Figure 1A

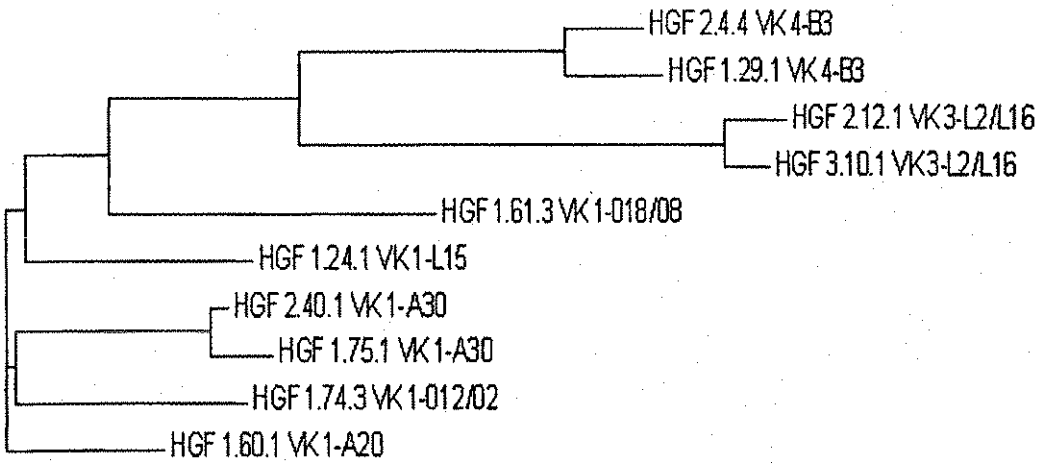

HGF 2.4.4 VK4-B3
HGF 1.29.1 VK4-B3
HGF 2.12.1 VK3-L2/L16
HGF 3.10.1 VK3-L2/L16
HGF 1.61.3 VK1-018/08
HGF 1.24.1 VK1-L15
HGF 2.40.1 VK1-A30
HGF 1.75.1 VK1-A30
HGF 1.74.3 VK1-012/02
HGF 1.60.1 VK1-A20

Figure 1B

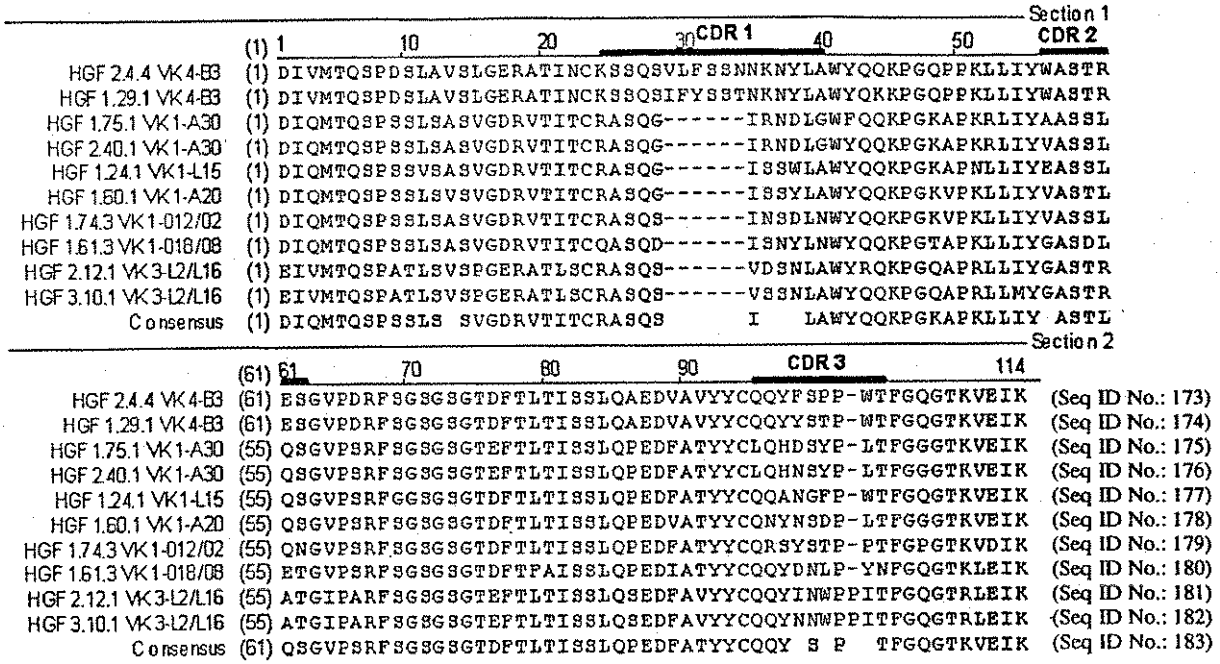

Section 1
CDR 1
CDR 2
HGF 2.4.4 VK4-B3 (1) DIVMTQSPDSLAVSLGERATINCKSSQSVLFSSNNKNYLAWYQQKPGQPPKLLIYWASTR
HGF 1.29.1 VK4-B3 (1) DIVMTQSPDSLAVSLGERATINCKSSQSIFYSSTNKNYLAWYQKKPGQPPKLLIYWASTR
HGF 1.75.1 VK1-A30 (1) DIQMTQSPSSLSASVGDRVTITCRASQG------IRNDLGWFQQKPGKAPKRLIYAASSL
HGF 2.40.1 VK1-A30 (1) DIQMTQSPSSLSASVGDRVTITCRASQG------IRNDLGWYQQKPGKAPKRLIYVASSL
HGF 1.24.1 VK1-L15 (1) DIQMTQSPSSVSASVGDRVTITCRASQG------ISSWLAWYQQKPGKAPNLLIYEASSL
HGF 1.60.1 VK1-A20 (1) DIQMTQSPSSLSVSVGDRVTITCRASQG------ISSYLAWYQQKPGKVPKLLIYVASTL
HGF 1.74.3 VK1-012/02 (1) DIQMTQSPSSLSASVGDRVTITCRASQS------INSDLNWYQQKPGKVPKLLIYVASSL
HGF 1.61.3 VK1-018/08 (1) DIQMTQSPSSLSASVGDRVTITCQASQD------ISNYLNWYQQKPGTAPKLLIYGASDL
HGF 2.12.1 VK3-L2/L16 (1) EIVMTQSPATLSVSPGERATLSCRASQS------VDSNLAWYRQKPGQAPRLLIYGASTR
HGF 3.10.1 VK3-L2/L16 (1) EIVMTQSPATLSVSPGERATLSCRASQS------VSSNLAWYQQKPGQAPRLLMYGASTR
Consensus (1) DIQMTQSPSSLS SVGDRVTITCRASQS I LAWYQQKPGKAPKLLIY ASTL
Section 2
CDR 3
HGF 2.4.4 VK4-B3 (61) ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYFSPP-WTFGQGTKVEIK (Seq ID No.: 173)
HGF 1.29.1 VK4-B3 (61) ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP-WTFGQGTKVEIK (Seq ID No.: 174)
HGF 1.75.1 VK1-A30 (55) QSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHDSYP-LTFGGGTKVEIK (Seq ID No.: 175)
HGF 2.40.1 VK1-A30 (55) QSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP-LTFGGGTKVEIK (Seq ID No.: 176)
HGF 1.24.1 VK1-L15 (55) QSGVPSRFGGSGSGTDFTLTISSLQPEDFATYYCQQANGFP-WTFGQGTKVEIK (Seq ID No.: 177)
HGF 1.60.1 VK1-A20 (55) QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQNYNSDP-LTFGGGTKVEIK (Seq ID No.: 178)
HGF 1.74.3 VK1-012/02 (55) QNGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRSYSTP-PTFGPGTKVDIK (Seq ID No.: 179)
HGF 1.61.3 VK1-018/08 (55) ETGVPSRFSGSGSGTDFTFAISSLQPEDIATYYCQQYDNLP-YNFGQGTKLEIK (Seq ID No.: 180)
HGF 2.12.1 VK3-L2/L16 (55) ATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYINWPPITFGQGTRLEIK (Seq ID No.: 181)
HGF 3.10.1 VK3-L2/L16 (55) ATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPITFGQGTRLEIK (Seq ID No.: 182)
Consensus (61) QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQY S P TFGQGTKVEIK (Seq ID No.: 183)

Figure 2A

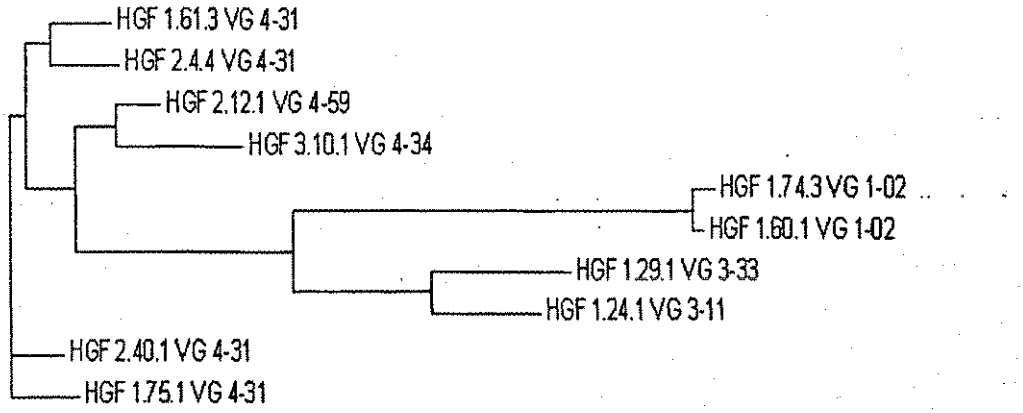
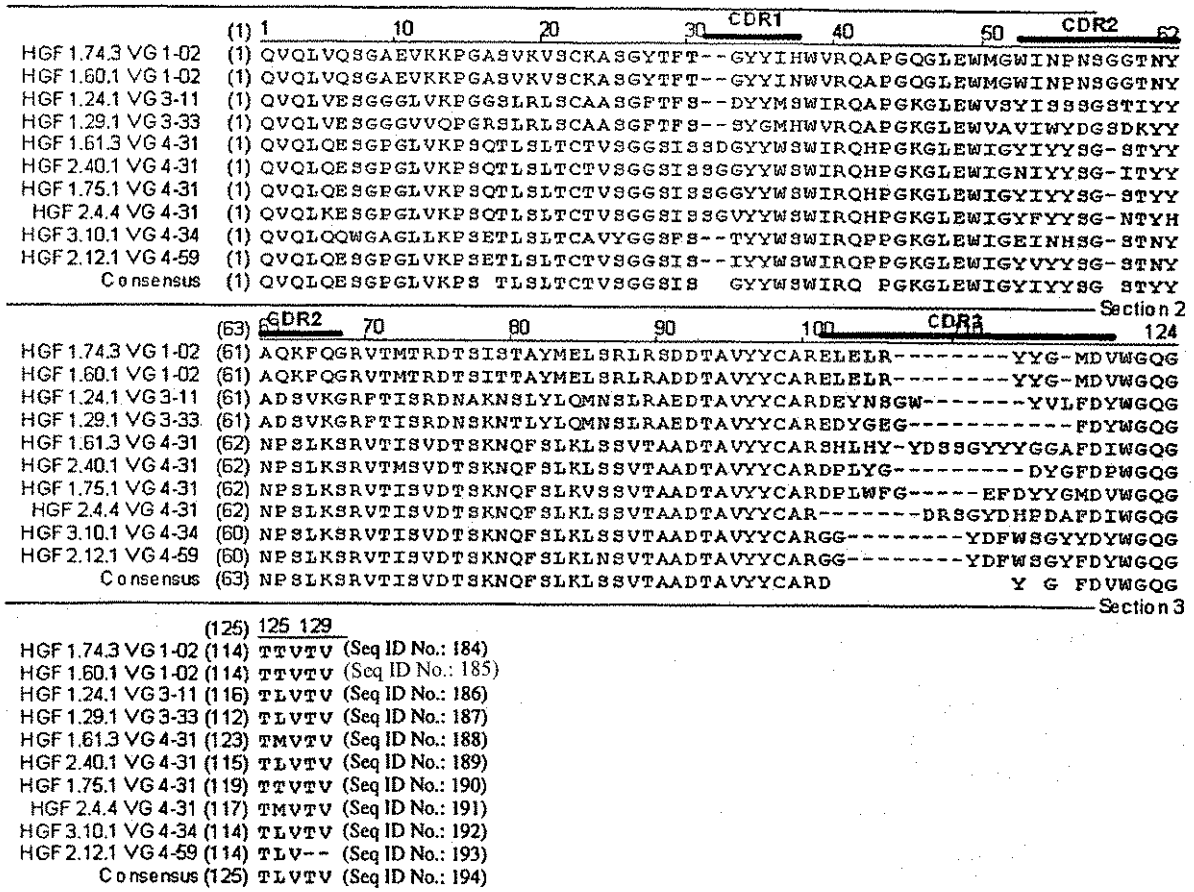

HGF 1.61.3 VG 4-31
HGF 2.4.4 VG 4-31
HGF 2.12.1 VG 4-59
HGF 3.10.1 VG 4-34
HGF 1.74.3 VG 1-02
HGF 1.60.1 VG 1-02
HGF 1.29.1 VG 3-33
HGF 1.24.1 VG 3-11
HGF 2.40.1 VG 4-31
HGF 1.75.1 VG 4-31

Figure 2B



(125) 125 129
HGF 1.74.3 VG 1-02 (114) TTVTV (Seq ID No.: 184)
HGF 1.60.1 VG 1-02 (114) TTVTV (Seq ID No.: 185)
HGF 1.24.1 VG 3-11 (116) TLVTV (Seq ID No.: 186)
HGF 1.29.1 VG 3-33 (112) TLVTV (Seq ID No.: 187)
HGF 1.61.3 VG 4-31 (123) TMVTV (Seq ID No.: 188)
HGF 2.40.1 VG 4-31 (115) TLVTV (Seq ID No.: 189)
HGF 1.75.1 VG 4-31 (119) TTVTV (Seq ID No.: 190)
HGF 2.4.4 VG 4-31 (117) TMVTV (Seq ID No.: 191)
HGF 3.10.1 VG 4-34 (114) TLVTV (Seq ID No.: 192)
HGF 2.12.1 VG 4-59 (114) TLV-- (Seq ID No.: 193)
Consensus (125) TLVTV (Seq ID No.: 194)

Figure 3

HGF 1.24.1 Light chain V region (Vk, 1-L15)

ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCCCAGGTTCCAGATGC
GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCT
AACCTCCTGATCTATGAAGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCGGCGGCAGTGGA
TCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGT
CAACAGGCTAACGGTTTCCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA (SEQ ID NO: 01)

HGF 1.24.1 Heavy chain V region (Vh, H3-11)-huIgG2 C region)

ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGCTATTATAAAAGGTGTCCAGTGTCAGGTGCAG
CTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGG
GTTTCATACATTAGTAGTAGTGGTAGTACCATATACTACGCAGACTCTGTGAAGGGCCGATTCACC
ATCTCCAGGGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG
GCCGTGTATTACTGTGCGAGAGATGAGTATAACAGTGGCTGGTACGTCCTCTTTGACTACTGGGGC
CAGGGAACCCTGGTCACCGTCTCTAGT (SEQ ID NO: 02)

HGF 1.29.1 Light chain V region (Vk, 4-B3)

ATGGTGTTGCAGACCCAGGTCTTCATTTCTCTGTTGCTCTGGATCTCTGATGCCTACGGAGACATC
GTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG
TCCAGCCAGAGTATTTTTTACAGCTCCACCAATAAGAACTACTTAGCTTGGTATCAGAAGAAACCG
GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGGTTC
AGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCA
GTTTATTACTGTCAGCAATATTATAGTACTCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATC
AAA (SEQ ID NO: 03)

HGF 1.29.1 Heavy chain V region (Vh, 3-33)- huIgG2 C region

ATGGAGTTTGGGCTGAACTGGGTTTTCCTCGTTGCTCTTTTAAGAGGTGTCCAGTGTCAGGTGCAG
CTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCT
GGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCGGGCAAGGGACTGGAGTGG
GTGGCAGTTATATGGTATGATGGAAGTGATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG
GCTGTGTATTACTGTGCGAGAGAGGACTACGGCGAGGGTTTTGACTACTGGGGCCAGGGAACCCTG
GTCACCGTCTCTAGT (SEQ ID NO: 04)

HGF 1.60.1 Light chain V region (Vk, 1-A20)

ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGACTCCTGCTGCTCTGGCTCCCAGATACCAGATGT
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGTATCTGTCGGAGACAGAGTCACCATCACT
TGCCGGGCGAGTCAGGGCATTAGCAGTTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCT
AAGCTCCTGATCTATGTTGCATCCACTTTGCAATCAGGGGTCCCGTCTCGGTTCAGTGGCAGTGGA
TCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT
CAAAACTATAACAGTGACCCGCTCACTTTCGGCGGCGGGACCAAGGTGGAGATCAAA (SEQ ID NO: 05)

Figure 3 (continued)

HGF 1.60.1 Heavy chain V region (Vh, H1-02)- huIgG2 C region

ATGGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCCACAGGAGCCCACTCCCAGGTGCAG
CTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT
GGATACACCTTCACCGGCTACTATATAAACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGG
ATGGGATGGATCAACCCTAACAGTGGTGGCACAAACTATGCACAGAAGTTTCAGGGCAGGGTCACC
ATGACCAGGGACACGTCCATCACCACAGCCTACATGGAGCTGAGCAGGCTGAGAGCTGACGACACG
GCCGTGTACTACTGTGCGAGAGAACTGGAACTACGCTACTACGGTATGGACGTCTGGGGCCAAGGG
ACCACGGTCACCGTCTCTAGT (SEQ ID NO: 06)

HGF 1.61.3 Light chain V region (Vk, 1-018/08)

ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCTCAGGTGCCAGATGT
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGCCAGGCGAGTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGGACAGCCCCT
AAACTCCTGATCTACGGTGCATCCGATTTGGAAACGGGGGTCCCATCAAGGTTCAGTGGAAGTGGA
TCTGGGACAGATTTTACTTTCGCCATCAGCAGCCTGCAGCCTGAAGATATTGCAACATATTACTGT
CAACAGTATGATAATCTCCCGTACAATTTTGGCCAGGGGACCAAGCTGGAGATCAAA (Seq.
ID NO: 07)

HGF 1.61.3 Heavy chain V region (Vh, 4-31)- huIgG2 C region

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAG
CTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT
GGTGGCTCCATCAGCAGTGATGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTG
GAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTC
ACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGAC
ACGGCCGTCTATTACTGTGCGAGATCCCACCTTCATTACTATGATAGTAGTGGTTATTACTACGGC
GGTGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTAGT (SEQ ID NO: 08)

HGF 1.74.3 Light chain V region (Vk, 1-012/02)

ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCGAGGTGCCAGATGT
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGCCGGGCAAGTCAGAGCATTAACAGCGATTTAAATTGGTATCAGCAGAAACCAGGGAAAGTCCCT
AAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGTTCAGTGGCAGTGGA
TCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGT
CAACGGAGTTACAGTACCCCTCCCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA (SEQ
ID NO: 09)

HGF 1.74.3 Heavy chain V region (Vh, VG1-02)- huIgG2 C region

ATGGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCCACAGGAGCCCACTCCCAGGTGCAG
CTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT
GGATACACCTTCACCGGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGG
ATGGGATGGATCAACCCTAACAGTGGTGGCACAAACTATGCACAGAAGTTTCAGGGCAGGGTCACC
ATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGAGCAGGCTGAGATCTGACGACACG
GCCGTGTATTACTGTGCGAGAGAACTGGAACTACGCTACTACGGTATGGACGTCTGGGGCCAAGGG
ACCACGGTCACCGTCTCTAGT (SEQ ID NO: 10)

Figure 3 (continued)

HGF 1.75.1 Light chain V region (Vk, 1-A30)

ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCCCAGGTGCCAGGTGT
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGGTTTCAGCAGAAACCAGGGAAAGCCCCT
AAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGAATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGT
CTACAGCATGATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA (SEQ ID NO: 11)

HGF 1.75.1 Heavy chain V region (Vh, VG4-31)- huIgG2 C region

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAG
CTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT
GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTG
GAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTT
ACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGGTGAGCTCTGTGACTGCCGCGGAC
ACGGCCGTGTATTACTGTGCGAGAGACCCACTATGGTTCGGGGAGTTCGACTACTACGGTATGGAC
GTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT (SEQ ID NO: 12)

HGF 2.4.4 Light chain V region (Vk, 4-B3)

ATGGTGTTGCAGACCCAGGTCTTCATTTCTCTGTTGCTCTGGATCTCTGGTGCCTACGGGGACATC
GTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG
TCCAGCCAGAGTGTTTTATTCAGCTCCAACAATAAGAATTACTTAGCTTGGTATCAGCAGAAACCA
GGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTC
AGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCA
GTTTATTACTGTCAGCAATATTTTAGTCCTCCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATC
AAA (SEQ ID NO: 13)

HGF 2.4.4 Heavy chain V region (Vh, VG 4-31)- huIgG2 C region

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGATCCTGTCCCAGGTGCAG
CTGAAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT
GGTGGCTCCATCAGCAGTGGTGTTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTG
GAGTGGATTGGGTACTTCTATTATAGTGGGAACACCTACCACAACCCGTCCCTCAAGAGTCGAGTG
ACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGAC
ACGGCCGTGTATTACTGTGCGAGAGATCGTAGTGGCTACGATCACCCTGATGCTTTTGATATCTGG
GGCCAAGGGACAATGGTCACCGTCTCTAGT (SEQ ID NO: 14)

HGF 2.12.1 Light chain V region (Vk, 3-L2/L16)

ATGGAAGCCCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACTGGAGAAATA
GTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTGACAGCAACTTAGCCTGGTACCGGCAGAAACCTGGCCAGGCTCCCAGGCTC
CTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGG
ACTGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAG
TATATTAACTGGCCTCCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA (SEQ ID NO: 15)

Figure 3 (continued)

HGF 2.12.1 Heavy chain V region (Vh4-59)- huIgG2 C region

ATGAAACACCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAG
CTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCT
GGTGGCTCCATCAGTATTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGG
ATTGGGTATGTCTATTACAGTGGGAGCACCAATTACAACCCCTCCCTCAAGAGTCGAGTCACCATA
TCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAACTCTGTGACCGCTGCGGACACGGCC
GTGTATTACTGTGCGAGAGGGGGATACGATTTTTGGAGTGGTTATTTTGACTACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCTAGT (SEQ ID NO: 16)

HGF 2.40.1 Light chain V region (Vk, 1A20)

ATGGACATGAGGGTGCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCCCAGGTGCCAGGTGT
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCT
AAGCGCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGAATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGT
CTACAACATAATAGTTACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA (SEQ
ID NO: 17)

HGF 2.40.1 Heavy chain V region (Vh, VG 4-31)- huIgG2 C region

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAG
CTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT
GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGTCAGCACCCAGGGAAGGGCCTG
GAGTGGATTGGGAACATCTATTACAGTGGGATCACCTACTACAACCCGTCCCTCAAGAGTCGAGTT
ACCATGTCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGTTCTGTGACTGCCGCGGAC
ACGGCCGTGTATTACTGTGCGAGAGATCCCCTCTACGGTGACTACGGGTTCGACCCCTGGGGCCAG
GGAACCCTGGTCACCGTCTCTAGT (SEQ ID NO: 18)

HGF 3.10.1 Light chain V region (Vk, 3-L2/L16)

ATGGAAGCCCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACTGGAGAAATA
GTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCTGGGGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC
CTCATGTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGG
ACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAG
TATAATAACTGGCCTCCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA (SEQ ID NO:
19)

HGF 3.10.1 Heavy chain V region (Vh, VG 4-34)- huIgG1 C region

ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAG
CTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTAT
GGTGGGTCCTTCAGTACTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGG
ATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGAGTCACCATA
TCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCT
GTGTATTACTGTGCGAGAGGGGGGTACGATTTTTGGAGTGGTTATTATGACTACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCTAGT (SEQ ID NO: 20)

Figure 3 (continued)

Human Kappa Constant Region

CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACT
GCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGAT
AACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTAC
AGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA
GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA

(SEQ ID NO: 21)

Human IgG1 Constant Region

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAG
CCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCA
CCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC
ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG
GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT
GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCC
AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGG
GAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
TGA (SEQ ID NO: 22)

Human IgG2 Constant Region

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGC
GCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAG
CCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCA
GCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAAC
AGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGG
CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC
AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG
CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTAC
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ
ID NO: 23)

Figure 4

HGF 1.24.1 Light chain V region (Vk, 1-L15)
MDMRVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAP
NLLIYEASSLQSGVPSRFGGSGSGTDFTLTISSLQPEDFATYYCQQANGFPWTFGQGTKVEIK
(SEQ ID NO: 24)

HGF 1.24.1 Heavy chain V region (Vh, H3-11)-huIgG2 C region
MEFGLSWVFLVAIIKGVQCQVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEW
VSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDEYNSGWYVLFDYWG
QGTLVTVSS (SEQ ID NO: 25)

HGF 1.29.1 Light chain V region (Vk, 4-B3)
MVLQTQVFISLLLWISDAYGDIVMTQSPDSLAVSLGERATINCKSSQSIFYSSTNKNYLAWYQKKP
GQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPWTFGQGTKVEI
K (SEQ ID NO: 26)

HGF 1.29.1 Heavy chain V region (Vh, 3-33)- huIgG2 C region
MEFGLNWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW
VAVIWYDGSDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDYGEGFDYWGQGTL
VTVSS (SEQ ID NO: 27)

HGF 1.60.1 Light chain V region (Vk, 1-A20)
MDMRVPAQLLGLLLLWLPDTRCDIQMTQSPSSLSVSVGDRVTITCRASQGISSYLAWYQQKPGKVP
KLLIYVASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQNYNSDPLTFGGGTKVEIK
(SEQ ID NO: 28)

HGF 1.60.1 Heavy chain V region (Vh, H1-02)- huIgG2 C region
MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYINWVRQAPGQGLEW
MGWINPNSGGTNYAQKFQGRVTMTRDTSITTAYMELSRLRADDTAVYYCARELELRYYGMDVWGQG
TTVTVSS (SEQ ID NO: 29)

HGF 1.61.3 Light chain V region (Vk, 1-018/08)
MDMRVPAQLLGLLLLWLSGARCDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGTAP
KLLIYGASDLETGVPSRFSGSGSGTDFTFAISSLQPEDIATYYCQQYDNLPYNFGQGTKLEIK
(SEQ ID NO: 30)

HGF 1.61.3 Heavy chain V region (Vg, 4-31)- huIgG2 C region
MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSQTLSLTCTVSGGSISSDGYYWSWIRQHPGKGL
EWIGYIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSHLHYYDSSGYYYG
GAFDIWGQGTMVTVSS (SEQ ID NO: 31)

HGF 1.74.3 Light chain V region (Vk, 1-012/02)
MDMRVPAQLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSINSDLNWYQQKPGKVP
KLLIYVASSLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQRSYSTPPTFGPGTKVDIK
(SEQ ID NO: 32)

HGF 1.74.3 Heavy chain V region(Vh, VG1-02)-huIgG2 C region
MDWTWRILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEW
MGWINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARELELRYYGMDVWGQG
TTVTVSS (SEQ ID NO: 33)

Figure 4 (continued)

HGF 1.75.1 Light chain V region (Vk, 1-A30)
MDMRVPAQLLGLLLLWFPGARCDIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWFQQKPGKAP
KRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHDSYPLTFGGGTKVEIK
(SEQ ID NO: 34)

HGF 1.75.1 Heavy chain V region (Vh, VG4-31)-huIgG2 C region
MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGL
EWIGYIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKVSSVTAADTAVYYCARDPLWFGEFDYYGMD
VWGQGTTVTVSS **(SEQ ID NO: 35)**

HGF 2.4.4 Light chain V region (Vk, 4-B3)
MVLQTQVFISLLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLFSSNNKNYLAWYQQKP
GQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYFSPPWTFGQGTKVEI
K **(SEQ ID NO: 36)**

HGF 2.4.4 Heavy chain V region (Vh, VG 4-31)-huIgG2 C region
MKHLWFFLLLVAAPRWILSQVQLKESGPGLVKPSQTLSLTCTVSGGSISSGVYYWSWIRQHPGKGL
EWIGYFYYSGNTYHNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRSGYDHPDAFDIW
GQGTMVTVSS **(SEQ ID NO: 37)**

HGF 2.12.1 Light chain V region (Vk, 3-L2/L16)
MEAPAQLLFLLLLWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVDSNLAWYRQKPGQAPRL
LIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYINWPPITFGQGTRLEIK
(SEQ ID NO: 38)

HGF 2.12.1 Heavy chain V region (Vg, 4-59)- huIgG2 C region
MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISIYYWSWIRQPPGKGLEW
IGYVYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLNSVTAADTAVYYCARGGYDFWSGYFDYWGQG
TLVTVSS **(SEQ ID NO: 39)**

HGF 2.40.1 Light chain V region (Vk, 1A20)
MDMRVPAQLLGLLLLWFPGARCDIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAP
KRLIYVASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK
(SEQ ID NO: 40)

HGF 2.40.1 Heavy chain V region (Vh, VG 4-31)-huIgG2 C region
MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGL
EWIGNIYYSGITYYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDPLYGDYGFDPWGQ
GTLVTVSS **(SEQ ID NO: 41)**

HGF 3.10.1 Light chain V region (Vk, 3-L2/L16)
MEAPAQLLFLLLLWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRL
LMYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPITFGQGTRLEIK
(SEQ ID NO: 42)

HGF 3.10.1 Heavy chain V region (Vh, VG 4-34)-huIgG1 C region
MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSTYYWSWIRQPPGKGLEW
IGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYDFWSGYYDYWGQG
TLVTVSS **(SEQ ID NO: 43)**

Figure 4 (continued)

Human Kappa Constant Region

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY
SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC **(SEQ ID NO: 44)**

Human IgG1 Constant Region

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD
TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 45)

Human IgG2 Constant Region

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 46)

Figure 5A

Light Chain Variable Region Amino Acid Sequences for CDR1, CDR2, and CDR3

Antibody	CDR1	CDR2	CDR3
1.24.1	RASQGISSWLA (SEQ ID NO. 60)	EASSLQS (SEQ ID NO. 70)	QQANGFPWT (SEQ ID NO. 80)
1.29.1	KSSQSIFYSSTNKNYLA (SEQ ID NO. 61)	WASTRES (SEQ ID NO. 71)	QQYYSTPWT (SEQ ID NO. 81)
1.60.1	RASQGISSYLA (SEQ ID NO. 62)	VASTLQS (SEQ ID NO. 72)	QNYNSDPLT (SEQ ID NO. 82)
1.61.3	QASQDISNYLN (SEQ ID NO. 63)	GASDLET (SEQ ID NO. 73)	QQYDNLPYN (SEQ ID NO. 83)
1.74.3	RASQSINSDLN (SEQ ID NO. 64)	VASSLQN (SEQ ID NO. 74)	QRSYSTPPT (SEQ ID NO. 84)
1.75.1	RASQGIRNDLG (SEQ ID NO. 65)	AASSLQS (SEQ ID NO. 75)	LQHDSYPLT (SEQ ID NO. 85)
2.4.4	KSSQSVLFSSNNKNYLA (SEQ ID NO. 66)	WASTRES (SEQ ID NO. 76)	QQYFSPPWT (SEQ ID NO. 86)
2.12.1	RASQSVDSNLA (SEQ ID NO. 67)	GASTRAT (SEQ ID NO. 77)	QQYINWPPIT (SEQ ID NO. 87)
2.40.1	RASQGIRNDLG (SEQ ID NO. 68)	VASSLQS (SEQ ID NO. 78)	LQHNSYPLT (SEQ ID NO. 88)
3.10.1	RASQSVSSNLA (SEQ ID NO. 69)	GASTRAT (SEQ ID NO. 79)	QQYNNWPPIT (SEQ ID NO. 89)

Light chain CDR1 consensus sequence (CDR1a) (SEQ ID NO: 166): a b c d e f g h i j k l m n o p q, where wherein amino acid a is selected from lysine, arginine, or glutamine; amino acid b is selected from serine or alanine; amino acid c is serine, amino acid d is glutamine; amino acid e is selected from serine, glycine, or aspartic acid; amino acid f is selected from valine or isoleucine or is not present; amino acid g is selected from leucine or phenylalanine or is not present; amino acid h is selected from phenylalanine or tyrosine or is not present; amino acid i is serine or not present; amino acid j is serine or not present; amino acid k is selected from asparagine, threonine, or not present; amino acid l is selected from asparagine, isoleucine, or valine; amino acid m is selected from lysine, arginine, asparagine, or aspartic acid; amino acid n is selected from asparagine or serine; amino acid o is selected from tyrosine, aspartic acid, tryptophan, or asparagine; amino acid p is leucine; and amino acid q is selected from alanine, glycine, or asparagine

Light chain CDR2 consensus sequence (CDR2a) (SEQ ID NO: 167): r s t u v w x, wherein amino acid r is selected from tryptophan, alanine, valine, glutamic acid, or glycine; amino acid s is alanine, amino acid t is serine, amino acid u is selected from threonine, serine, or aspartic acid; amino acid v is selected from arginine or leucine; amino acid w is selected from glutamic acid, glutamine, or alanine; and amino acid x is selected from serine, asparagine, or threonine

Light chain CDR3 consensus sequence (CDR3a) (SEQ ID NO: 168): y z a' b' c' d' e' f' g' h', wherein amino acid y is selected from glutamine or leucine; amino acid z is selected from glutamine, asparagine, or arginine; amino acid a' is selected from tyrosine, histidine, alanine, or serine; amino acid b' is selected from phenylalanine, tyrosine, aspartic acid, asparagine, or isoleucine; amino acid c' is selected from serine, glycine, or asparagine; amino acid d' is selected from proline, tyrosine, threonine, phenylalanine, aspartic acid, leucine, or tryptophan; amino acid e' is proline; amino acid f' is proline or is not present; amino acid g' is tryptophan, leucine, proline, tyrosine, or isoleucine; and amino acid h' is threonine or asparagine

Figure 5B

Heavy Chain Variable Region Amino Acid Sequences for CDR1, CDR2, and CDR3

Antibody	CDR1	CDR2	CDR3
1.24.1	DYYMS (SEQ ID NO. 90)	YISSSGSTIYYADSVKG (SEQ ID NO. 100)	DEYNSGWYVLFDY (SEQ ID NO. 110)
1.29.1	SYGMH (SEQ ID NO. 91)	VIWYDGSDKYYADSVKG (SEQ ID NO. 101)	EDYGEGFDY (SEQ ID NO. 111)
1.60.1	GYYIN (SEQ ID NO. 92)	WINPNSGGTNYAQKFQG (SEQ ID NO. 102)	ELELRYYGMDV (SEQ ID NO. 112)
1.61.3	SDGYYWS (SEQ ID NO. 93)	YIYYSGSTYYNPSLKS (SEQ ID NO. 103)	SHLHYYDSSGYYYGGAFDI (SEQ ID NO. 113)
1.74.3	GYYIH (SEQ ID NO. 94)	WINPNSGGTNYAQKFQG (SEQ ID NO. 104)	ELELRYYGMDV (SEQ ID NO. 114)
1.75.1	SGGYYWS (SEQ ID NO. 95)	YIYYSGSTYYNPSLKS (SEQ ID NO. 105)	DPLWFGEFDYYGMDV (SEQ ID NO. 115)
2.4.4	SGVYYWS (SEQ ID NO. 96)	YFYYSGNTYHNPSLKS (SEQ ID NO. 106)	DRSGYDHPDAFDI (SEQ ID NO. 116)
2.12.1	IYYWS (SEQ ID NO. 97)	YVYYSGSTNYNPSLKS (SEQ ID NO. 107)	GGYDFWSGYFDY (SEQ ID NO. 117)
2.40.1	SGGYYWS (SEQ ID NO. 98)	NIYYSGITYYNPSLKS (SEQ ID NO. 108)	DPLYGDYGFDP (SEQ ID NO. 118)
3.10.1	TYYWS (SEQ ID NO. 99)	EINHSGSTNYNPSLKS (SEQ ID NO. 109)	GGYDFWSGYYDY (SEQ ID NO. 119)

Heavy chain CDR1 consensus sequence (CDR1b) (SEQ ID NO: 169): a b c d e f g, wherein amino acid a is serine or is not present; amino acid b is selected from aspartic acid or glycine, or is not present; amino acid c is selected from aspartic acid, glycine, serine, valine, threonine, or isoleucine; amino acid d is tyrosine; amino acid e is selected from tyrosine or glycine; amino acid f is selected from isoleucine, methionine, or tryptophan; and amino acid g is selected from histidine, asparagine, or serine

Heavy chain CDR2 consensus sequence (CDR2b) (SEQ ID NO: 170): h i j k l m n o p q r s t u v w x, wherein amino acid h is selected from tryptophan, tyrosine, valine, asparagine, or glutamic acid; amino acid i is selected from isoleucine, phenylalanine, or valine; amino acid j is selected from asparagine, serine, tryptophan, or tyrosine; amino acid k is selected from proline, serine, tyrosine, or histidine; amino acid l is selected from asparagine, serine, or aspartic acid; amino acid m is selected from serine or glycine; amino acid n is selected from glycine or serine, or is not present; amino acid o is selected from glycine, threonine, aspartic acid, serine, isoleucine, or asparagine; amino acid p is selected from threonine, isoleucine, or lysine; amino acid q is selected from asparagine or tyrosine; amino acid r is selected from tyrosine or histidine; amino acid s is selected from alanine or asparagine; amino acid t is selected from glutamine, aspartic acid, or proline; amino acid u is selected from lysine or serine; amino acid v is selected from phenylalanine, valine, or leucine; amino acid w is selected from glutamine or lysine, and amino acid x is selected from glycine or serine

Heavy chain CDR3 consensus sequence (CDR3b) (SEQ ID NO: 171): y z a' b' c' d' e' f' g' h' i' j' k' l' m' n' o' p' q' r', wherein amino acid y is selected from glutamic acid, aspartic acid, serine, or glycine, or is not present; amino acid z is selected from leucine, glutamic acid, aspartic acid, histidine, proline, or glycine, or is not present; amino acid a' is selected from glutamic acid, tyrosine, or leucine, or is not present; amino acid b' is selected from leucine, asparagine, glycine, histidine, tyrosine, or tryptophan, or is not present; amino acid c' is selected from arginine, serine, glutamic acid, tyrosine, glycine, or phenylalanine, or is not present; amino acid d' is glycine or is not present; amino acid e' is selected from tryptophan or tyrosine, or is not present; amino acid f' is aspartic acid or is not present; amino acid g' is selected from serine or arginine, or is not present; amino acid h' is serine or is not present; amino acid i' is selected from glycine or tyrosine, or is not present; amino acid j' is selected from tyrosine, glutamic acid, or aspartic acid, or is not present; amino acid k' is selected from tyrosine, phenylalanine, or aspartic acid, or is not present; amino acid l' is selected from tyrosine, aspartic acid, histidine, or tryptophan, or is not present; amino acid m' is selected from tyrosine, glycine, aspartic acid, proline, or serine, or is not present; amino acid n' is selected from glycine, valine, tyrosine, or aspartic acid, or is not present; amino acid o' is selected from leucine, alanine, glycine, or tyrosine, or is not present; amino acid p' is selected from methionine, phenylalanine, or tyrosine; amino acid q' is aspartic acid, and amino acid r' is selected from valine, tyrosine, isoleucine, or proline

Figure 6A

ID	~Kd (M)	ka (1/Ms)	kd (1/s)
3.10.1	4.7E-10	6.5E+04	3.0E-05
2.4.4	9.9E-11	2.7E+05	2.7E-05
2.12.1	2.2E-10	1.3E+05	2.8E-05
1.29.1	7.9E-10	6.2E+04	4.8E-05
1.75.1	7.8E-10	3.6E+04	2.8E-05
1.74.3	3.6E-10	1.3E+05	4.7E-05

Figure 6B

ID	K_D (pM)
2.4.4	< 10
1.29.1	34 +/- 15
1.74.2	41 +/- 13
2.12.1	54 +/- 7

Figure 7

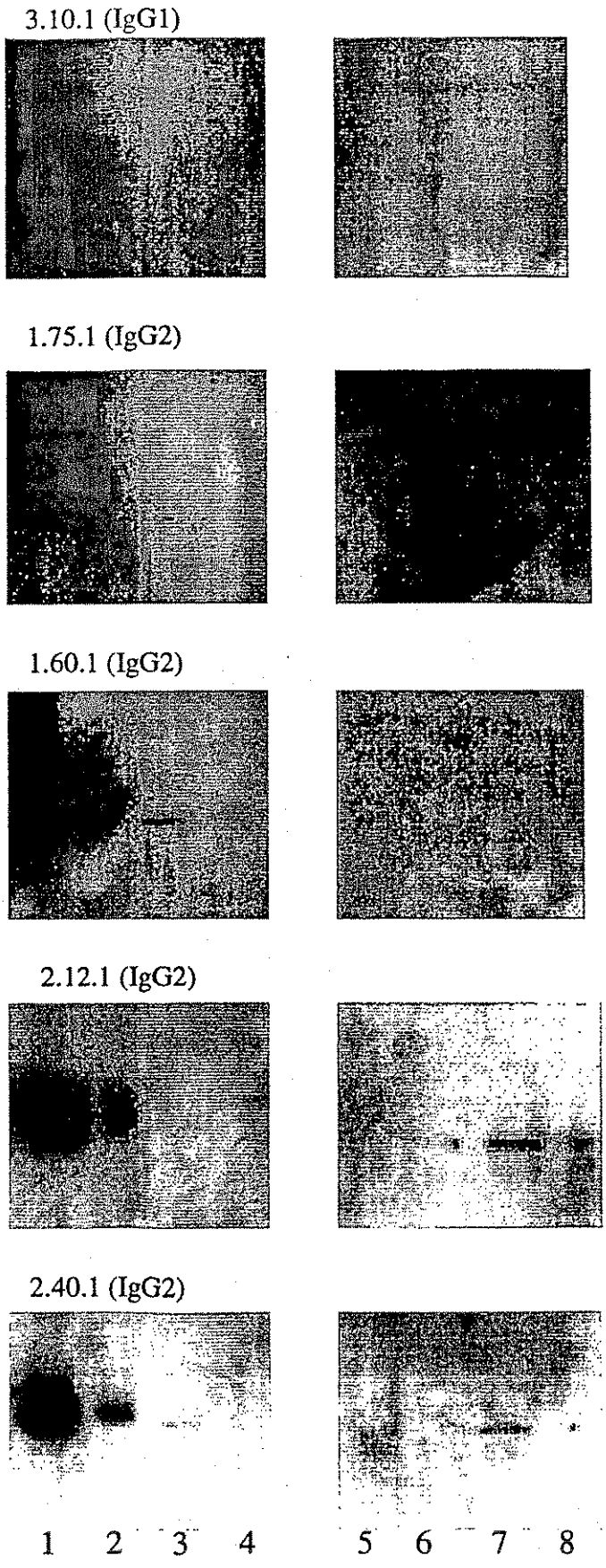


Figure 7 (continued)

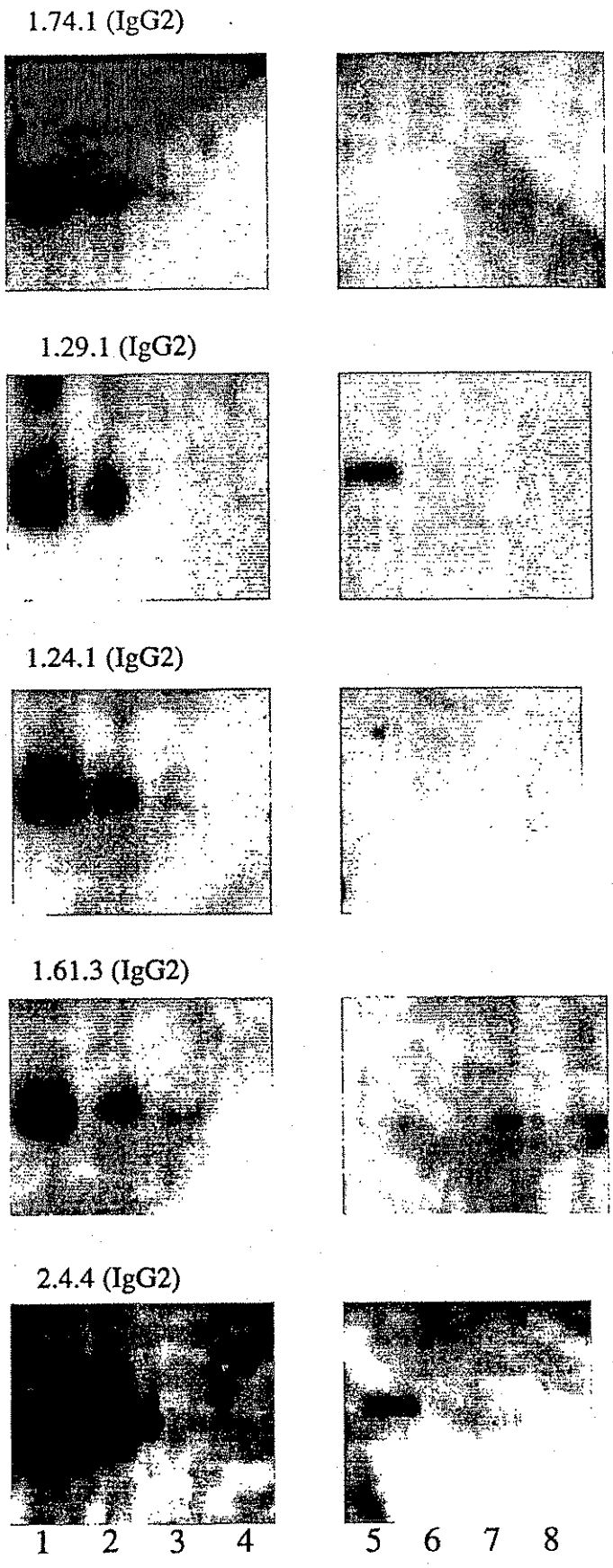


Figure 8

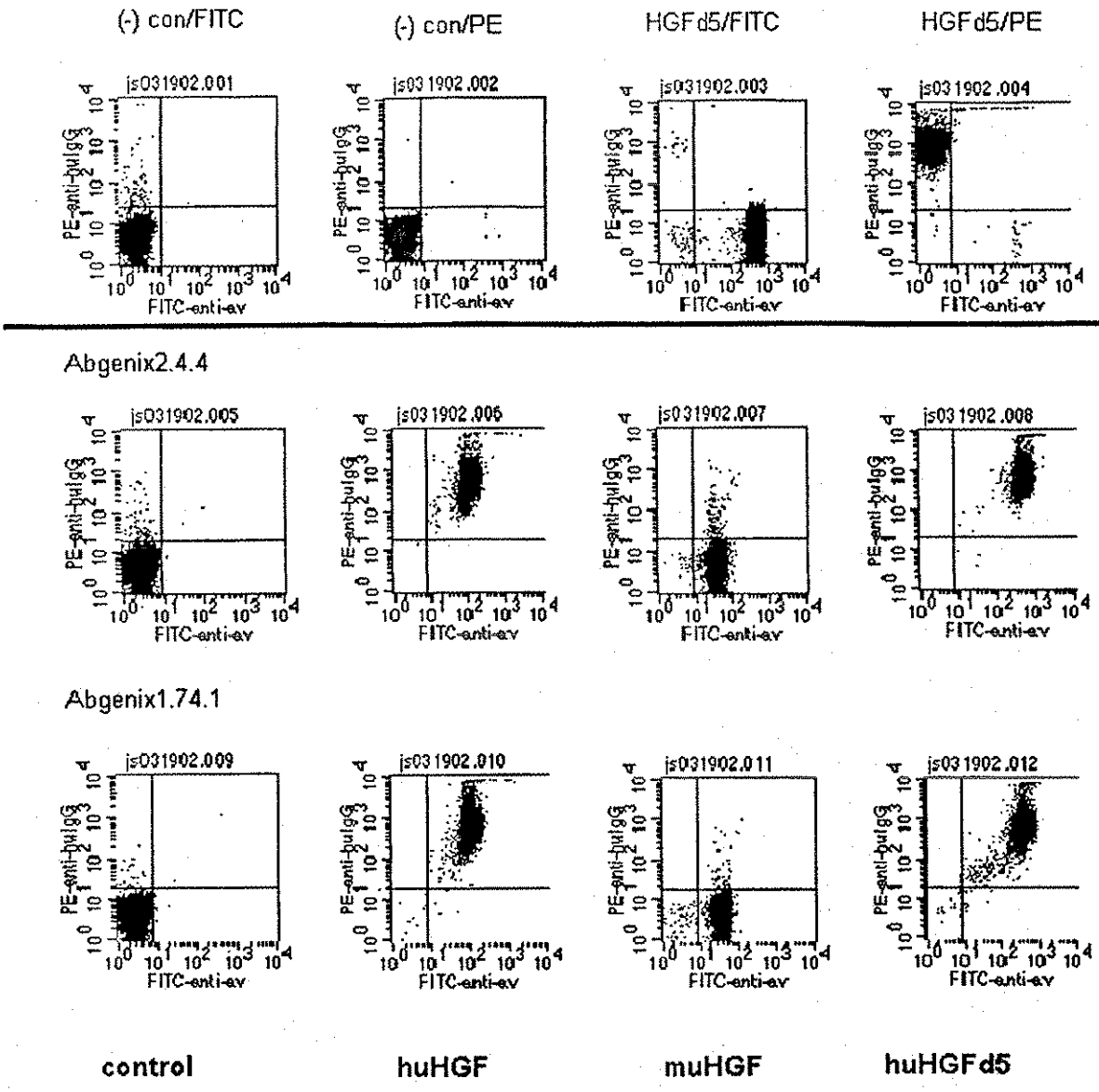

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(-) con/PE
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HGFd5/PE
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js031902.002
js031902.003
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PE-anti-huIgG
FITC-anti-ev
Abgenix2.4.4
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js031902.006
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js031902.008
Abgenix1.74.1
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huHGFd5

Figure 8 (continued)

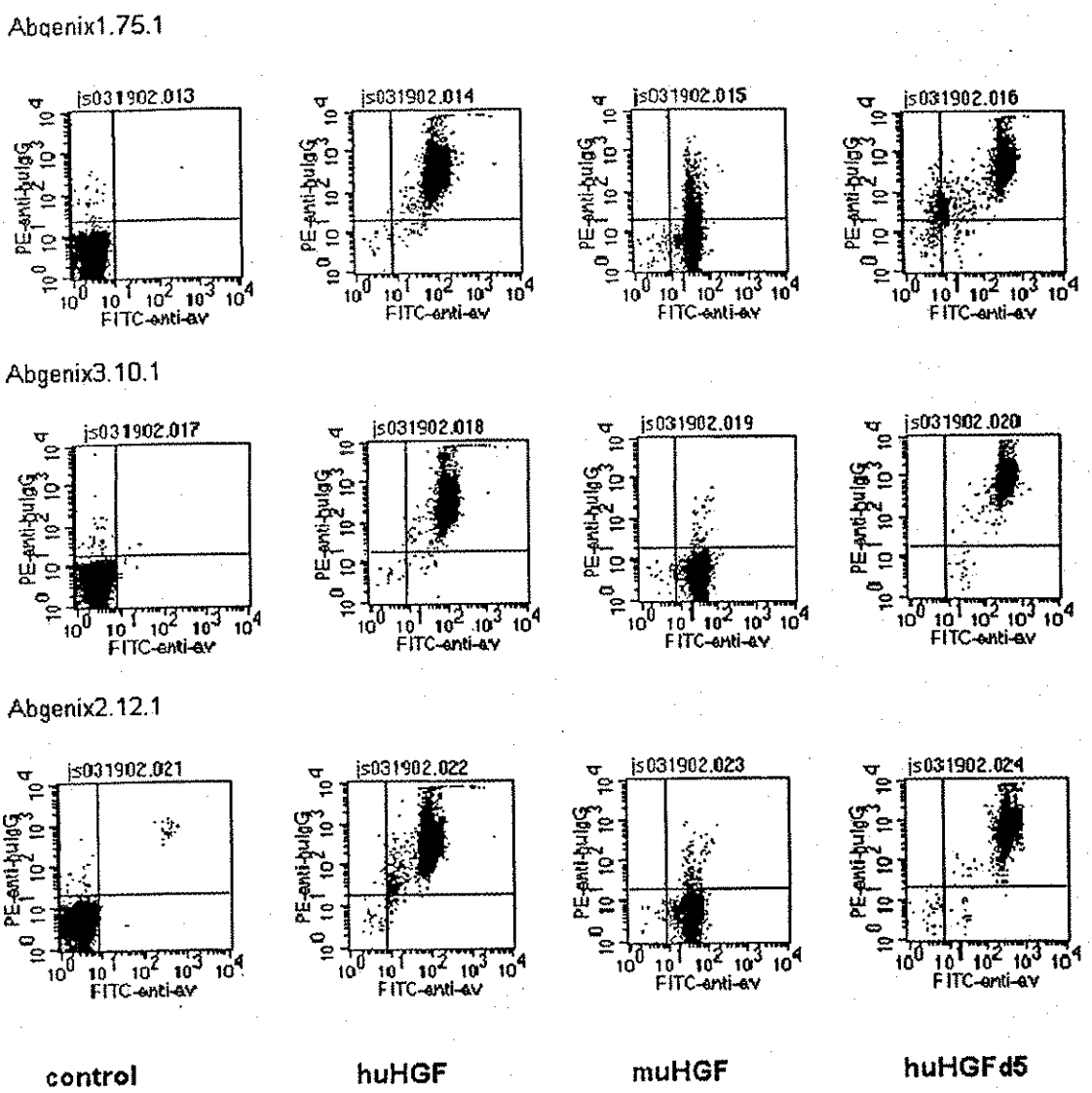


Figure 9A

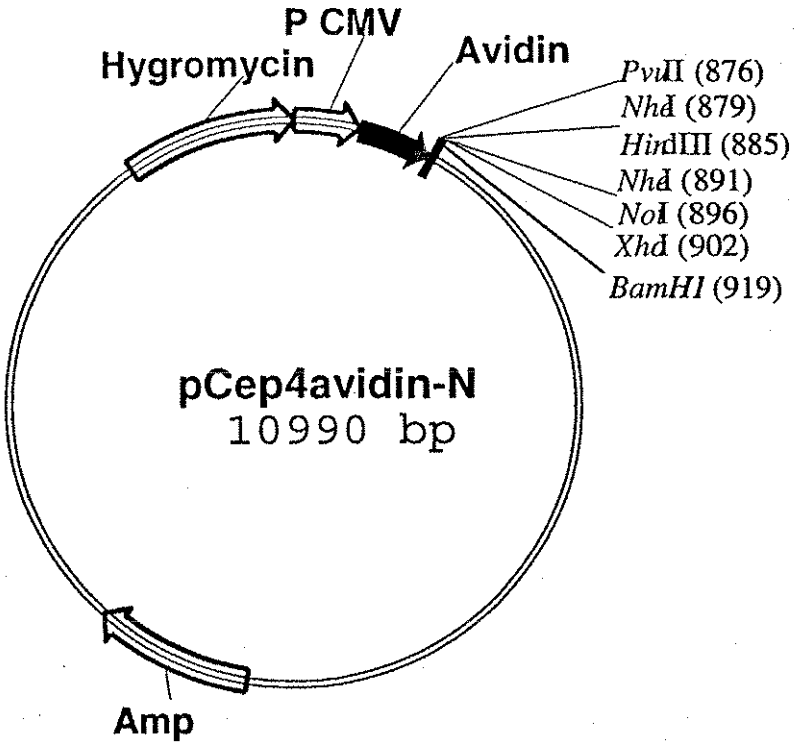

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Avidin
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NheI (879)
HindIII (885)
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XhoI (902)
BamHI (919)
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10990 bp
Amp

Figure 9B

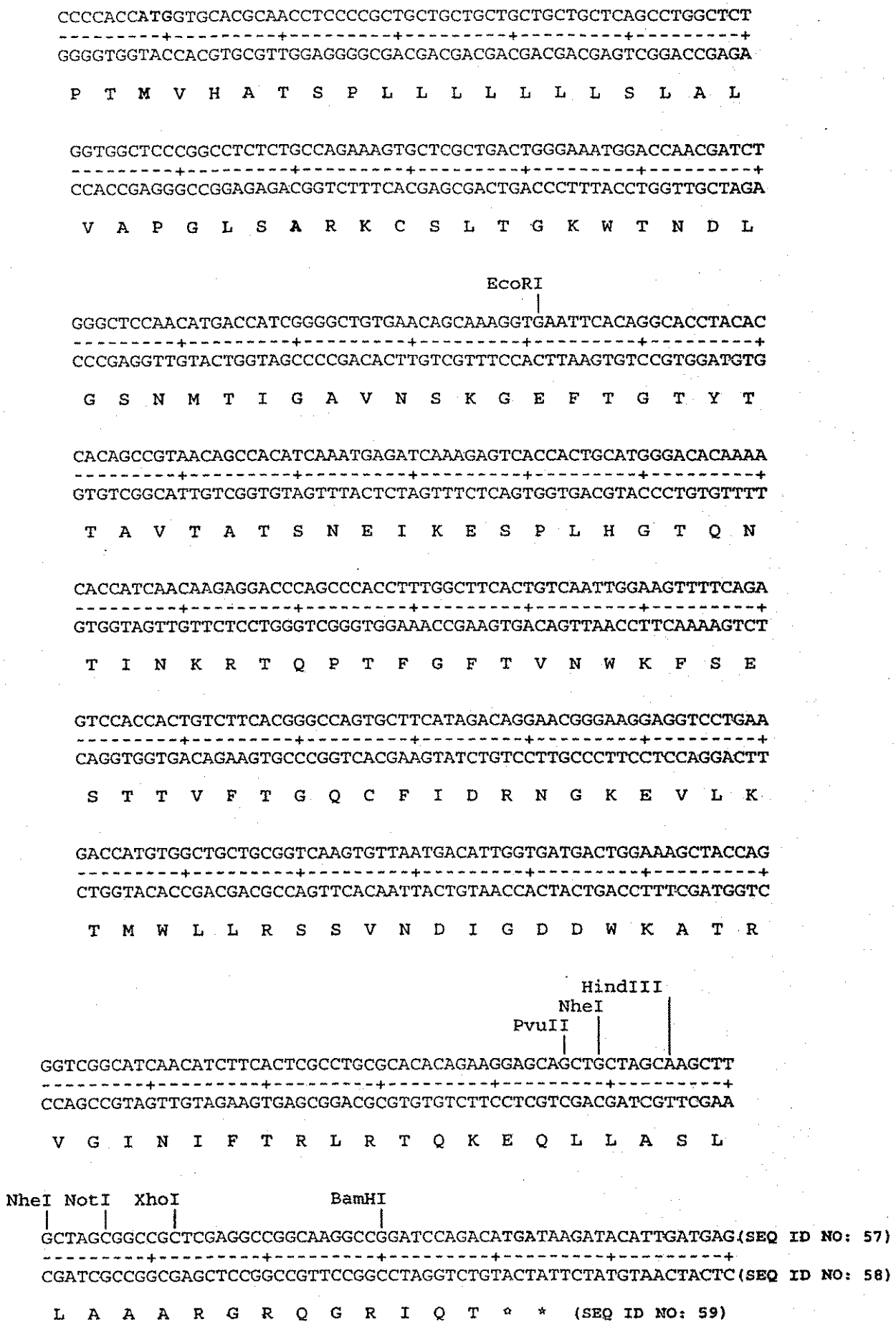

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EcoRI
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G S N M T I G A V N S K G E F T G T Y T
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T A V T A T S N E I K E S P L H G T Q N
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V G I N I F T R L R T Q K E Q L L A S L
NheI NotI XhoI BamHI
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L A A A R G R Q G R I Q T * * (SEQ ID NO: 59)

Figure 10A

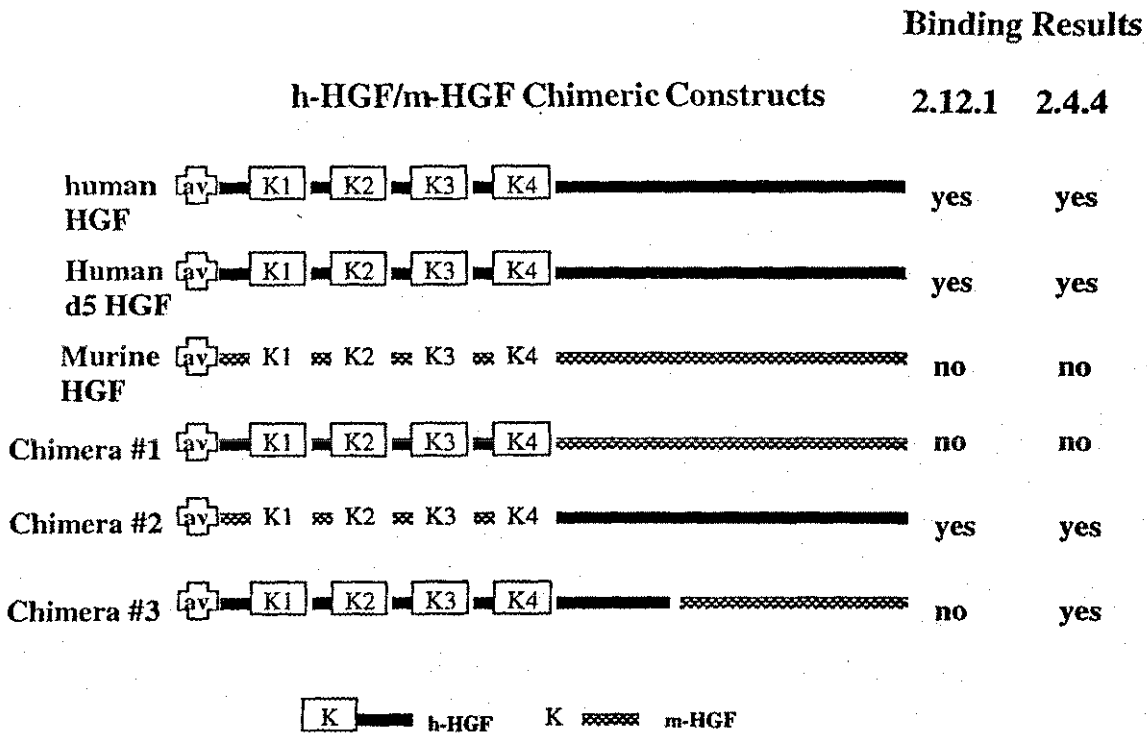

Binding Results
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2.4.4
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K2
K3
K4
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yes
Human d5 HGF
av
K1
K2
K3
K4
yes
yes
Murine HGF
av
K1
K2
K3
K4
no
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h-HGF
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m-HGF

Figure 10B

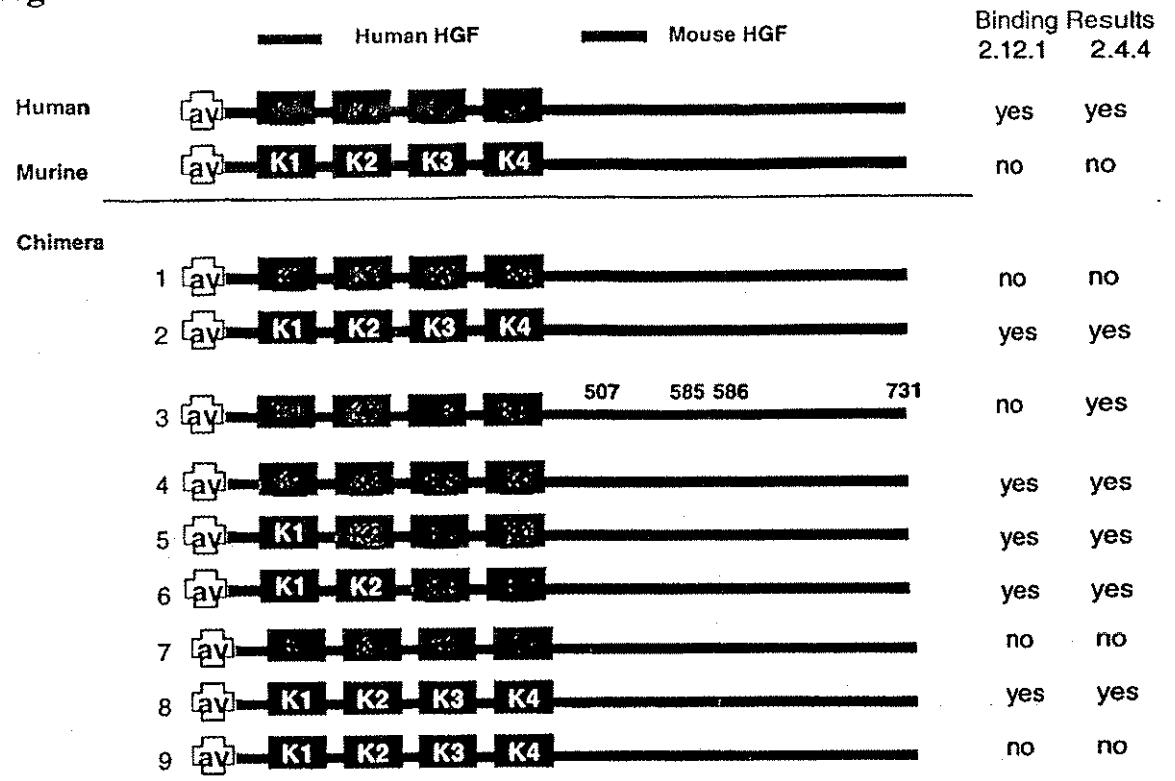


Figure 10C

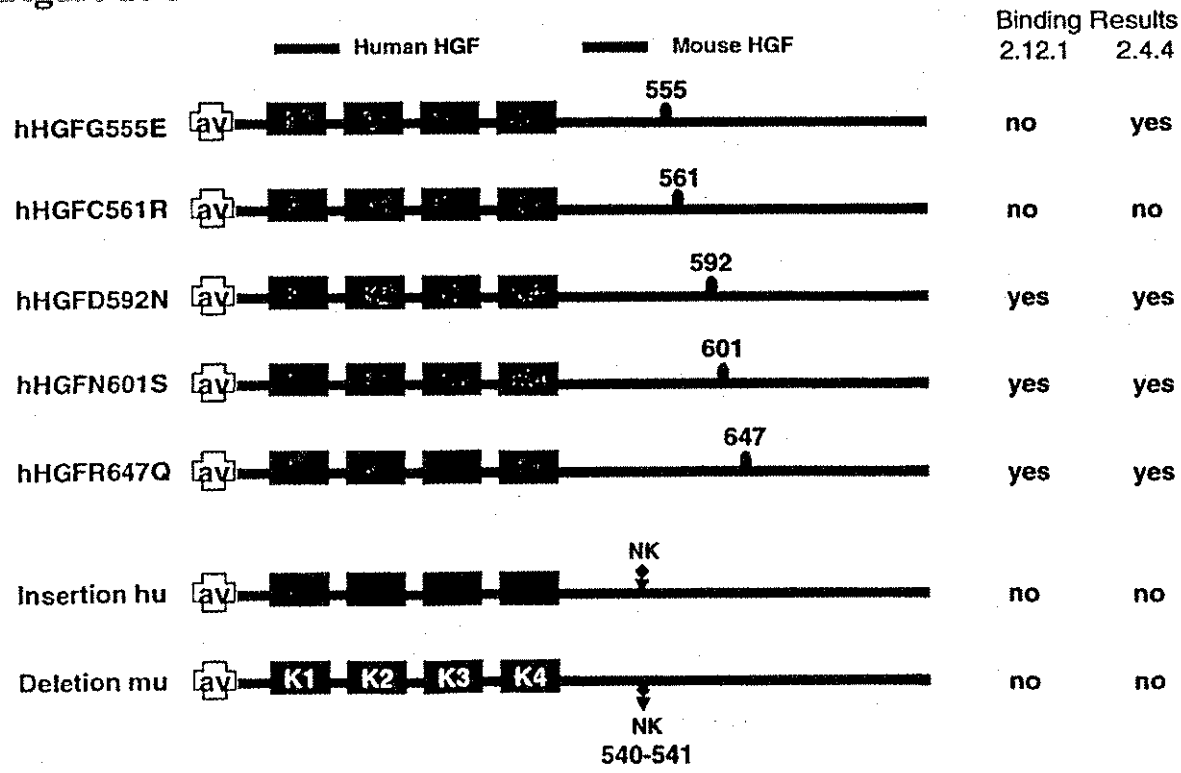


Figure 10D

```
                  451                                                 500
human HGF   (450) PWCYTGNPLIPWDYCPISRCEGDTTPTIVNLDHPVISCAKTKQLRVVNGI
mouse HGF   (451) PWCYTGNPLIPWDYCPISRCEGDTTPTIVNLDHPVISCAKTKQLRVVNGI
Consensus   (451) PWCYTGNPLIPWDYCPISRCEGDTTPTIVNLDHPVISCAKTKQLRVVNGI
                  501                                                 550
human HGF   (500) PTRTNIGWMVSLRYRNKHICGGSLIKESWVLTARQCFPSR--DLKDYEAW
mouse HGF   (501) PTQTTVGWMVSLKYRNKHICGGSLIKESWVLTARQCFPARNKDLKDYEAW
Consensus   (501) PT T IGWMVSLKYRNKHICGGSLIKESWVLTARQCFPAR  DLKDYEAW
                  551                                                 600
human HGF   (548) LGIHDVHGRGDEKCKQVLNVSQLVYGPEGSDLVLMKLARPAVLDDFVSTI
mouse HGF   (551) LGIHDVHERGEEKRKQILNISQLVYGPEGSDLVLLKLARPAILDNFVSTI
Consensus   (551) LGIHDVH RGDEK KQILNISQLVYGPEGSDLVLLKLARPAILD FVSTI
                  601                                                 650
human HGF   (598) DLPNYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHR
mouse HGF   (601) DLPSYGCTIPEKTTCSIYGWGYTGLINADGLLRVAHLYIMGNEKCSQHHQ
Consensus   (601) DLP YGCTIPEKTSCSIYGWGYTGLIN DGLLRVAHLYIMGNEKCSQHH
                  651                                                 700
human HGF   (648) GKVTLNESEICAGAEKIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGC
mouse HGF   (651) GKVTLNESELCAGAEKIGSGPCEGDYGGPLICEQHKMRMVLGVIVPGRGC
Consensus   (651) GKVTLNESEICAGAEKIGSGPCEGDYGGPLICEQHKMRMVLGVIVPGRGC
                  701                          731
human HGF   (698) AIPNRPGIFVRVAYYAKWIHKIILTYKVPQS (SEQ ID NO. 120)
mouse HGF   (701) AIPNRPGIFVRVAYYAKWIHKVILTYKL---- (SEQ ID NO. 121)
Consensus   (701) AIPNRPGIFVRVAYYAKWIHKIILTYKL     (SEQ ID NO. 122)
```

Figure 11A

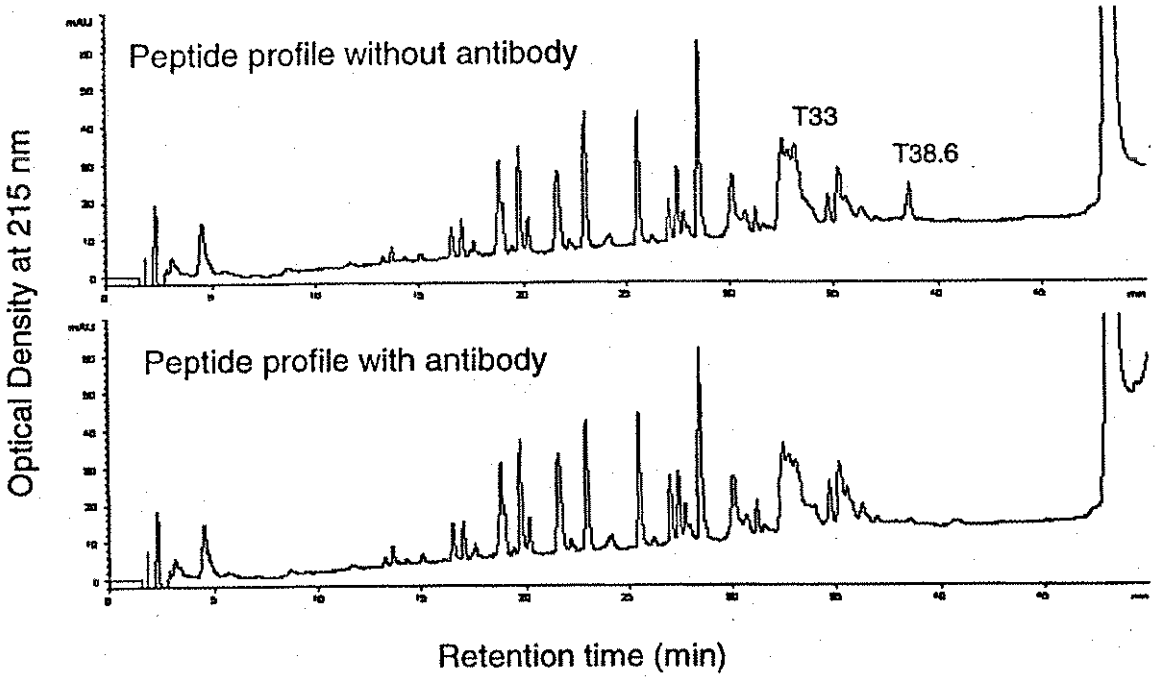


Figure 11B

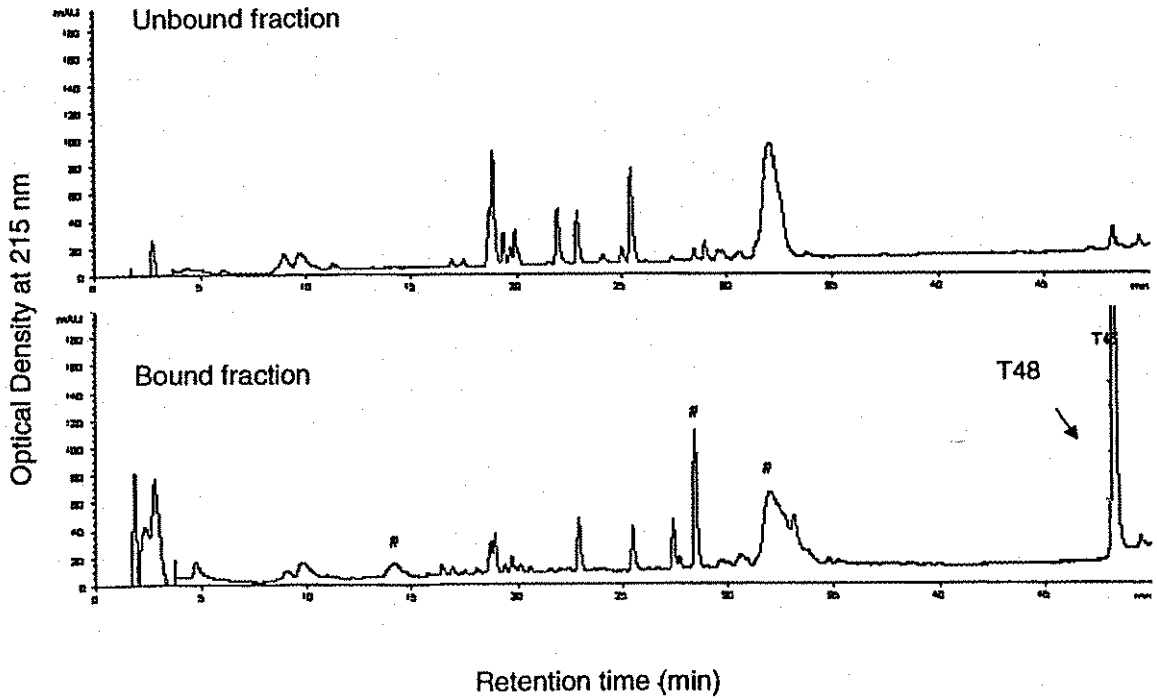


Figure 11C

T38.6= V V N G I P T R ----------H G R (calc. mass=7152) obs. mass=7165 (SEQ ID NO. 161)

G I P T R T----------H G R (calc. Mass= 6840) obs mass= ~6878 (SEQ ID NO. 162)

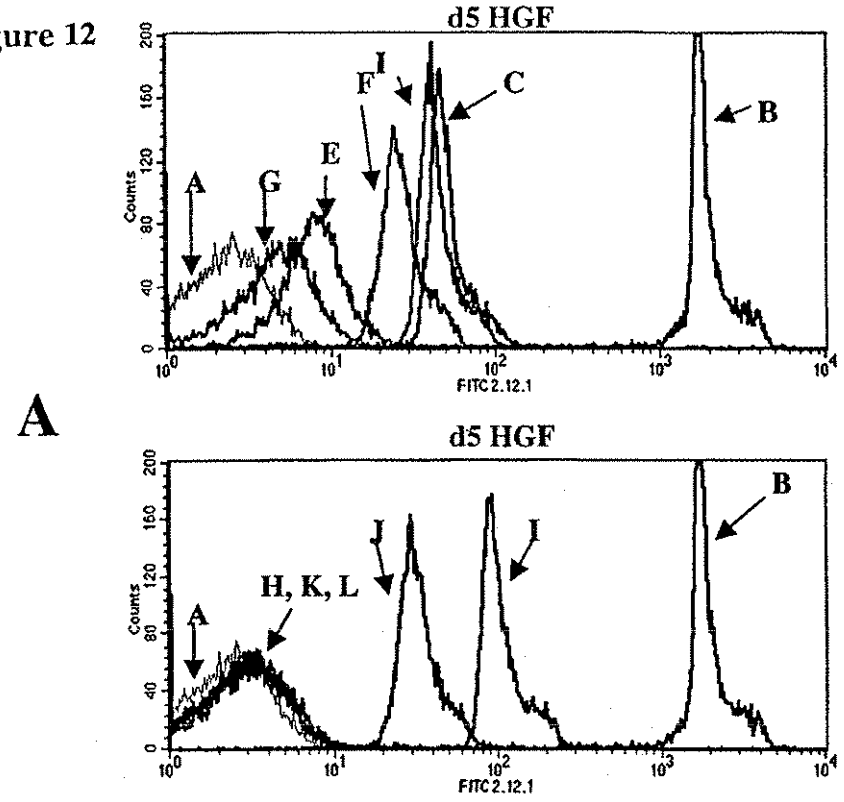
T33= V N T L D Q ----------? (SEQ ID NO. 163)

Predicted protected peptides from peak T38.6:

VVNGIPTRTNIGWMVSLRYRNKHICGGSLIKESWVLTARQCFPSRDLKDYEAWLGIHDVHGR
(SEQ ID NO. 164)

GIPTRTNIGWMVSLRYRNKHICGGSLIKESWVLTARQCFPSRDLKDYEAWLGIHDVHGR
(SEQ ID NO. 165)

Figure 12


d5 HGF
A
G
E
F
I
C
B
Counts
FITC 2.12.1
d5 HGF
A
H, K, L
J
I
B
Counts
FITC 2.12.1

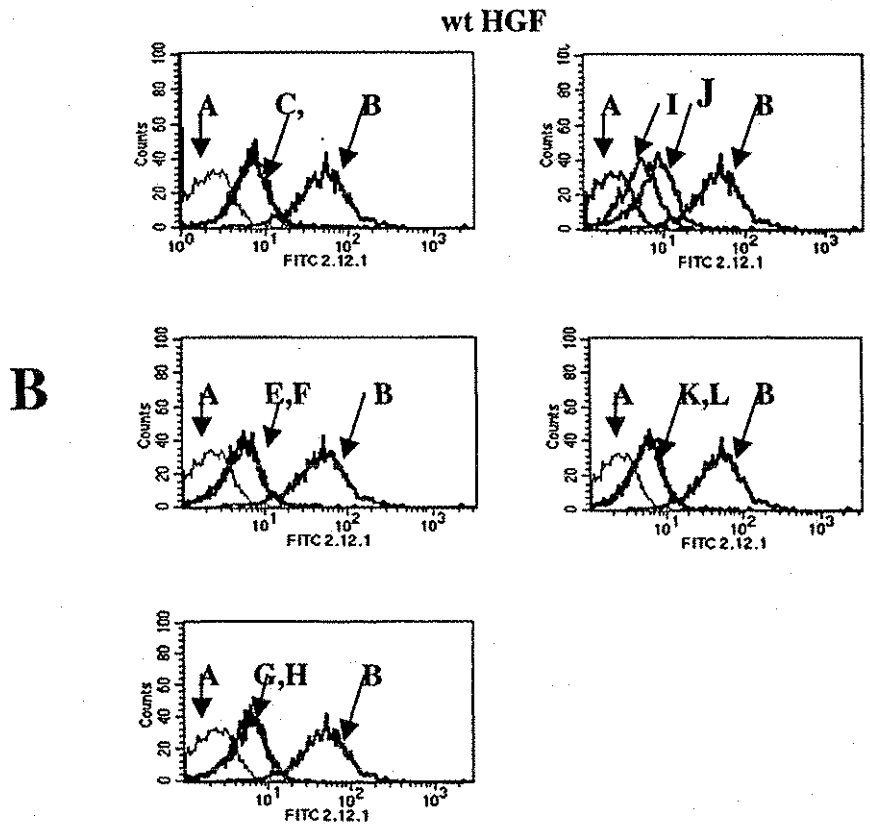
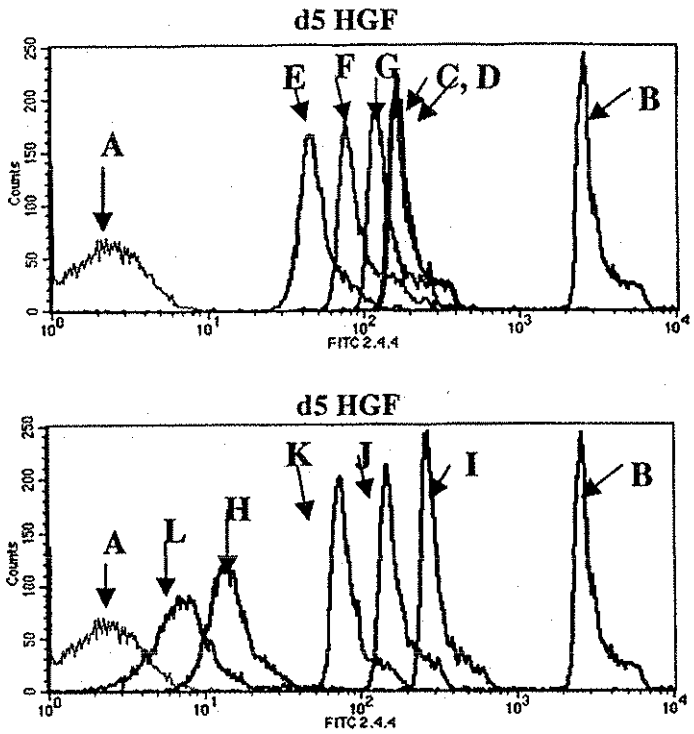

wt HGF
A
C,
B
A
I
J
B
A
E,F
B
A
K,L
B
A
G,H
B
Counts
FITC 2.12.1

Figure 12

C


d5 HGF
A
E
F
G
C, D
B
Counts
FITC 2.4.4
d5 HGF
A
L
H
K
J
I
B
Counts
FITC 2.4.4

D

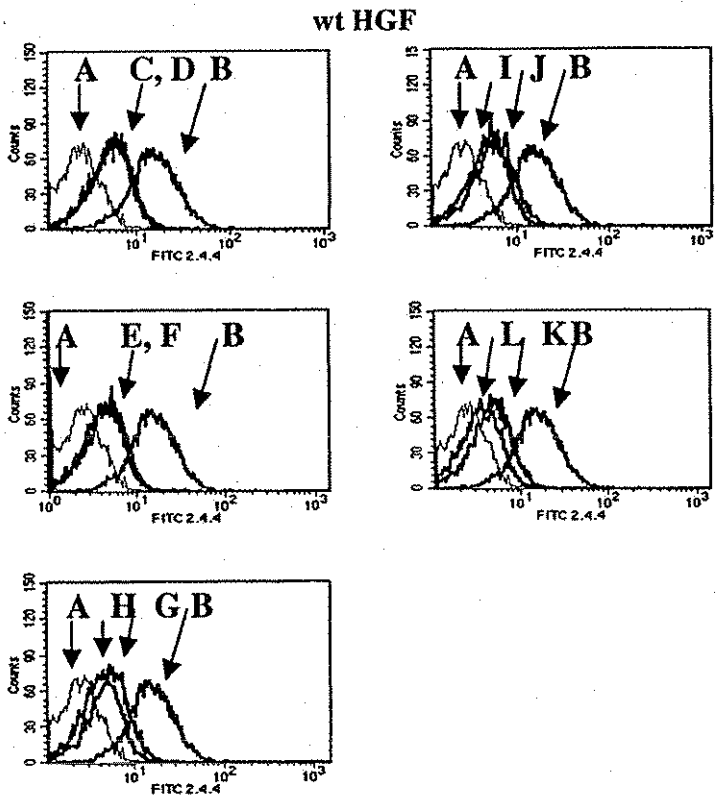

wt HGF
A C, D B
A I J B
A E, F B
A L K B
A H G B
Counts
FITC 2.4.4

Figure 13

ID	IC50 IP (nM)
3.10.1	0.9
2.40.1	1.0
1.75.1	1.0
2.12.1	2.1
1.24.1	2.6
1.29.1	3.2
1.74.1	3.7
1.60.2	4.5
2.4.4	5.1

ID	IC50 IP (nM)
3.10.1	0.37
2.12.1	0.52
1.75.1	0.72
1.29.1	1.93
1.74.1	2.31
1.61.3	2.59
1.24.1	9.36

Figure 14

Experiment #1

ID	IC50 IP (nM)
1.75.1	0.34
2.12.1	0.49
2.40.1	0.51
3.10.1	0.64
1.24.1	0.64
1.29.1	1.18
2.4.4	1.24
1.74.1	1.25

Experiment #2

ID	IC50 IP (nM)
1.61.3	0.28
1.24.1	0.40
1.75.1	0.59
1.29.1	0.88
1.60.1	1.06
1.74.1	2.17

Figure 15

Experiment #1

ID	IC50 IP (nM)
1.24.1	15
1.60.1	15
1.29.1	23
2.4.4	33
2.12.1	57
3.10.1	137

Experiment #2

ID	IC50 IP (nM)
2.4.4	8
1.61.3	17
1.29.1	21
2.12.1	34
2.40.1	59
3.10.1	133
1.60.1	215
1.74.1	>666
1.75.1	>666

Figure 16A

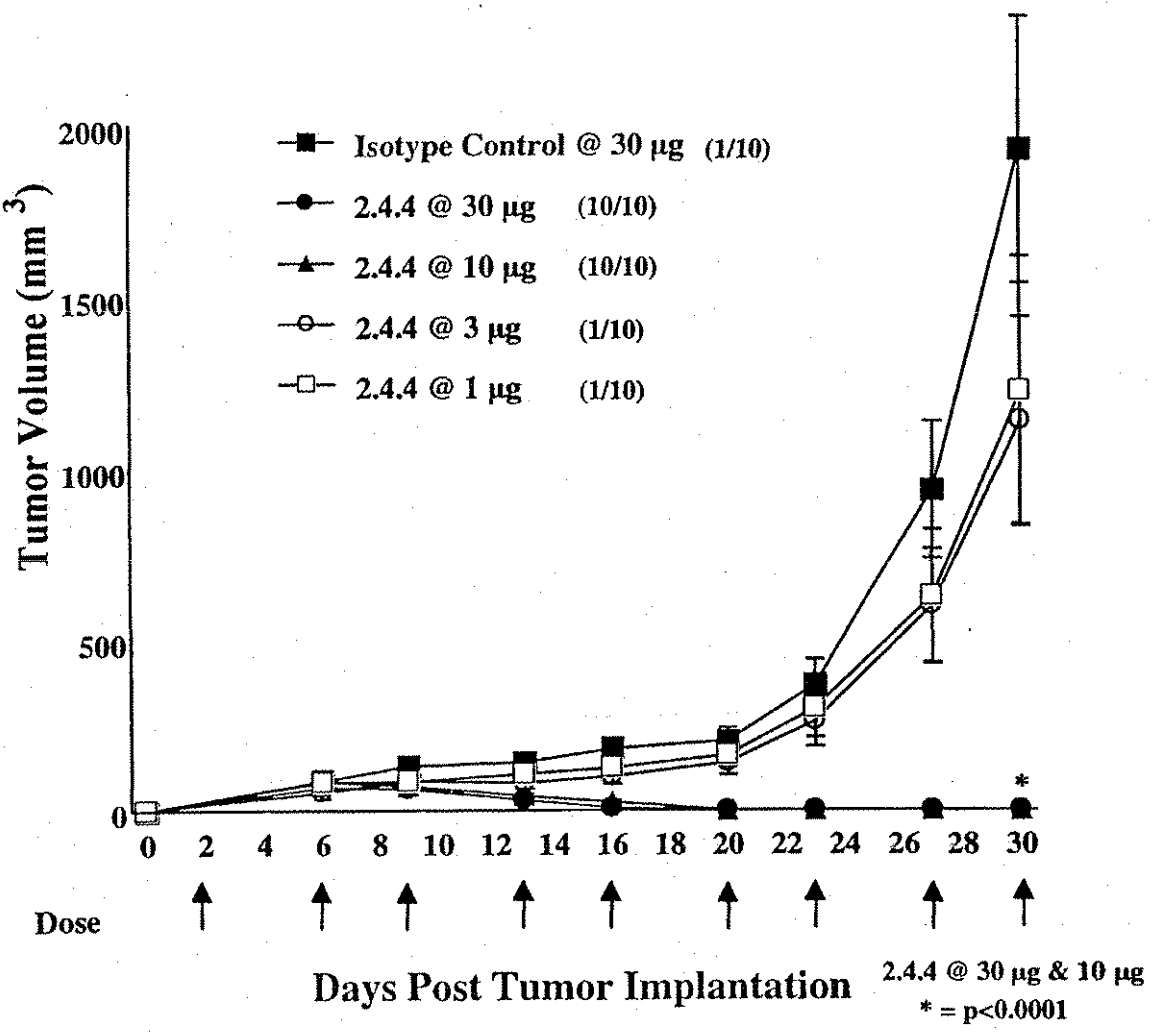

Isotype Control @ 30 µg (1/10)
2.4.4 @ 30 µg (10/10)
2.4.4 @ 10 µg (10/10)
2.4.4 @ 3 µg (1/10)
2.4.4 @ 1 µg (1/10)
Tumor Volume (mm 3)
2000
1500
1000
500
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
*
Dose
Days Post Tumor Implantation
2.4.4 @ 30 µg & 10 µg
* = p<0.0001

Figure 16B

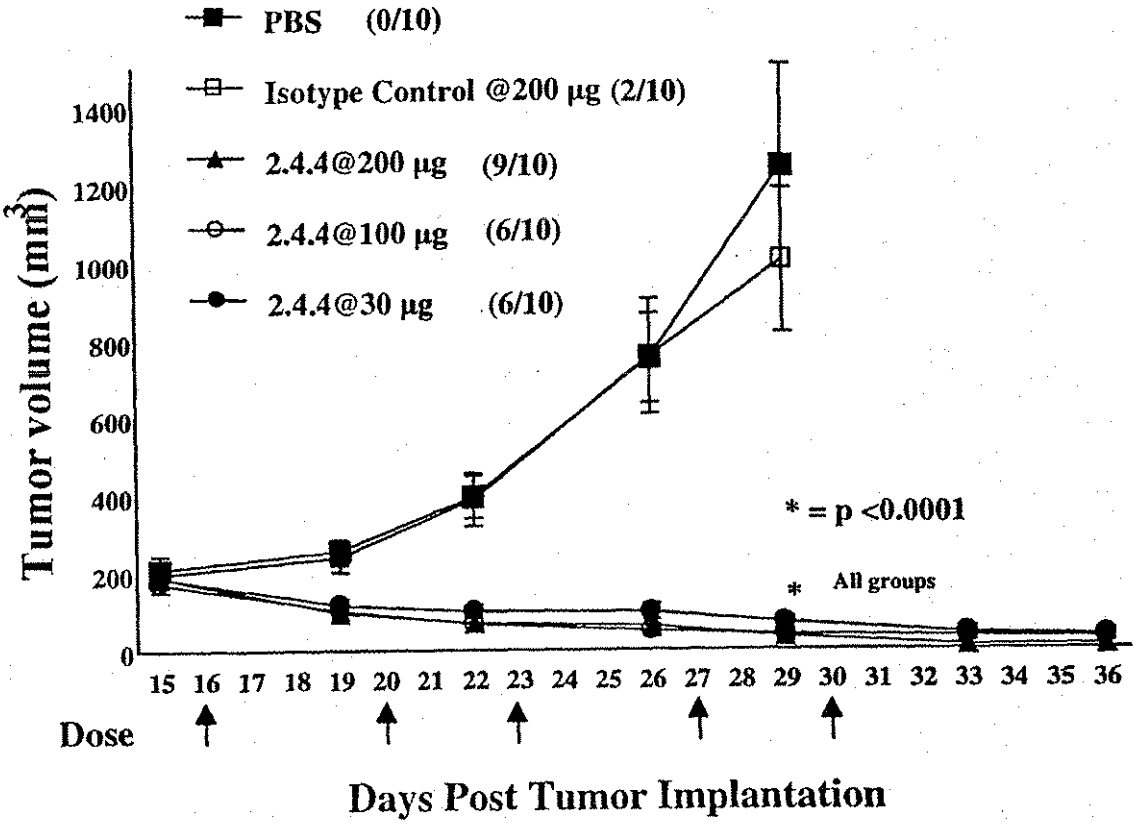

PBS (0/10)
Isotype Control @200 µg (2/10)
2.4.4@200 µg (9/10)
2.4.4@100 µg (6/10)
2.4.4@30 µg (6/10)
Tumor volume (mm3)
1400
1200
1000
800
600
400
200
0
* = p <0.0001
* All groups
15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36
Dose
Days Post Tumor Implantation

Figure 16C

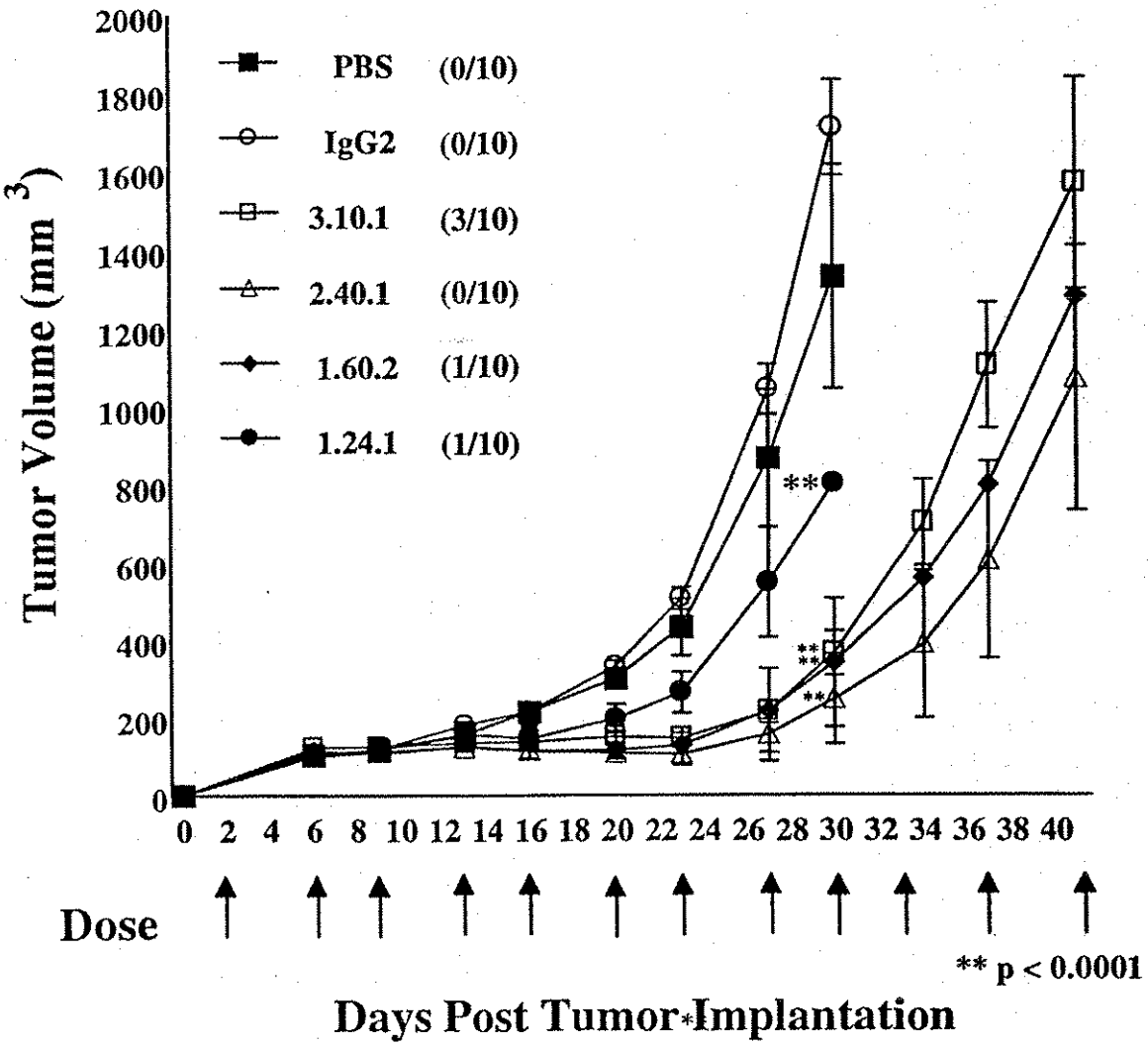

Tumor Volume (mm 3)
2000
1800
1600
1400
1200
1000
800
600
400
200
0
PBS (0/10)
IgG2 (0/10)
3.10.1 (3/10)
2.40.1 (0/10)
1.60.2 (1/10)
1.24.1 (1/10)
**
**
**
**
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40
Dose
** p < 0.0001
Days Post Tumor Implantation

Figure 16D

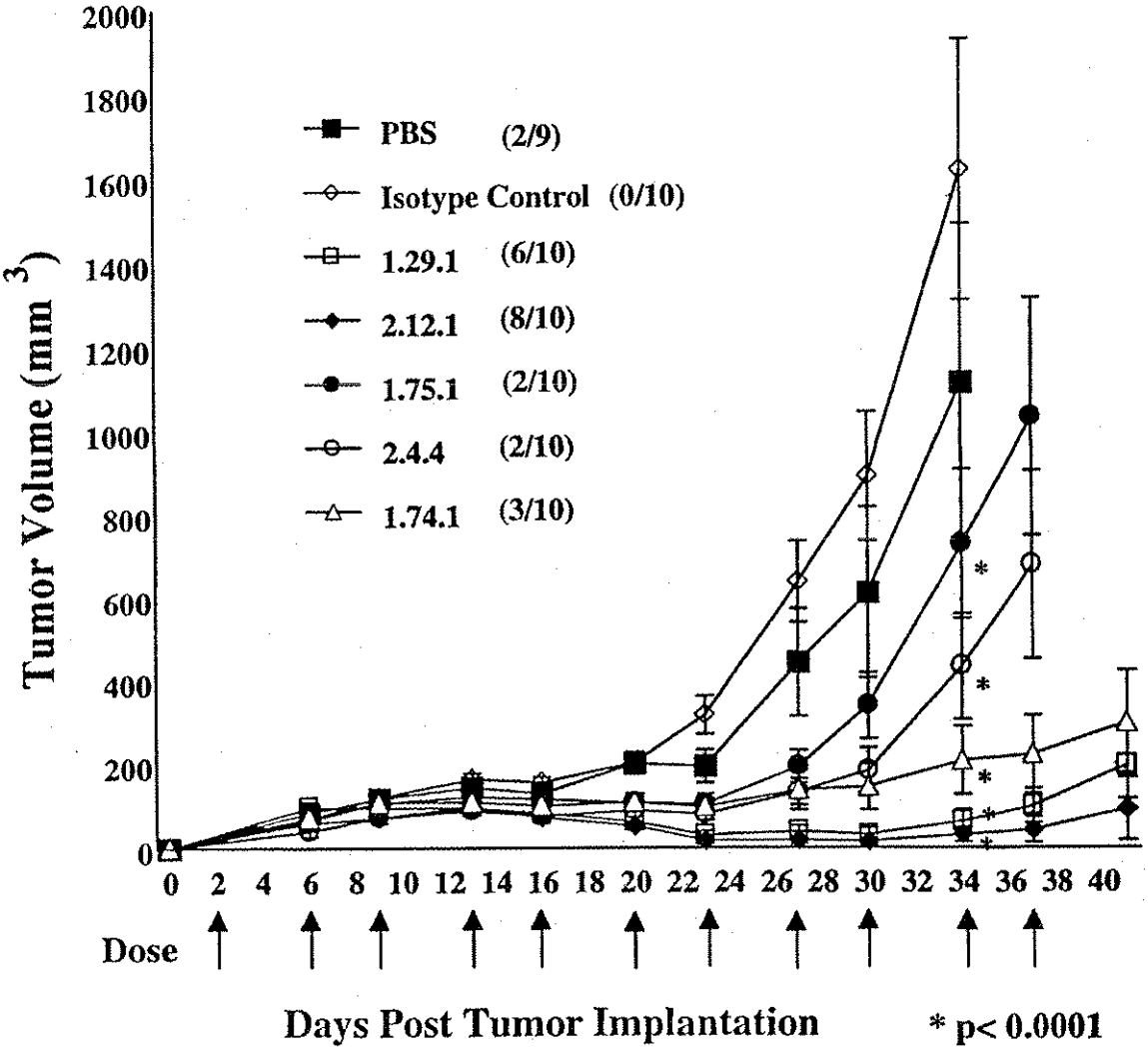

Tumor Volume (mm 3)
2000
1800
1600
1400
1200
1000
800
600
400
200
0
PBS (2/9)
Isotype Control (0/10)
1.29.1 (6/10)
2.12.1 (8/10)
1.75.1 (2/10)
2.4.4 (2/10)
1.74.1 (3/10)
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40
Dose
Days Post Tumor Implantation
* p< 0.0001

Figure 16E

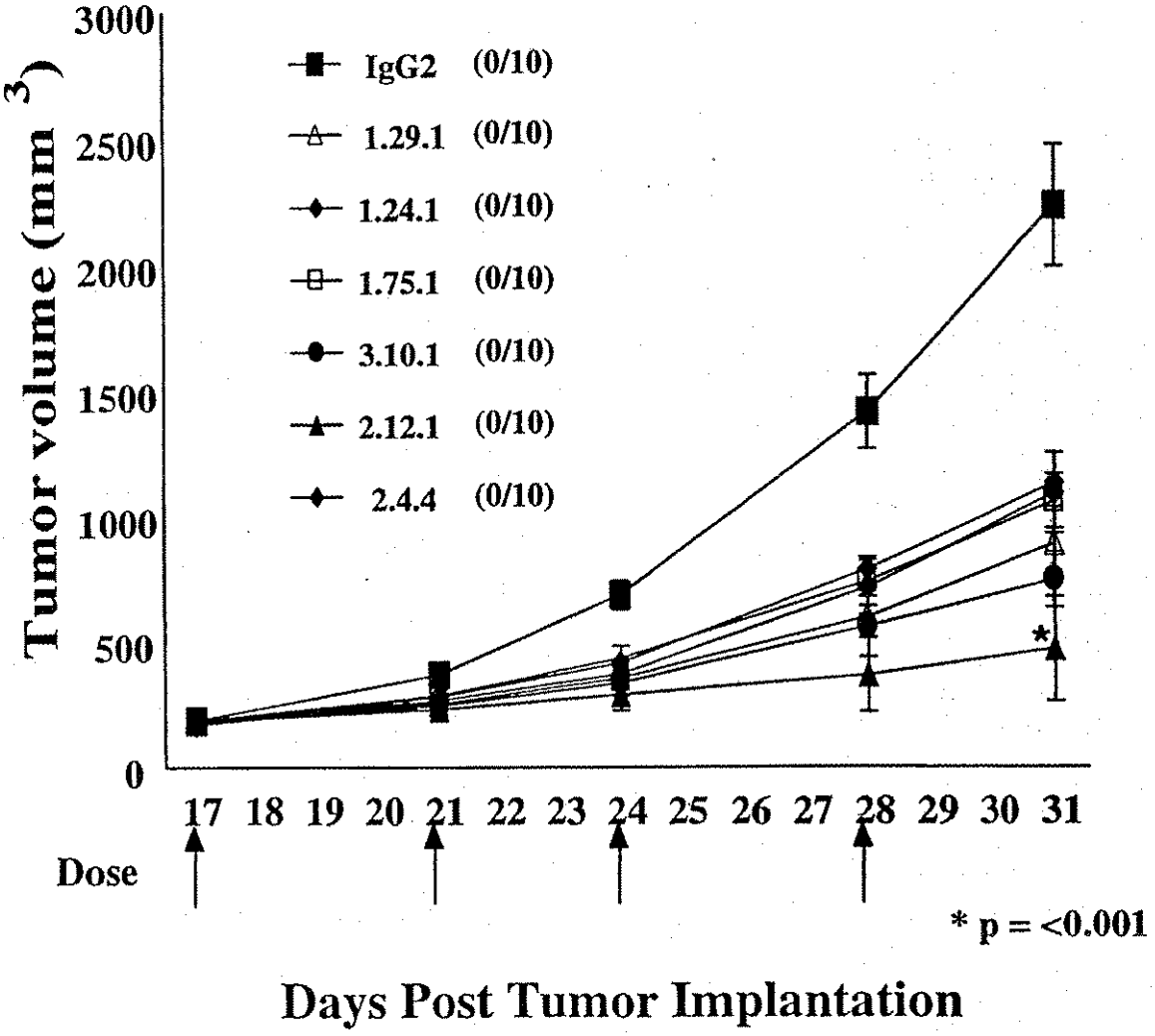
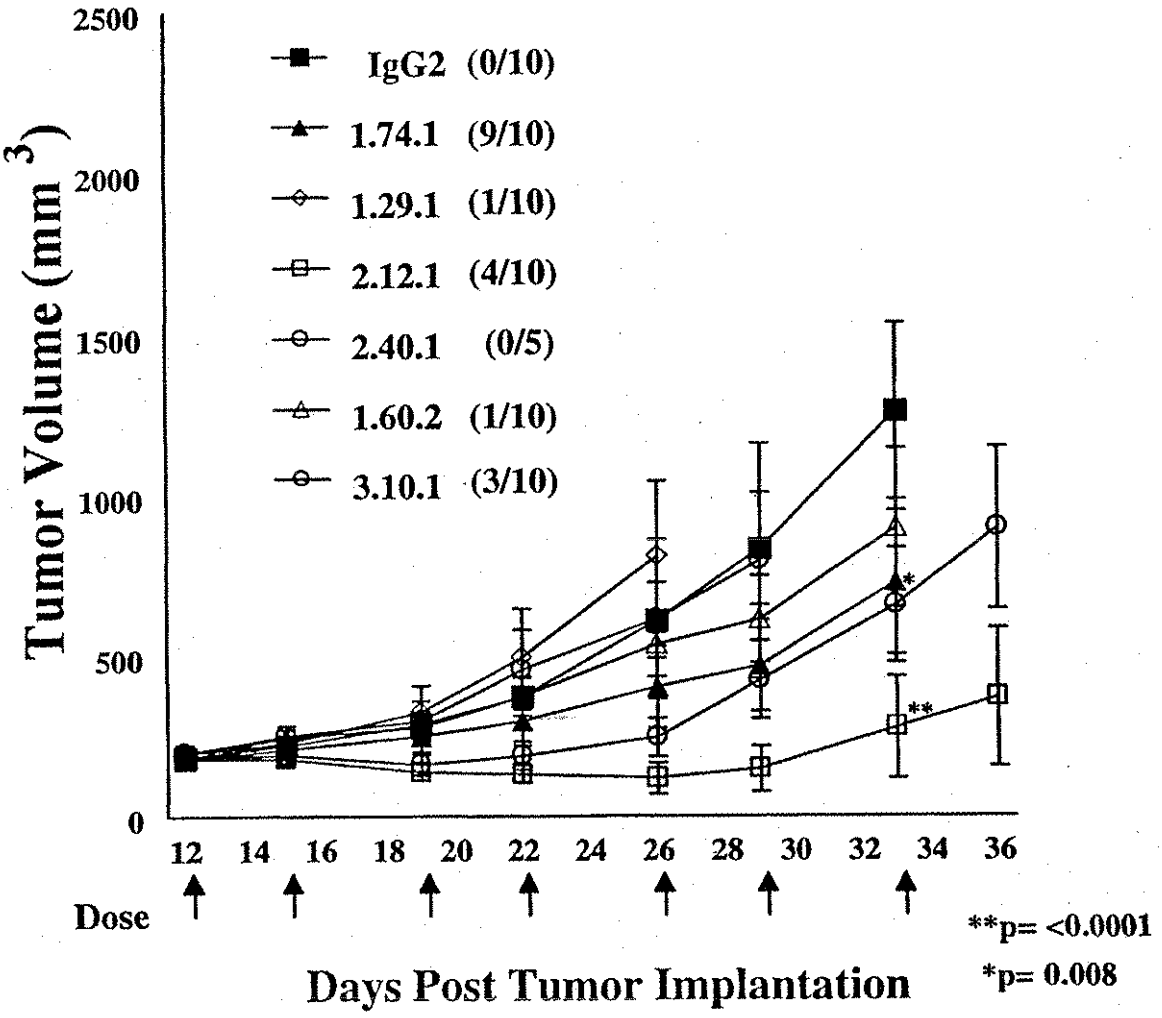

Tumor volume (mm 3)
3000
2500
2000
1500
1000
500
0
IgG2 (0/10)
1.29.1 (0/10)
1.24.1 (0/10)
1.75.1 (0/10)
3.10.1 (0/10)
2.12.1 (0/10)
2.4.4 (0/10)
*
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31
Dose
* p = <0.001
Days Post Tumor Implantation

Figure 16F


2500
2000
1500
1000
500
0
Tumor Volume (mm 3)
IgG2 (0/10)
1.74.1 (9/10)
1.29.1 (1/10)
2.12.1 (4/10)
2.40.1 (0/5)
1.60.2 (1/10)
3.10.1 (3/10)
*
**
12 14 16 18 20 22 24 26 28 30 32 34 36
Dose
Days Post Tumor Implantation
**p= <0.0001
*p= 0.008