FIG. 1F is a line graph showing insulin levels (mg/dl) vs. time (minutes) during an insulin tolerance test (ITT). This test was performed after 3 weeks of treatment in obese mice on HFD with vehicle (diamonds) or anti-aP2 monoclonal antibodies (0.75 IU/kg insulin) (CA33; squares) (CA15; triangles). ** $p < 0.01$.

FIG. 1G is a bar graph showing body weight (g) at week 0 (open bars) or week 4 (solid bars) in mice treated with vehicle or anti-aP2 monoclonal antibodies CA33, CA13, CA15, CA23, or H3. Weight was measured in the fed state. * $p < 0.05$.

FIG. 2A is a bar graph of the signal interaction (nm) as determined by octet analysis for the anti-aP2 antibodies CA33 and H3 against aP2 (black bars) compared to the related proteins FABP3 (gray bars) and FABP5/Mal1 (light gray bars).

FIG. 2B is a bar graph of plasma aP2 levels (ng/ml) as determined by ELISA in HFD-fed mice treated with vehicle, CA33, or H3 for 3 weeks (n=10 mice per group). Mice had been on HFD for 12 weeks before the experiment was initiated. A Western blot to detect aP2 in serum from three mice from each group (vehicle, CA33, or H3) is shown in the inset. ** $p < 0.01$.

FIG. 2C is a table of antibody crossblocking of H3 vs. CA33, CA13, CA15, and CA23 as determined by Biacore analysis. ++ = complete blocking; + = partial blocking; - = no crossblocking.

FIG. 2D shows the epitope sequence of aP2 residues involved in the interaction with CA33 and H3, as identified by hydrogen-deuterium exchange mass spectrometry (HDX). Interacting residues are underlined. The indicated interaction of CA33 with first alpha helix beta sheet of aP2 on residues 9-17, 20-28 and 118-132 of Seq. ID. No. 2, which partially overlapped with the aP2 epitope on residues 21-41 of Seq. ID. No. 2 identified for H3.

FIG. 2E is a superimposed image of the Fab of CA33 co-crystallized with aP2 and the Fab of H3 co-crystallized with aP2.

FIG. 2F is a high resolution mapping of CA33 epitope on aP2. Interacting residues in both molecules are indicated. Hydrogen bonds are shown as dashed lines. The side chain of K10 in aP2 forms a hydrophobic interaction with the phenyl side chain of Y92.

FIG. 2G is a line graph showing paranaric acid binding to aP2 (relative fluorescence) vs. pH in the presence of IgG control antibody (circles) or CA33 antibody (squares).

FIG. 2H is a graph showing CA33 binding to aP2 (resonance units) vs. time (seconds) in response to increasing concentrations of lipid-loaded aP2.

FIG. 26A is a bar graph of triglycerides in lipoprotein fractions (mg/dl) (total lipoprotein, very low-density lipoprotein (VLDL), low-density lipoprotein (LDL), or high-density lipoprotein (HDL)) in ApoE knockout mice treated with PBS (triangles), CA33 (squares), or CA15 (circles) for six weeks. Particle size distribution of the lipoproteins was determined by fast-performance liquid chromatography (FPLC), using pooled samples of plasma. * $p < 0.05$.

FIG. 26B is a bar graph of triglycerides in lipoprotein fractions (mg/dl) (total lipoprotein, very low-density lipoprotein (VLDL), low-density lipoprotein (LDL), or high-density lipoprotein (HDL)) in ApoE knockout mice treated with PBS (triangles), CA33 (squares), or CA15 (circles) for twelve weeks. Particle size distribution of the lipoproteins was determined by fast-performance liquid chromatography (FPLC), using pooled samples of plasma. * $p < 0.05$.

FIGS. 27-28 are further discussed in Example 4 below.

FIG. 27 provides anti-human aP2 humanized kappa light chain variable region antibody fragments, wherein the 909 sequence (Seq. ID. No. 445) is rabbit variable light chain sequence, and the 909 gL1 (Seq. ID. No. 446), gL10 (Seq. ID. 448), gL13 (Seq. ID. No. 487), gL50 (Seq. ID No. 488), gL54 (Seq. ID. No. 450), and gL55 (Seq. ID. No. 452) sequences are humanized grafts of 909 variable light chain using IGKV1-17 (Seq. ID. No. 506) human germline as the acceptor framework. The CDRs are shown in bold/underlined, while the applicable donor residues are shown in bold/italic and are highlighted: 2V, 3V, 63K and 70D. The mutation in CDRL3 to remove a Cysteine residue is shown in bold/underlined and is highlighted: 90A.

FIG. 28 provides anti-human aP2 humanized heavy chain variable region antibody fragments, wherein the 909 sequence (Seq. ID. No. 454) is rabbit variable heavy chain sequence, and the 909gH1 (Seq. ID. No. 455), gH14 (Seq. ID. NO.457), gH15 (Seq. ID. No. 459), gH61 (Seq. ID. No. 461), and gH62 (Seq. ID. No. 463) sequences are humanized grafts of 909 variable heavy chain using IGHV4-4 (Seq. ID. No. 481) human germline as the acceptor framework. The CDRs are shown in bold/underlined. The two residue gap in framework 3, in the loop between beta sheet strands D and E, is highlighted in gH1: 75 and 76. Applicable donor residues are shown in bold/italic and are highlighted: 23T, 67F, 71K, 72A, 73S, 74T, 77T, 78V, 79D, 89T, and 91F. The mutation in CDRH2 to remove a Cysteine residue is shown in bold/underlined and is highlighted: 59S. The mutation in CDRH3 to remove a potential Aspartate isomerization site is shown in bold/underlined and is highlighted: 98E. The N-terminal Glutamine residue is replaced with Glutamic acid, and is shown in bold and highlighted: 1E.

FIGS. 29-31 are further discussed in Example 5 below.

FIG. 29 is an illustration representing key contact points between aP2 and a murine derived anti-aP2 antibody. As is shown in the figure, substitution of particular amino acid residues with CDR regions of the heavy and light chains resulted in a reduction in the affinity of the altered antibodies in comparison with the parent antibody H3.

FIG. 30A provides amino acid substitutions for inducing a reduction in binding affinity in a murine derived anti-aP2 antibody compared to the parent antibody H3, where g1 = wild-type parent H3. Binding affinities (μM) are shown for CA33 and two reduced affinity H3-like antibodies.

FIG. 30B provides the protein sequence of the heavy chain detailing the amino acid substitutions for inducing a reduction in binding affinity in a murine derived anti-aP2 antibody compared to the parent antibody H3, where g1 = wild-type parent H3 (Seq. ID. No. 482), g19 = W33A, Y52S (Seq.ID. No. 483), and g20 = W33A, Y52S and Y98F (Seq. ID. No. 484). The CDRs are underlined and the amino acid substitutions are shown in bold.

FIG. 30C provides the protein sequence of the light chain detailing the amino acid substitutions for inducing a reduction in binding affinity in a murine derived anti-aP2 antibody compared to the parent antibody H3, where g1 = wild-type parent H3 (Seq. ID. No. 485), and g11 = W91A (Seq. ID. No. 486). The CDRs are underlined and the amino acid substitutions are shown in bold.

FIG. 31 is a table indicating affinity data against human and mouse aP2 for murine derived anti-aP2 antibodies that have been mutated to reduce binding affinity. Binding affinities (KD) are shown for two clones for each antibody (APP5168/PB1172 and APP5169/PB1171) and average binding affinity (KD) is shown (μM).

FIGS. 32 – 46 are further discussed in Example 6 below.

FIG. 32 illustrates that aP2 regulates gluconeogenic gene expression in a FoxO1-dependent manner. Primary hepatocytes were incubated with or without 50 μg/ml of aP2 in the presence or absence of 2 μM forskolin (fsk) for 3h (FIGS. 32A, 32B, 32C, 32D, and 32E) or 6h (FIG. 32F). FIGS. 32A and 32B show the impact of forskolin stimulation on the effect of aP2 on gluconeogenic gene expression (G6pc and Pck1 respectively) in hepatocytes, as well as the role of aP2 lipid binding in this process (n=4). mut: lipid binding mutant, delip: delipidated aP2, WT: lipid-loaded aP2. FIG. 32C illustrates the screening of transcription factors by siRNA mediated knockdown and the effect on forskolin and aP2-stimulated *G6pc* expression (n=4). FIG. 32D illustrates the effect of adenovirus-mediated FoxO1 knockdown

on aP2-mediated *G6pc* expression (n=4). FIG. 32E illustrates the knockdown efficiency at protein levels for FoxO1.

FIG. 32F illustrates the effect of aP2 stimulation of FHRE luciferase activity in primary hepatocytes (n=6). FIG. 32G illustrates glucose production from hepatocytes following adenovirus-mediated FoxO1 knockdown and aP2 stimulation (n=5). Data are expressed as the mean ± SEM. *, ** and NS denote $p < 0.05$, $p < 0.01$ and no significant difference, respectively, determined by Student's t-test.

FIG. 33 illustrates that aP2 alters fatty acid metabolism to regulate gluconeogenic gene expression. FIGS. 33A and 33B show the tabulated results for *G6pc* and *Pck1* expression, respectively, from primary hepatocytes preincubated with vehicle or 50 μM Etomoxir for 30 min and stimulated with 50 μg/ml of aP2 in the presence or absence of 2 μM of forskolin (fsk) for 3 h (n=4). FIGS. 33C and 33D show the results obtained when primary hepatocytes were stimulated with 50 μg/ml of aP2 for 2 h, and stimulated with 150 μM palmitate (FIG. 33C) or 150 μM oleate (FIG. 33D) for the indicated amount of time to measure oxygen consumption rate (OCR, FIG. 33C, n=6) or fatty acid uptake (FIG 33D, n=5). FIGS. 33E and 33F illustrate the mRNA levels obtained for *G6pc* and *Pck1*, respectively, when primary hepatocytes were stimulated with 50 μg/ml of aP2 for 2 h and the cells were further stimulated with 50 μg/ml of aP2 in the presence or absence of 2 μM of forskolin (fsk)/100 μM palmitate for 3 h (n=4). FIGS. 33G and 33H illustrate the mRNA levels obtained for *G6pc* and *Pck1*, respectively, when primary hepatocytes were preincubated with 5 μM Triacsin C for 30 min and further treated as in FIG. 33D with or without the same concentrations of Triacsin C (n=4). FIG. 33I illustrates the level of nuclear fatty acyl-CoA (pmol/10^6 cells) in primary hepatocytes after they were treated with either vehicle or aP2. Data are expressed as the mean ± SEM. *, ** and NS denote $p < 0.05$, $p < 0.01$ and no significant difference, respectively, determined by Student's t-test.

FIG. 34 demonstrates the existence of a novel FoxO1/CtBP2 transcriptional complex regulated by aP2. Primary hepatocytes were stimulated with 50 μg/ml of aP2 (FIGS. 34 A, B, H, L, M and N) in the presence or absence of 2 μM of forskolin (fsk) for 3 h (FIGS. 34 A and B) or 90 min (FIGS. 34 H, K, M and N). FIGS. 34A and 34B show the effects of adenovirus-mediated CtBP1 and CtBP2 knockdown on aP2-induced expression of *G6pc* and *Pck1*, respectively (n=4). FIG. 34C shows the PxDLS-like motifs in human and mouse FoxO sequences as indicated by the rectangles: mouse FOXO1 amino acids 571 to 610 (Seq. ID. No. 603), mouse FOXO3 amino acids 581 to 610 (Seq. ID. No. 604), mouse FOXO4 amino acids 411 to 480 (Seq. ID. No. 605), mouse FOXO6 amino acids 481 to 520 (Seq. ID. No. 606),

human FOXO1 amino acids 581 to 620 (Seq. ID. No. 607), human FOXO3 amino acids 591 to 630 (Seq. ID. No. 608), human FOXO4 amino acids 451 to 490 (Seq. ID. No. 609), human FOXO6 amino acids 411 to 451 (Seq. ID. No. 610).

FIG. 34D and 34E show endogenous FoxO1/CtBP complex in primary hepatocytes shown by reciprocal coimmunoprecipitation of CtBP or FoxO1, respectively. FIGS. 34F and 34G illustrate the critical role of the PxDL motif in the FoxO1/CtBP2 complex. HEK293 cells

of both heavy and light chain V-regions were created by modifying the VH and VK genes by oligonucleotide-directed mutagenesis, including, in some cases, mutations within CDRs to modify potential aspartic acid isomerisation sites or remove unpaired Cysteine residues. These genes were cloned into vectors to enable expression of humanized 909 IgG4P (human IgG4 containing the hinge stabilising mutation S241P, Angal et al., Mol Immunol. 1993, 30(1):105-8) antibodies in mammalian cells. The variant humanized antibody chains, and combinations thereof, were expressed and assessed for their potency relative to the parent antibody, their biophysical properties and suitability for downstream processing, leading to the selection of heavy and light chain grafts shown in Figures 27 and 28.

Human V-region IGKV1-17 (A30) plus JK4 J-region was chosen as the acceptor for antibody 909 light chain CDRs. The light chain framework residues in grafts gL1 (Seq. ID No. 446), gL10 (Seq. ID No. 448), gL54 (Seq. ID No. 450) and gL55 (Seq. ID No. 452) are all from the human germline gene, with the exception of residues 2, 3, 63 and 70 (Kabat numbering), where the donor residues Valine (2V), Valine (3V), Lysine (63K) and Aspartic acid (70D) were retained, respectively. Retention of residues 2, 3, 63 and 70 was essential for full potency of the humanized antibody. Residue 90 in CDRL3 of the gL10 graft, gL54 graft, and gL55 graft was mutated from a Cysteine (90C) to a Serine (90S), Glutamine (90Q), and Histidine (H90) residue, respectively, thus removing the unpaired Cysteine residue from the gL10, gL54, and gL55 sequence.

Human V-region IGHV4-4 plus JH4 J-region was chosen as the acceptor for the heavy chain CDRs of antibody 909. In common with many rabbit antibodies, the VH gene of antibody 909 is shorter than the selected human acceptor. When aligned with the human acceptor sequence, framework 1 of the VH region from antibody 909 (Seq. ID No. 454) lacks the N-terminal residue, which is retained in the humanised antibody (Figure 28). Framework 3 of the 909 rabbit VH region also lacks two residues (75 and 76) in the loop between beta sheet strands D and E: in graft gH1 (Seq. ID No. 455) the gap in framework 3 is conserved, whilst in graft gH14 (Seq. ID No. 457), gH15 (Seq. ID No. 459), gH61 (Seq. ID No. 461), and gH62 (Seq. ID No. 463) the gap is filled with the corresponding residues (Lysine 75, 75K; Asparagine 76, 76N) from the selected human acceptor sequence (Figure 28). The heavy chain framework residues in grafts gH1 and gH15 are all from the human germline gene, with the exception of residues 23, 67, 71, 72, 73, 74, 77, 78, 79, 89 and 91 (Kabat numbering), where the donor residues Threonine

What is claimed is:

1. A humanized anti-adipocyte protein 2 (aP2) monoclonal antibody, or antigen binding agent, comprising:

(a) a light chain variable region comprising:

(i) a CDR-L1 complementarity determining region (CDR) comprising an amino acid sequence of Seq. ID No. 7;

(ii) a CDR-L2 CDR comprising an amino acid sequence of Seq. ID No. 8; and,

(iii) a CDR-L3 CDR comprising an amino acid sequence selected from the group consisting of Seq. ID No. 9, Seq. ID No. 10, Seq. ID No. 11, and Seq. ID No. 12; and

(b) a heavy chain variable region comprising:

(i) a CDR-H1 CDR comprising an amino acid sequence of Seq. ID No.14;

(ii) a CDR-H2 CDR comprising an amino acid sequence selected from the group consisting of Seq. ID No. 16 and Seq. ID No. 17; and,

(iii) a CDR-H3 CDR comprising an amino acid sequence selected from the group consisting of Seq. ID No. 19 and Seq. ID No. 20.

2. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-L3 CDR comprises the amino acid sequence of Seq. ID No. 9.

3. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-L3 CDR comprises the amino acid sequence of Seq. ID No. 10.

4. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-L3 CDR comprises the amino acid sequence of Seq. ID No. 11.

5. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-L3 CDR comprises the amino acid sequence of Seq. ID No. 12.

6. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 16.

7. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 17.

8. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 19.

9. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 20.

10. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H1 CDR comprises the amino acid sequence of Seq. ID No. 14, the

CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 16, and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 19.

11. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H1 CDR comprises the amino acid sequence of Seq. ID No. 14, the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 17, and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 19.

12. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H1 CDR comprises the amino acid sequence of Seq. ID No. 14, the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 16, and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 20.

13. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H1 CDR comprises the amino acid sequence of Seq. ID No. 14, the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 17, and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 20.

14. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the light chain variable region comprises an amino acid sequence selected from Seq. ID No. 446, Seq. ID No. 448, Seq. ID No. 487, Seq. ID No. 488, Seq. ID No. 450, and Seq. ID No. 452.

15. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the heavy chain variable region comprises an amino acid sequence of Seq. ID No. 455.

16. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the light chain variable region comprises the amino acid sequence of Seq. ID No. 446 and the heavy chain variable region comprises the amino acid sequence of Seq. ID No. 459.

17. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 2, wherein the heavy chain variable region comprises the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 16 and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 19.

18. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 2, wherein the heavy chain variable region comprises the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 17 and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 20.

19. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 3, wherein the heavy chain variable region comprises the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 16 and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 19.

20. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 3, wherein the heavy chain variable region comprises the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 17 and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 20.

21. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 4, wherein the heavy chain variable region comprises the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 16 and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 19.

22. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 4, wherein the heavy chain variable region comprises the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 17 and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 20.

23. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 5, wherein the heavy chain variable region comprises the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 16 and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 19.

24. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 5, wherein the heavy chain variable region comprises the CDR-H2 CDR comprises the amino acid sequence of Seq. ID No. 17 and the CDR-H3 CDR comprises the amino acid sequence of Seq. ID No. 20.

25. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the heavy chain variable region comprises an amino acid sequence of Seq. ID No. 459.

26. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the heavy chain variable region comprises an amino acid sequence of Seq. ID No. 457.

27. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the heavy chain variable region comprises an amino acid sequence of Seq. ID No. Seq. ID No. 461

28. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the heavy chain variable region comprises an amino acid sequence of Seq. ID No. 463.

29. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 15, wherein the light chain variable region comprises an amino acid sequence of Seq. ID No. 446.

30. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 25, wherein the light chain variable region comprises an amino acid sequence of Seq. ID No. 446.

31. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 26, wherein the light chain variable region comprises an amino acid sequence of Seq. ID No. 446.

32. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 27, wherein the light chain variable region comprises an amino acid sequence of Seq. ID No. 446.

33. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 28, wherein the light chain variable region comprises an amino acid sequence of Seq. ID No. 446.

34. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, further comprising a human kappa light chain constant region.

35. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 34, wherein the light chain variable region and human kappa light chain constant region amino acid sequence is selected from the group consisting of Seq. ID No. 447, Seq. ID No. 449, Seq. ID No. 489, Seq. ID No. 490, Seq. ID No. 451, and Seq. ID No. 453.

36. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, further comprising a human IgG4 heavy chain constant region.

37. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 36, wherein in the IgG4 heavy chain constant region comprises a proline substitution at amino acid 241.

38. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 37, wherein the heavy chain variable region and human IgG4 heavy chain constant region amino acid sequence is selected from the group consisting of Seq. ID No. 456, Seq. ID No. 458, Seq. ID No. 460, Seq. ID No. 462, and Seq. ID No. 464.

39. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 14, wherein the light chain variable region comprises Seq. ID No. 446.

40. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 14, wherein the light chain variable region comprises Seq. ID No. 448.

41. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 14, wherein the light chain variable region comprises Seq. ID No. 450.

42. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 14, wherein the light chain variable region comprises Seq. ID No. 452.

43. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 14, wherein the light chain variable region comprises Seq. ID No. 487.

44. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 14, wherein the light chain variable region comprises Seq. ID No. 488.

45. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-L1 CDR, CDR-L2 CDR, and CDR-L3 CDR are grafted into a human IGKV1-17 acceptor sequence comprising the amino acid sequence of Seq. ID No. 506.

46. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 45, wherein the human IGKV1-17 acceptor sequence comprises one or more amino acid substitutions selected from valine at amino acid 2, valine at amino acid 3, lysine at amino acid 63, and aspartic acid at amino acid 70.

47. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 1, wherein the CDR-H1 CDR, CDR-H2 CDR, and CDR-H3 CDR are grafted into a human IGHV4-4 acceptor sequence comprising the amino acid sequence of Seq. ID No. 481.

48. The humanized anti-aP2 monoclonal antibody, or antigen binding agent, of claim 47, wherein the human IGHV4-4 acceptor sequence comprises one or more amino acid substitutions selected from the group consisting of threonine at amino acid 23, phenylalanine at amino acid 67, lysine at amino acid 71, alanine at amino acid 72, serine at amino acid 73, threonine at amino acid 74, threonine at amino acid 77, valine at amino acid 78, aspartic acid at amino acid 79, threonine at amino acid 89, and phenylalanine at amino acid 91.