FIG. 2B

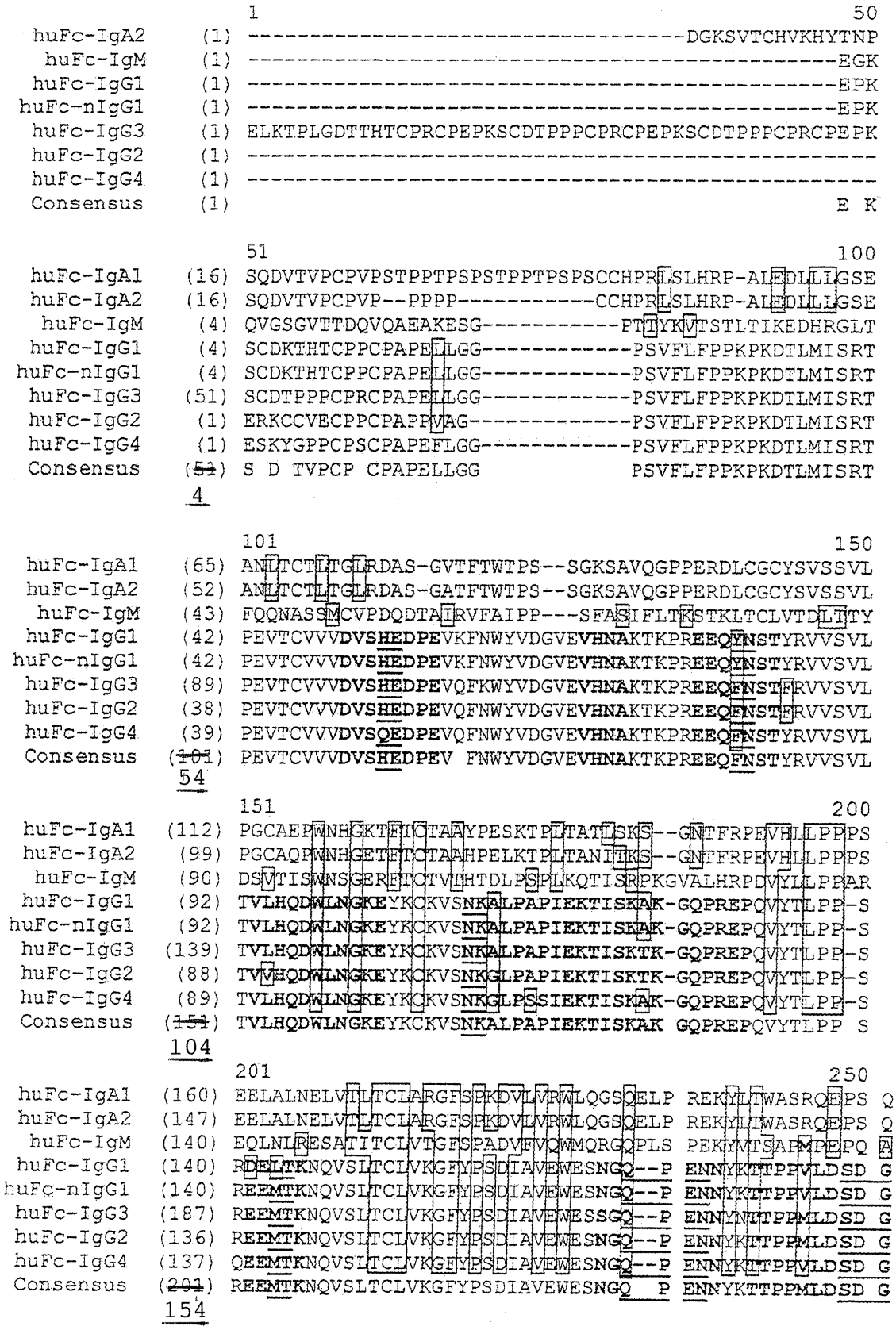

1 50
huFc-IgA2 (1) ----------DGKSVTCHVKHYTNP
huFc-IgM (1) ----------EGK
huFc-IgG1 (1) ----------EPK
huFc-nIgG1 (1) ----------EPK
huFc-IgG3 (1) ELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPK
huFc-IgG2 (1) ----------
huFc-IgG4 (1) ----------
Consensus (1) E K
51 100
huFc-IgA1 (16) SQDVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRP-ALEDLLLGSE
huFc-IgA2 (16) SQDVTVPCPVP--PPPP----------CCHPRLSLHRP-ALEDLLLGSE
huFc-IgM (4) QVGSGVTTDQVQAEAKESG----------PTTYKVTSTLTIKEDHRGLT
huFc-IgG1 (4) SCDKTHTCPPCPAPELLGG----------PSVFLFPPKPKDTLMISRT
huFc-nIgG1 (4) SCDKTHTCPPCPAPELLGG----------PSVFLFPPKPKDTLMISRT
huFc-IgG3 (51) SCDTPPPCPRCPAPELLGG----------PSVFLFPPKPKDTLMISRT
huFc-IgG2 (1) ERKCCVECPPCPAPPVAG----------PSVFLFPPKPKDTLMISRT
huFc-IgG4 (1) ESKYGPPCPSCPAPEFLGG----------PSVFLFPPKPKDTLMISRT
Consensus (51) S D TVPCP CPAPELLGG PSVFLFPPKPKDTLMISRT
4
101 150
huFc-IgA1 (65) ANLTCTLTGLRDAS-GVTFTWTPS--SGKSAVQGPPERDLCGCYSVSSVL
huFc-IgA2 (52) ANLTCTLTGLRDAS-GATFTWTPS--SGKSAVQGPPERDLCGCYSVSSVL
huFc-IgM (43) FQQNASSMCVPDQDTAIRVFAIPP---SFASIFLTKSTKLTCLVTDLTTY
huFc-IgG1 (42) PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
huFc-nIgG1 (42) PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
huFc-IgG3 (89) PEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRVVSVL
huFc-IgG2 (38) PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVL
huFc-IgG4 (39) PEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVL
Consensus (101) PEVTCVVVDVSHEDPEV FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVL
54
151 200
huFc-IgA1 (112) PGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS--GNTFRPEVHLLPPPS
huFc-IgA2 (99) PGCAQPWNHGETFTCTAAHPELKTPLTANITKS--GNTFRPEVHLLPPPS
huFc-IgM (90) DSVTISWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAR
huFc-IgG1 (92) TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPP-S
huFc-nIgG1 (92) TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPP-S
huFc-IgG3 (139) TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK-GQPREPQVYTLPP-S
huFc-IgG2 (88) TVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK-GQPREPQVYTLPP-S
huFc-IgG4 (89) TVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK-GQPREPQVYTLPP-S
Consensus (151) TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPP S
104
201 250
huFc-IgA1 (160) EELALNELVTLTCLARGFSPKDVLVRWLQGSQELP REKYLTWASRQEPS Q
huFc-IgA2 (147) EELALNELVTLTCLARGFSPKDVLVRWLQGSQELP REKYLTWASRQEPS Q
huFc-IgM (140) EQLNLRESATITCLVTGFSPADVFVQWMQRGQPLS PEKYVTSAPMPEPQ A
huFc-IgG1 (140) RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--P ENNYKTTPPVLDSD G
huFc-nIgG1 (140) REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ--P ENNYKTTPPVLDSD G
huFc-IgG3 (187) REEMTKNQVSLTCLVKGFYPSDIAVEWESSGQ--P ENNYNTTPPMLDSD G
huFc-IgG2 (136) REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ--P ENNYKTTPPMLDSD G
huFc-IgG4 (137) QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ--P ENNYKTTPPVLDSD G
Consensus (201) REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ P ENNYKTTPPMLDSD G
154

FIG. 2C

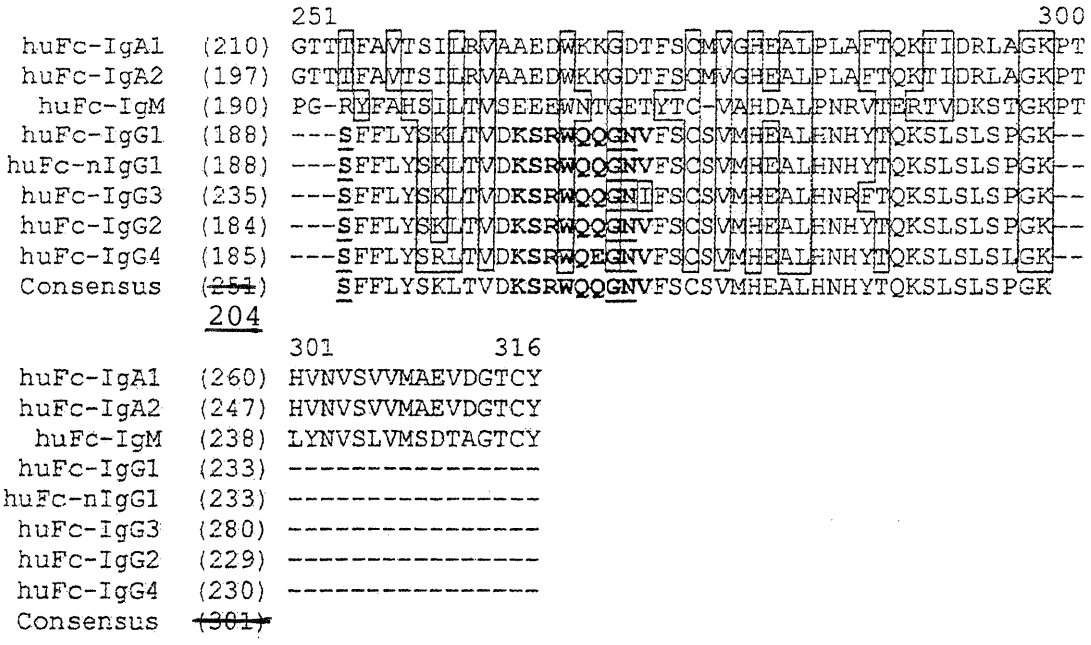
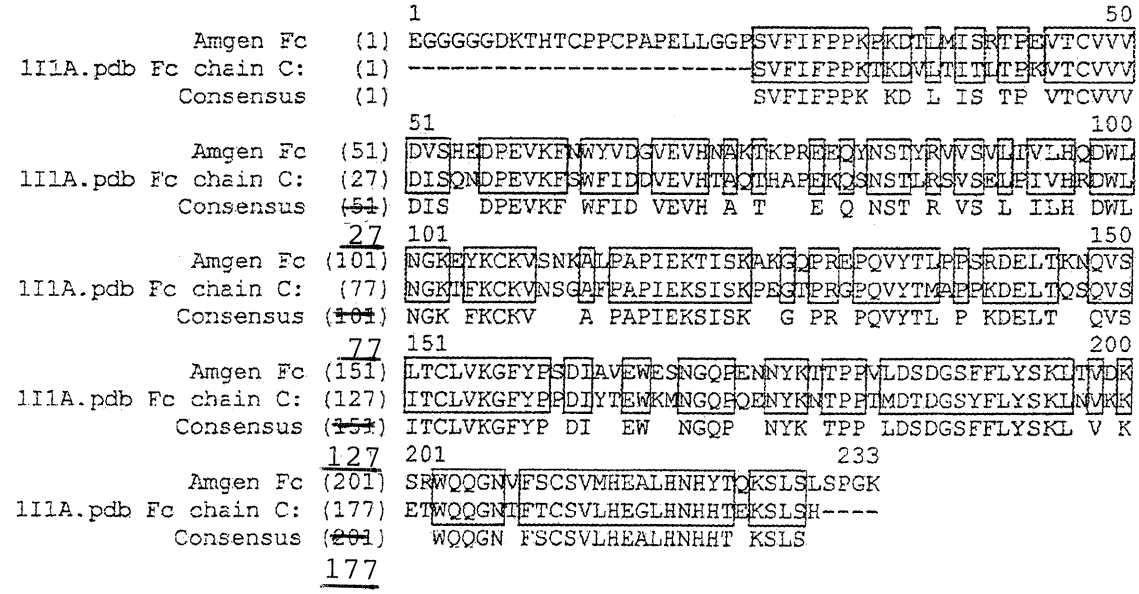

251
300
huFc-IgA1 (210) GTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPT
huFc-IgA2 (197) GTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPT
huFc-IgM (190) PG-RVFAHSILTVSEEEWNTGETYTC-VAHDALPNRVTERTVDKSTGKPT
huFc-IgG1 (188) ---SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK--
huFc-nIgG1 (188) ---SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK--
huFc-IgG3 (235) ---SFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK--
huFc-IgG2 (184) ---SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK--
huFc-IgG4 (185) ---SFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK--
Consensus (251) SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
204
301
316
huFc-IgA1 (260) HVNVSVVMAEVDGTCY
huFc-IgA2 (247) HVNVSVVMAEVDGTCY
huFc-IgM (238) LYNVSLVMSDTAGTCY
huFc-IgG1 (233) ----------
huFc-nIgG1 (233) ----------
huFc-IgG3 (280) ----------
huFc-IgG2 (229) ----------
huFc-IgG4 (230) ----------
Consensus (301)

FIG. 2D


1
50
Amgen Fc (1) EGGGGGDKTHTCPPCPAPELLGGPSVFIFPPKPKDTLMISRTPEVTCVVV
1I1A.pdb Fc chain C: (1) ----------SVFIFPPKTKDVLTITLTPKVTCVVV
Consensus (1) SVFIFPPK KD L IS TP VTCVVV
51
100
Amgen Fc (51) DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
1I1A.pdb Fc chain C: (27) DISQNDPEVKFSWFIDDVEVHTAQTHAPEKQSNSTLRSVSELPIVHRDWL
Consensus (51) DIS DPEVKF WFID VEVH A T E Q NST R VS L ILH DWL
27
101
150
Amgen Fc (101) NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS
1I1A.pdb Fc chain C: (77) NGKTFKCKVNSGAFPAPIEKSISKPEGTPRGPQVYTMAPPKDELTQSQVS
Consensus (101) NGK FKCKV A PAPIEKSISK G PR PQVYTL P KDELT QVS
77
151
200
Amgen Fc (151) LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
1I1A.pdb Fc chain C: (127) ITCLVKGFYPPDIYTEWKMNGQPQENYKNTPPIMDTDGSYFLYSKLNVKK
Consensus (151) ITCLVKGFYP DI EW NGQP NYK TPP LDSDGSFFLYSKL V K
127
201
233
Amgen Fc (201) SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1I1A.pdb Fc chain C: (177) ETWQQGNIFTCSVLHEGLHNHHTEKSLSH----
Consensus (201) WQQGN FSCSVLHEALHNHHT KSLS
177