Figure 1A.

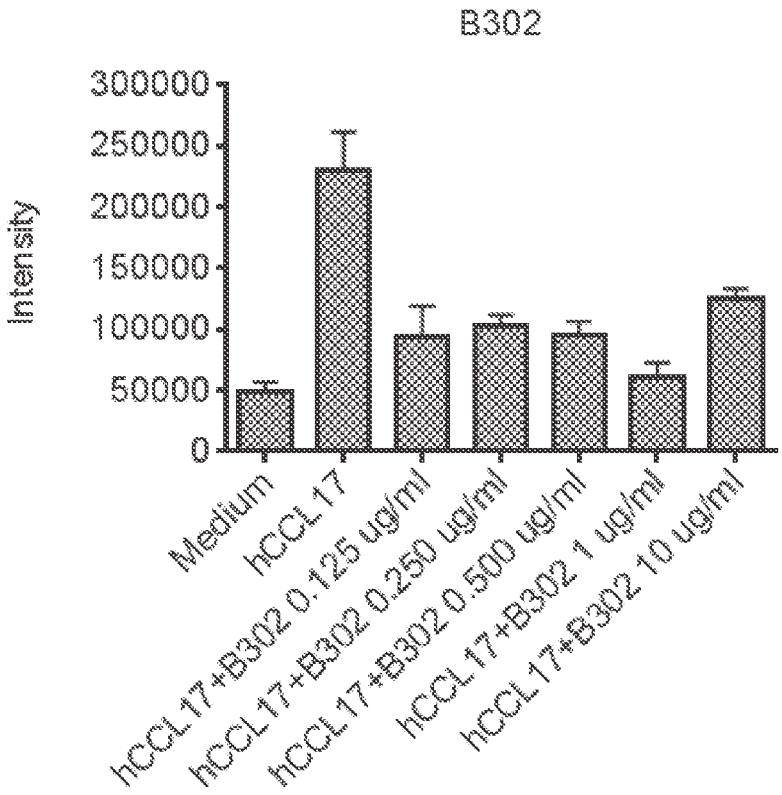

B302
Intensity
300000
250000
200000
150000
100000
50000
0
Medium
hCCL17
hCCL17+B302 0.125 ug/ml
hCCL17+B302 0.250 ug/ml
hCCL17+B302 0.500 ug/ml
hCCL17+B302 1 ug/ml
hCCL17+B302 10 ug/ml

Figure 1B.

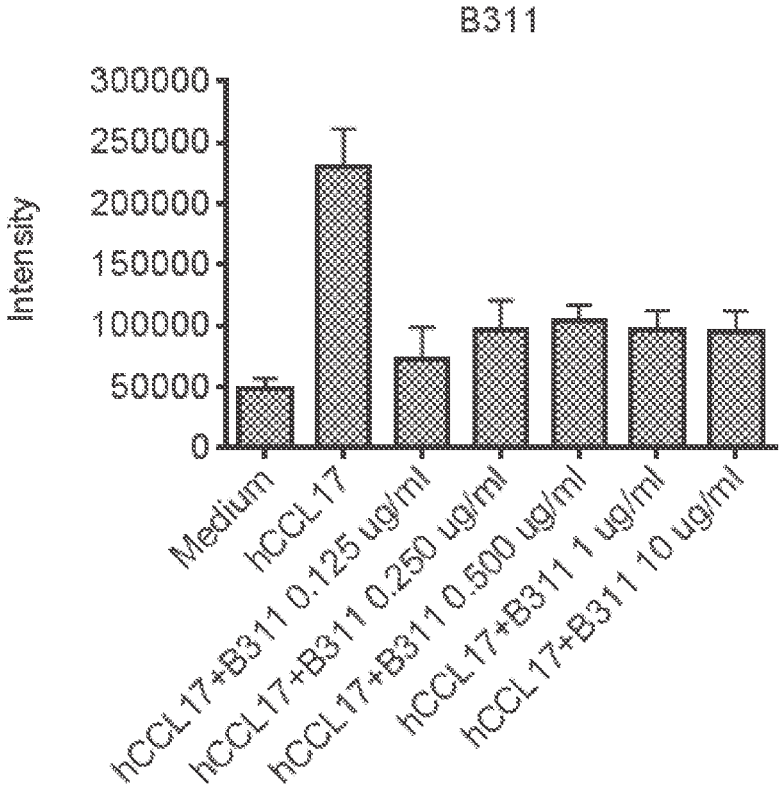

B311
Intensity
300000
250000
200000
150000
100000
50000
0
Medium
hCCL17
hCCL17+B311 0.125 ug/ml
hCCL17+B311 0.250 ug/ml
hCCL17+B311 0.500 ug/ml
hCCL17+B311 1 ug/ml
hCCL17+B311 10 ug/ml

Figure 1C.

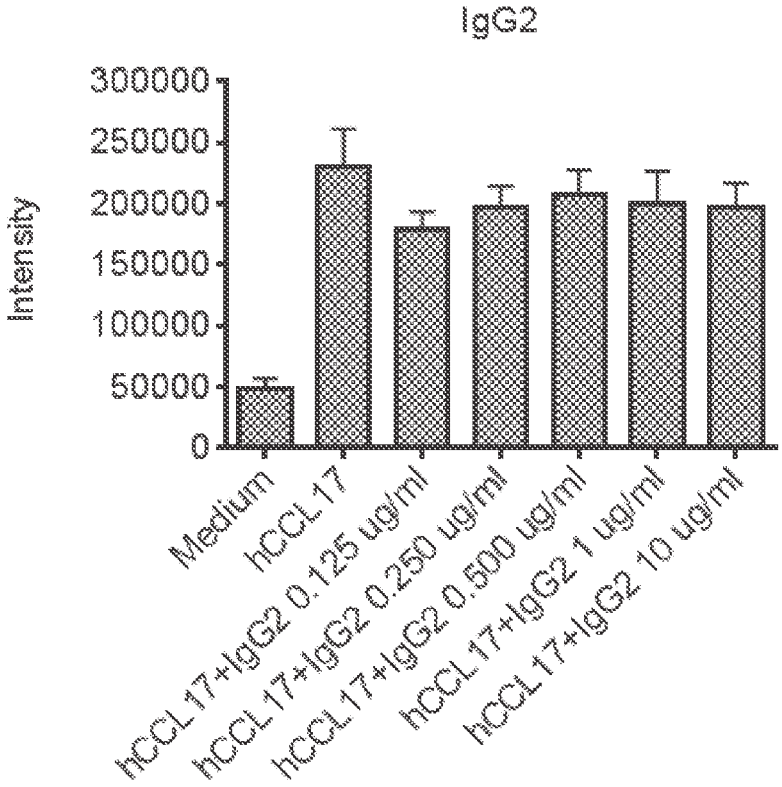

IgG2
Intensity
300000
250000
200000
150000
100000
50000
0
Medium
hCCL17
hCCL17+IgG2 0.125 ug/ml
hCCL17+IgG2 0.250 ug/ml
hCCL17+IgG2 0.500 ug/ml
hCCL17+IgG2 1 ug/ml
hCCL17+IgG2 10 ug/ml

Figure 1D.

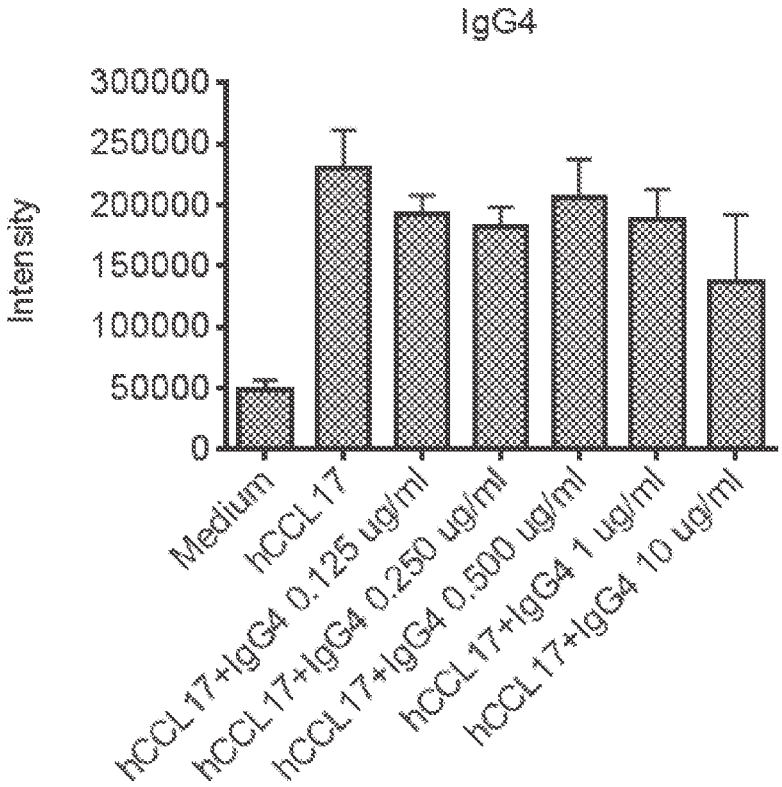

IgG4
Intensity
300000
250000
200000
150000
100000
50000
0
Medium
hCCL17
hCCL17+IgG4 0.125 ug/ml
hCCL17+IgG4 0.250 ug/ml
hCCL17+IgG4 0.500 ug/ml
hCCL17+IgG4 1 ug/ml
hCCL17+IgG4 10 ug/ml

Figure 2A.

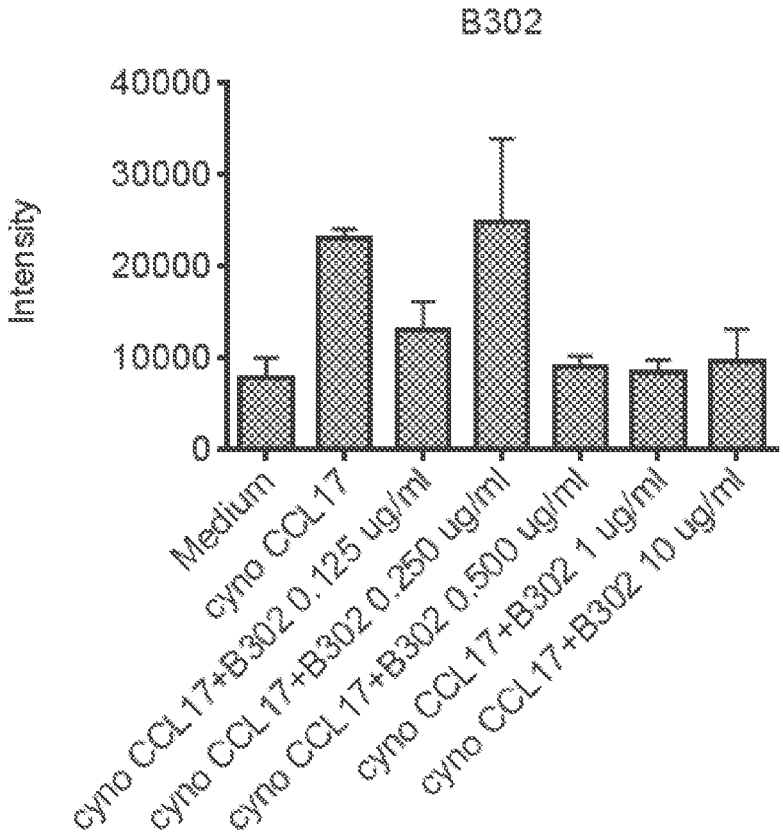

B302
Intensity
40000
30000
20000
10000
0
Medium
cyno CCL17
cyno CCL17+B302 0.125 ug/ml
cyno CCL17+B302 0.250 ug/ml
cyno CCL17+B302 0.500 ug/ml
cyno CCL17+B302 1 ug/ml
cyno CCL17+B302 10 ug/ml

Figure 2B.

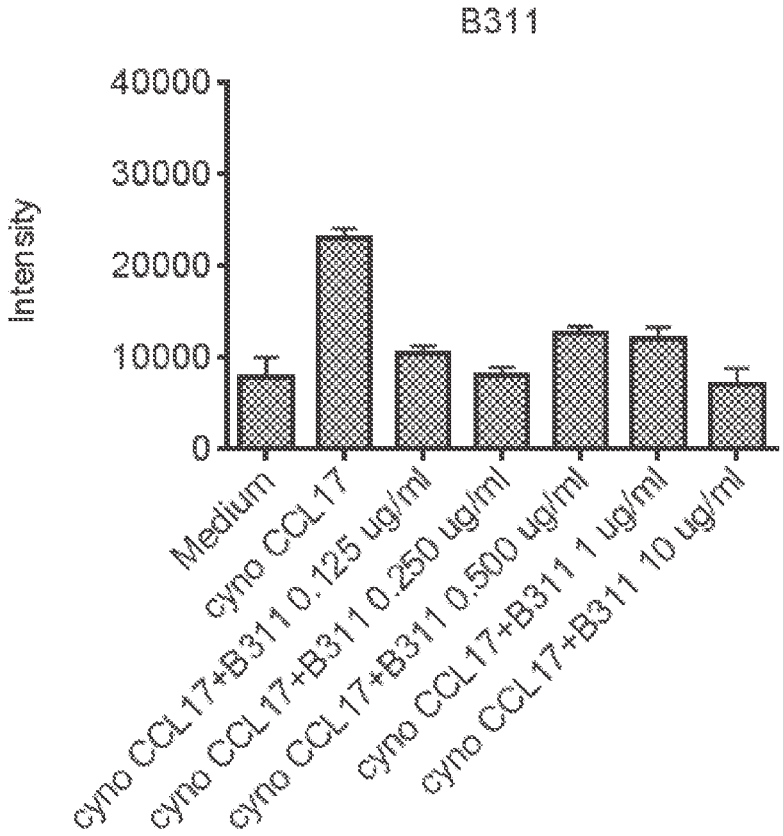

B311
Intensity
40000
30000
20000
10000
0
Medium
cyno CCL17
cyno CCL17+B311 0.125 ug/ml
cyno CCL17+B311 0.250 ug/ml
cyno CCL17+B311 0.500 ug/ml
cyno CCL17+B311 1 ug/ml
cyno CCL17+B311 10 ug/ml

Figure 2C.

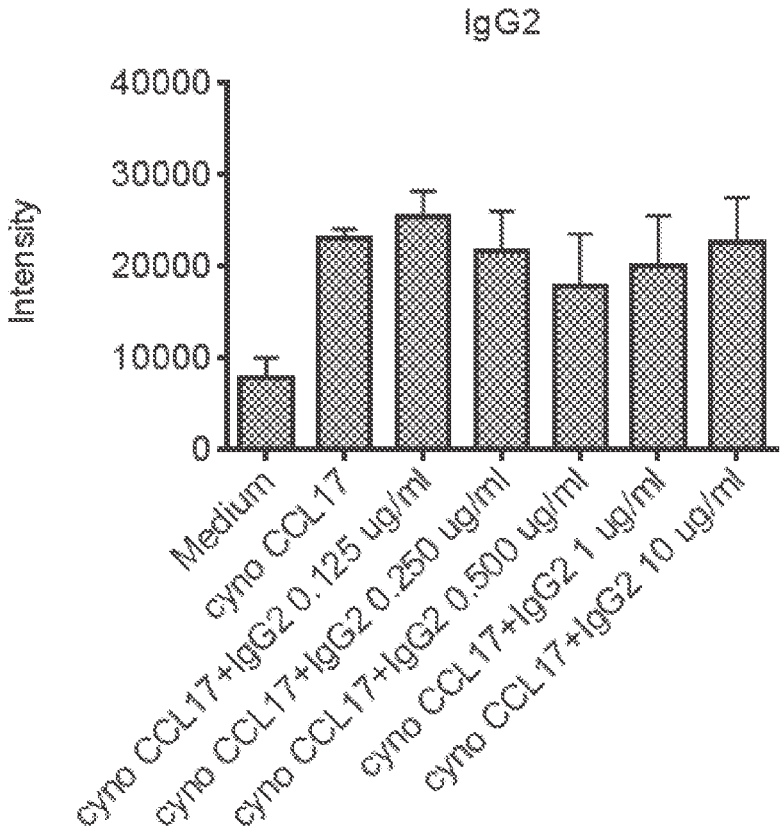

IgG2
Intensity
40000
30000
20000
10000
0
Medium
cyno CCL17
cyno CCL17+IgG2 0.125 ug/ml
cyno CCL17+IgG2 0.250 ug/ml
cyno CCL17+IgG2 0.500 ug/ml
cyno CCL17+IgG2 1 ug/ml
cyno CCL17+IgG2 10 ug/ml

Figure 2D.

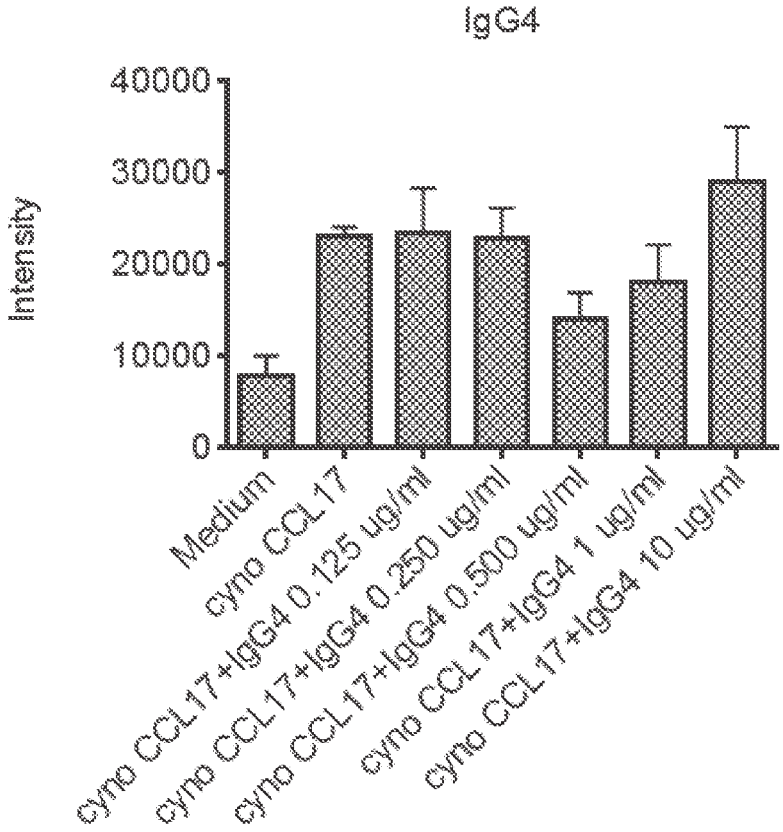

IgG4
Intensity
40000
30000
20000
10000
0
Medium
cyno CCL17
cyno CCL17+IgG4 0.125 ug/ml
cyno CCL17+IgG4 0.250 ug/ml
cyno CCL17+IgG4 0.500 ug/ml
cyno CCL17+IgG4 1 ug/ml
cyno CCL17+IgG4 10 ug/ml

Figure 3.

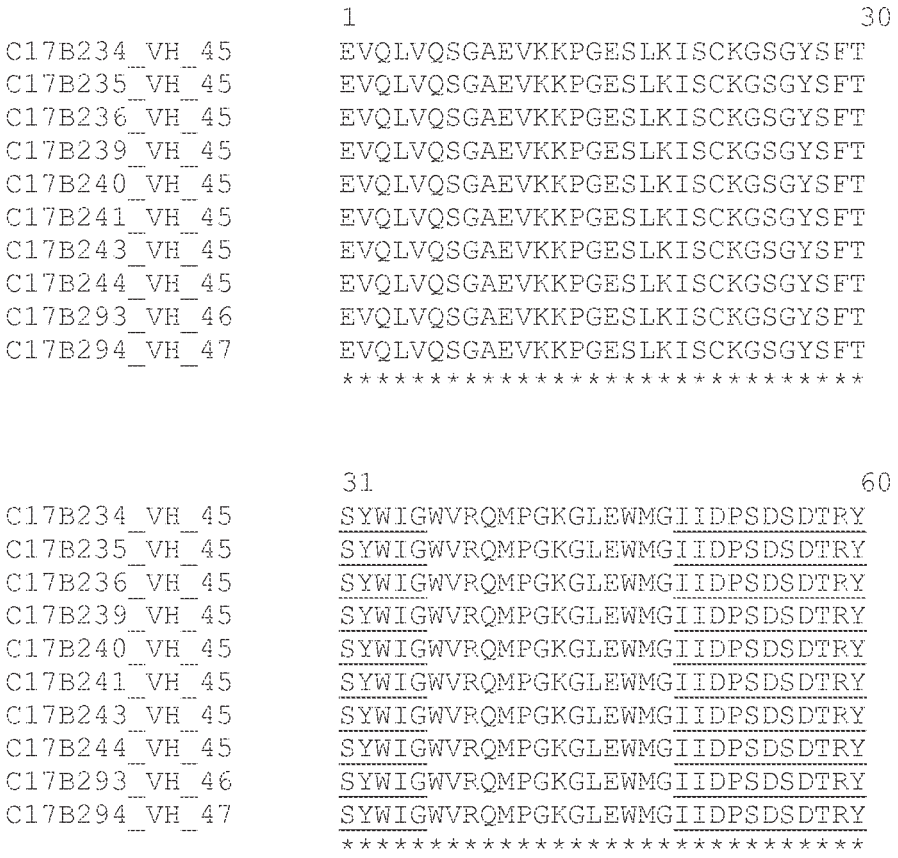

1 30
C17B234_VH_45 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B235_VH_45 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B236_VH_45 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B239_VH_45 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B240_VH_45 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B241_VH_45 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B243_VH_45 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B244_VH_45 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B293_VH_46 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
C17B294_VH_47 EVQLVQSGAEVKKPGESLKISCKGSGYSFT
31 60
C17B234_VH_45 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B235_VH_45 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B236_VH_45 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B239_VH_45 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B240_VH_45 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B241_VH_45 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B243_VH_45 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B244_VH_45 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B293_VH_46 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY
C17B294_VH_47 SYWIGWVRQMPGKGLEWMGIIDPSDSDTRY

Figure 3 cont'd.

```
                        61                                  90
C17B234_VH_45           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B235_VH_45           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B236_VH_45           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B239_VH_45           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B240_VH_45           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B241_VH_45           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B243_VH_45           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B244_VH_45           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B293_VH_46           SPSFQGQVTISADKSISTAYLQWSSLKASD
C17B294_VH_47           SPSFQGQVTISADKSISTAYLQWSSLKASD
                        ********************************

                        91                                  121
C17B234_VH_45           TAMYYCARVGPADVWDSFDYWGQGTLVTVSS
C17B235_VH_45           TAMYYCARVGPADVWDSFDYWGQGTLVTVSS
C17B236_VH_45           TAMYYCARVGPADVWDSFDYWGQGTLVTVSS
C17B239_VH_45           TAMYYCARVGPADVWDSFDYWGQGTLVTVSS
C17B240_VH_45           TAMYYCARVGPADVWDSFDYWGQGTLVTVSS
C17B241_VH_45           TAMYYCARVGPADVWDSFDYWGQGTLVTVSS
C17B243_VH_45           TAMYYCARVGPADVWDSFDYWGQGTLVTVSS
C17B244_VH_45           TAMYYCARVGPADVWDSFDYWGQGTLVTVSS
C17B293_VH_46           TAMYYCARVGPADVWDAFDYWGQGTLVTVSS
C17B294_VH_47           TAMYYCARVGPADVWDTFDYWGQGTLVTVSS
                        ****************:***************
```

Figure 4.

VH consensus sequence (SEQ ID NO: 75)

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIDPSDSDT

RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARVGPADVWDX$_1$FDYWGQGT

LVTVSS

wherein

X_1 is S, A or T

HCDR1 squence

SYWIG (SEQ ID NO: 4)

HCDR2 sequence

IIDPSDSDTRYSPSFQG (SEQ ID NO: 5)

HCDR3 consensus sequence

VGPADVWDX$_1$FDY (SEQ ID NO: 71),

wherein

X_1 is S, A or T

Figure 5.


1 30
C17B234_VL_50 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B235_VL_51 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B236_VL_52 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B239_VL_55 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B240_VL_56 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B241_VL_57 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B243_VL_59 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B244_VL_60 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B293_VL_62 DIVMTQSPDSLAVSLGERATINCKSSQSVL
C17B294_VL_62 DIVMTQSPDSLAVSLGERATINCKSSQSVL
31 60
C17B234_VL_50 LSFDNINKLAWYQQKPGQPPKLLIYNASTR
C17B235_VL_51 YSFYNFNALAWYQQKPGQPPKLLIYHASTR
C17B236_VL_52 LSPWNSNQLAWYQQKPGQPPKLLIYGASTR
C17B239_VL_55 SSFTNTNTLAWYQQKPGQPPKLLIYHASTR
C17B240_VL_56 YSHVNYNALAWYQQKPGQPPKLLIYNASTR
C17B241_VL_57 NSFTNNNALAWYQQKPGQPPKLLIYEASTR
C17B243_VL_59 NSFDNKNDLAWYQQKPGQPPKLLIYEASTR
C17B244_VL_60 SSITNVNDLAWYQQKPGQPPKLLIYTASTR
C17B293_VL_62 LSFDNINKLAWYQQKPGQPPKLLIYDASTR
C17B294_VL_62 LSFDNINKLAWYQQKPGQPPKLLIYDASTR

Figure 5 cont'd.

```
                    61                                  90
C17B234_VL_50       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B235_VL_51       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B236_VL_52       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B239_VL_55       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B240_VL_56       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B241_VL_57       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B243_VL_59       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B244_VL_60       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B293_VL_62       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
C17B294_VL_62       ESGVPDRFSGSGSGTDFTLTISSLQAEDVA
                    ******************************
```

```
                    91                      113
C17B234_VL_50       VYYCQQFYSVPSTFGQGTKVEIK
C17B235_VL_51       VYYCQQFYATPFTFGQGTKVEIK
C17B236_VL_52       VYYCQQYYLIPSTFGQGTKVEIK
C17B239_VL_55       VYYCQQYLIYPSTFGQGTKVEIK
C17B240_VL_56       VYYCQQYYTLPATFGQGTKVEIK
C17B241_VL_57       VYYCQQTNSIPLTFGQGTKVEIK
C17B243_VL_59       VYYCQQHWQTPLTFGQGTKVEIK
C17B244_VL_60       VYYCQQYYHDPFTFGQGTKVEIK
C17B293_VL_62       VYYCQQFYSVPSTFGQGTKVEIK
C17B294_VL_62       VYYCQQFYSVPSTFGQGTKVEIK
                    ******     * ***********
```

Figure 6A.

VL consensus sequence (SEQ ID NO: 76):

DIVMTQSPDSLAVSLGERATINCKSSQSVLX$_1$SX$_2$X$_3$NX$_4$NX$_5$LAWYQQKPGQPPKLLIY X$_6$ASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQX$_7$X$_8$X$_9$X$_{10}$PX$_{11}$TFGQGT KVEIK; wherein

X$_1$ is L, Y, S or N;

X$_2$ is F, P, H or I;

X$_3$ is D, Y, W, T or V;

X$_4$ is I, F, S, T, Y, N, K or V;

X$_5$ is K, A, Q, T or D;

X$_6$ is N, H, G, E, T or D;

X$_7$ is F, Y, T or H;

X$_8$ is Y, L, N or W;

X$_9$ is S, A, L, I, T, Q or H;

X$_{10}$ is V, T, I, Y, L or D; and

X$_{11}$ is S, F, A or L.

Figure 6B.

LCDR1 consensus sequence:

KSSQSVLX$_1$SX$_2$X$_3$NX$_4$NX$_5$LA (SEQ ID NO: 72),

wherein

X$_1$ is L, Y, S or N;

X$_2$ is F, P, H or I;

X$_3$ is D, Y, W, T or V;

X$_4$ is I, F, S, T, Y, N, K or V; and

X$_5$ is K, A, Q, T or D.

LCDR2 consensus sequence:

X$_1$ASTRE (SEQ ID NO: 73),

wherein

X$_1$ is N, H, G, E, T or D.

LCDR3 consensus sequence

QQX$_1$X$_2$X$_3$X$_4$PX$_5$T (SEQ ID NO: 74);

wherein

X$_1$ is F, Y, T or H;

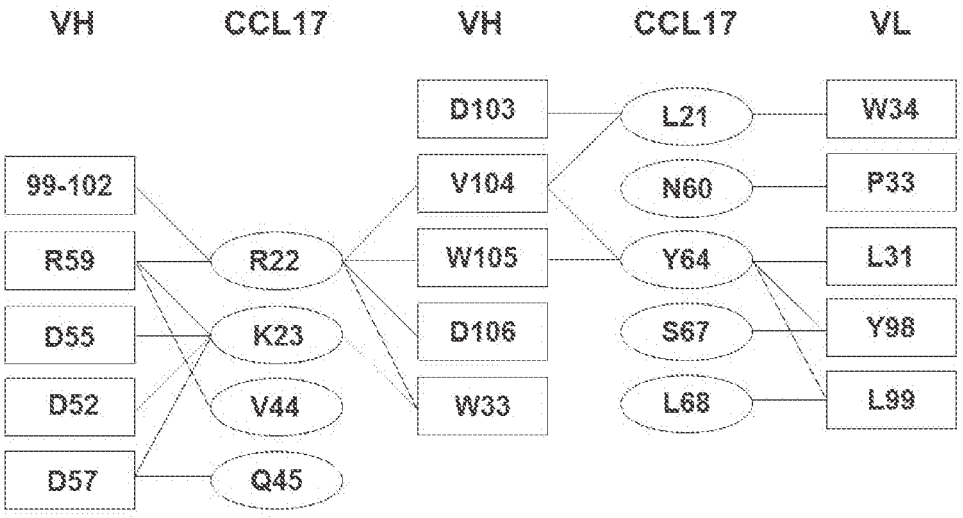
X$_2$ is Y, L, N or W;

X$_3$ is S, A, L, I, T, Q or H;

X$_4$ is V, T, I, Y, L or D; and

X$_5$ is S, F, A or L.

Figure 7.


VH
CCL17
VH
CCL17
VL
99-102
R59
D55
D52
D57
R22
K23
V44
Q45
D103
V104
W105
D106
W33
L21
N60
Y64
S67
L68
W34
P33
L31
Y98
L99