

FIGURE 1

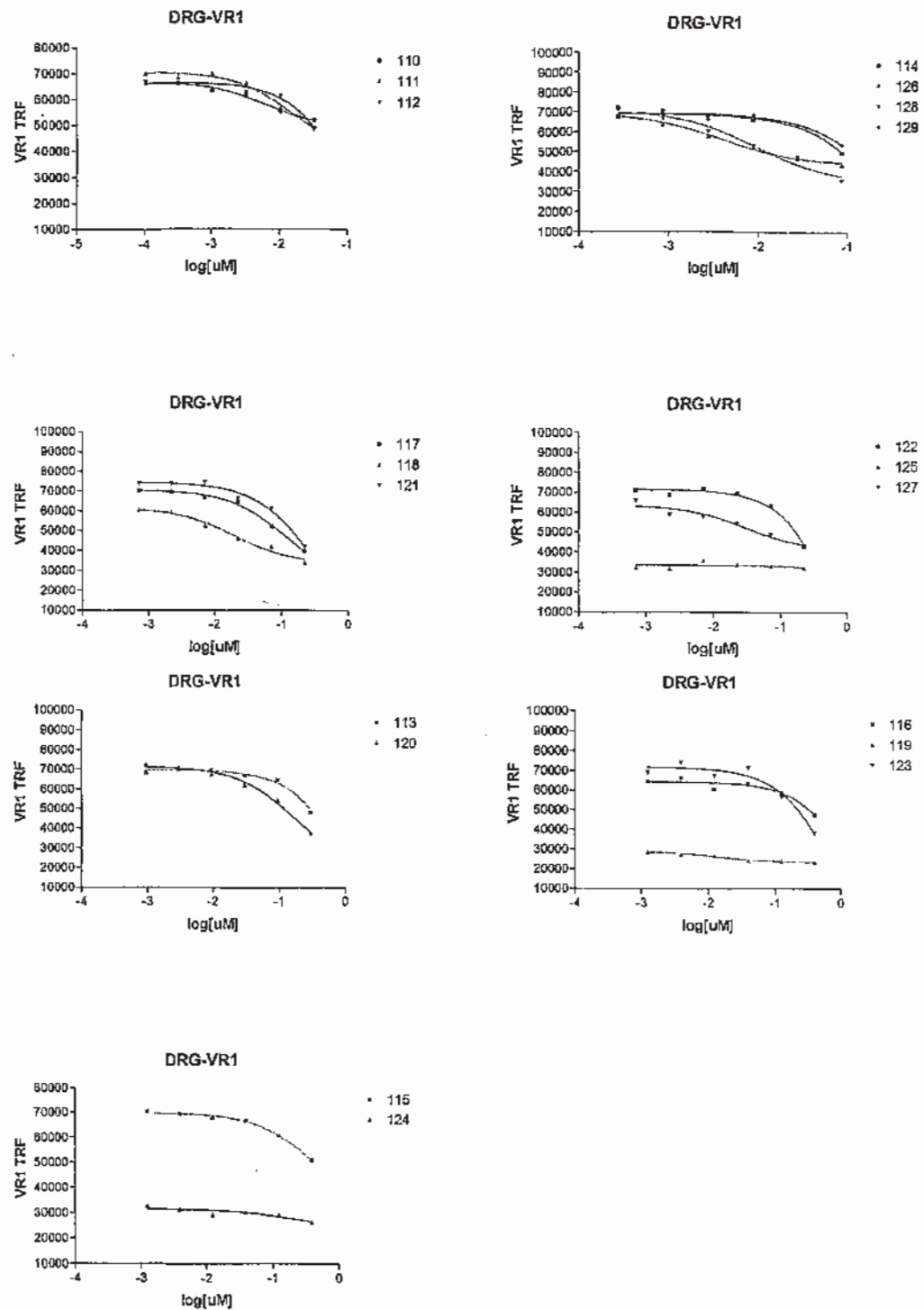


FIGURE 2

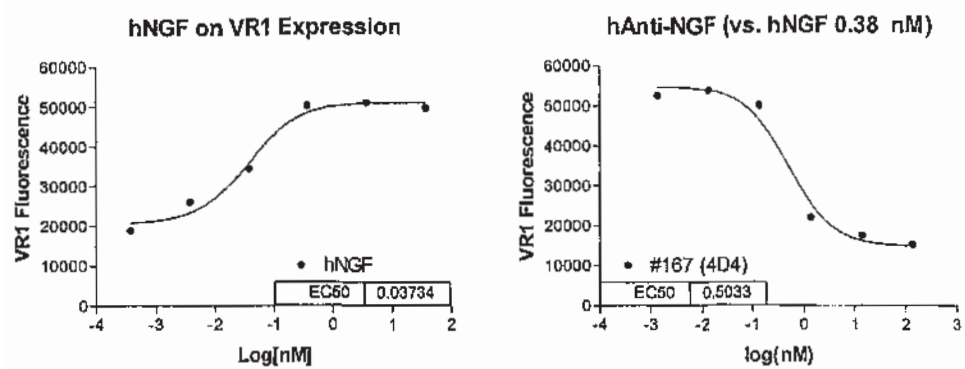


FIGURE 3

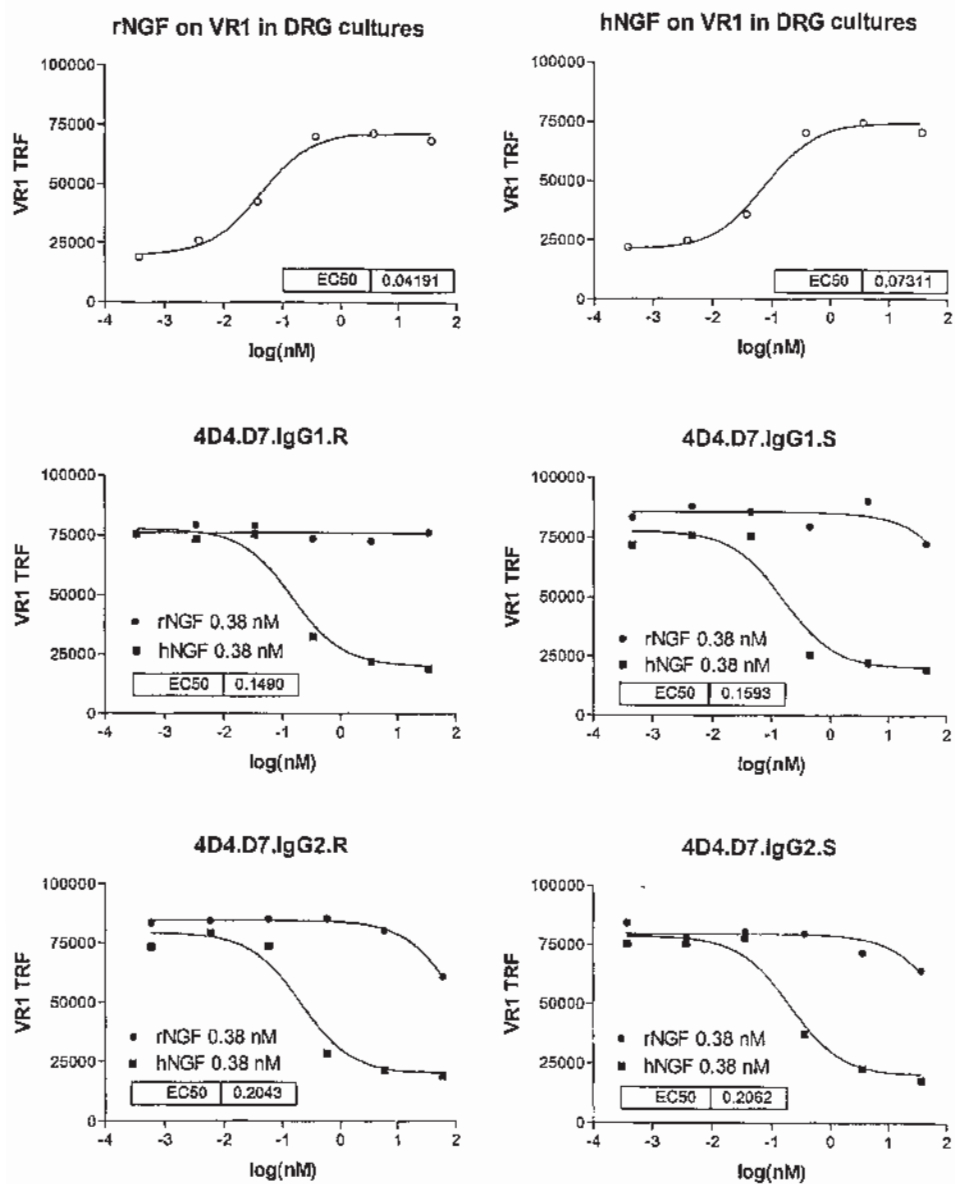


FIGURE 4

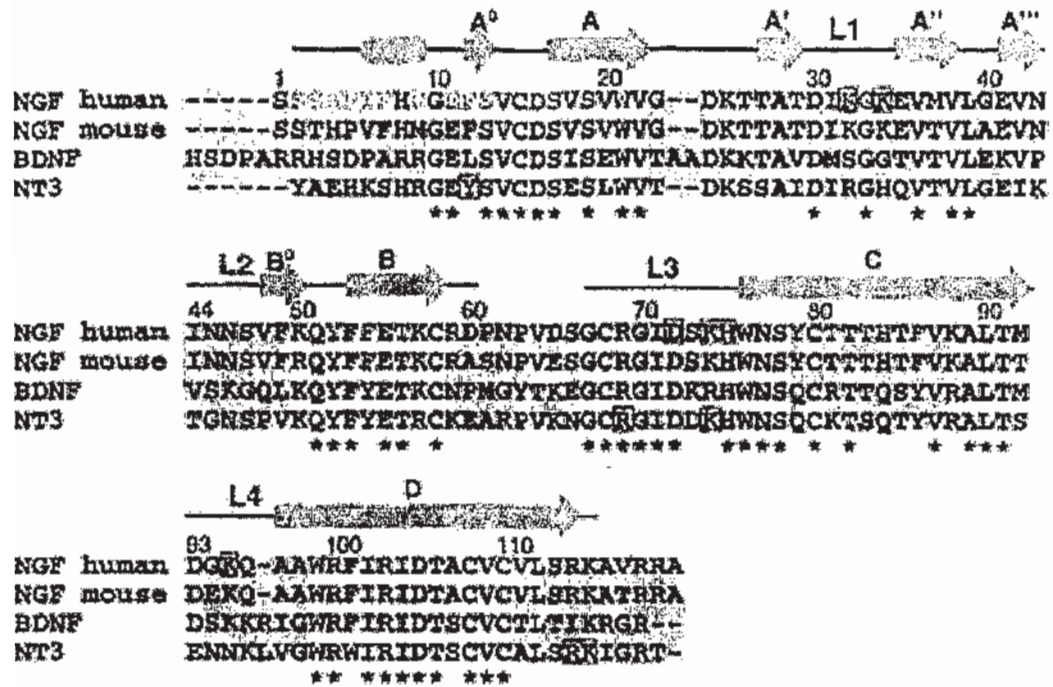


FIGURE 5

NGF CDR1 heavy chain alignments/ % identity

(1) 1 5
 14D10 HC CDR1 (1) DYAMH
 6H9 HC CDR1 (1) DYAMH
 7H2 HC CDR1 (1) DYAMH
 4G6 HC CDR1 (1) DYGMN
 14D11 HC CDR1 (1) TYWLG
 4D4 HC CDR1 (1) SYGMN

	14D10 HC CDR1	6H9 HC CDR1	7H2 HC CDR1	4G6 HC CDR1	14D11 HC CDR1	4D4 HC CDR1
14D10 HC CDR1	100	100	100	60	20	40
6H9 HC CDR1		100	100	60	20	40
7H2 HC CDR1			100	60	20	40
4G6 HC CDR1				100	20	60
14D11 HC CDR1					100	20
4D4 HC CDR1						100

FIGURE 6

NGF CDR2 heavy chain alignments/% identity

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(1) 1 17
14D10 HC CDR2 (1) GTSWNRGIIGYADSVRG
6H9 HC CDR2 (1) GTSWNRGIIGYAGSVRG
7H2 HC CDR2 (1) GTSWNRGIIGYADSVRG
4G6 HC CDR2 (1) DINWNGGSTGYADSVRG
4D4 HC CDR2 (1) YISRSSTTFYADSVRG
14D11 HC CDR2 (1) IIVPGDSDTKYSPSFQG

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	14D10 HC CDR2	6H9 HC CDR2	14D11 HC CDR2	4D4 HC CDR2	4G6 HC CDR2	7H2 HC CDR2
14D10 HC CDR2	100	94	24	59	70	82
6H9 HC CDR2		100	24	53	65	76
14D11 HC CDR2			100	24	29	24
4D4 HC CDR2				100	47	53
4G6 HC CDR2					100	70
7H2 HC CDR2						100

FIGURE 7

NGF CDR3 heavy chain alignments/% identity

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(1) 1 17
14D10 HC CDR3 (1) GYYGSGRPGYFYVMDV
6H9 HC CDR3 (1) GYYGSGRPGYFYVMDV
14D11 HC CDR3 (1) -NYYGSGTYVYVYGMNV
4G6 HC CDR3 (1) --EQWLDPYVYVYGMNV
4D4 HC CDR3 (1) -VYS-SGWHVSDY-FDY
7H2 HC CDR3 (1) ---EGSGR---YYNFDY

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	14D10 HC CDR3	6H9 HC CDR3	14D11 HC CDR3	4G6 HC CDR3	4D4 HC CDR3	7H2 HC CDR3
14D10 HC CDR3	100	100	35	41	18	18
6H9 HC CDR3		100	35	41	18	18
14D11 HC CDR3			100	53	29	35
4G6 HC CDR3				100	18	29
4D4 HC CDR3					100	41
7H2 HC CDR3						100

FIGURE 8

NGF CDR1 light chain alignments/% identity

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(1) 1 12
14D11 LC CDR1 (1) RASQGVSSWIA-
4G6 LC CDR1 20031028340 (1) RASQGVSSWIA-
4D4 LC CDR1 (1) RASQGVSSWIA-
4G6 LC CDR1 20031028351 (1) RASQGVSSWIA-
14D10 LC CDR1 (1) RASQGVSSWIA-
4G6 LC CDR1 20031000528 (1) RASQGVSSWIA-
4G6 LC CDR1 20031071526 (1) RASQGVSSWIA-
6H9 LC CDR1 (1) RASQGVSSWIA-
7H2 LC CDR1 (1) RASQGVSSWIA-
NGF 4G6 LC CDR1 20031028344 (1) RASQGVSSWIA-

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	14D11 LC CDR1	4G6 LC CDR1 20031028340	4D4 LC CDR1	4G6 LC CDR1 20031028351	14D10 LC CDR1	4G6 LC CDR1 20031000528	4G6 LC CDR1 20031071526	6H9 LC CDR1
14D11 LC CDR1	100	92	83	75	42	67	42	42
4G6 LC CDR1 20031028340		100	92	83	50	75	50	50
4D4 LC CDR1			100	83	50	75	50	50
4G6 LC CDR1 20031028351				100	58	92	58	58
14D10 LC CDR1					100	67	83	83
4G6 LC CDR1 20031000528						100	67	67
4G6 LC CDR1 20031071526							100	100
6H9 LC CDR1								100
7H2 LC CDR1								
NGF 4G6 LC CDR1 20031028344								

FIGURE 9

NGF CDR2 light chain alignments/% identity

(1) 1 7
 14D11 LC CDR2 (1) PASSAGE
 4G6 LC CDR2 20031028340 (1) PASSAGE
 4D4 LC CDR2 (1) PASSAGE
 4G6 LC CDR2 20031000528 (1) PASSAGE
 4G6 LC CDR2 20031028351 (1) PASSAGE
 6H9 LC CDR2 (1) PASSAGE
 14D10 LC CDR2 (1) PASSAGE
 4G6 LC CDR2 20031071526 (1) PASSAGE
 7H2 LC CDR2 (1) PASSAGE
 NGF 4G6 LC CDR2 20031028344 (1) PASSAGE

	14D11 LC CDR2	4G6 LC CDR2 20031028340	4D4 LC CDR2	4G6 LC CDR2 20031000528	4G6 LC CDR2 20031028351	6H9 LC CDR2	14D10 LC CDR2	4G6 LC CDR2 20031071526	7H2 LC CDR2	NGF 4G6 LC CDR2 20031028344
14D11 LC CDR2	100	100	71	28	28	43	43	43	43	43
4G6 LC CDR2 20031028340		100	71	28	28	43	43	43	43	43
4D4 LC CDR2			100	43	43	43	43	43	43	43
4G6 LC CDR2 20031000528				100	100	71	71	71	71	71
4G6 LC CDR2 20031028351					100	71	71	71	71	71
6H9 LC CDR2						100	86	86	86	86
14D10 LC CDR2							100	100	100	100
4G6 LC CDR2 20031071526								100	100	100
7H2 LC CDR2									100	100
NGF 4G6 LC CDR2 20031028344										100

FIGURE 10

NGF CDR3 light chain alignments/% identity

(1) 1 9
 14D10 LC CDR3 (1) QQYGSSSPYT
 7H2 LC CDR3 (1) QQYGSS-XT
 6H9 LC CDR3 (1) QQYGSSPYT
 4G6 LC CDR3 20031000528 (1) QQRSNWPHWT
 4G6 LC CDR3 20031028351 (1) QQRSNWPHWT
 14D11 LC CDR3 (1) QQANSPHWT
 4D4 LC CDR3 (1) QQYNAPPHWT
 4G6 LC CDR3 20031028340 (1) QQYNAPPHWT
 4G6 LC CDR3 20031071526 (1) QQYNAPPHWT
 NGF 4G6 LC CDR3 20031028344 (1) QQYGSSSPYT

	14D10 LC CDR3	7H2 LC CDR3	6H9 LC CDR3	4G6 LC CDR3 20031000528	4G6 LC CDR3 20031028351	14D11 LC CDR3	4D4 LC CDR3	4G6 LC CDR3 20031028340	4G6 LC CDR3 20031071526	NGF 4G6 LC CDR3 20031028344
14D10 LC CDR3	100	89	100	44	33	56	56	67	67	100
7H2 LC CDR3		100	89	33	33	44	44	56	56	89
6H9 LC CDR3			100	44	33	56	56	67	67	100
4G6 LC CDR3 20031000528				100	78	56	44	56	56	44
4G6 LC CDR3 20031028351					100	33	33	33	33	33
14D11 LC CDR3						100	67	78	78	56
4D4 LC CDR3							100	78	78	56
4G6 LC CDR3 20031028340								100	100	67
4G6 LC CDR3 20031071526									100	67
NGF 4G6 LC CDR3 20031028344										100

FIGURE 11

Alignment of light chain variable regions of mAbs 4G6, 7H2, 14D10, 14D11, 4G6, 4D4

		CDR 1	CDR 2	Section 1			
	(1)	10	20	30	40	50	67
4D4 VK	(1)	AIQLTQSPSSRLASVGDPRVTITCRASQGVSS-ALAYVQKRPQAPRLIYDASSLRSPSPRPSGSG					
NGF 4G6 kappa 20031071526 rc V region	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
NGF 4G6 LC 20031028344 v region	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
NGF 4G6 LC 20031028340 v region	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
NGF 4G6 LC 20031028351 v region	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
NGF LC 4G6 GR5' pCR4 20031000528 V region#2	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
NGF 14D10 LC 20031028386 rc v region	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
NGF 14D11 lc 20031028405 rc v region	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
NGF 6H9 Hu kappa V region no sp 2002120980	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
NGF 7H2 Hu kappa 2002120984 V region no sp	(1)	EIVLTQSPGTLISLSPGERATLSCRASQGVSSSYLAHYQKRPQAPRLIYDASSLRATIPDRPSGSG					
							Section 2
	(68)	BB	BO	CDR 3	108		
4D4 VK	(67)	SGTDFTLTISLQPEDFATYYCQYNSYPTFGQSTKVEIK					
NGF 4G6 kappa 20031071526 rc V region	(68)	SGTDFTLTISLQPEDFAVYYCQYNSYPTFGQSTKVEIK					
NGF 4G6 LC 20031028344 v region	(68)	SGTDFTLTISLQPEDFAVYYCQYNSYPTFGQSTKVEIK					
NGF 4G6 LC 20031028340 v region	(67)	SGTDFTLTISLQPEDFATYYCQYNSYPTFGQSTKVEIK					
NGF 4G6 LC 20031028351 v region	(67)	SGTDFTLTISLQPEDFAVYYCQYNSYPTFGQSTKVEIK					
NGF LC 4G6 GR5' pCR4 20031000528 V region#2	(67)	SGTDFTLTISLQPEDFAVYYCQYNSYPTFGQSTKVEIK					
NGF 14D10 LC 20031028386 rc v region	(68)	SGTDFTLTISLQPEDFAVYYCQYNSYPTFGQSTKVEIK					
NGF 14D11 lc 20031028405 rc v region	(67)	SGTDFTLTISLQPEDFAVYYCQYNSYPTFGQSTKVEIK					
NGF 6H9 Hu kappa V region no sp 2002120980	(68)	SGTDFTLTISLQPEDFAVYYCQYNSYPTFGQSTKVEIK					
NGF 7H2 Hu kappa 2002120984 V region no sp	(68)	SGTDFTLTISLQPEDFAVYYCQYNSYPTFGQSTKVEIK					

FIGURE 12

Alignment of heavy chain variable regions of mAbs 4D4,
4G6, 14D10, 14D11, 7H2, 6H9

	(1)	10	20	30	40	50	60
4D4 VH	(1)	EVQLVESGGGLVQPGGSLRL	3CAAAGPTLH	9YGMH	WVROAPGKGL	EVV	SI
NGF 14D10 HC 20031071581 v region	(1)	EVQLVESGGGLVQPGGSLRL	3CAASGPTLH	9YGMH	WVROAPGKGL	EVV	SI
NGF 6H9 HC Hu-Rat 2002120864 final V region	(1)	EVQLVESGGGLVQPGGSLRL	3CAASGPTLH	9YGMH	WVROAPGKGL	EVV	SI
NGF 7H2 Hu-Rat IgG2b.5 2002118141 final V region	(1)	EVQLVESGGGLVQPGGSLRL	3CAASGPTLH	9YGMH	WVROAPGKGL	EVV	SI
NGF 14D11 HC race 20031028394rc V region	(1)	EVQLVESGGGLVQPGGSLRL	3CAASGPTLH	9YGMH	WVROAPGKGL	EVV	SI
NGF 4G6 HC pCR4TOPO 20031028326r V region	(1)	EVQLVESGGGLVQPGGSLRL	3CAASGPTLH	9YGMH	WVROAPGKGL	EVV	SI
Section 2							
	(57)	57	60	80	100	127	
4D4 VH	(57)	RFTISRDNARNSLYLQMS	SLRAEDTALYYCAR	---	VYSSGMHVSDFD	YWGQGITLVTS	
NGF 14D10 HC 20031071581 v region	(57)	RFTISRDNARNSLYLQMS	SLRAEDTALYYCAR	---	VYSSGMHVSDFD	YWGQGITLVTS	
NGF 6H9 HC Hu-Rat 2002120864 final V region	(57)	RFTISRDNARNSLYLQMS	SLRAEDTALYYCAR	---	VYSSGMHVSDFD	YWGQGITLVTS	
NGF 7H2 Hu-Rat IgG2b.5 2002118141 final V region	(57)	RFTISRDNARNSLYLQMS	SLRAEDTALYYCAR	---	VYSSGMHVSDFD	YWGQGITLVTS	
NGF 14D11 HC race 20031028394rc V region	(57)	RFTISRDNARNSLYLQMS	SLRAEDTALYYCAR	---	VYSSGMHVSDFD	YWGQGITLVTS	
NGF 4G6 HC pCR4TOPO 20031028326r V region	(57)	RFTISRDNARNSLYLQMS	SLRAEDTALYYCAR	---	VYSSGMHVSDFD	YWGQGITLVTS	