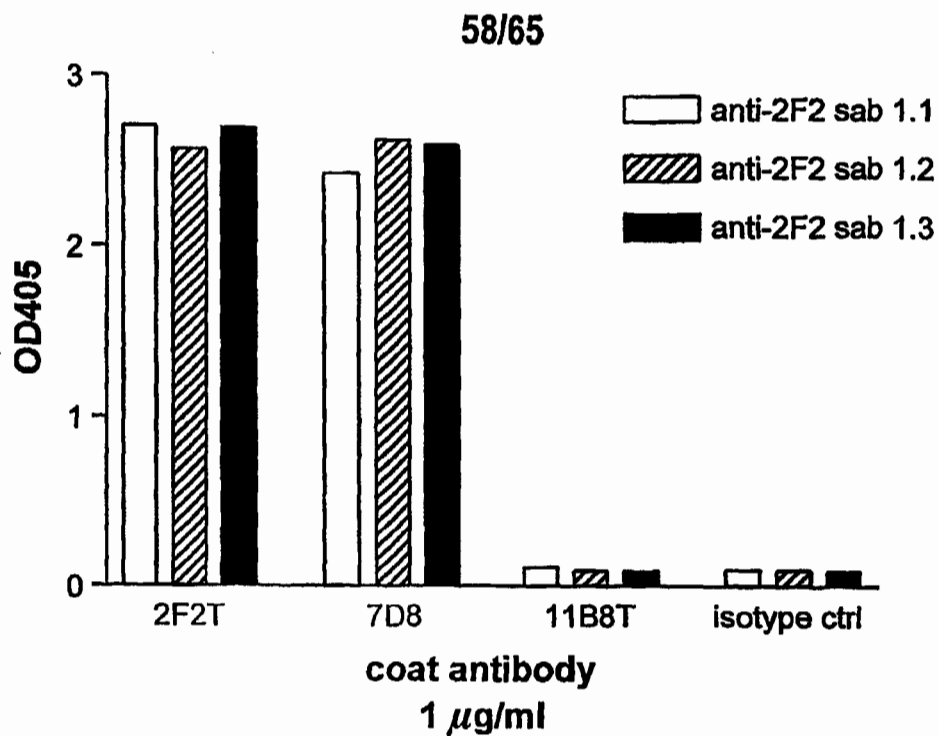


Fig. 50

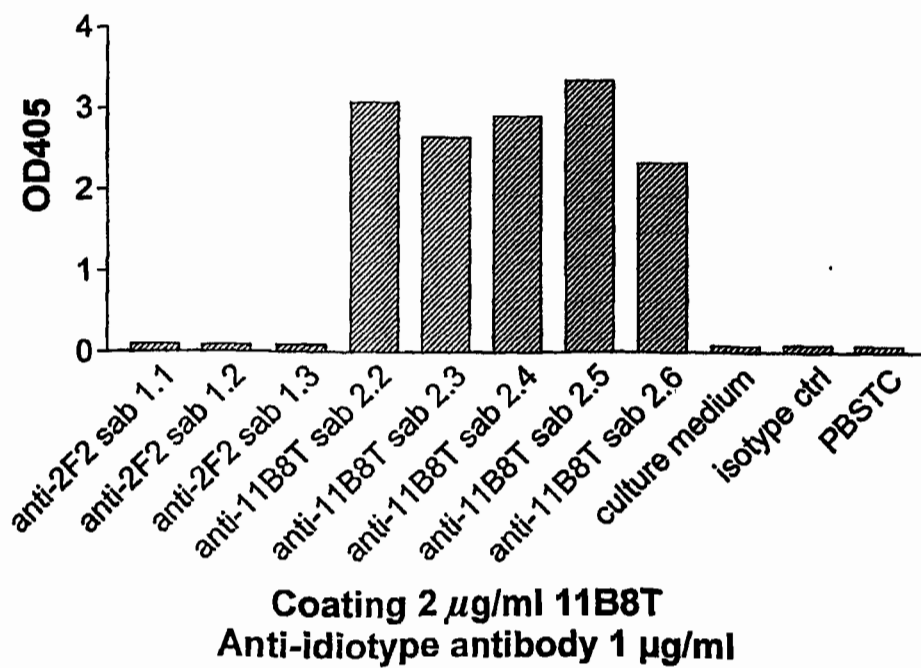
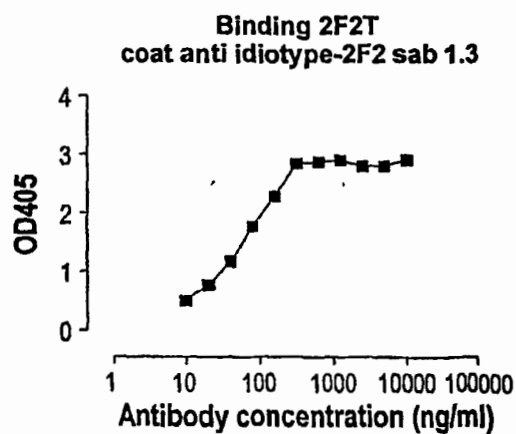
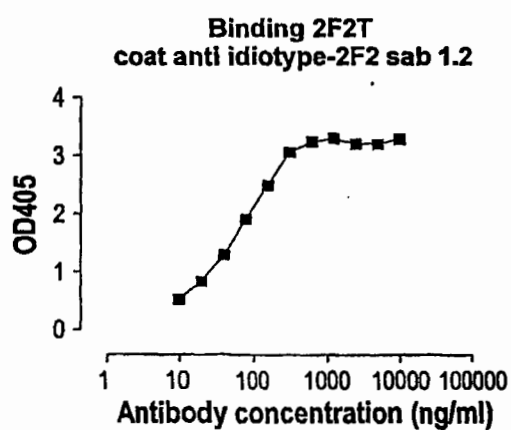
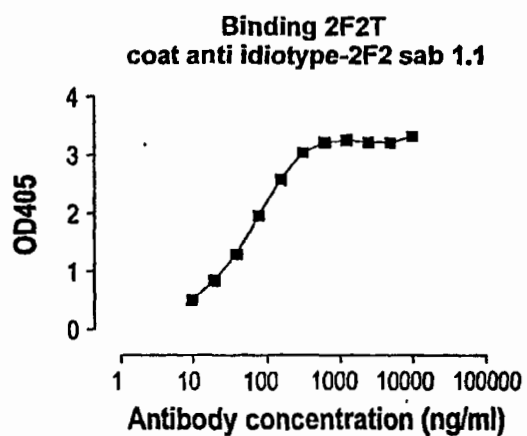


Fig. 51

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*Fig. 52*

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Translation of 2F2 VH

1 MFLGLSWIFL LAILKGVQCE VOLVESGGGL VQGRSLRLS CAASGFTFND
 51 YAMHWVRQAP GKGLEWVSTI SWNSGSIGYA DSVKGRFTIS RDNAKKSLYL
 101 QMNSLRAEDT ALYYCAKDTQ YGNYYYGMDV WGQGTTVTVS S

Translation of 2F2VL

1 MEAPAQLLFL LLLWLPDITG EIVLTQSPAT LSLSPGERAT LSCRASQSVS
 51 SYLAWYQOKP GOAPRLLIYD ASNRTGIPA RFSGSGSGTD FTLTISSELP
 101 EDFAVYYCQQ RSNWETFGQ GTRLEIK

CDR1

CDR2

CDR3

Fig. 53

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2F2 VH

```

1  ATGGAG TTGGGA CTGAGC TGGATT TTCCCTT TTGGCT ATTTTA AAAGGT GTCCAG
55  TGTGAA GTGCAG CTGGTG GAGTCT GGGGGA GGCTTG GTACAG CCTGGC AGGTCC
109 CTGAGA CTCTCC TGTGCA GCCTCT GGATTC ACCTTT AATGAT TATGCC ATGCAC
163 TGGGTC CGGCAA GCTCCA GGAAG GGCCTG GAGTGG GTCCTA ACTATT AGTTGG
217 AATAGT GGTTC ATAGGC TATGCG GACTCT GTGAAG GGCCGA TTCACC ATCTCC
271 AGAGAC AACGCC AAGAAG TCCCTG TATCTG CAAATG AACAGT CTGAGA GCTGAG
325 GACACG GCCTTG TATTAC TGTGCA AAAGAT ATACAG TACGGC AACTAC TACTAC
379 GGTATG GACGTC TGGGGC CAAGGG ACCACG GTCACC GTCTCC TCAG

```

2F2VL

```

1  ATGGAA GCCCCA GCTCAG CTCTCT TCCTC CTGCTA CTCTGG CTCCCA GATACC
55  ACCGGA GAAATT GTGTTG ACACAG TCTCCA GCCACC CTGTCT TTGTCT CCAGGG
109 GAAAGA GCCACC CTCTCC TGCAGG GCCAGT CAGAGT GTTAGC AGCTAC TTAGCC
163 TGGTAC CAACAG AAACCT GGCCAG GCTCCC AGGCTC CTCATC TATGAT GCATCC
217 AACAGG GCCACT GGCAAT CCAGCC AGGTTT CGTGGC AGTGGG TCTGGG ACAGAC
271 TTCACT CTCACC ATCAGC AGCCTA GAGCCT GAAGAT TTTGCA GTTTAT TACTGT
325 CAGCAG CGTAGC AACTGG CCGATC ACCTTC GGCCAA GGGACA CGACTG GAGATT
379 AAAC

```

Fig. 54

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Translation of 7D8VH

1 MELGLSWIFL LAILKGVOCE VOLVESGGGL VQDDRSLRLS CAASGFTTFH
 51 YAMFWVRQAP GKGLEWVSTI SWNSGTIGYA DSVKGRFTIS RDNAKNSLYL
 101 OMNSLRAEDT ALYYCAKDTQ YGNYYGMDV WGQGTTVTVS S

Translation of 7D8VL

1 MEAPAQLLFL LLLWLPDTG EIVLTQSPAT LSLSPGERAT LSCRASQSVS
 51 SYLAWYQQKPGQAPRLIYD ASNRATGIPA RFSGSGSGTD FTLTSSLEP
 101 EDFAVYCCQ RSNWRTTFGQ GTRLEIK

CDR1
 CDR2
 CDR3

Fig. 55

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7D8VH

```

1  ATGGAG TTGGGA CTGAGC TGGATT TTCCTT TTGGCT ATTTA AAAGGT GTCCAG
55  TGTGAA GTGCAG CTGGTG GAGTCT GGGGGA GGCTTG GTACAG CCTGAC AGGTCC
109 CTGAGA CTCCTC TGTGCA GCCTCT GGATTC ACCTTT CATGAT TATGCC ATGCAC
163 TGGGTC CGGCAA GCTCCA GGAAG GGCCTG GAGTGG GTCCTA ACTATT AGTTGG
217 AATAGT GGTACC ATAGGC TATGCG GACTCT GTGAAG GGCCGA TTCACC ATCTCC
271 AGAGAC AACGCC AAGAAC TCCCTG TATCTG CAAATG AACAGT CTGAGA GCTGAG
325 GACACG GCCTTG TATTAC TGTGCA AAAGAT ATACAG TACGGC AACTAC TACTAC
379 GGTATG GACGTC TGGGGC CAAGGG ACCACG GTCACC GTCTCC TCAG

```

7D8VH

```

1  ATGGAA GCCCCA GCTCAG CTTCTC TTCCCTC CTGCTA CTCTGG CTCCCA GATACC
55  ACCGGA GAAATT GTGTTG ACACAG TCTCCA GCCACC CTGTCT TTGTCT CCAGGG
109 GAAAGA GCCACC CTCCTC TGCAGG GCCAGT CAGAGT GTTAGC AGCTAC TTAGCC
163 TGGTAC CAACAG AAACCT GGCCAG GCTCCC AGGCTC CTCATC TATGAT GCATCC
217 AACAGG GCCACT GGCATC CCAGCC AGGTC AGTGGC AGTGGG TCTGGG ACAGAC
271 TTCACT CTCACC ATCAGC AGCCTA GAGCCT GAAGAT TTTGCA GTTTAT TACTGT
325 CAGCAG CGTAGC AACTGG CCGATC ACCTTC GGCCAA GGGACA CGACTG GAGATT
379 AAAC

```

Fig. 56

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Translation of VHCD2011B8

1 MELGLSWVFL VAILKGVQCE VOLVQSGGGL VHPGGSRLRS CTGSGFTFFSY
 51 HAMHWVRQAP GKGLEWVSII GTGGVTYYAD SVKGRFTISR DNVKNSLYLQ
 101 MNSLRAEDMA VYICARDYYC AGSEYDGLYG MDYWGQGT TVSS

Translation of VLCD2011B8

1 MEAPAQLLFL LLLWLPDTTG EIVLTQSPAT LSLSPGERAT LSCRASQSVS
 51 SYIAWYQOKP GOAPRLLIYD ASNRTGIPA RFSGSGSGTD FTLTSSLEP
 101 EDFAVYCCQ RSDWPLTFEGG GTKVEIK

CDR1
 CDR2
 CDR3

Fig. 57

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VHCD2011B8

```

1  ATGGAG TTGGGG CTGAGC TGGGTT TTCCTT GTTGCT ATATTA AAAGGT GTCCAG
55  TGTGAG GTTCAG CTGGTG CAGTCT GGGGGA GGCTTG GPACAT CCTGGG GGTCC
109 CTGAGA CTCTCC TGTACA GGCTCT GGATTC ACCTTC AGTTAC CATGCT ATGCAT
163 TGGGTT CGCCAG GCTCCA GGA AAA GGCTCT GAATGG GTATCA ATTATT GGGACT
217 GGTGGT GTCACA TACTAT GCAGAC TCCGTG AAGGGC CGATTG ACCATC TCCAGA
271 GACAAAT GTCAAG AACTCC TTGTAT CTTC AA ATGAAC AGCCTG AGAGCC GAGGAC
325 ATGGCT GTGTAT TACTGT GCAAGA GATTAC TATGGT CGGGGG AGTTTT TATGAC
379 GGCCTC TACGGT ATGGAC GTCTGG GGCCAA GGGACC ACGGTC ACCGTC TCCTCA
433 G

```

VLCD2011B8

```

1  ATGGAA GCCCCA GCACAG CTCTC TTCTC CTGCTA CTCGG CTCCTA GATACC
55  ACCGGA GAAATT GTGTG ACACAG TCTCCA GCCACC CTGTCT TTGTCT CCAGGG
109 GAAAGA GCCACC CTCTCC TGCAGG GCCAGT CAGAGT GTTAGC AGCTAC TTAGCC
163 TGGTAC CAACAG AAACCT GGCCAG GCTCCC AGGCTC CTCATC TATGAT GCATCC
217 AACAGG GCCACT GGCAAT CCAGCC AGGTTG AGTGGG TCTGGG ACAGAC
271 TTCACT CTCACC ATCAGC AGCCTA GAGCCT GAAGAT TTTGCA GTTTAT TACTGT
325 CAGCAG CGTAGC GACTGG CCGCTC ACTTTC GCGGGA GGGACC AAGGTG GAGATC
379 AAAC

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Fig. 58

GMI-055PC

SEQUENCE LISTING

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<151> 2002-10-17

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tgtgcagcct ctggattcac ctttaatgat tatgccatgc actgggtccg gcaagctcca 180
gggaagggcc tggagtgggt ctcaactatt agttggaata gtggttccat aggctatgcg 240
gactctgtga agggccgatt caccatctcc agagacaacg ccaagaagtc cctgtatctg 300
caaatgaaca gtctgagagc tgaggacacg gccttgattt actgtgcaaa agatatacag 360
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 20           25           30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35           40           45
Asn Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50           55           60
Glu Trp Val Ser Thr Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala
 65           70           75           80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys
 85           90           95
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
100          105          110
Tyr Tyr Cys Ala Lys Asp Ile Gln Tyr Gly Asn Tyr Tyr Tyr Gly Met
115          120          125
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
130          135          140

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GMI-055PC

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 <212> PRT
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 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45
 Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 50 55 60
 Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95
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 <212> DNA
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 caaatgaaca gtctgagagc tgaggacacg gccttgatt actgtgcaaa agatatacag 360
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 Pro Asp Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 His Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Thr Ile Ser Trp Asn Ser Gly Thr Ile Gly Tyr Ala
 65 70 75 80
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
 100 105 110
 Tyr Tyr Cys Ala Lys Asp Ile Gln Tyr Gly Asn Tyr Tyr Tyr Gly Met
 115 120 125
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 130 135 140

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 ctctcctgca gggccagtc gagtgtagc agctacttag cctggtagca acagaaacct 180
 ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240
 aggttcagtg gcagtggtgc tgggacagac ttcactctca ccatcagcag cctagagcct 300
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 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45
 Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 50 55 60
 Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
 65 70 75 80

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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95
 Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser
 100 105 110
 Asn Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 115 120 125

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 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Gly Ser Gly Phe Thr Phe
 35 40 45
 Ser Tyr His Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Ile Ile Gly Thr Gly Gly Val Thr Tyr Tyr Ala Asp
 65 70 75 80
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Asn Ser
 85 90 95
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
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GMI-055PC

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aggttcagtg gcagtgggtc tgggacagac ttactcttca ccatcagcag cctagagcct 300
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      20              25              30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
      35              40              45
Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
      50              55              60
Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
      65              70              75              80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
      85              90              95
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser
      100             105             110
Asp Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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<210> 13

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<212> PRT

<213> Homo sapiens

<400> 13

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<210> 14

<211> 17

<212> PRT

<213> Homo sapiens

<400> 14

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Gly

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<210> 15

<211> 13

<212> PRT

<213> Homo sapiens

GMI-055PC

<400> 15

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1 5 10

<210> 16

<211> 11

<212> PRT

<213> Homo sapiens

<400> 16

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1 5 10

<210> 17

<211> 7

<212> PRT

<213> Homo sapiens

<400> 17

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1 5

<210> 18

<211> 9

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<400> 18

Gln Gln Arg Ser Asn Trp Pro Ile Thr
1 5

<210> 19

<211> 6

<212> PRT

<213> Homo sapiens

<400> 19

His Asp Tyr Ala Met His
1 5

<210> 20

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1 5 10 15
Gly

GMI-055PC

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<213> Homo sapiens

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1 5 10

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1 5 10

<210> 23
<211> 7
<212> PRT
<213> Homo sapiens

<400> 23
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1 5

<210> 24
<211> 9
<212> PRT
<213> Homo sapiens

<400> 24
Gln Gln Arg Ser Asn Trp Pro Ile Thr
1 5

<210> 25
<211> 6
<212> PRT
<213> Homo sapiens

<400> 25
Ser Tyr His Ala Met His
1 5

<210> 26
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GMI-055PC

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<400> 27

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Val

<210> 28

<211> 11

<212> PRT

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<400> 28

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1 5 10

<210> 29

<211> 7

<212> PRT

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<400> 29

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 30

<211> 9

<212> PRT

<213> Homo sapiens

<400> 30

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GMI-055PC

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27

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<220>
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 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp
 65 70 75 80
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser
 85 90 95
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr
 100 105 110
 Tyr Cys Ala Arg
 115

<210> 55
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 55
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 1 5 10 15
 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
 20 25 30

GMI-055PC

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
   35                               40                               45
Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
   50                               55                               60
Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
  65                               70                               75                               80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                               85                               90                               95
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser
                               100                               105                               110
Asn Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
  115                               120                               125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
  130                               135

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<213> Homo sapiens

<400> 56

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Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly
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  20                               25                               30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
  35                               40                               45
Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
  50                               55                               60
Glu Trp Val Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala
  65                               70                               75                               80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
  85                               90                               95
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
  100                               105                               110
Tyr Tyr Cys Ala Lys Asp Ile Asp Tyr Tyr Tyr Tyr Tyr Tyr Gly Met
  115                               120                               125
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
  130                               135                               140

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<210> 57

<211> 127

<212> PRT

<213> Homo sapiens

<400> 57

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
  1                               5                               10                               15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
  20                               25                               30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
  35                               40                               45
Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
  50                               55                               60

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GMI-055PC

Arg	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Ala
65					70					75					80
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser
			85						90					95	
Ser	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser
			100					105						110	
Asn	Trp	Pro	Ile	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	
		115					120						125		