

**A1 clone**

QSVLTQPPSVSAAPGQQRVSISCSGRSSNIASHDVFVWYQQLPGTAPKVMYETNKRPGIPDRFSGSKSGTSATLDIA  
GLQTGDEADYYCGAWDSGLTGMLFGGGTKVTVL (SEQ ID NO:1)

LC-CDR1: SGRSSNIASHDVF (SEQ ID NO:9)

LC-CDR2: ETNKRPGW (SEQ ID NO:10)

LC-CDR3: GAWDSGLTGML (SEQ ID NO:11)

**C2 clone**

SYELTQPPSVSVAPGKTTTRITCGGDNIGRKSVHWYQQRPGQAPLLVLVYDDGDRPSGIPDRFSGNSGNTATLTISGT  
QAMDEADYYCQAWDSTVVFGGGTRLTVL (SEQ ID NO:2)

LC-CDR1: GGDNIGRKSVH (SEQ ID NO:12)

LC-CDR2: DDGDRPS (SEQ ID NO:13)

LC-CDR3: QAWDSTV (SEQ ID NO:14)

**Figure 1**

C4 clone

QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNNYVSWYQQLPGTAPKLLIYDNNERLSGIPDRFSGSKSGTSATLGISG  
 LQTGDEADYYCGTWDSSLVVF~~GGG~~TKLTVL (SEQ ID NO:3)

LC-CDR1: SGSSSNIGNNNYVS (SEQ ID NO:15)

LC-CDR2: DNNERLS (SEQ ID NO:16)

LC-CDR3: GTWDSSLVWV (SEQ ID NO:17)

H12 clone and H12 GL clone

QSVLTQPPSVSGAPGQQRVTISCTIGSSSNIGAGYDVHWWYQQLPGTAPKLLIY~~GNSNRPS~~GVPDRFSGSKSGTSASLAI  
 TGLQAEDEADYYCQSYDSSL~~SGSYVVF~~GGGTKLTVL (SEQ ID NO:4)

LC-CDR1: TGSSSNIGAGYDVH (SEQ ID NO:18)

LC-CDR2: GNSNRPS (SEQ ID NO:19)

LC-CDR3: QSYDSSLSGSYV (SEQ ID NO:20)

Figure 1 (cont.)

**A1 clone**

QVQLQQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRAPGGGLEWMGRIIPILGIANYAQKFQGRVTITADKSTS  
TAYMELSSLRSEDTAVYYCARGSGSLYAFDIWGQGTMTVSS (SEQ ID NO:5)

HC-CDR1: SYAIS (SEQ ID NO:21)  
HC-CDR2: RIIPILGIANYAQKFQG (SEQ ID NO:22)  
HC-CDR3: GGSYGSLYAFDI (SEQ ID NO:23)

**C2 clone**

QVQLQQSGAEVKKPGSSVKVCKASGGTFSSYAISWVRAPGGGLEWMGRIIPILGIANYAQKFQGRVTITADKSTS  
TAYMELSSLRSEDTAVYYCARGSGSLYAFDIWGQGTMTVSS (SEQ ID NO:6)

HC-CDR1: SYAIS (SEQ ID NO:21)  
HC-CDR2: RIIPILGIANYAQKFQG (SEQ ID NO:22)  
HC-CDR3: GGSYGSLYAFDI (SEQ ID NO:23)

**Figure 2**

C4 clone

QVQLQQSGAEVKKPGSSVKVSKASGGTFSSYAISWVRQAPGQGLEWMGRIPILGIANYAQKFQGRVTITADKSTST  
 TAYMELSSLRSEDTAVYYCARGGYGGNSLYAFDIWGQGTMTVSS (SEQ ID NO:7)

|          |                   |                |
|----------|-------------------|----------------|
| HC-CDR1: | SYAIS             | (SEQ ID NO:21) |
| HC-CDR2: | RIIPILGIANYAQKFQG | (SEQ ID NO:22) |
| HC-CDR3: | GGYGGNSLYAFDI     | (SEQ ID NO:24) |

H12 clone

EVQLVQSGAEVKKPGASVKVSKASGGTFSSYAISWVRQAPGQGLEWMGRIPILGIANYAQKFQGRVTITADKSTST  
 AYMELSSLRSEDTAVYYCARSGHGYSGAFDYGQGT (SEQ ID NO:8)

|          |                   |                |
|----------|-------------------|----------------|
| HC-CDR1: | SYAIS             | (SEQ ID NO:21) |
| HC-CDR2: | RIIPILGIANYAQKFQG | (SEQ ID NO:22) |
| HC-CDR3: | SGHGYSGAFDY       | (SEQ ID NO:25) |

Figure 2 (cont.)

H12 GL clone

QVQLVQSGAEVKKPGSSVKVSCSKASGGTFSSYAISWVRQAPGQGLEWMGRIPILGIANYAQKFQGRVTITADKSTSTAYMELSSLR  
SED~~TAVYYCAR~~SGHGYSGAFDYWGQGTLVTVSS (SEQ ID NO:35)

HC-CDR1: SYAIS (SEQ ID NO:21)

HC-CDR2: RIIPILGIANYAQKFQG (SEQ ID NO:22)

HC-CDR3: SGHGYSGAFDY (SEQ ID NO:25)

Figure 2 (cont.)

| Clone                     | CDR 1                            | CDR 2                               | CDR 3                                                                                                                                                                                                                                                                                                                                                                                                                             |
|---------------------------|----------------------------------|-------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Light Chain</b>        |                                  |                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| <b>A1</b>                 | SGRSSNIASHDVF<br>(SEQ ID NO:9)   | ETNKRPW<br>(SEQ ID NO:10)           | GAWDSTGLTGM<br>(SEQ ID NO:11)                                                                                                                                                                                                                                                                                                                                                                                                     |
| <b>C2</b>                 | GGDNIGRKSVH<br>(SEQ ID NO:12)    | DDGDRPS<br>(SEQ ID NO:13)           | QAWDSTVV<br>(SEQ ID NO:14)                                                                                                                                                                                                                                                                                                                                                                                                        |
| <b>C4</b>                 | SGSSSNIGNNYVS<br>(SEQ ID NO:15)  | DNNERLS<br>(SEQ ID NO:16)           | GTWDSSLSVVV<br>(SEQ ID NO:17)                                                                                                                                                                                                                                                                                                                                                                                                     |
| <b>H12 and<br/>H12_GL</b> | TGSSSNIGAGYDVH<br>(SEQ ID NO:18) | GNSNRPS<br>(SEQ ID NO:19)           | QSYDSSLSGSYVV<br>(SEQ ID NO:20)                                                                                                                                                                                                                                                                                                                                                                                                   |
| <b>Heavy Chain</b>        |                                  |                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| <b>A1</b>                 | SYAIS<br>(SEQ ID NO:21)          | RIIPILGIANYAQKFQG<br>(SEQ ID NO:22) | GGSYGSLYAFDI<br>(SEQ ID NO:23)                                                                                                                                                                                                                                                                                                                                                                                                    |
| <b>C2</b>                 | SYAIS<br>(SEQ ID NO:21)          | RIIPILGIANYAQKFQG<br>(SEQ ID NO:22) | GGSYGSLYAFDI<br>(SEQ ID NO:23)                                                                                                                                                                                                                                                                                                                                                                                                    |
| <b>C4</b>                 | SYAIS<br>(SEQ ID NO:21)          | RIIPILGIANYAQKFQG<br>(SEQ ID NO:22) | GGYGNSLYAFDI<br>(SEQ ID NO:24)                                                                                                                                                                                                                                                                                                                                                                                                    |
| <b>H12 and<br/>H12_GL</b> | SYAIS<br>(SEQ ID NO:21)          | RIIPILGIANYAQKFQG<br>(SEQ ID NO:22) | SGHGYSYGAFDY<br>(SEQ ID NO:25)                                                                                                                                                                                                                                                                                                                                                                                                    |
| <b>Consensus</b>          | SYAIS<br>(SEQ ID NO:21)          | RIIPILGIANYAQKFQG<br>(SEQ ID NO:22) | X <sub>1</sub> X <sub>2</sub> X <sub>3</sub> X <sub>4</sub> X <sub>5</sub> X <sub>6</sub> SX <sub>7</sub> X <sub>8</sub> AFDX <sub>9</sub><br>X <sub>1</sub> = no amino acid or G<br>X <sub>2</sub> = G or S<br>X <sub>3</sub> = G or Y<br>X <sub>4</sub> = S, G or H<br>X <sub>5</sub> = Y or G<br>X <sub>6</sub> = G, N or Y<br>X <sub>7</sub> = L or Y<br>X <sub>8</sub> = Y or G<br>X <sub>9</sub> = I or Y<br>(SEQ ID NO:26) |

**Figure 3**

**Light chain variable domains****A1 clone**

&gt;A1\_aa\_L

QSVLTQPPSVSAAPGQRVSISSGRSSNIASHDVFWYQQLPGTAPKIVMYETNKRPGIPDRFSGSKS  
GTSATLDIAGLQTGDEADYYCGAWDSGLTGMLFGGGTKVTVL [SEQ ID NO. 1]

&gt;A1\_ntd\_L

CAGTCTGTGTTGACGCAGCCTCCCTCAGTGTCTGCGGCCCCAGGACAGAGAGTCTCCATCTCCTGCTCTGGGAGG  
AGCTCCAACATTGCCAGTCATGATGTTTTCTGGTACCAGCAACTCCCAGGAACAGCCCCAAAATCGTCATGTAT  
GAACTAATAAACGTCCCTGGGGGATTCTGACCGATTCTCCGGCTCCAAGTCTGGCACGTCCGCCACCCTGGAC  
ATCGCCGGACTCCAGACTGGGGACGAGGCCGACTATTACTGCGGAGCATGGGATAGCGGCCTGACTGGTATGCTG  
TTCGGCGAGGGACCAAGGTGACCGTCCTA [SEQ ID NO. 27]

**C2 clone**

&gt;C2\_aa\_L

SYELTQPPSVSVAPGKTTTRITCGGDNIGRKSVHWYQQRPQAPLLLVYDDGDRPSGIPDRFSGSNSGN  
TATLTISGTQAMDEADYYCQAWDSTVVFGGGTRLTVL [SEQ ID NO. 2]

&gt;C2\_ntd\_L

TCCTATGAGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGACCAGGATTACCTGTGGGGGAGAC  
AACATTGGACGTAAAAGTGTCCATTGGTATCAGCAGAGGCCAGGCCAGGCCCCCTCTCCTCCTCGTCTATGATGAT  
GGCGACCGGCCCTCAGGGATCCCTGACCGATTCTCTGGCTCCAACCTCTGGGAACACAGCCACTCTGACCATCAGC  
GGGACCCAGGCTATGGATGAGGCTGACTATTACTGTGAGCGGTGGGACAGCACCGTGGTATTCGGCGGAGGGACC  
AGACTGACCGTCCTG [SEQ ID NO. 28]

**C4 clone**

&gt;C4\_aa\_L

QSVVTQPPSVSAAPGQKVTIISGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNERLSGIPDRFSGSKS  
GTSATLGISGLQTGDEADYYCGTWDSSLSVVFVGGGTKLTVL [SEQ ID NO. 3]

&gt;C4\_ntd\_L

CAGTCTGTGTCGTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAAGGTCACCATCTCCTGCTCTGGAAGT  
AGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTAT  
GACAATAATGAGCGACTCTCAGGGATTCTGACCGATTCTCTGGTTCCAAGTCTGGCACGTGAGCCACCCTGGGC  
ATCAGCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGCACATGGGATAGTAGCCTGAGTGTCTGGTA  
TTCGGCGGAGGGACCAAGCTGACCGTCCTA [SEQ ID NO. 29]

**Figure 4**

**H12 clone and H12 GL clone**

&gt;H12\_aa\_L

QSVLTQPPSVSGAPGQRTIISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSK  
SGTSASLAITGLQAEDEADYYCQSYDSSLGSGSYVVFGGGTKLTVL [SEQ ID NO. 4]

&gt;H12\_ntd\_L

CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCAC  
TGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCTTCCAGGAACAGCCC  
CCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAG  
TCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCA  
GTCCTATGACAGCAGCCTGAGTGGTTCTTATGTGGTATTTCGGCGGAGGGACCAAGCTGACCGTCTTA  
[SEQ ID NO. 30]

**Heavy chain variable domains****A1 clone**

&gt;A1\_aa\_H

QVQLQQSGAEVKKPGSSVKVSKASGGTFSSYAISWVRQAPQGQLEWMGRIIPILGIANYAQKFQGRV  
TITADKSTSTAYMELSSLRSEDTAVYYCARGGSYGSLYAFDIWGQGTMTVTSS [SEQ ID NO. 5]

&gt;A1\_ntd\_H

CAGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTGAAGGTCTCCTGCAAGGCTTCT  
GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAAGG  
ATCATCCCTATCCTTGGTATAGCAAACACGCACAGAAGTTCAGGGCAGAGTCACGATTACCGCGACAAATCC  
ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGC  
AGCTATGGTTCTCTCTATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCAAGC [SEQ ID  
NO. 31]

**C2 clone**

&gt;C2\_aa\_H

QVQLQQSGAEVKKPGSSVKVSKASGGTFSSYAISWVRQAPQGQLEWMGRIIPILGIANYAQKFQGRV  
TITADKSTSTAYMELSSLRSEDTAVYYCARGGSYGSLYAFDIWGQGTMTVTSS [SEQ ID NO. 6]

&gt;C2\_ntd\_H

CAGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTGAAGGTCTCCTGCAAGGCTTCT  
GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAAGG  
ATCATCCCTATCCTTGGTATAGCAAACACGCACAGAAGTTCAGGGCAGAGTCACGATTACCGCGACAAATCC  
ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGC  
AGCTATGGTTCTCTCTATGCTTTTGATATCTGGGGCCAAGGGACCAGGGTCACCGTCTCAAGC [SEQ ID  
NO. 32]

**Figure 4 (cont.)**

**C4 clone**

&gt;C4\_aa\_H

QVQLQQSGAEVKKPGSSVKVSKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANAYAQKFQGRV  
 TITADKSTSTAYMELSSLRSEDVAVYYCARGGYGGSNLYAFDIWGQGTMTVSS [SEQ ID NO.  
 7]

&gt;C4\_ntd\_H

CAGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGTCTCGGTGAAGGTCTCCTGCAAGGCTTCT  
 GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAAGG  
 ATCATCCCTATCCTTGGTATAGCAAACCTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCC  
 ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGGGGGGGC  
 TACGGTGGTAACCTTGTATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCCTCA [SEQ ID  
 NO. 33]

**H12 clone**

&gt;H12\_aa\_H

EVQLVQSGAEVKKPGASVKVSKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANAYAQKFQGRV  
 TITADKSTSTAYMELSSLRSEDVAVYYCARSGHGYSYGAFDYWGQGT [SEQ ID NO. 8]

&gt;H12\_ntd\_H

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAA  
 GGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTG  
 AGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACCTACGCACAGAAGTTCCAGGGCAGAGTC  
 ACGATTACCGCGGACAAATCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC  
 GGCCGTGTATTACTGTGCGAGGTGAGGGCATGGATACAGCTATGGAGCTTTTGACTACTGGGGCCAGG  
 GCACCCTG [SEQ ID NO. 34]

**Figure 4 (cont.)**

**H12\_GL clone**

&gt;H12\_GL\_aa\_H

QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKFQGRVTITADKS  
TSTAYMELSSLRSEDTAVYYCARSGHGYSYGAFDYWGQGTLVTVSS [SEQ ID NO. 35]

&gt;H12\_GL\_ntd\_H

CAGGTGCAGCTGGTGCAATCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTCTCCTGCAAGGCTTCT  
GGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAAGG  
ATCATCCCTATCCTTGGTATAGCAAACCTACGCACAGAAGTTCAGGGCAGAGTCACGATTACCGCGGACAAATCC  
ACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGGTCAGGG  
CATGGATACAGCTATGGAGCTTTTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCAAGC [SEQ ID  
NO. 36]**Figure 4 (cont.)**

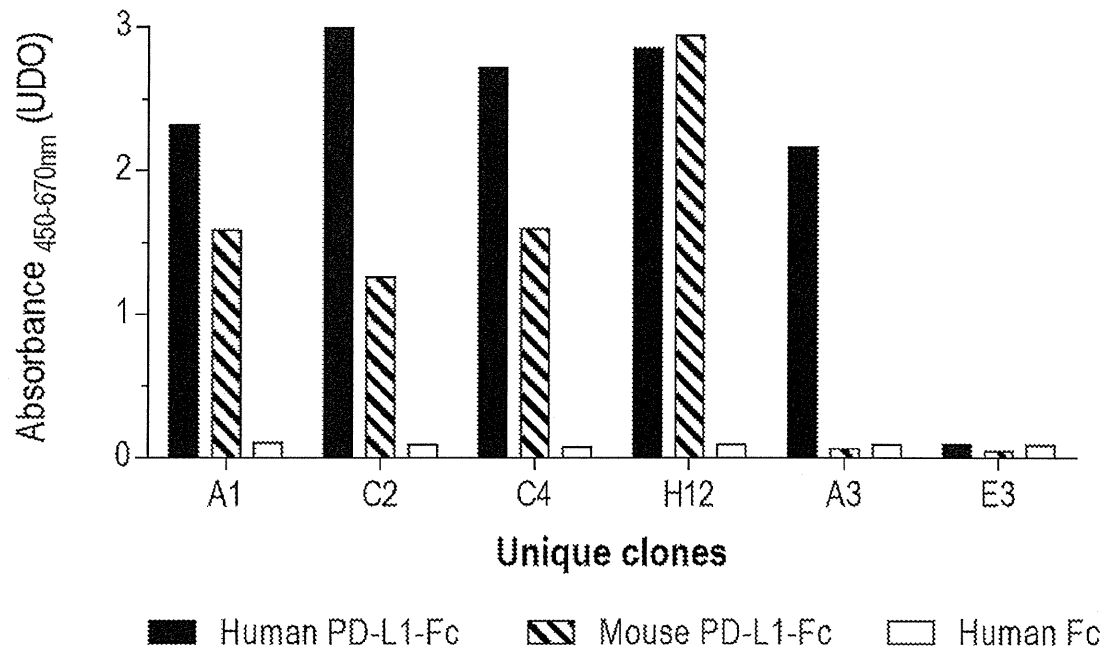


Figure 5

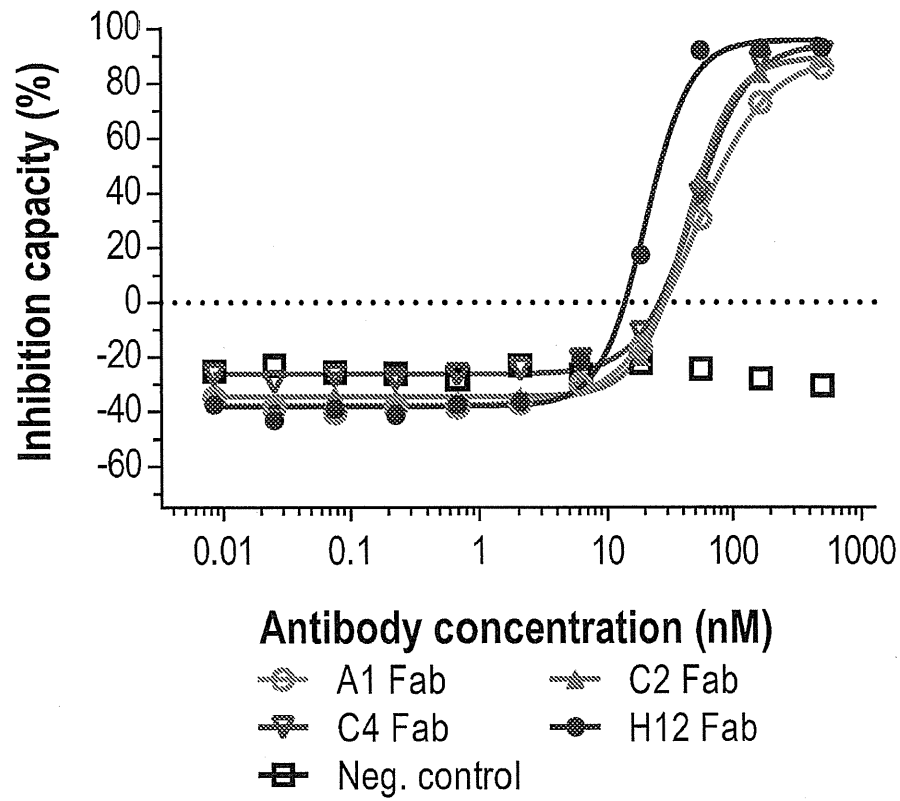


Figure 6

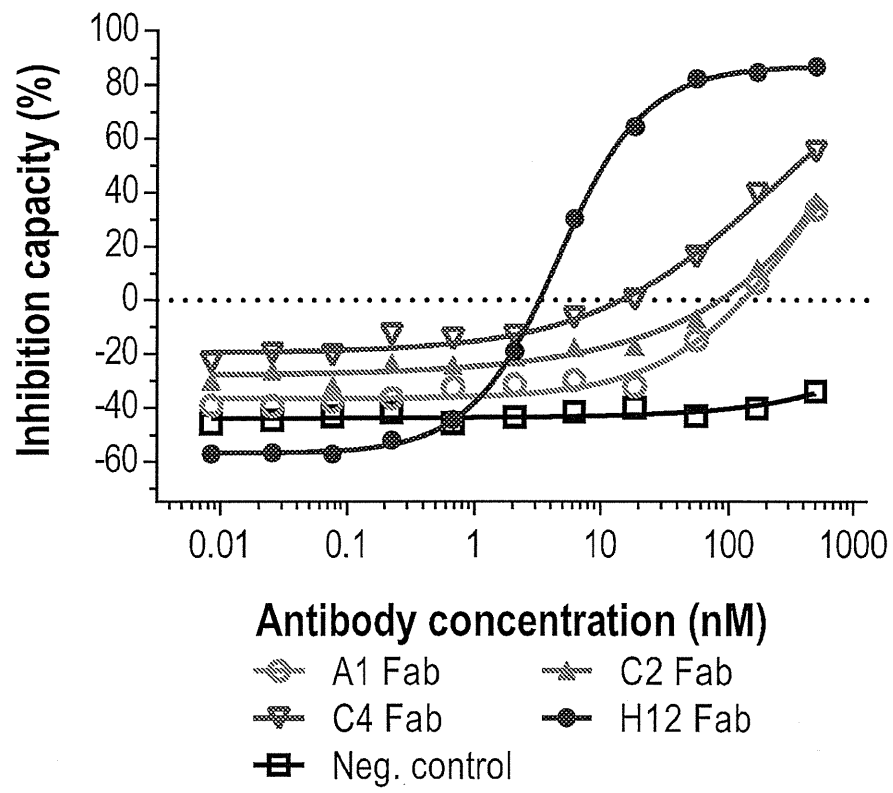


Figure 7

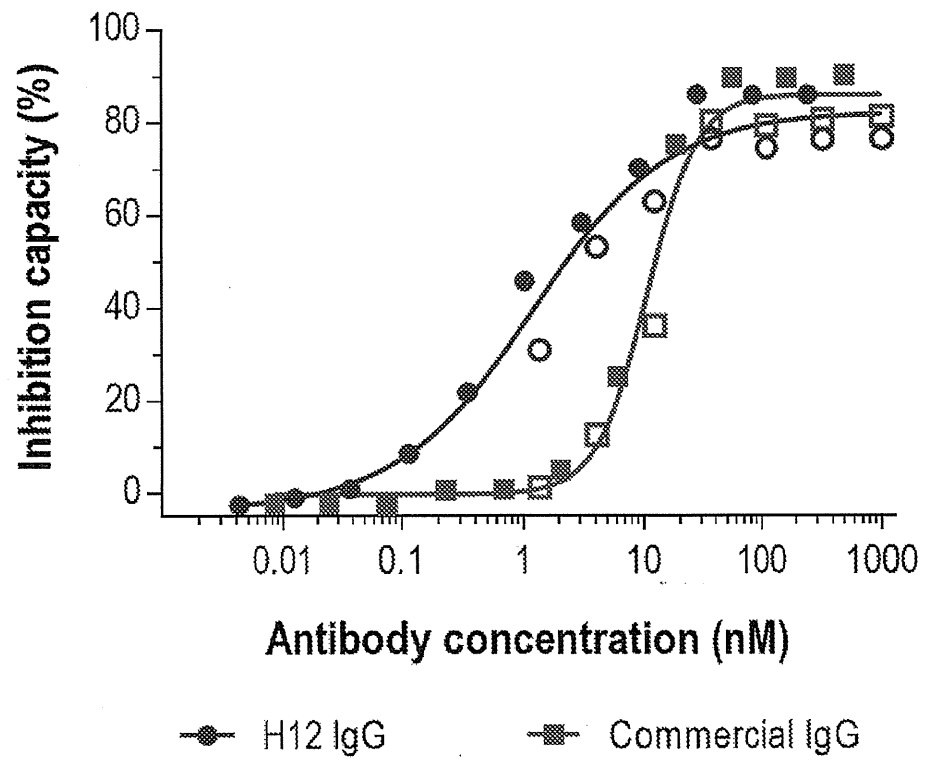


Figure 8

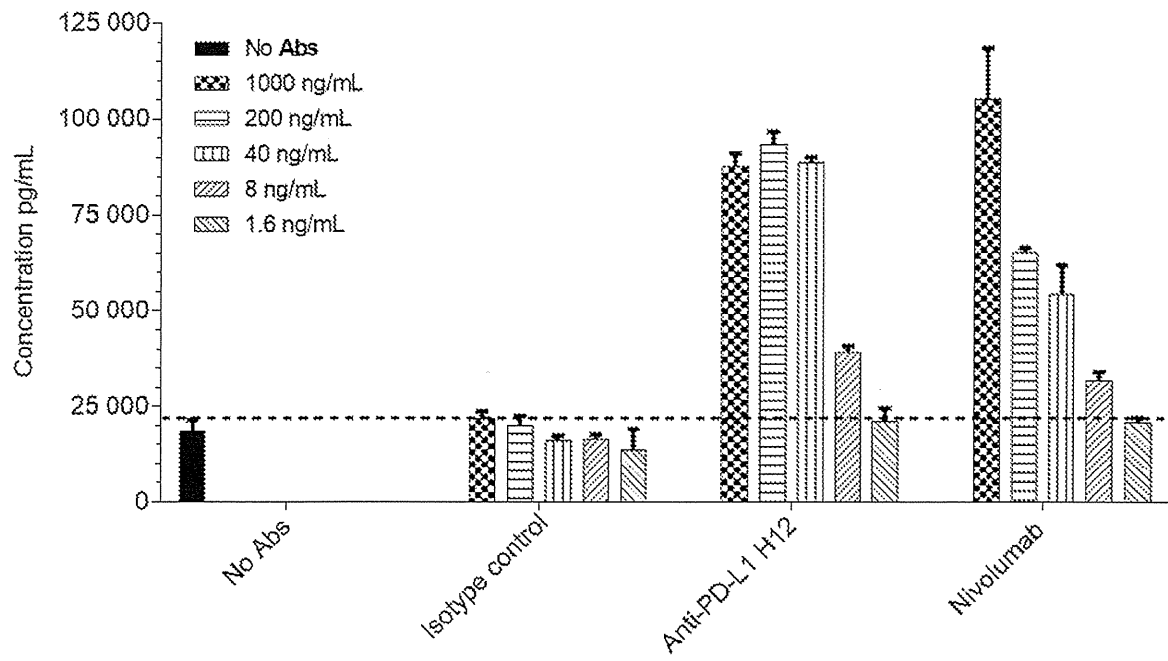


Figure 9

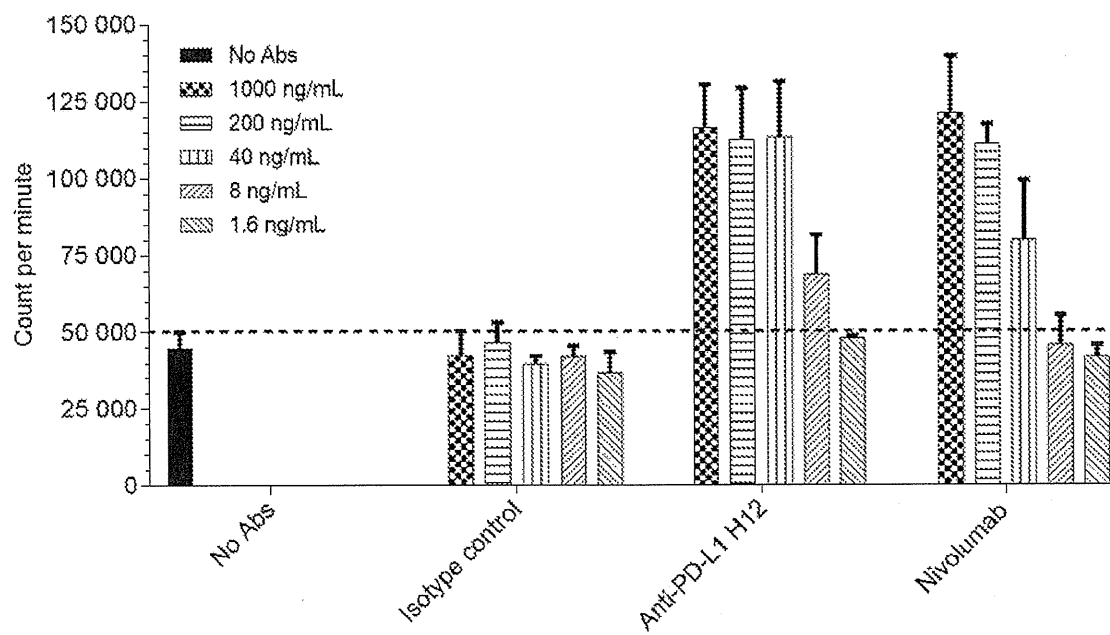


Figure 10

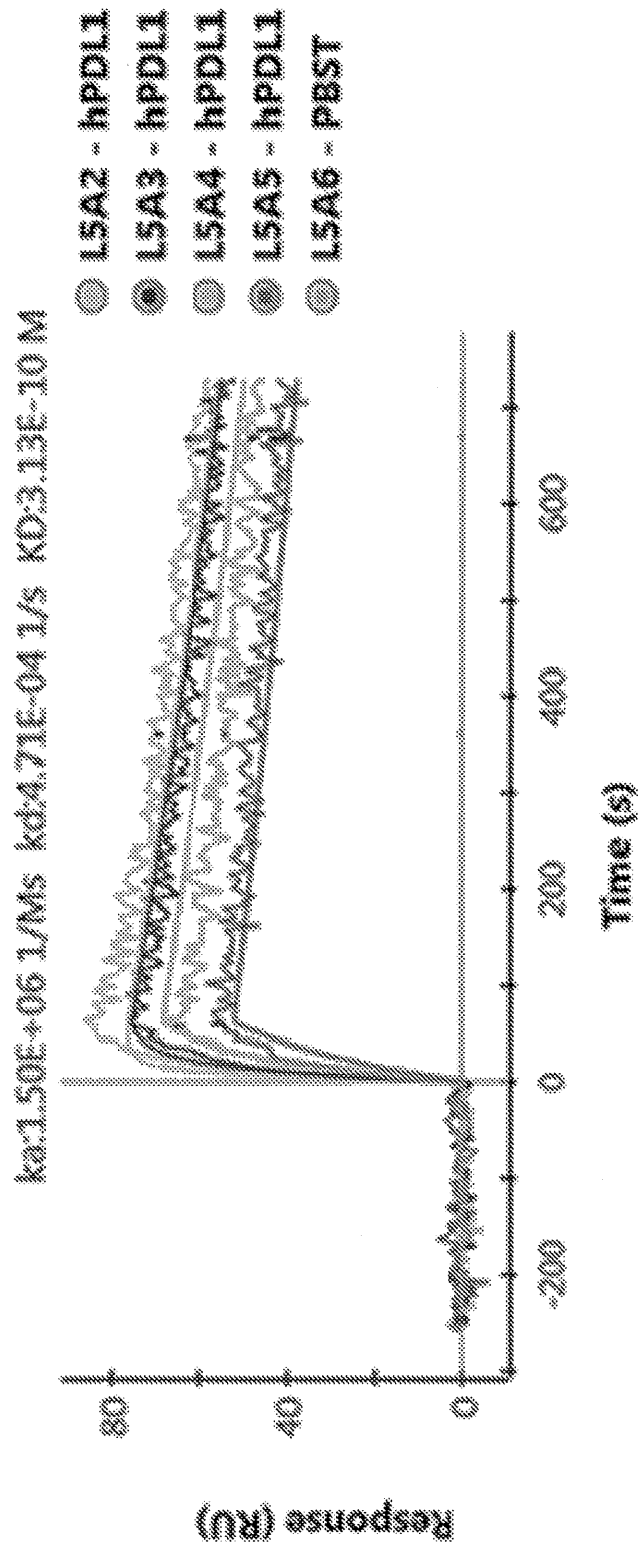


Figure 11

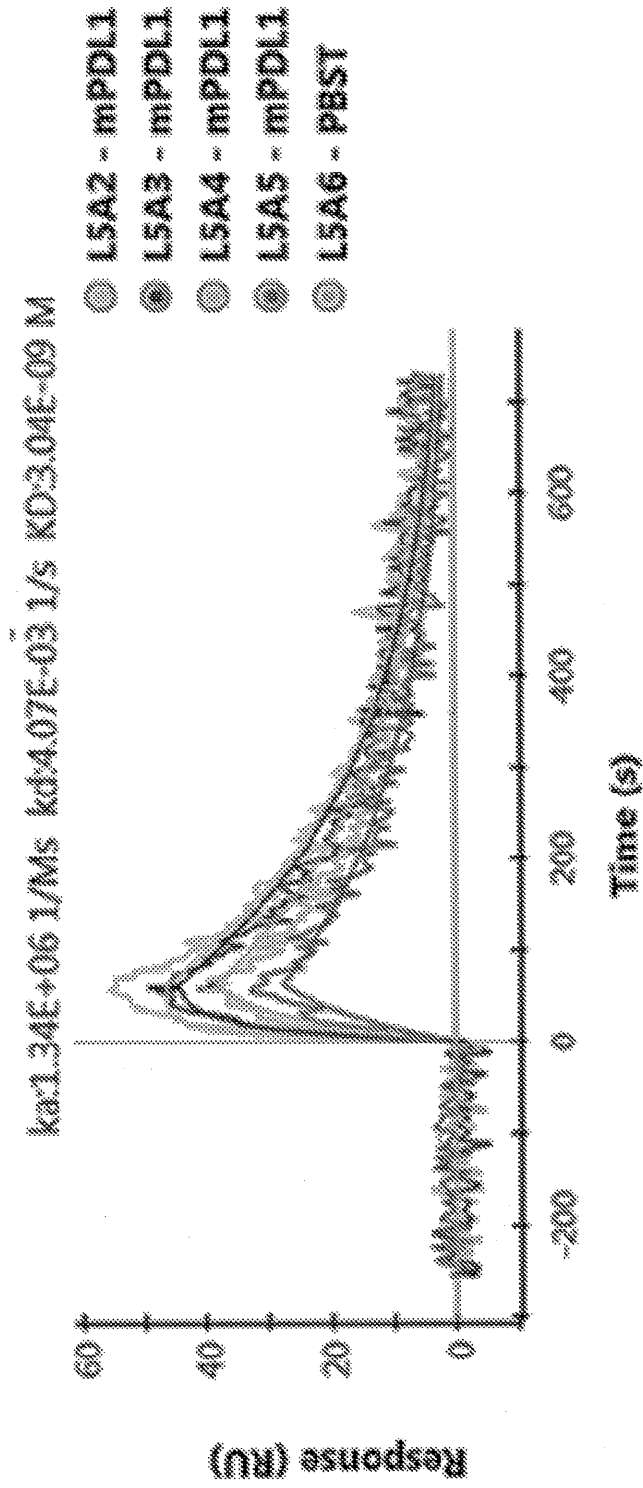


Figure 12

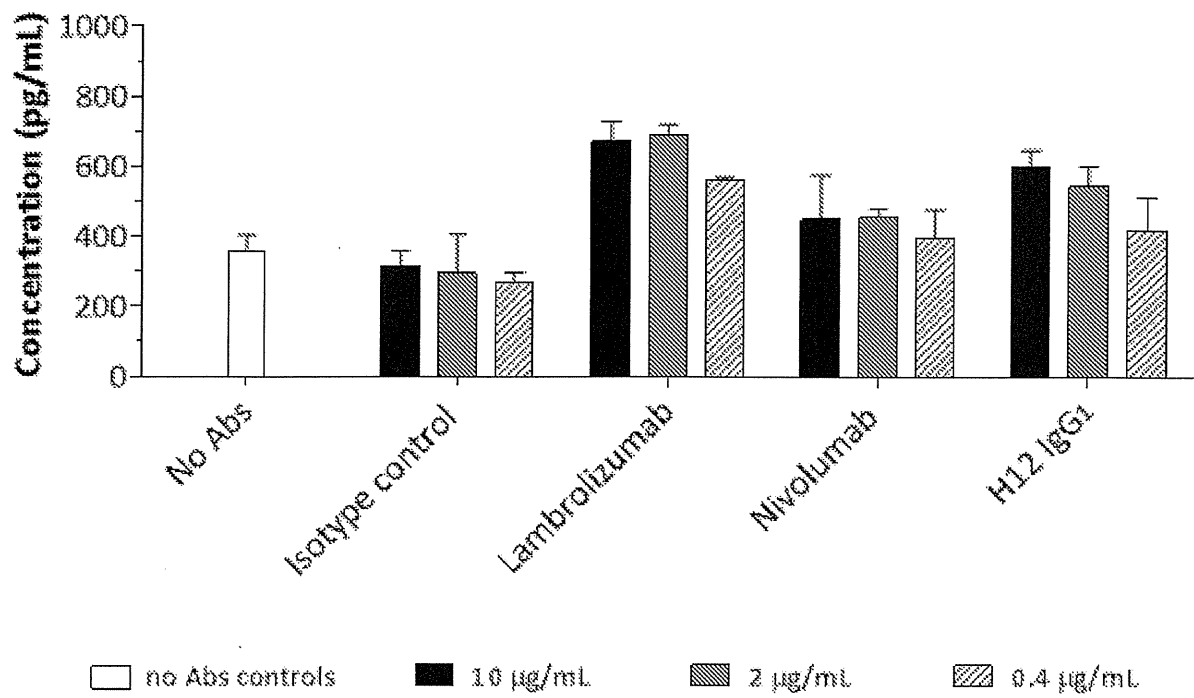


Figure 13A

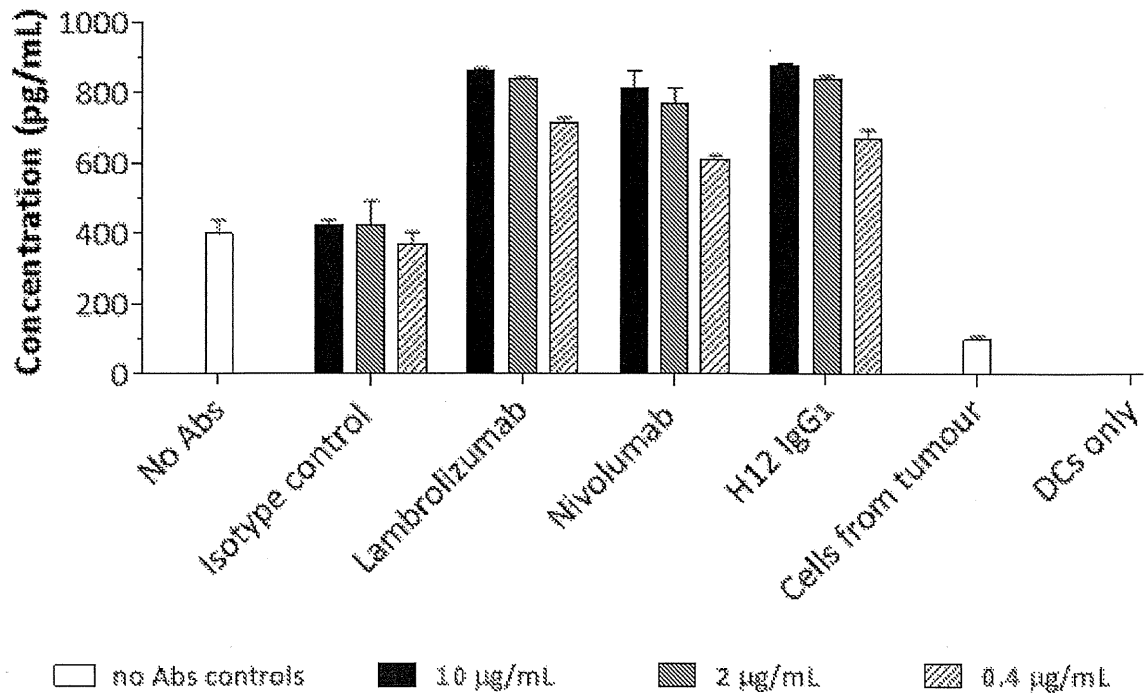


Figure 13B

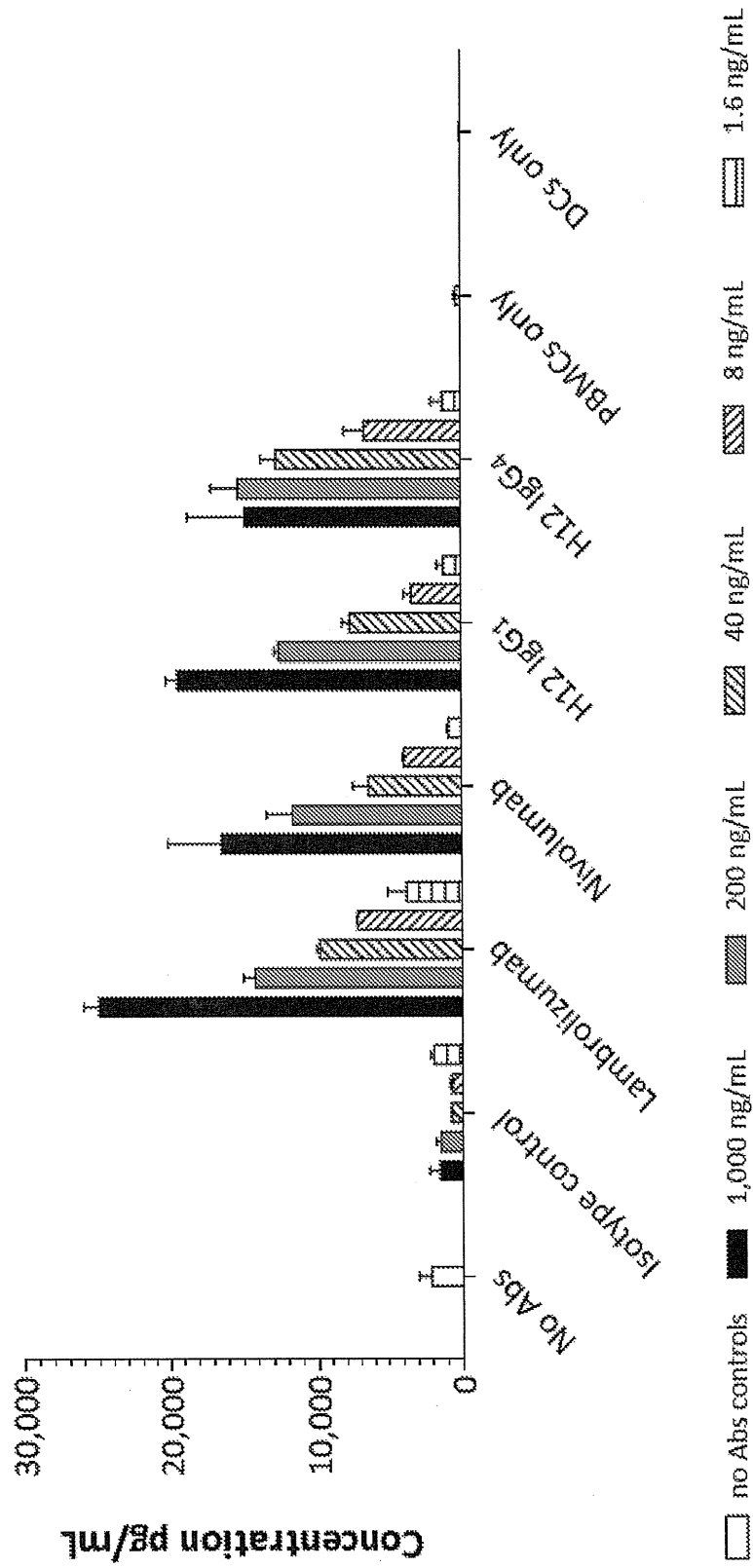


Figure 14

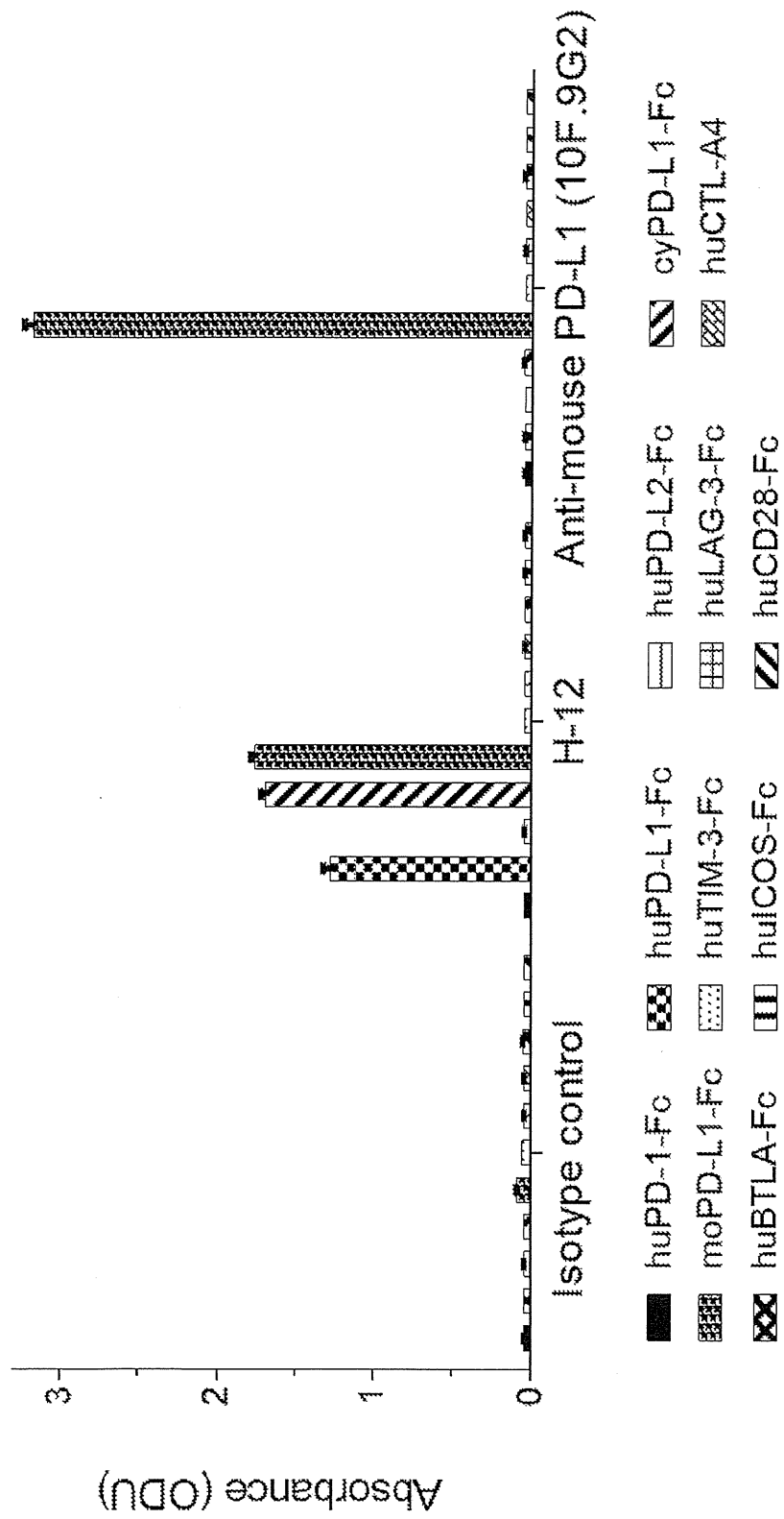


Figure 15

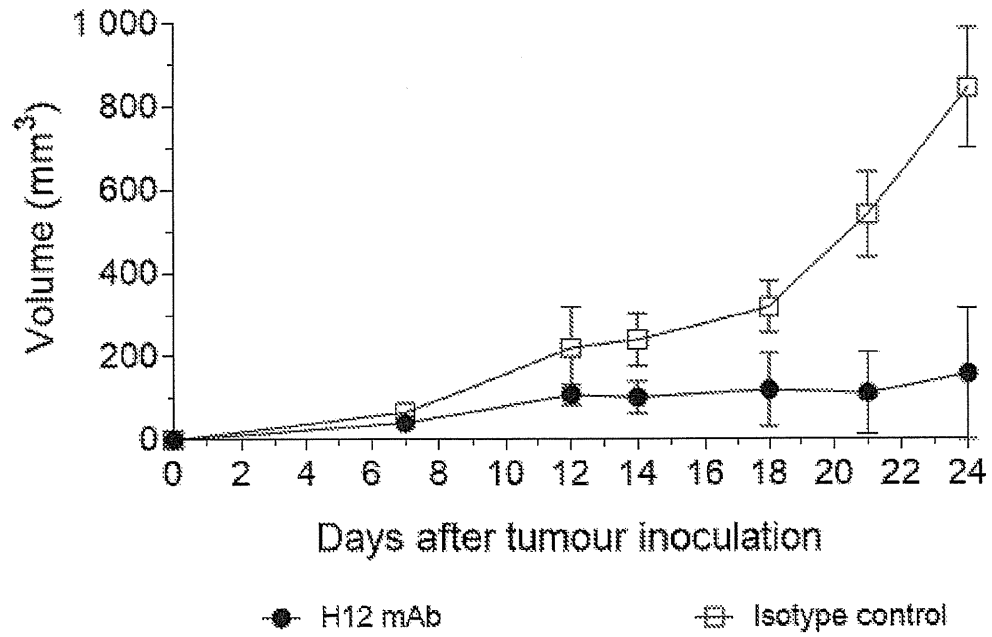


Figure 16A

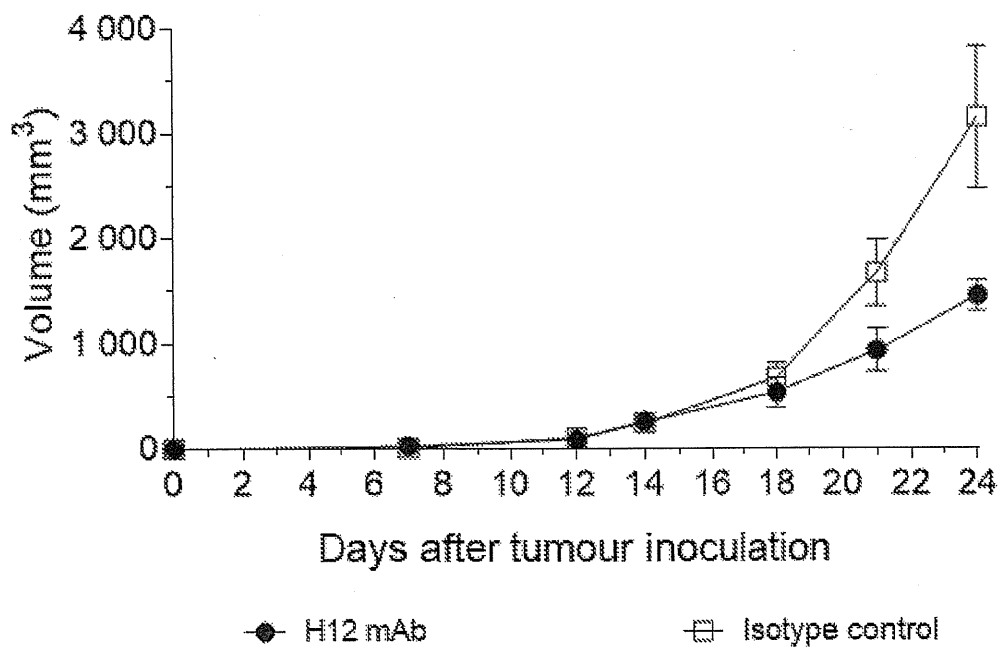


Figure 16B

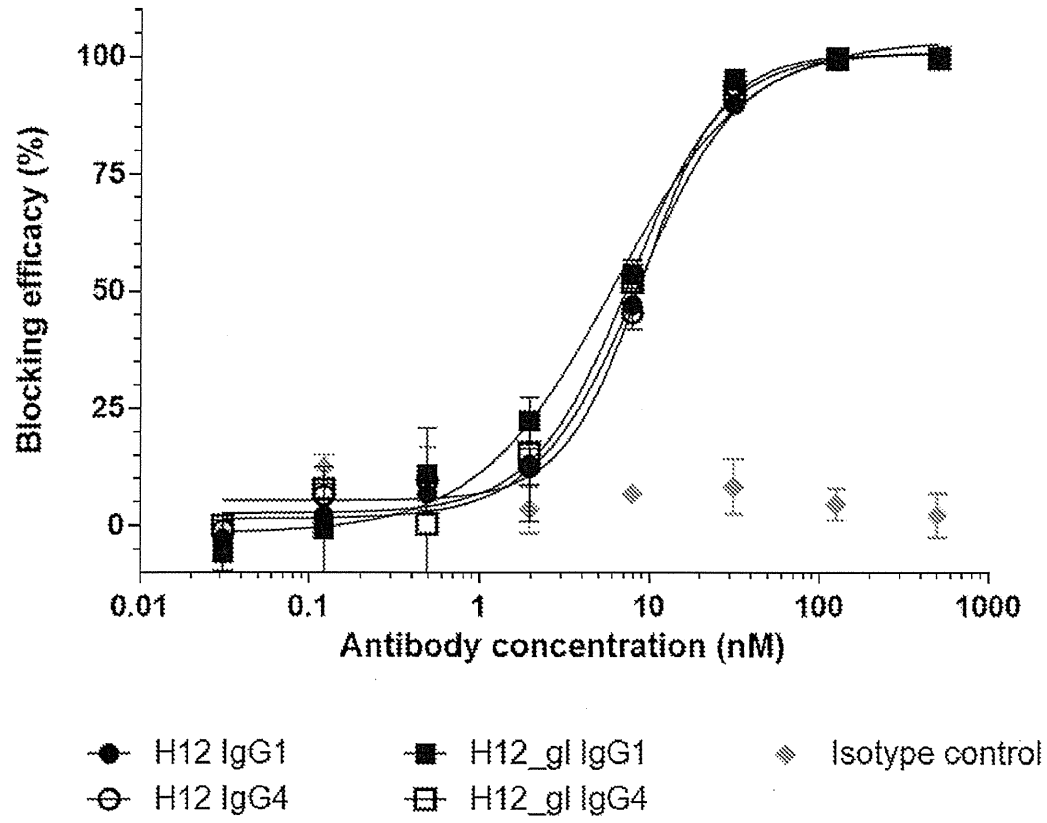


Figure 17

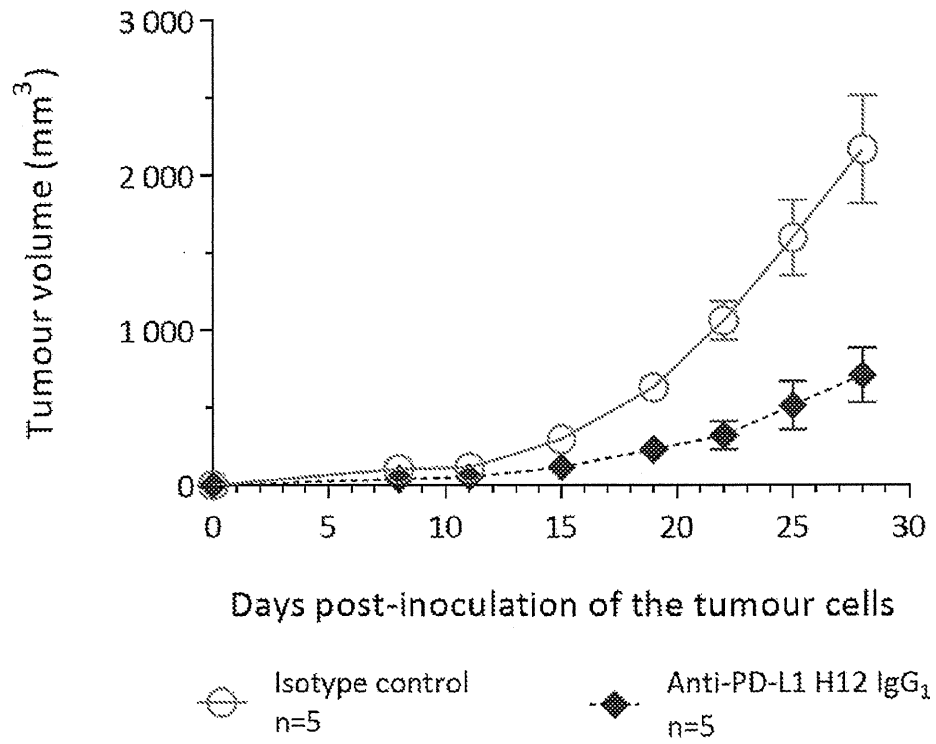


Figure 18A

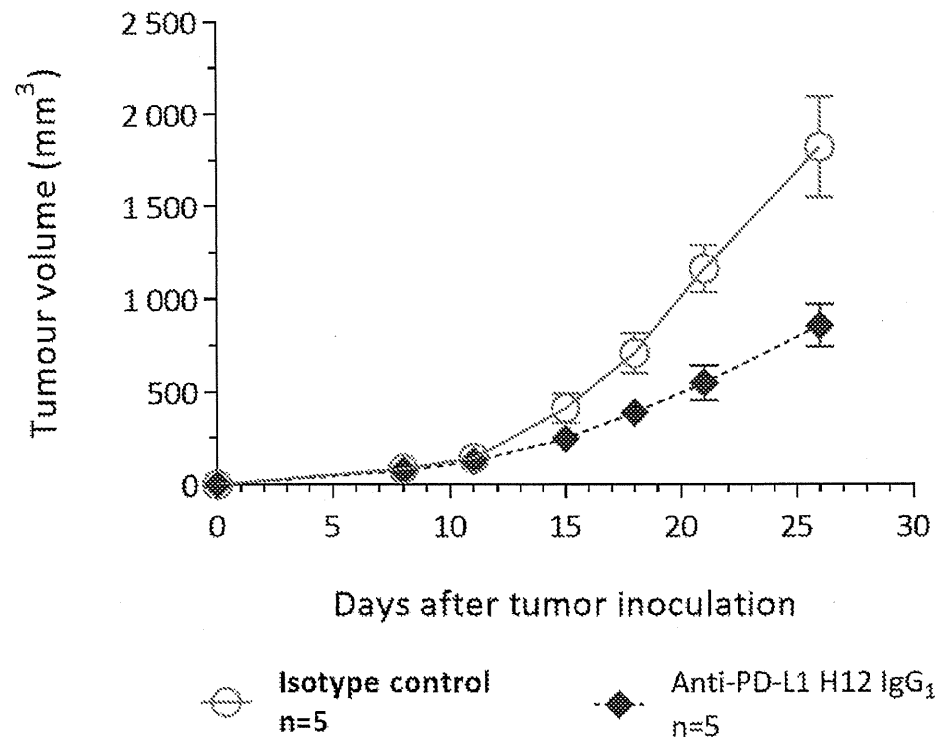


Figure 18B

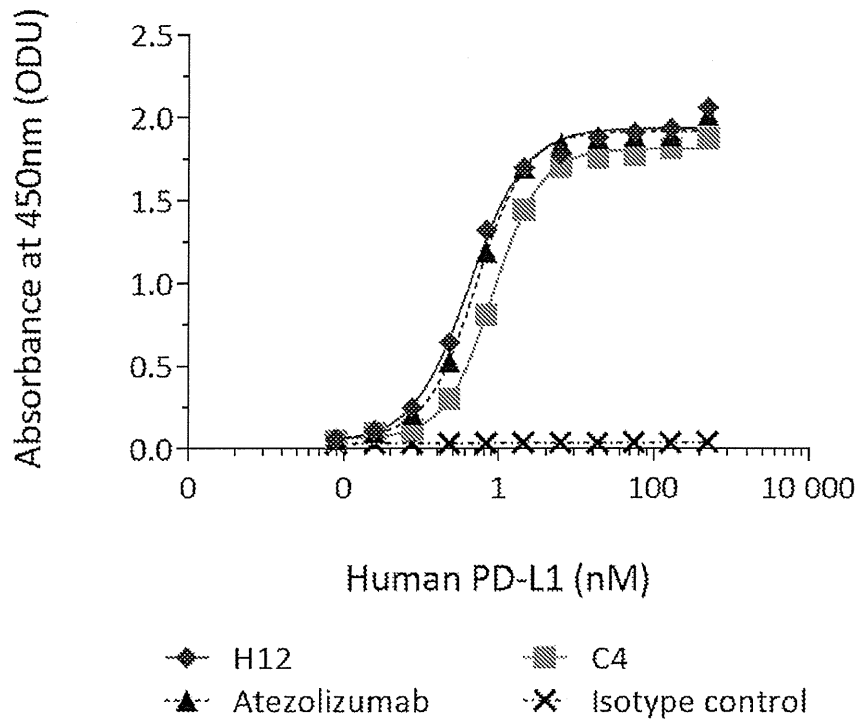


Figure 19A

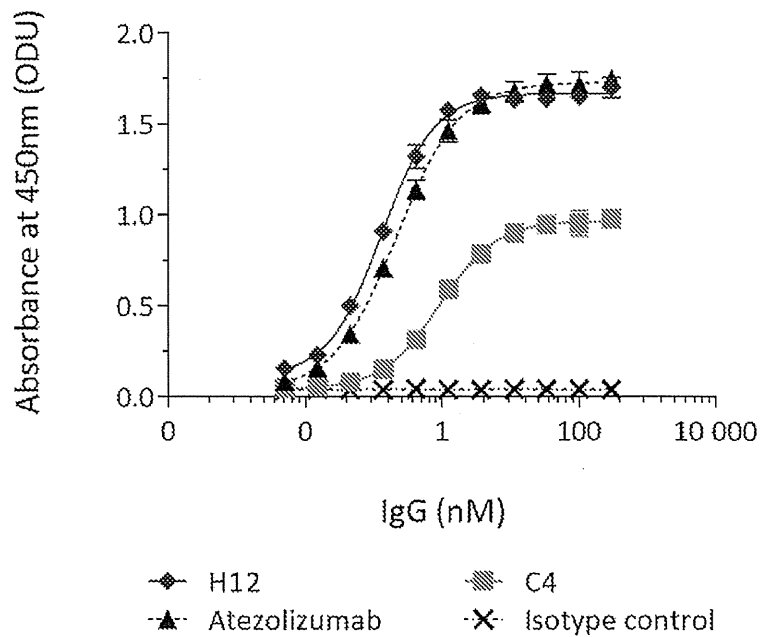


Figure 19B

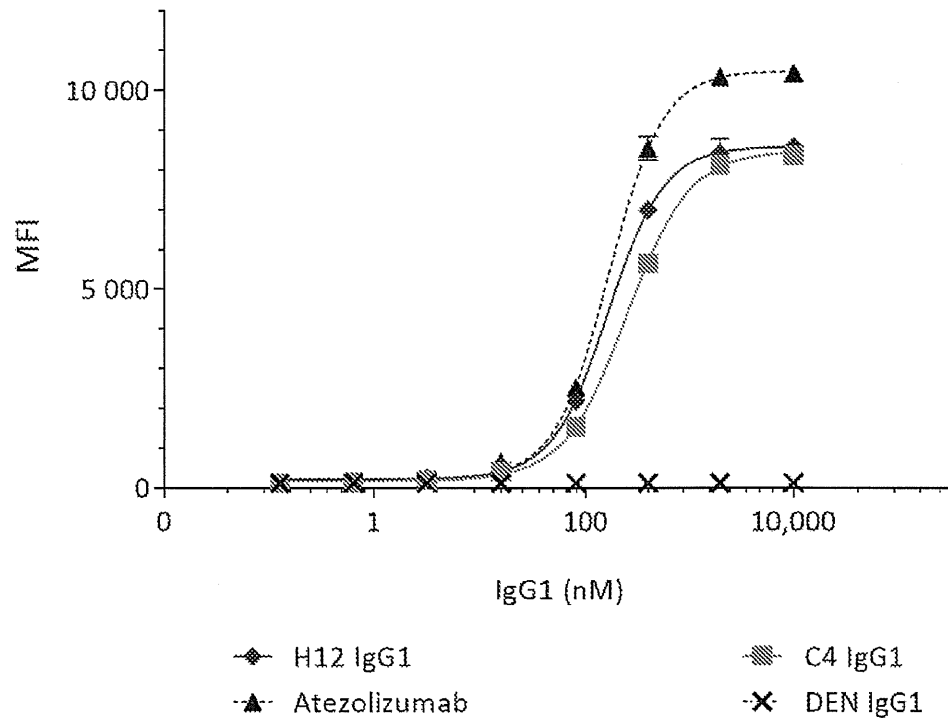


Figure 20

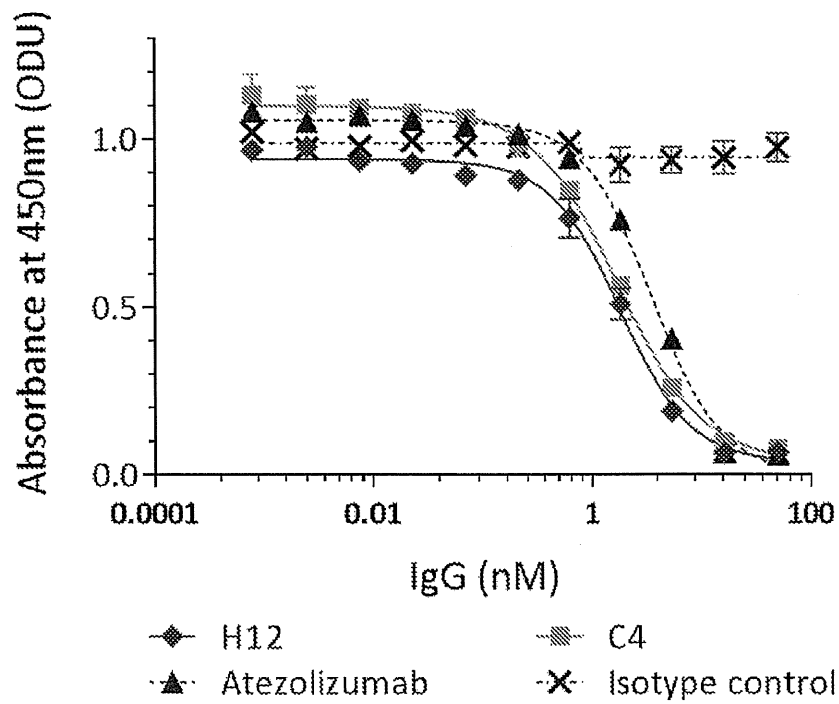


Figure 21