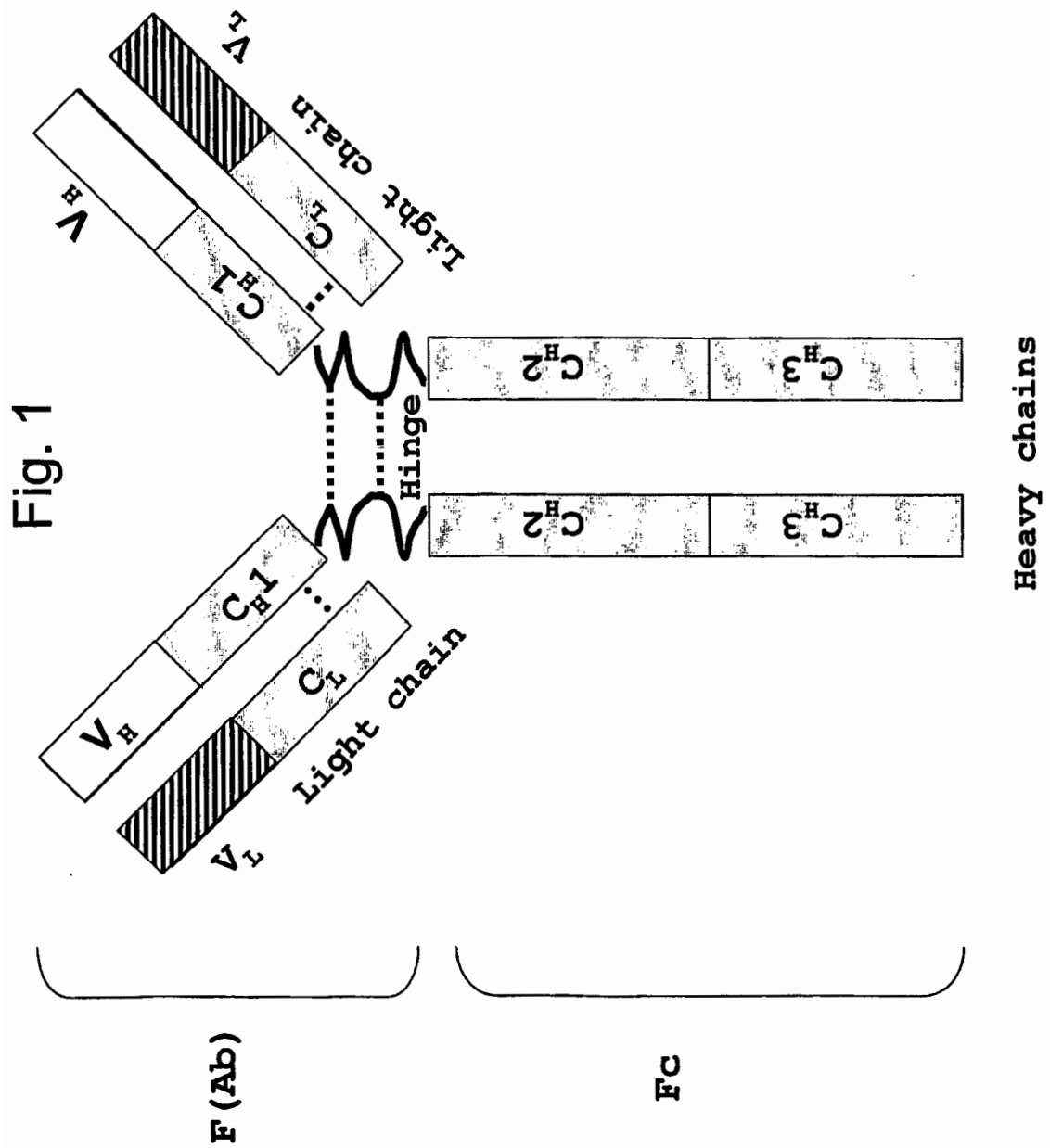
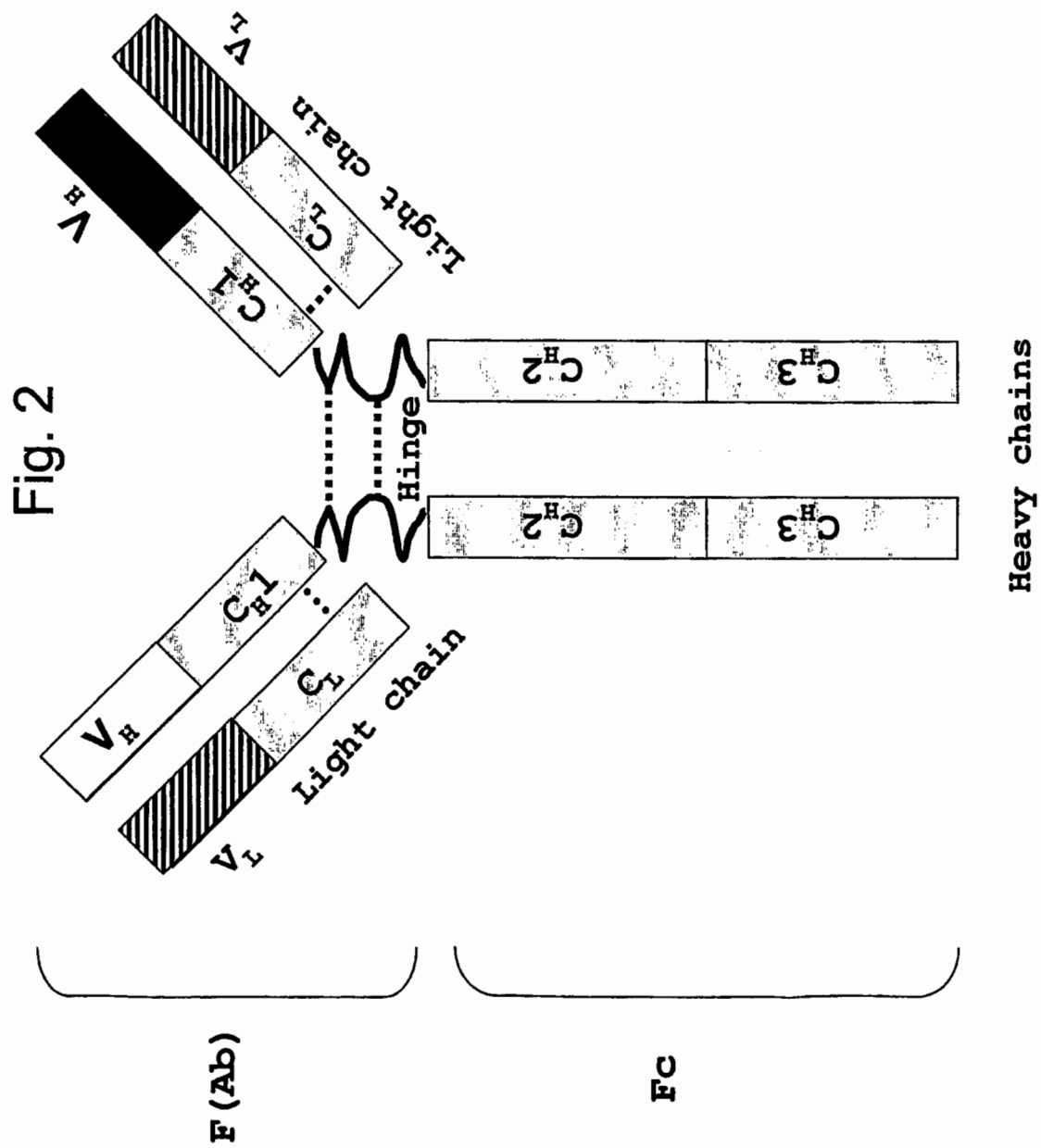


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Fig. 3

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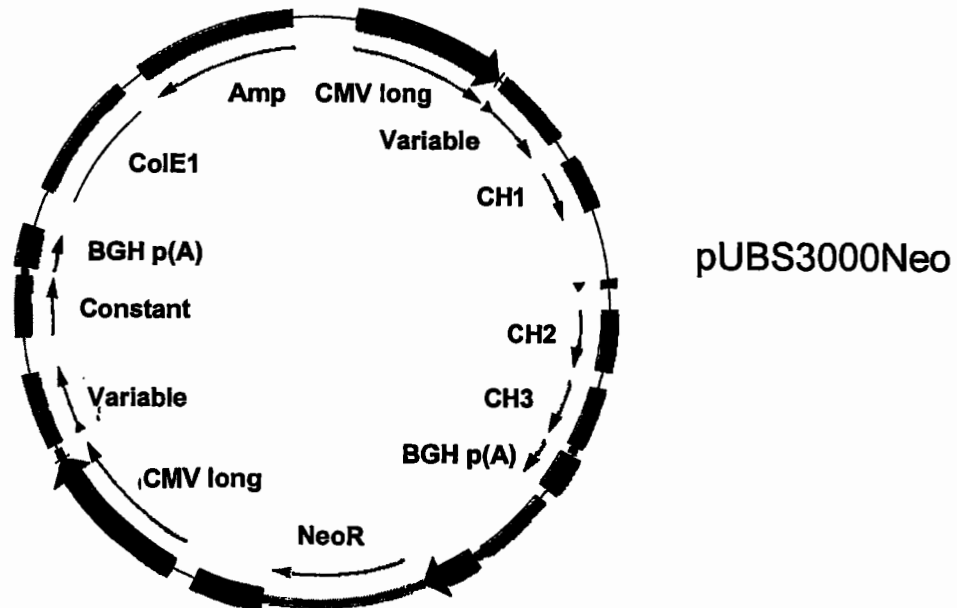
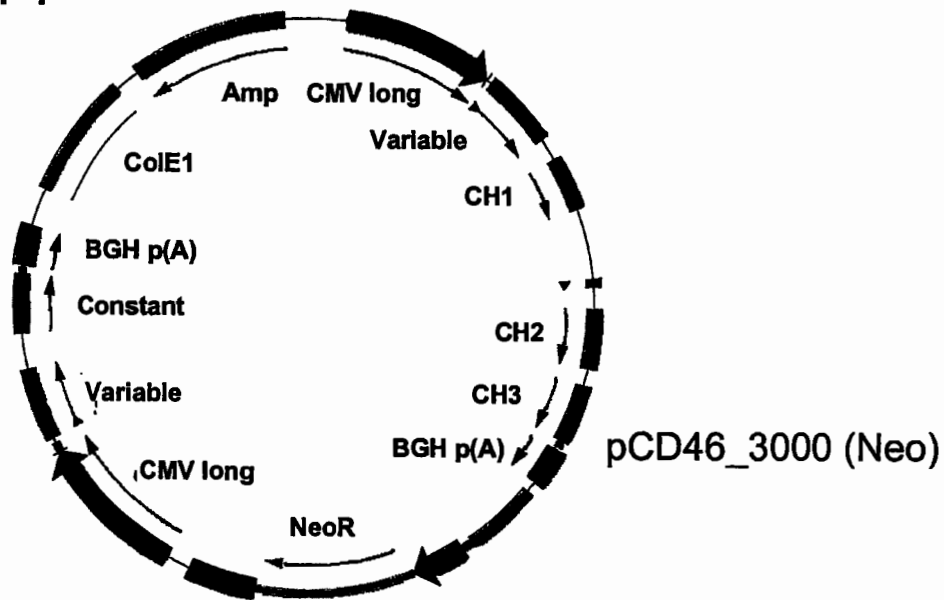
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K53-VL
02-237-VL
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GAAATTGAGCTCACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCC
GACATCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCC
** ** * * *
TCCATCTCCTGCAGGCTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACCTATTGGAT
TCCATCTCCTGCAGGCTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACCTATTGGAT
TCCATCTCCTGCAGGCTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACCTATTGGAT
*****
TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTTCTAATCGG
TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTTCTAATCGG
TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTTCTAATCGG
*****
GCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAA
GCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAA
GCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAA
*****
ATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCATGCAAGCTCTACAACT
ATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCATGCAAGCTCTACAACT
ATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCATGCAAGCTCTACAACT
*****
TTCACCTTTCGGCCCTGGGACCAAGGTGGAGATCAAA
TTCACCTTTCGGCCCTGGGACCAAGGTGGAGATCAAA
TTCACCTTTCGGCCCTGGGACCAAGGTGGAGATCAAA
*****

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K53-VH
02-237-VH
UBS54-VH

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Fig. 4



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Fig. 5

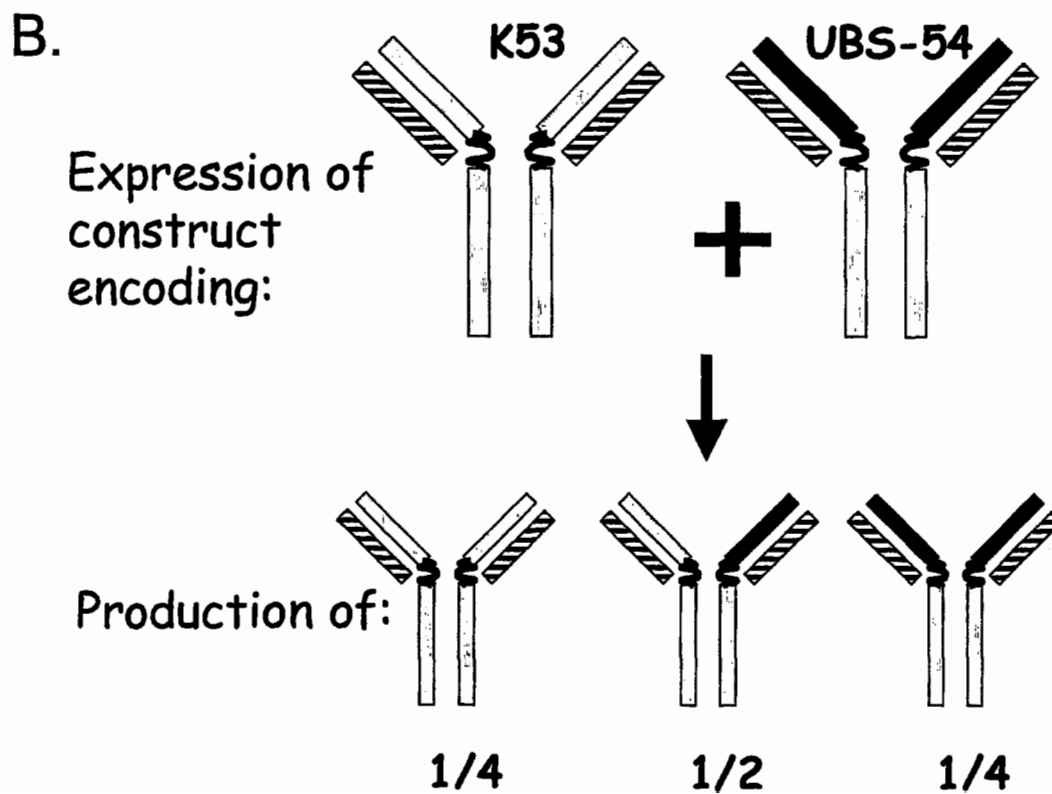
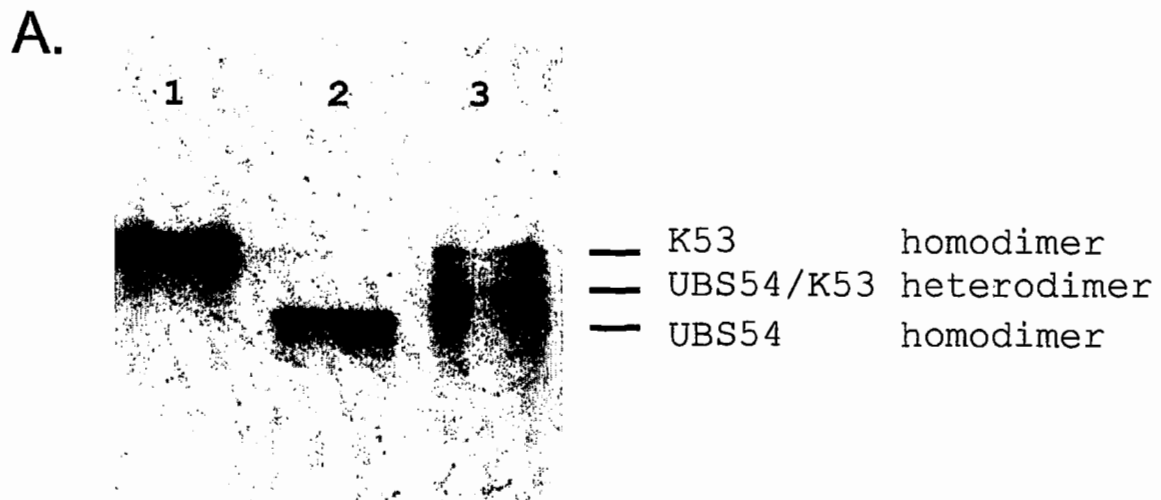
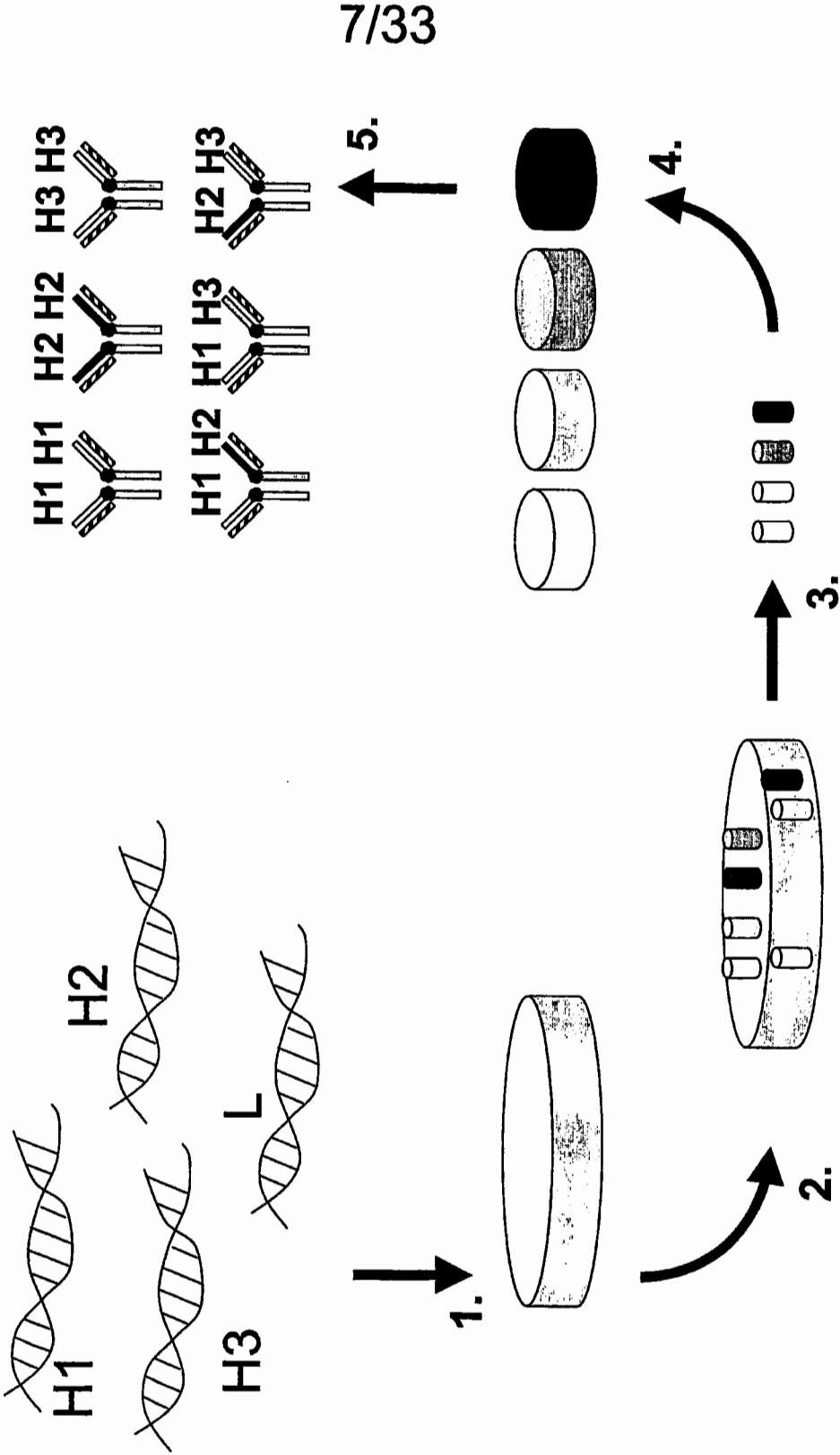


Fig. 6



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Fig. 7

Anti-CD22 V_H fragment (Phage B28)
M A E V Q L V E S G G G V R P G G S L R L S C .
1 ATGGCCGAGGTGCAGCTGGTGGAGTCTGGGGAGGTGTGTACGGCTGGAGGTCCTGAGACTCTCCTG
. A A S G F T F D D Y G M S W V R Q A P G K G L E .
72 TGCAGCCTCTGGATTACCTTTGATGATTATGGCATGAGCTGGTCCGCCAAGCTCCAGGGAAGGGGCTGG
. W V S G I N W N G G S T G Y A D S V K G R F T
143 AGTGGTCTCTGGTATTAAATTGGAATGGTGTAGCACAGGTTATGCAGACTCTGTGAAGGCCGATTACCC
I S R D N A K N S L Y L Q M N S L R A E D T A V .
214 ATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAAAATGAACAGTCTGAGAGCCGAGGACACGGCCGT
. Y Y C A R G F L R F A S S W F D Y W G Q G T L V .
285 GTATTACTGTGCAAGAGGCTTTCTTCTGTTTCTCCTCTGTTGACTATTGGGGCCAAAGGTACCCCTGG
. T V S R
356 TCACCGTCTCGAGA

Anti-CD72 V_H fragment (Phage II-2)
M A Q V Q L V Q S G A E V K K P G A S V K V S C .
1 ATGGCCCGAGGTGCAGCTGGTGCAGTCTGGGGCTGAGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTG
. K A S G Y T F T S Y Y M H W V R Q A P G Q G L E .
72 CAAGGCATCTGGATACACCTTCACCAGCTACTATATGCAGTGGTGGACAGGCCCCCTGGACAAGGGCTTG
. W M G I I N P S G G G T S Y A Q K F Q G R V T
143 AGTGGATGGGAATAATCAACCCCTAGTGGTGGCACAAGCTACGCACAGAAGTCCAGGGCAGAGTCACC
M T R D T S T S T V Y M E L S S L R S E D T A V .
214 ATGACCGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGT
. Y Y C A R D Y Y V T Y D S W F D S W G Q G T L V .
285 GTATTACTGTGCAAGAGACTACTATGTTACGTATGATTCTCTGTTGACTCTCTGGGGCCAAAGGTACCCCTGG
. T V S R
356 TCACCGTCTCGAGA

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Fig. 7, cont'dAnti-Class II V_H fragment (Phage I-2)

```

      M A E V Q L V E S G G L V Q P G R S L R L S C .
1  ATGCCGAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGTACAGCCTGGCAGTCCCTGAGACTCTCCTG
   . A A S G F T F D D Y A M H W V R Q A P G K G L E .
72 TGCAGCCTCTGGATTACCTTTGATGATTATGCCATGCACCTGGGTCCGGCAAGCTCCAGGGAAGGCGCTGG
   . W V S G I S W N S G S I G Y A D S V K G R F T
143 AGTGGGTCTCAGGTATTAGTTGGAATAGTGGTAGCATAGGCTATGCGGACTCTGTGAAGGCCGATTACCC
   I S R D N A K N S L Y L Q M N S L R A E D T A V .
214 ATCTCCAGAGACAACGCCCAAGAACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCTGAGGACACGGCCGT
   . Y Y C A R D L Y L A H F D Y W G Q G T L V T V S .
285 GTATTACTGTGCAAGGACCTTTATCTTGCGCATTTTGACTACTGGGGCCCAAGGTACCCCTGGTCACCGTCT
   . R
356 CGAGA

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Shared V_L sequence of Phages I-2, II-2 and B28

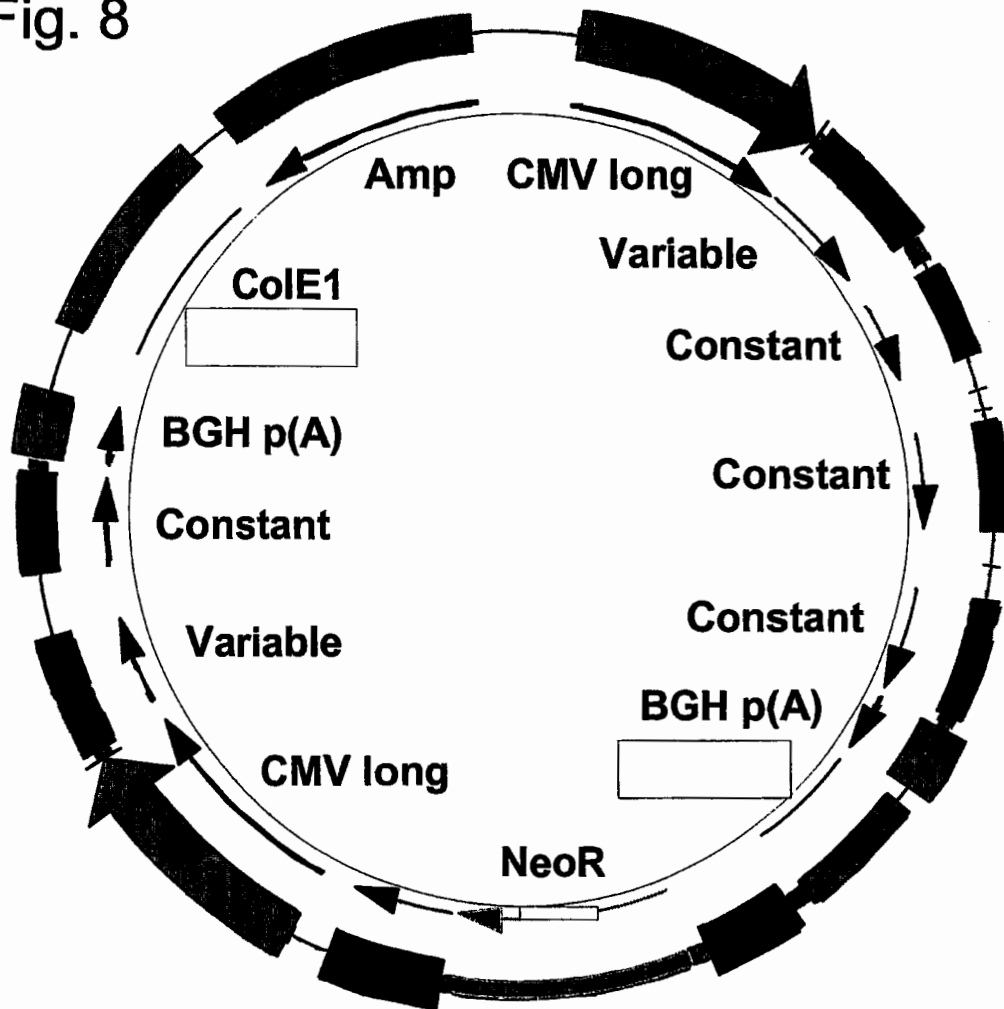
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      S S E L T Q D P A V S V A L G Q T V R I T C Q G .
1  TCGTCTGAGCTGACTCAGGACCCCTGCTGTCTGTGGCCCTTGGACAGACAGTCAGGATCACATGCCAAGG
   . D S L R S Y Y A S W Y Q Q K P G Q A P V L V I Y .
72 AGACAGCCTCAGAAGCTATTATGCAAGCTGGTACCAGCAGAAGCCAGGACAGGCCCTGTACTTGTCTATCT
   . G K N N R P S G I P D R F S G S S S G N T A S
143 ATGGTAAACAAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCAGCTCAGGAACACAGCTTCC
   L T I T G A Q A E D E A D Y Y C N S R D S S G N .
214 TTGACCATCACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAACTCCCGGACAGCAGTGGTAA
   . H V V F G G G T K L T V L G A A A
285 CCATGTGTATTTCGGGGAGGAGGACCAAGCTGACCGTCTAGGTGCGGCGCGCA

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Fig. 8



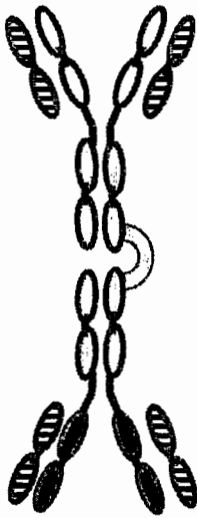
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Fig. 9

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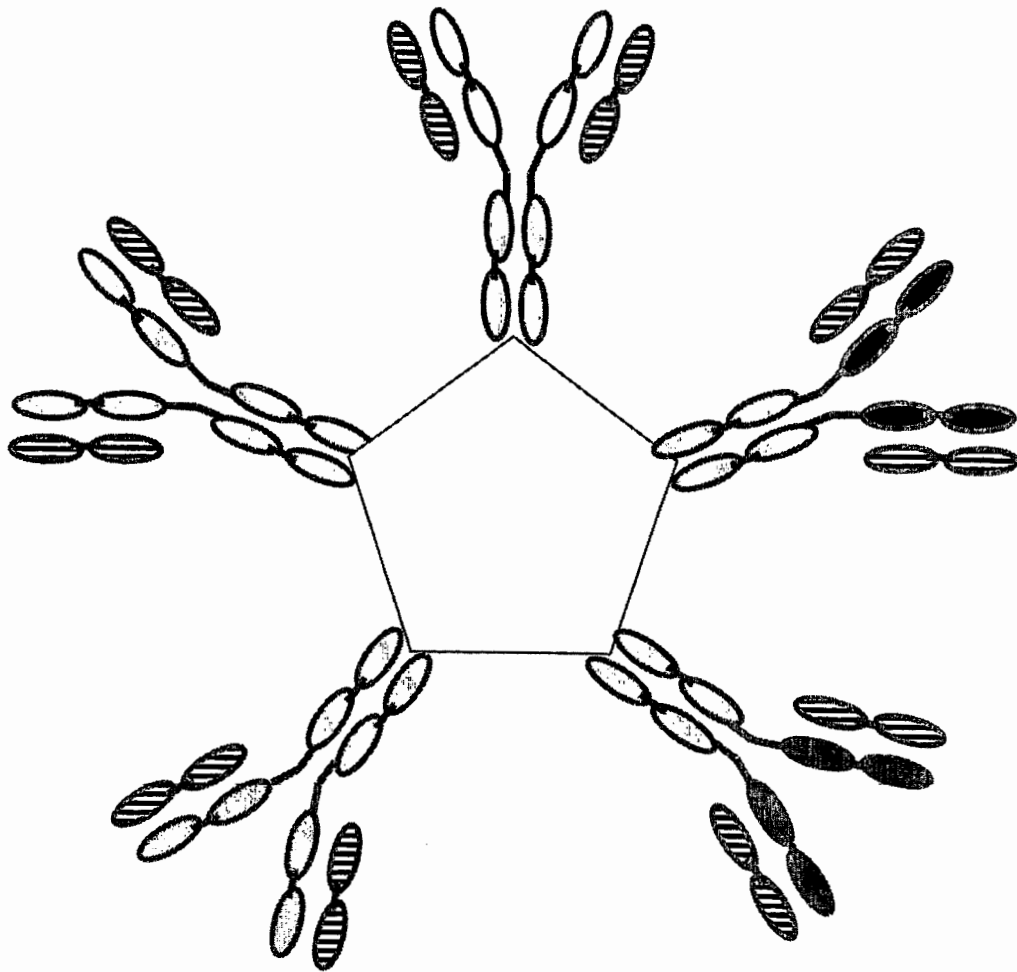


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Fig. 10

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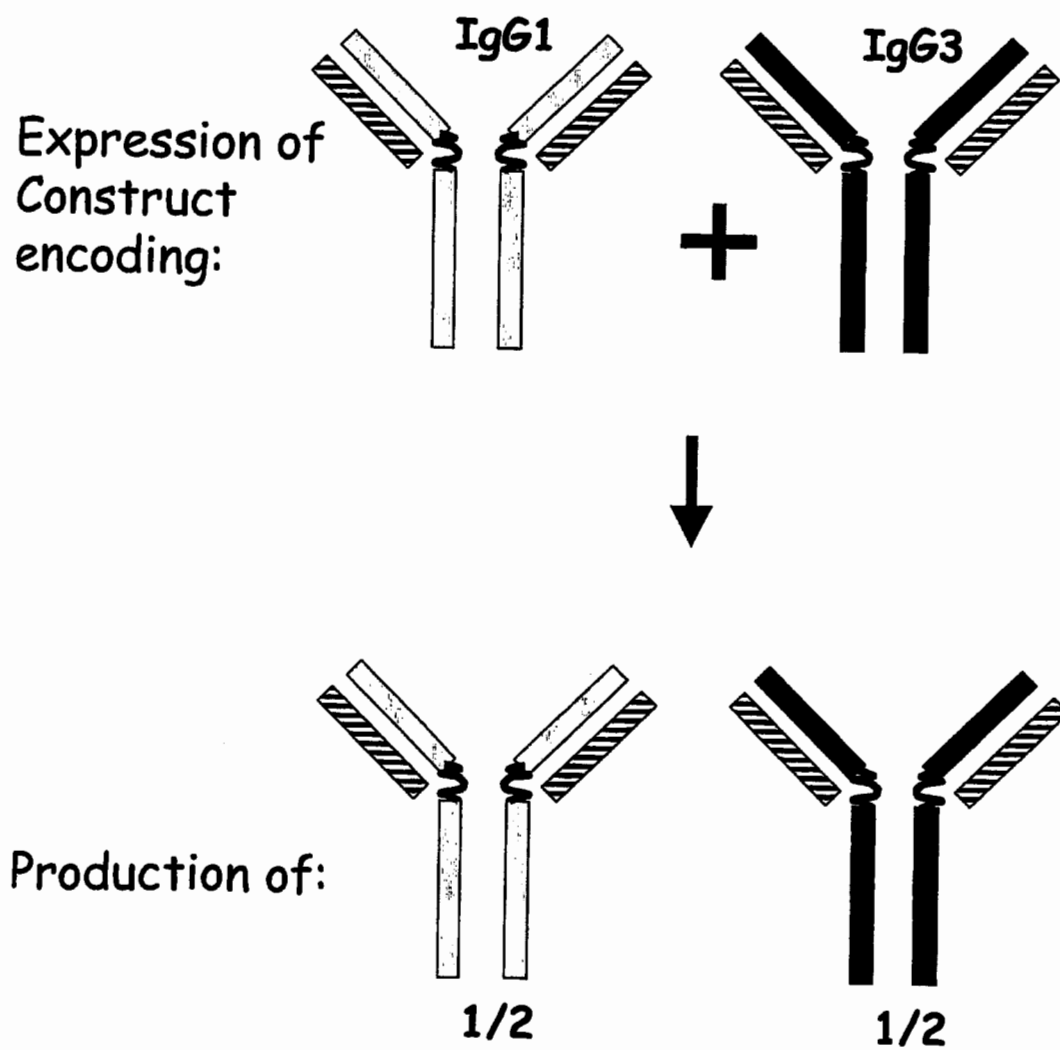


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Fig. 11



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Fig. 12

V_H sequence of K53 IgG

```
1      Q V Q L V Q S G A E V K K P G A S V K V  
      CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGGCCTCAGTGAAGGTC  
  
61     S C K A S G Y T F T S Y G I S W V R Q A  
      TCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGCTGGGTGCGACAGGCC  
  
121    P G Q G L E W M G W I S A Y N G N T N Y  
      CCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTTACAATGGTAACACAAACTAT  
  
181    A Q K L Q G R V T M T T D T S T S T A Y  
      GCACAGAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGCCTAC  
  
241    M E L R S L R S D D T A V Y Y C A R G M  
      ATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCAAGGGGCATG  
  
301    M R G V F D Y W G Q G T L V T V S T  
      ATGAGGGGTGTGTTTGA TACTACTGGGGCCAAGGTACCCCTGGTCACCGTCTCGACA
```

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Fig. 12, cont'd V_H sequence of 02-237 IgG

```
1      Q V Q L V Q S G A E V K K P G A S V K V  
      CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTC  
61     S C K A S G Y T F T S Y G I S W V R Q A  
      TCCTGCAAGGCTTCTGTTACACCTTTACCAGCTATGGTATCAGCTGGGTGCGACAGGCC  
121    P G Q G L E W M G W I S A Y N G N T N Y  
      CCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTTACAATGGTAACACAACTAT  
181    A Q K L Q G R V T M T T D T S T S T A Y  
      GCACAGAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGCCTAC  
241    M E L R S L R S D D T A V Y Y C A R G F  
      ATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCAAGGGGCTTT  
301    P R T S F D S W G Q G T L V T V S S  
      CCGGTACGTCGTTTGACTCCTGGGGCCAGGGCACCCCTGGTGACCGTCTCCTCA
```

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Fig. 12, cont'dV_H sequence of UBS54 IgG

```
1      Q V Q L V Q S G A E V K K P G S S V R V  
      CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTGAGGGTC  
61      S C K A S G G T F S S Y A I S W V R Q A  
      TCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGTGGTGGACAGGCC  
121     P G Q G L E W M G G I I P I F G T A N Y  
      CCTGGACAAGGGCTTGAGTGGATGGAGGGATCATCCCTATCTTTGGTACAGCAAACTAC  
181     A Q K F Q G R V T I T A D E S T S T A Y  
      GCACAGAAGTTCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTAC  
241     M E L S S L R S E D T A V Y Y C A R D P  
      ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCTGTGTATTACTGTGCAAGAGACCCG  
301     F L H Y W G Q G T L V T V S T  
      TTTCTTCACTATTGGGGCCCAAGGTACCCCTGGTCACCCGTCTCGACA
```

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Fig. 12, cont'dV_L sequence of K53 and UBS54 IgG

```
1      E I E L T Q S P L S L P V T P G E P A  
      GAAATTGAGCTCACTCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCCGGCC  
  
58     S I S C R S S Q S L L H S N G Y N Y L D  
      TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTGGAT  
  
118    W Y L Q K P G Q S P Q L L I Y L G S N R  
      TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGG  
  
178    A S G V P D R F S G S G S G T D F T L K  
      GCCTCCGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAA  
  
238    I S R V E A E D V G V Y Y C M Q A L Q T  
      ATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTCAAACT  
  
298    F T F G P G T K V E I K  
      TTCACTTTCGGCCCTGGGACCAAGGTGGAGATCAAA
```

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Fig. 12, cont'dV_L sequence of 02-237 IgG

```
1      D I V M T Q S P L S L P V T P G E P A  
      GACATCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCC  
58     S I S C R S S Q S L L H S N G Y N Y L D  
      TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTGGAT  
118    W Y L Q K P G Q S P Q L L I Y L G S N R  
      TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTTCTAATCGG  
178    A S G V P D R F S G S G S G T D F T L K  
      GCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAA  
238    I S R V E A E D V G V Y Y C M Q A L Q T  
      ATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAACT  
298    F T F G P G T K V E I K  
      TTCACTTTCGGCCCTGGGACCAAGGTGGAGATCAAA
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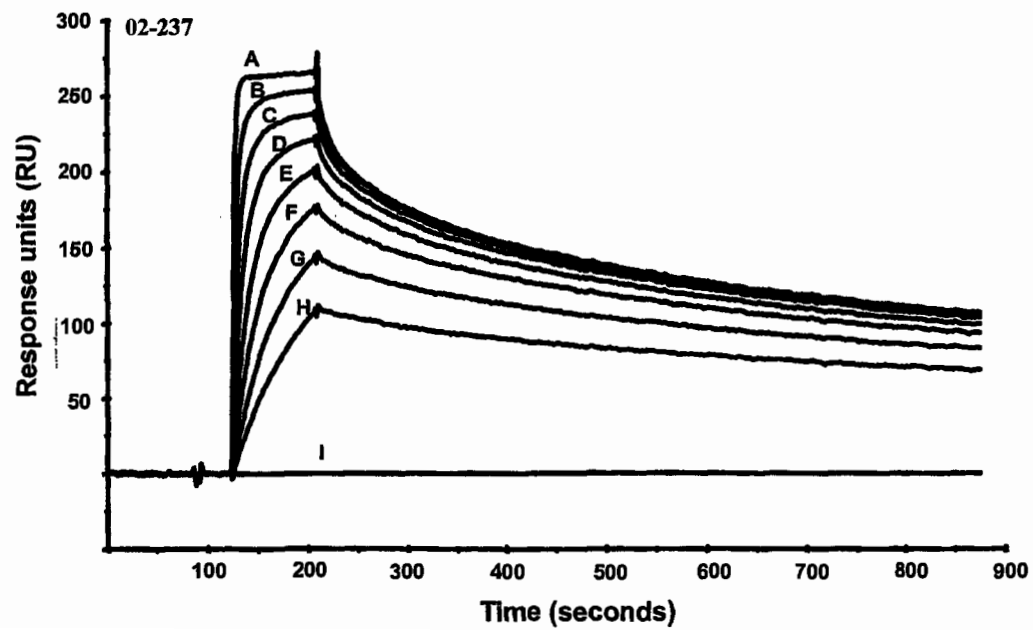
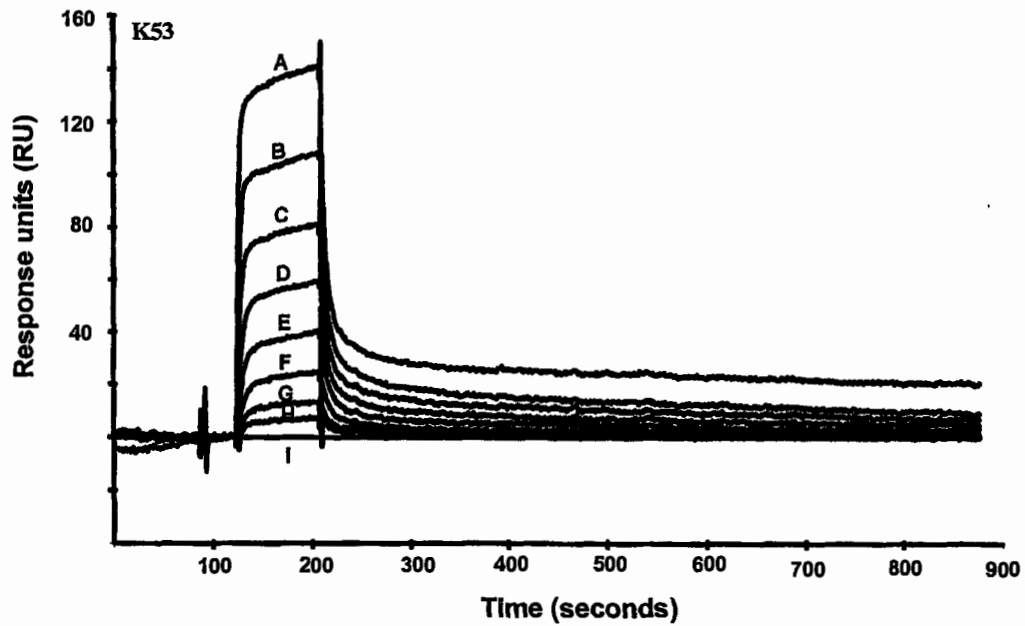
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FIG. 13

K53 VH	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMG	CDR1
UBS54 VH	1	QVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMG	
02-237	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMG	
		*****--**--*****	
K53 VH	50	WISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCAR	CDR2
UBS54	50	GIIPIFGNANYAQKFQGRVTITADESTSTAYMELSSLRSEDVAVYYCAR	
02-237	50	WISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCAR	
		-----**--*****--*_*-----**--*****	
K53 VH	99	GMMRGVFDYWGQGLVTVST	CDR3
UBS54 VH	99	DPFLH---YWGQGLVTVST	
02-237	99	GFPRTSFDSWGQGLVTVSS	
		-----**--*****--	

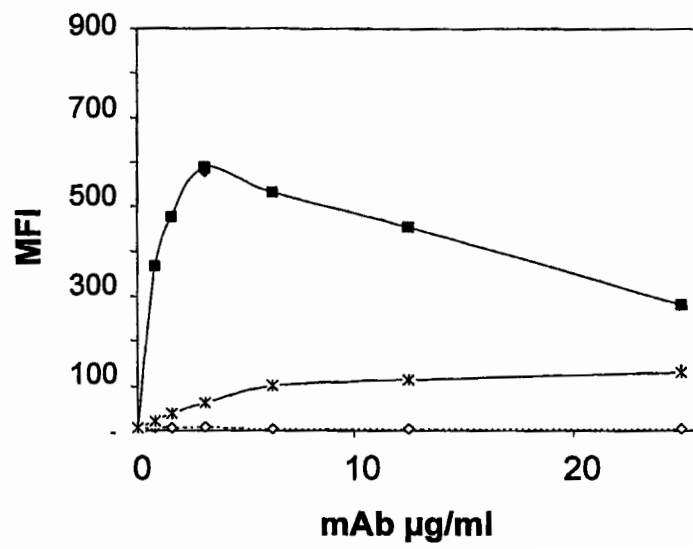
Fig. 14

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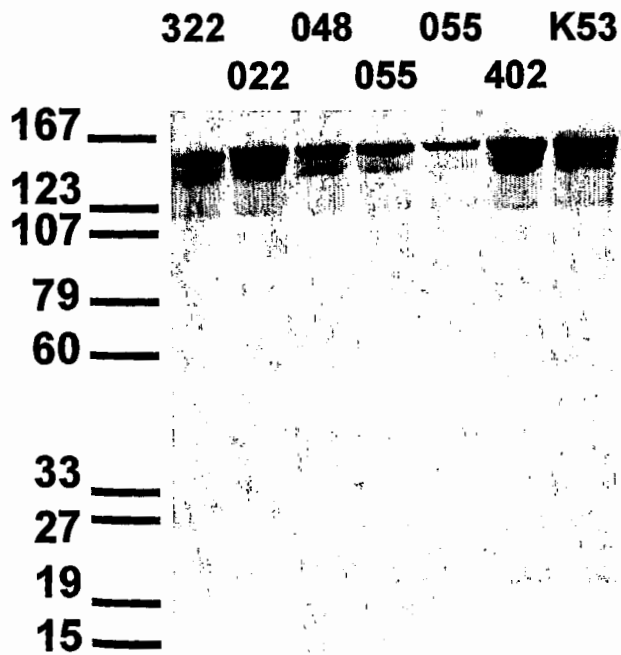
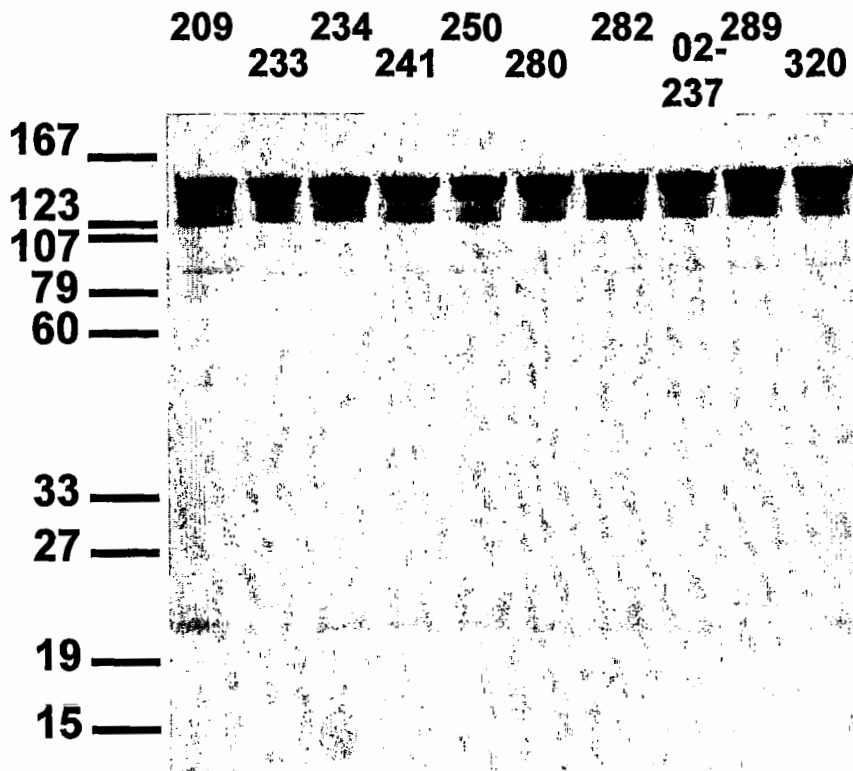
Fig. 15**21/33**

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Fig. 16A

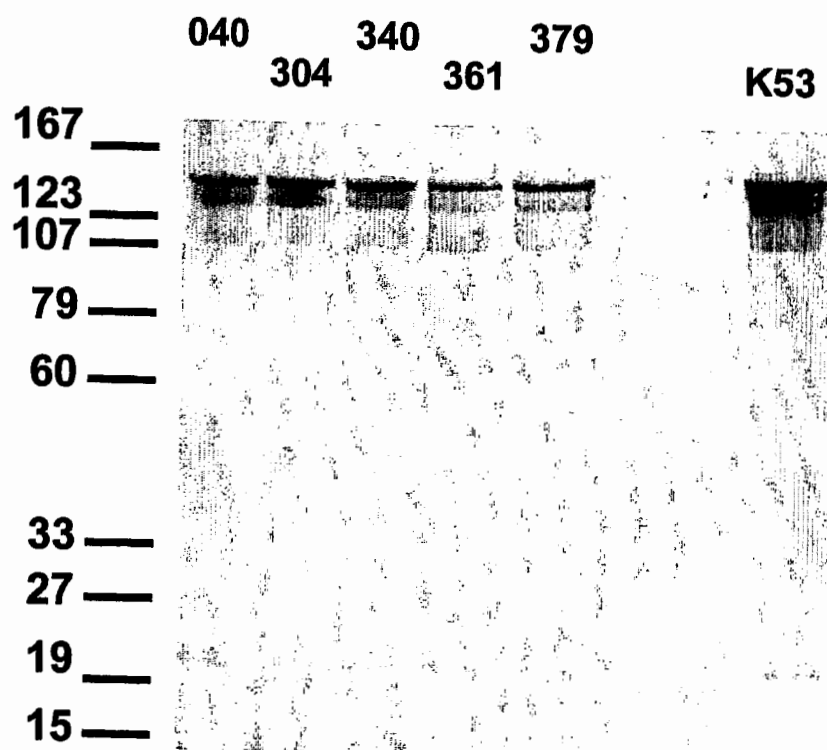


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Fig. 16A, cont'd

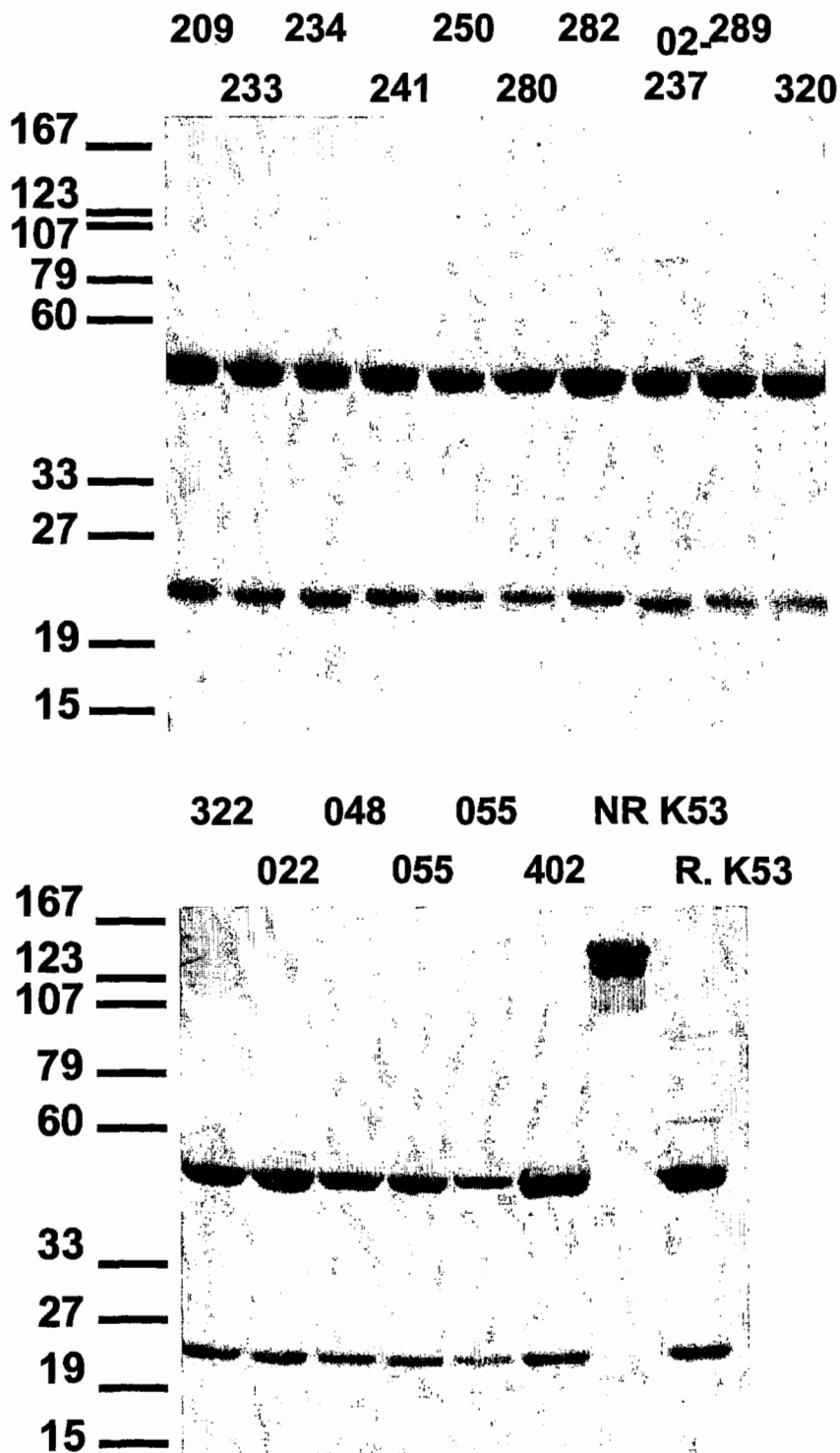


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Fig. 16B

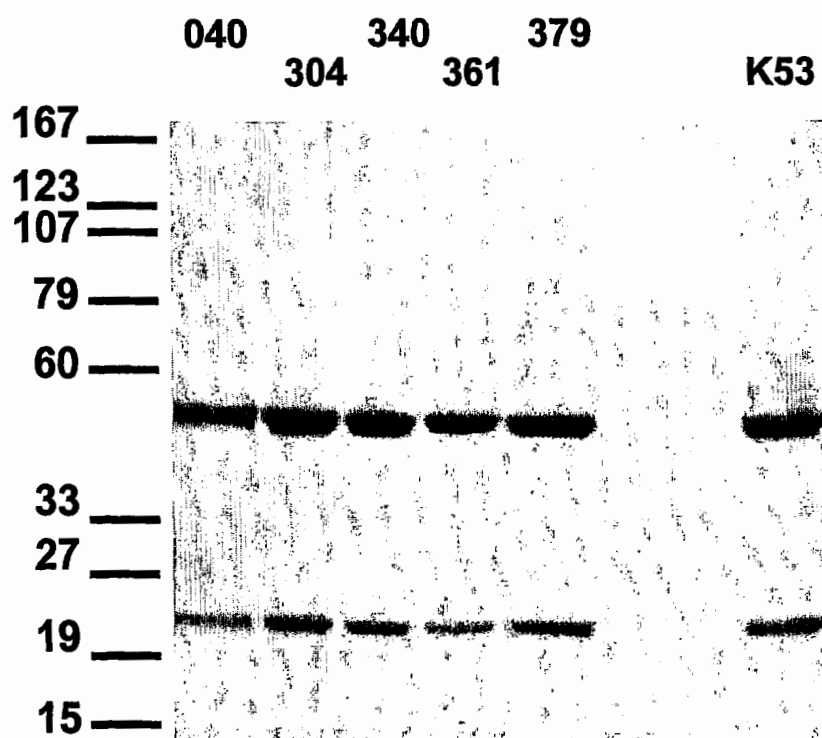


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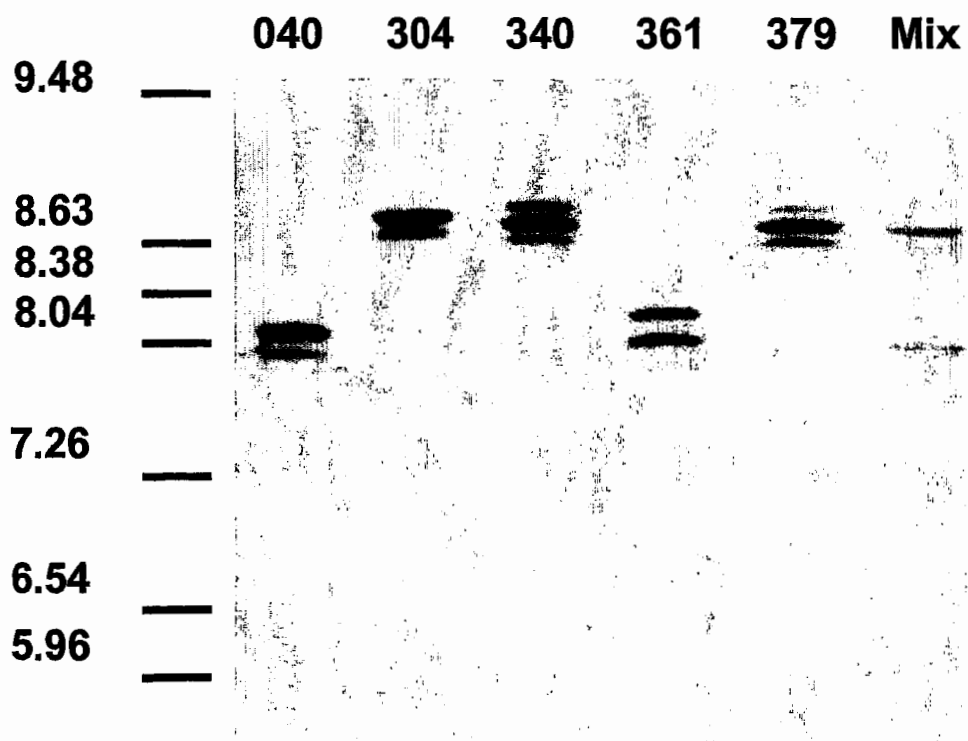
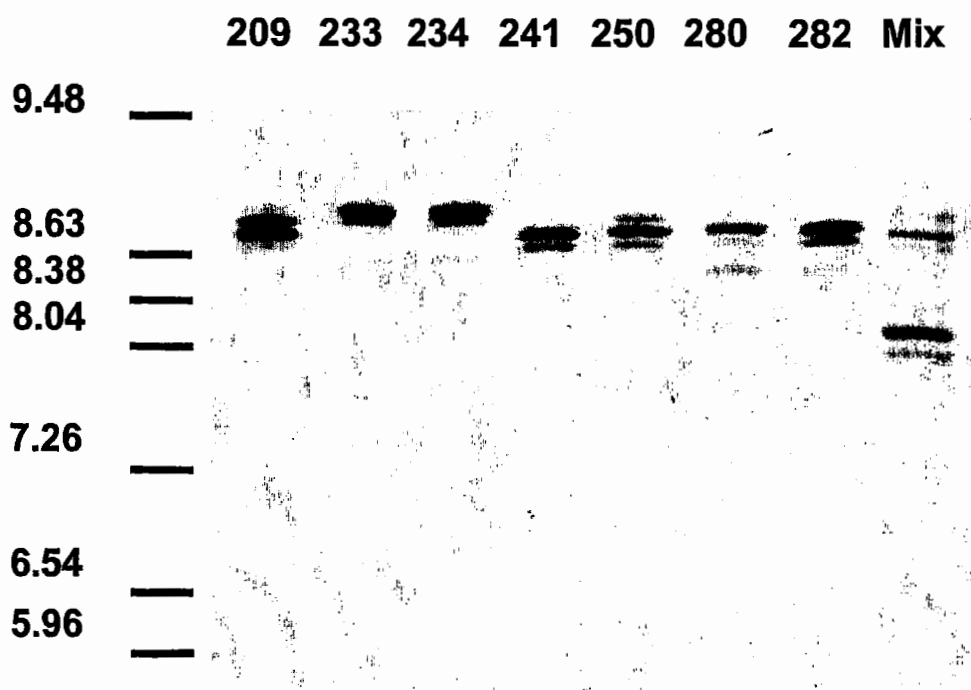
Fig. 16B, cont'd



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Fig. 17 **26/33**

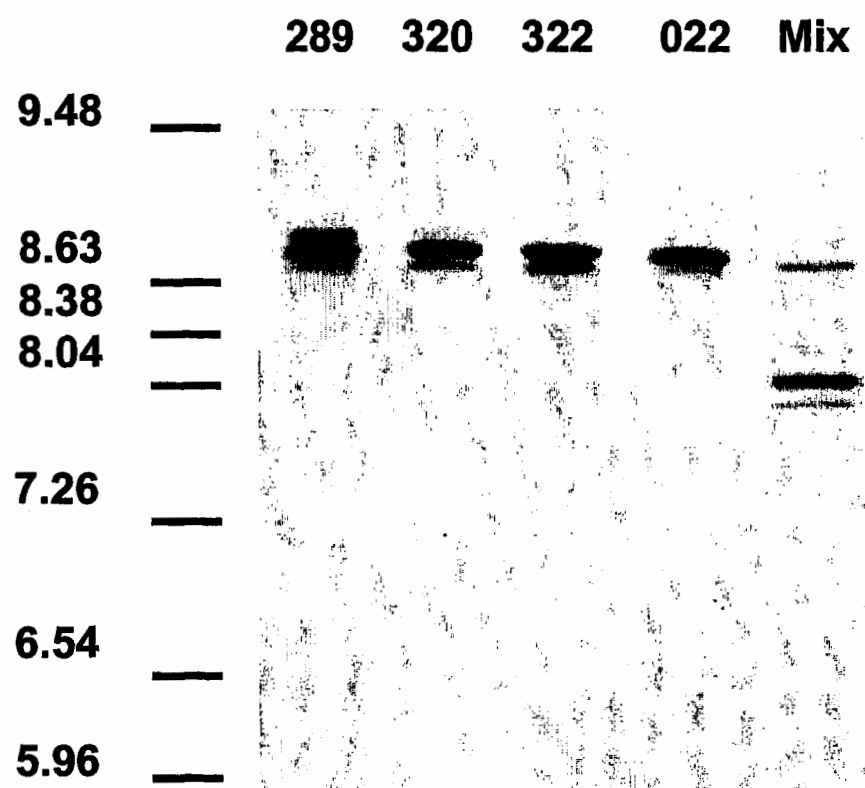


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Fig. 17, cont'd

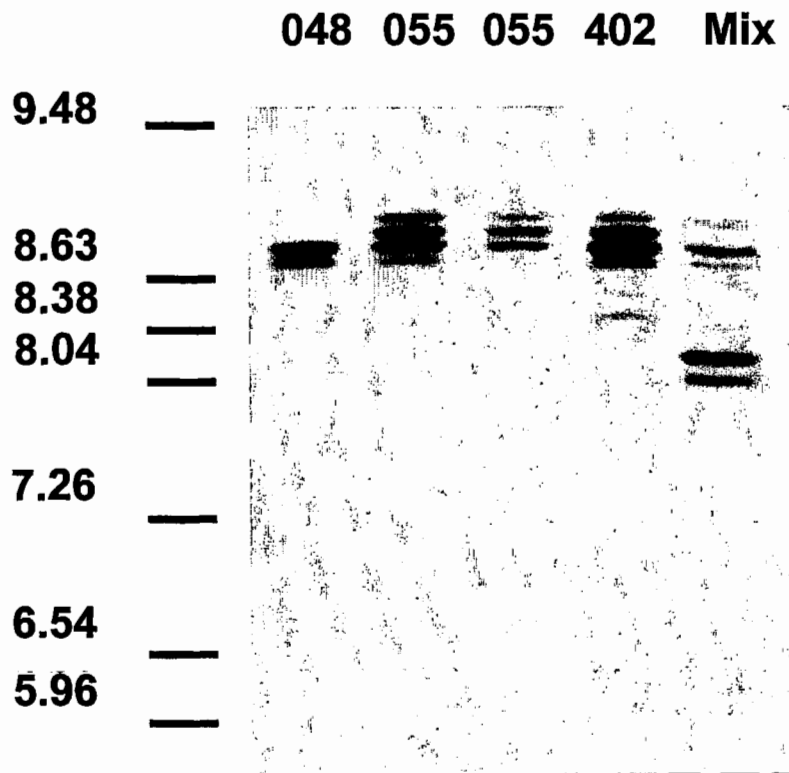


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Fig. 17, cont'd

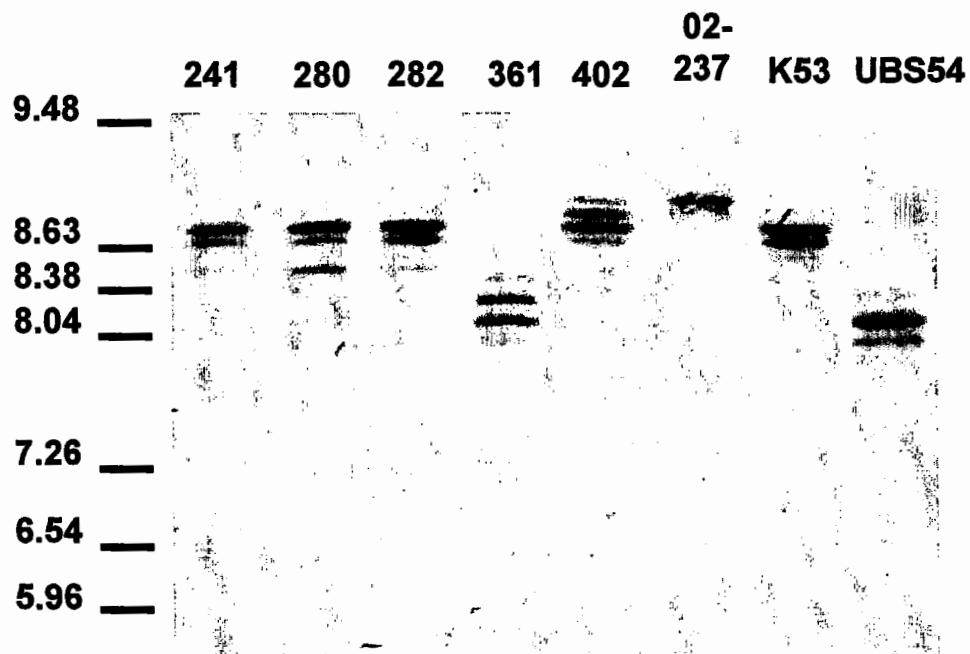


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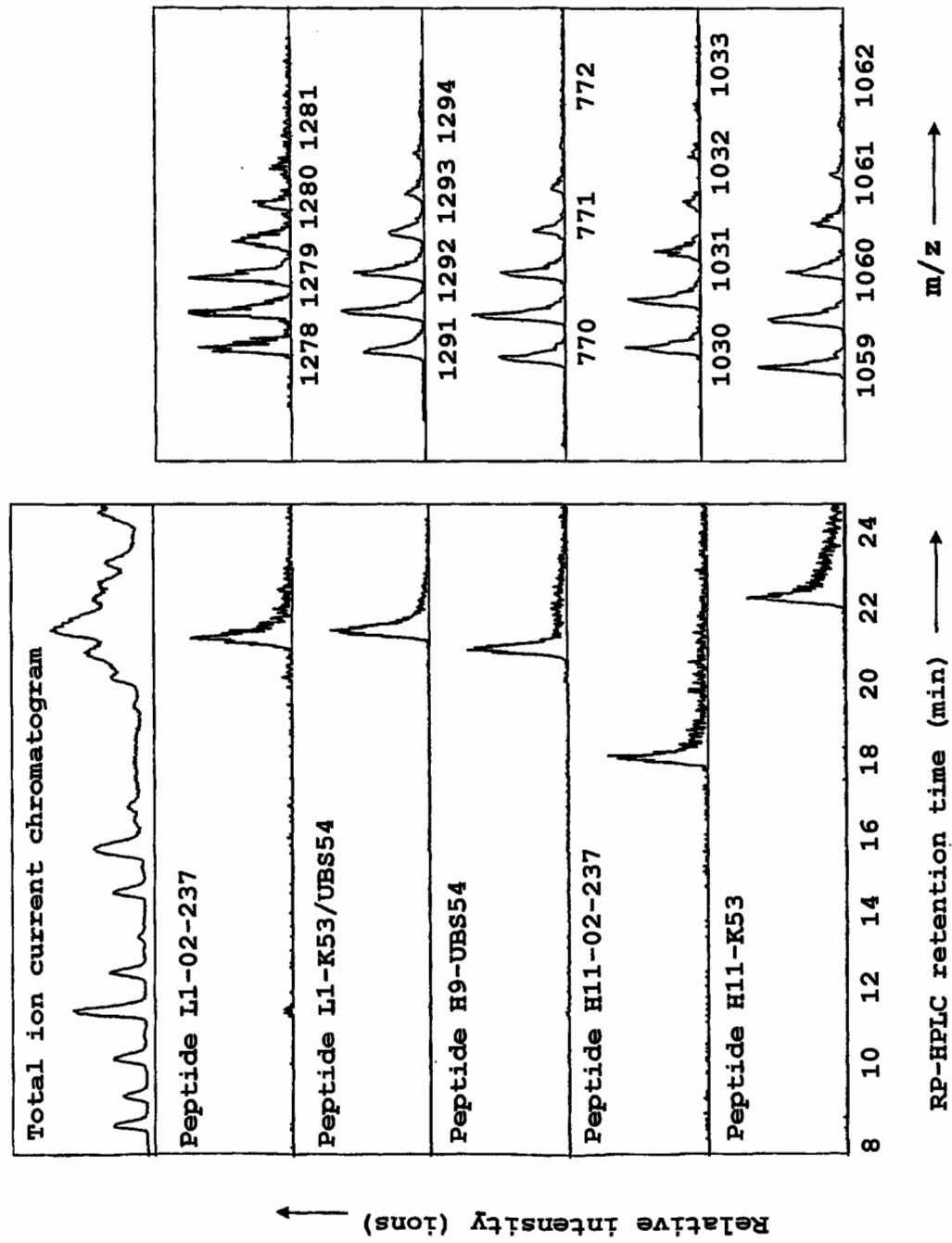
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Fig. 18



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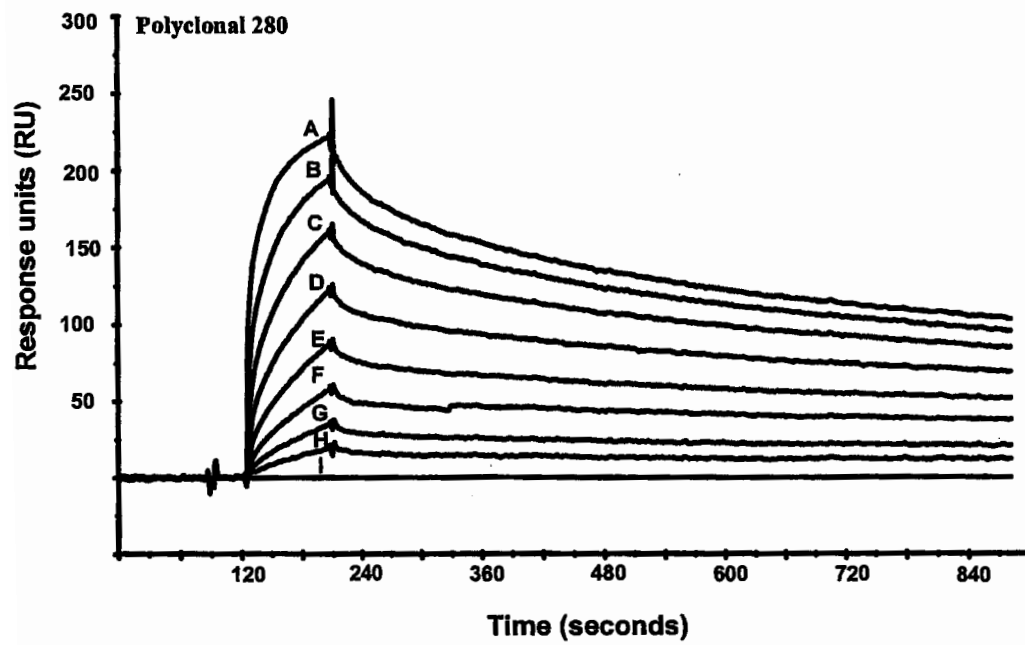
Fig. 19 peptide mapping of Polyclonal Poly1-280

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Fig. 20

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Fig. 21

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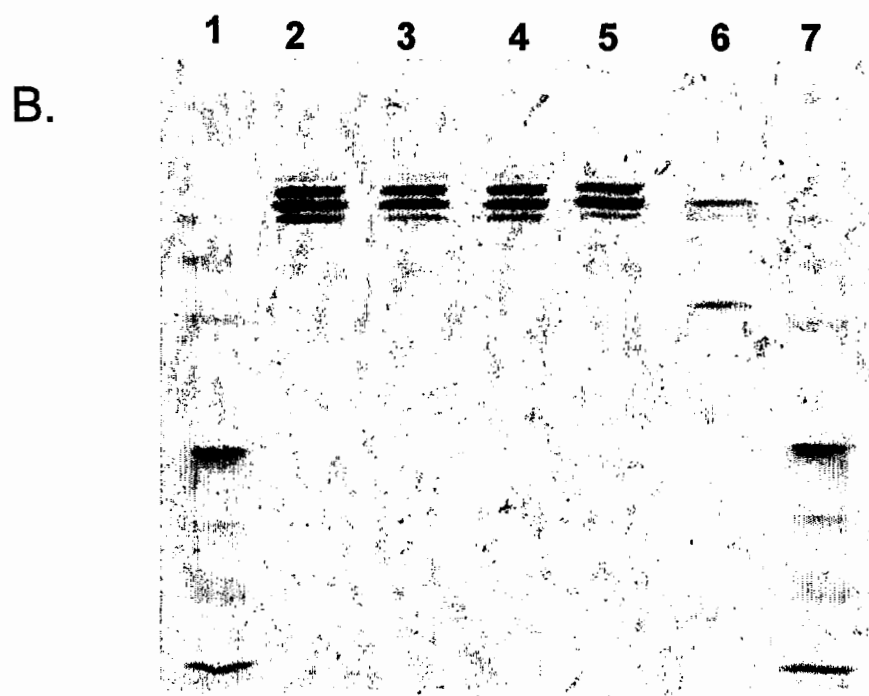
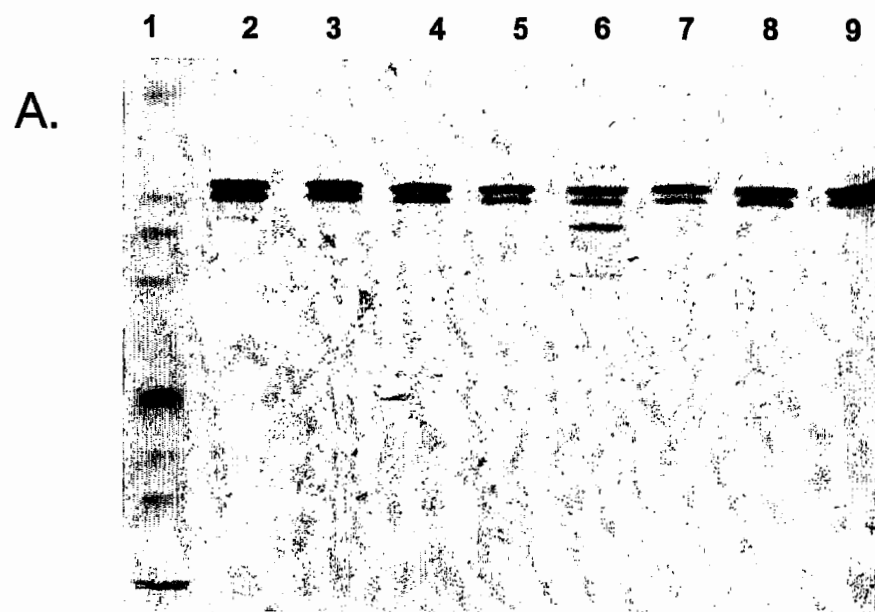
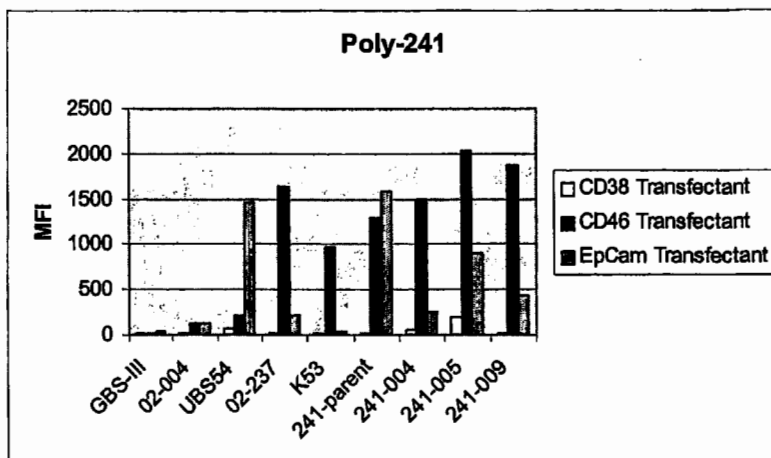


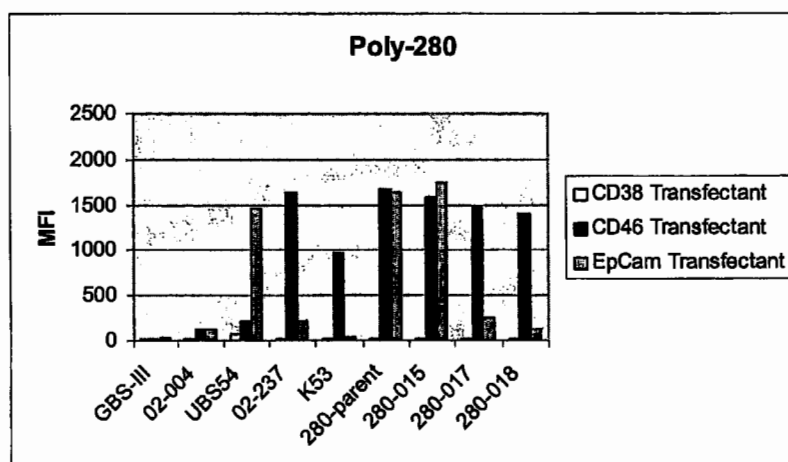
Fig. 22

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A.



B.



C.

