WHAT IS CLAIMED IS:

1. An isolated heavy chain variable region polypeptide comprising an HVR-H1, HVR-H2 and HVR-H3 sequence, wherein:

(a) the HVR-H1 sequence is GFTFSX_1SWIH (SEQ ID NO:1);

(b) the HVR-H2 sequence is AWIX_2PYGGSX_3YYADSVKG (SEQ ID NO:2);

(c) the HVR-H3 sequence is RHWPGGFDY (SEQ ID NO:3);

further wherein: X_1 is D or G; X_2 is S or L; X_3 is T or S.

2. The polypeptide of Claim 1 wherein X_1 is D; X_2 is S and X_3 is T.

3. The polypeptide of Claim 1 further comprising variable region heavy chain framework sequences juxtaposed between the HVRs according to the formula: (HC-FR1)-(HVR-H1)-(HC-FR2)-(HVR-H2)-(HC-FR3)-(HVR-H3)-(HC-FR4).

4. The polypeptide of Claim 3 wherein the framework sequences are derived from human consensus framework sequences.

5. The polypeptide of Claim 4 wherein the framework sequences are VH subgroup III consensus framework.

6. The polypeptide of Claim 5 wherein one or more of the framework sequences is the following:

HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4)

HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5)

HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6)

HC-FR4 is WGQGTLVTVSA (SEQ ID NO:7).

7. The isolated heavy chain polypeptide of Claim 1 in combination with a variable region light chain comprising an HVR-L1, HVR-L2 and HVR-L3, wherein:

(a) the HVR-L1 sequence is RASQ$X_4X_5X_6TX_7X_8$A (SEQ ID NOs:8);

(b) the HVR-L2 sequence is SASX_9LX_{10}S, and (SEQ ID NOs:9);

(c) the HVR-L3 sequence is QQ$X_{11}X_{12}X_{13}X_{14}PX_{15}$T (SEQ ID NOs:10);

further wherein: X_4 is D or V; X_5 is V or I; X_6 is S or N; X_7 is A or F; X_8 is V or L; X_9 is F or T; X_{10} is Y or A; X_{11} is Y, G, F, or S; X_{12} is L, Y, F or W; X_{13} is Y, N, A, T, G, F or I; X_{14} is H, V, P, T or I; X_{15} is A, W, R, P or T.

8. The polypeptide of Claim 7 wherein X_4 is D; X_5 is V; X_6 is S; X_7 is A; X_8 is V; X_9 is F; X_{10} is Y; X_{11} is Y; X_{12} is L; X_{13} is Y; X_{14} is H; X_{15} is A.

9. The polypeptide of Claim 7 further comprising variable region light chain framework sequences juxtaposed between the HVRs according to the formula: (LC-FR1)-(HVR-L1)-(LC-FR2)-(HVR-L2)-(LC-FR3)-(HVR-L3)-(LC-FR4).

10. The polypeptide of Claim 9 wherein the framework sequences are derived from human consensus framework sequences.

11. The polypeptide of Claim 10 wherein the framework sequences are VL kappa I consensus framework.

12. The polypeptide of Claim 11 wherein one or moreof the framework sequences is the following:

LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:13);
LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

13. An isolated anti-PD-L1 antibody or antigen binding fragment comprising a heavy chain and a light chain variable region sequence, wherein:

(a) the heavy chain comprises an HVR-H1, HVR-H2 and HVR-H3, wherein further:
(i) the HVR-H1 sequence is GFTFSX_1SWIH (SEQ ID NO:1);
(ii) the HVR-H2 sequence is AWIX_2PYGGSX_3YYADSVKG (SEQ ID NO:2);
(iii) the HVR-H3 sequence is RHWPGGFDY, and (SEQ ID NO:3);

(b) the light chain comprises an HVR-L1, HVR-L2 and HVR-L3, wherein further:
(iv) the HVR-L1 sequence is RASQ$X_4X_5X_6TX_7X_8$A (SEQ ID NOs:8);
(v) the HVR-L2 sequence is SASX_9LX_{10}S (SEQ ID NOs:9);
(vi) the HVR-L3 sequence is QQ$X_{11}X_{12}X_{13}X_{14}PX_{15}$T (SEQ ID NOs:10);

wherein: X_1 is D or G; X_2 is S or L; X_3 is T or S; X_4 may be D or V; X_5 may be V or I; X_6 may be S or N; X_7 may be A or F; X_8 may be V or L; X_9 may be F or T; X_{10} may be Y or A; X_{11} may be Y, G, F, or S; X_{12} may be L, Y, F or W; X_{13} may be Y, N, A, T, G, F or I; X_{14} may be H, V, P, T or I; X_{15} may be A, W, R, P or T.

14. The antibody or antibody fragment of Claim 13 wherein X_1 is D; X_2 is S and X_3 is T.

15. The antibody or antibody fragment of Claim 13, wherein X_4 = D, X_5 = V, X_6 = S, X_7 = A and X_8 = V, X_9 = F, and X_{10} = Y, X_{11} = Y, X_{12} = L, X_{13} = Y, X_{14} = H and X_{15} = A.

16. The antibody or antibody fragment of Claim 13, wherein X_1 = D, X_2 = S and X_3 = T, X_4 = D, X_5 = V, X_6 = S, X_7 = A and X_8 = V, X_9 = F, and X_{10} = Y, X_{11} = Y, X_{12} = L, X_{13} = Y, X_{14} = H and X_{15} = A.

17. The antibody or antibody fragment of any of Claims 13-16 further comprising:

(a) variable region heavy chain framework sequences juxtaposed between the HVRs according to the formula: (HC-FR1)-(HVR-H1)-(HC-FR2)-(HVR-H2)-(HC-FR3)-(HVR-H3)-(HC-FR4), and

(b) variable region light chain framework sequences juxtaposed between the HVRs according to the formula: (LC-FR1)-(HVR-L1)-(LC-FR2)-(HVR-L2)-(LC-FR3)-(HVR-L3)-(LC-FR4).

18. The antibody or antibody fragment of Claim 17 wherein the framework sequences are derived from human consensus framework sequences.

19. The antibody or antibody fragment of Claim 18 wherein the variable region heavy chain framework sequences are VH subgroup III consensus framework.

20. The antibody or antibody fragment of Claim 19 wherein one or more of the framework sequences is the following:

HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4);

HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5);

HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6);

HC-FR4 is WGQGTLVTVSA (SEQ ID NO:7).

21. The antibody or antibody fragment of Claim 18 wherein the variable region light chain framework sequences are VL kappa I consensus framework.

22. The antibody or antibody fragment of Claim 21 wherein one or more of the framework sequences is the following:

LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC, and (SEQ ID NO:13);
LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

23. The antibody of or antibody fragment of Claim 18 wherein:

(a) the variable heavy chain framework sequences are the following:
(i) HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4);
(ii) HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5);
(iii) HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6);
(iv) HC-FR4 is WGQGTLVTVSA; and (SEQ ID NO:7);

(b) the variable light chain framework sequences are the following:
(i) LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
(ii) LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
(iii) LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:13);
(iv) LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

24. The antibody or antibody fragment of Claim 23 further comprising a human constant region.

25. The antibody or antibody fragment of Claim 24, wherein the constant region is selected from the group consisting of IgG1, IgG2, IgG3 and IgG4.

26. The antibody of antibody fragment of Claim 25 wherein the constant region is IgG1.

27. The antibody or antibody fragment of Claim 23, further comprising murine constant region.

28. The antibody or antibody fragment of Claim 27 wherein the constant region is selected from the group consisting of IgG1, IgG2A, IgG2B and IgG3.

29. The antibody or antibody fragment of Claim 28, wherein the constant region is IgG2A.

30. The antibody or antibody fragment of Claim 25 or 28 having reduced or minimal effector function.

31. The antibody or antibody fragment of Claim 30, wherein the minimal effector function results from an effector-less Fc mutation.

32. The antibody or antibody fragment of Claim 31, wherein the effector-less Fc mutation is N297A.

33. The antibody or antibody fragment of Claim 31, wherein the effector-less Fc mutation is D265A/N297A.

34. The antibody or antibody fragment of Claim 30, wherein the minimal effector function results from aglycosylation.

35. An antibody or antigen binding fragment comprising a heavy chain and a light chain variable region sequence, wherein:

(a) the heavy chain comprises an HVR-H1, HVR-H2 and an HVR-H3, having at least 85% overall sequence identity to GFTFSDSWIH (SEQ ID NO:15), AWISPYGGSTYYADSVKG (SEQ ID NO:16) and RHWPGGFDY (SEQ ID NO:3), respectively, and

(b) the light chain comprises an HVR-L1, HVR-L2 and an HVR-L3, having at least 85% overall sequence identity to RASQDVSTAVA (SEQ ID NO:17), SASFLYS (SEQ ID NO:18) and QQYLYHPAT (SEQ ID NO:19), respectively.

36. The antibody or antibody fragment of Claim 35, wherein the sequence identity is at least 90%.

37. The antibody or antibody fragment of Claims 36 further comprising:

(a) variable region heavy chain (VH) framework sequences juxtaposed between the HVRs according to the formula: (HC-FR1)-(HVR-H1)-(HC-FR2)-(HVR-H2)-(HC-FR3)-(HVR-H3)-(HC-FR4), and

(b) variable region light chain (VL) framework sequences juxtaposed between the HVRs according to the formulat: (LC-FR1)-(HVR-L1)-(LC-FR2)-(HVR-L2)-(LC-FR3)-(HVR-L3)-(LC-FR4).

38. The antibody or antibody fragment of Claim 37, further comprising a VH and VL framework region derived from a human consensus sequence.

39. The antibody or antibody fragment of Claim 38, wherein the VH framework sequence is derived from a Kabat subgroup I, II, or III sequence.

40. The antibody or antibody fragment of Claim 39, wherein the VH framework sequence is a Kabat subgroup III consensus framework sequence.

41. The antibody or antibody fragment of Claim 40 wherein the VH framework sequences are the following:

HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4);
HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5);
HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6);
HC-FR4 is WGQGTLVTVSA (SEQ ID NO:7).

42. The antibody or antibody fragment of Claim 38, wherein the VL framework sequence is derived from a Kabat kappa I, II, III or IV subgroup sequence.

43. The antibody or antibody fragment of Claim 42 wherein the the VL framework sequence is a Kabat kappa I consensus framework sequence.

44. The antibody or antibody fragment of Claim 43 wherein the VL framework sequences are the following:

LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:13);

LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

45. An isolated anti-PD-L1 antibody or antigen binding fragment comprising a heavy chain and a light chain variable region sequence, wherein:

(a) the heavy chain sequence has at least 85% sequence identity to the heavy chain sequence: EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPG KGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLRAEDT AVYYCARRHWPGGFDYWGQGTLVTVSA (SEQ ID NO:20), and

(b) the light chain sequence has at least 85% sequence identity to the light chain sequence: DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGK APKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYLYH PATFGQGTKVEIKR (SEQ ID NO:21).

46. The antibody or antigen binding fragment of Claim 45, wherein the sequence identity is at least 90%.

47. An isolated anti-PD-L1 antibody or antigen binding fragment comprising a heavy chain and light chain variable region sequence, wherein:

(a) the heavy chain comprises the sequence: EVQLVESGGGLVQPGGSLRLS CAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTI SADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVS A (SEQ ID NO:20), and

(b) the light chain comprises the sequence: DIQMTQSPSSLSASVGDRVTITC RASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQYLYH PATFGQGTKVEIKR (SEQ ID NO:21).

48. A composition comprising the anti-PD-L1 antibody or antigen binding fragment of any of Claims 13-47 and at least one pharmaceutically-acceptable carrier.

49. An isolated nucleic acid encoding the polypeptide of any of Claims 1-11.

50. An isolated nucleic acid encoding a light chain or a heavy chain variable sequence of an anti-PD-L1 antibody or antigen binding fragment, wherein:

(a) the heavy chain further comprises and HVR-H1, HVR-H2 and an HVR-H3 sequence having at least 85% sequence identity to GFTFSDSWIH (SEQ ID

NO:15), AWISPYGGSTYYADSVKG (SEQ ID NO:16) and RHWPGGFDY (SEQ ID NO:3), respectively, or

(b) the light chain further comprises an HVR-L1, HVR-L2 and an HVR-L3 sequence having at least 85% sequence identity to RASQDVSTAVA (SEQ ID NO:17), SASFLYS (SEQ ID NO:18) and QQYLYHPAT (SEQ ID NO:19), respectively.

51. The nucleic acid of Claim 50, wherein sequence identity is 90%.

52. The nucleic acid of Claim 50, wherein the anti-PD-L1 antibody further comprises a VL and a VH framework region derived from a human consensus sequence.

53. The nucleic acid of Claim 52, wherein the VH sequence is derived from a Kabat subgroup I, II, or III sequence.

54. The nucleic acid of Claim 52, wherein the VL sequence is derived from a Kabat kappa I, II, III or IV subgroup sequence.

55. The nucleic acid of Claim 50, wherein the anti-PD-L1 antibody comprises a constant region derived from a murine antibody.

56. The nucleic acid of Claim 50, wherein the anti-PD-L1 antibody comprises a constant region derived from a human antibody.

57. The nucleic acid of Claim 56, wherein the constant region is IgG1.

58. The nucleic acid of Claim 57, having reduced or minimal effector function.

59. The nucleic acid of Claim 58, wherein the minimal effector function results from an effector-less Fc mutation.

60. The nucleic acid of Claim 59, wherein the effector-less Fc mutation is N297A.

61. A vector comprising the nucleic acid of any of claims 49-60.

62. A host cell comprising the vector of Claim 61.

63. The host cell of Claim 62 which is eukaryotic.

64. The host cell of Claim 63 which is mammalian.

65. The host cell of Claim 64 which is a Chinese Hamster Ovary (CHO) cell.

66. The host cell of Claim 62 which is prokaryotic.

67. The host cell of Claim 66 which is *E. coli*.

68. A process for making an anti-PD-L1 antibody comprising culturing the host cell of any of Claims 62-67 under conditions suitable for the expression of the vector encoding the anti-PD-L1 antibody or antigen binding fragment, and recovering the antibody or fragment.

69. An article of manufacture comprising the composition of Claim 48 and at least one BNCA molecule.

70. An article of manufacture comprising the composition of Claim 48 and at least one chemotherapeutic agent.

71. The article of manufacture according to Claim 70, wherein the chemotherapeutic agent is gemcitabine.

72. An article of manufacture comprising the composition of Claim 48 and at least one agonist to a positive costimulatory molecule.

73. The article of manufacture according to Claim 72, further comprising a BNCA antagonist.

74. An article of manufacture comprising the composition of Claim 48 and at least one antibiotic.

75. The article of manufacture according to Claim 74, wherein the antibiotic is an anti-viral agent.

76. The article of manufacture according to Claim 75, wherein anti-viral agent is a reverse transcriptase inhibitor.

77. The article of manufacture according to Claim 76, wherein the reverse transcriptase inhibitor is a polymerase inhibitor.

78. The article of manufacture according to Claim 75, wherein the anti-viral agent is a protease inhibitor.

79. An article of manufacture comprising the composition of Claim 48 and at least one vaccine.

80. A method of enhacing T-cell function comprising administration of an effective amount of the composition of Claim 48 to a dysfunctional T-cell.

81. A method of treating a T-cell dysfunctional disorder comprising administering a therapeutically effective amount of the composition of Claim 48 to a patient suffering from a T-cell dysfunctional disorder.

82. The method of Claim 81, wherein the T-cell dysfunctional disorder is infection.

83. The method of Claim 82, wherein the infection is chronic.

84. The method of Claim 81, wherein the T-cell dysfunctional disorder is tumor immunity.

85. The method of Claim 83, therein the chronic infection is persistent.

86. The method of Claim 83, wherein the chronic infection is latent.

87. The method of Claim 83, wherein the chronic infection is slow.

88. The method of Claim 82 wherein the infection results from a pathogen selected from the group consisting of bacteria, virus, fungi and protozoan.

89. The method of Claim 88 wherein the pathogen is a bacteria and the method further comprises the administration of an anti-bacterial agent.

90. The method of Claim 88, wherein the pathogen is virus and the method further comprises the administration of an anti-viral agent.

91. The method of Claim 88, wherein the pathogen is a fungi and the method further comprises the administration of an anti-fungal agent.

92. The method of Claim 88, wherein the pathogen is a protozoan and the method further comprising the administration of an anti-protozoan agent.

93. The method of Claim 88, further comprising the administration of a vaccine.

94. The method of Claim 84, wherein the method futher comprising the application of a treatment regimen selected from the group consisting of: radiation therapy, chemotherapy, targeted therapy, immunotherapy, hormonal therapy, angiogenesis inhibiton and palliative care.

95. The method of Claim 84, wherein the tumor immunity results from a cancer selected from the group consisting of: breast, lung, colon, ovarian, melanoma, bladder, kidney, liver, salivary, stomach, gliomas, thyroid, thymic, epithelial, head and neck cancers, gastric and pancreatic cancer.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid encoding a heavy chain variable region polypeptide that specifically binds to PD-L1 comprising an HVR-H1, HVR-H2 and HVR-H3 sequence, wherein:

(a) the HVR-H1 sequence is GFTFSX$_1$SWIH (SEQ ID NO:1);

(b) the HVR-H2 sequence is AWIX$_2$PYGGSX$_3$YYADSVKG (SEQ ID NO:2);

(c) the HVR-H3 sequence is RHWPGGFDY (SEQ ID NO:3);

further wherein: X$_1$ is D or G; X$_2$ is S or L; X$_3$ is T or S.

2. The nucleic acid of Claim 1 wherein X$_1$ is D; X$_2$ is S and X$_3$ is T.

3. The nucleic acid of Claim 1 further comprising variable region heavy chain framework sequences juxtaposed between the HVRs according to the formula: (HC-FR1)-(HVR-H1)-(HC-FR2)-(HVR-H2)-(HC-FR3)-(HVR-H3)-(HC-FR4).

4. The nucleic acid of Claim 3 wherein the framework sequences are human.

5. The nucleic acid of Claim 4 wherein the framework sequences are VH subgroup III consensus framework.

6. The nucleic acid of Claim 5 wherein one or more of the framework sequences is the following:

HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4)

HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5)

HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6)

HC-FR4 is WGQGTLVTVSA (SEQ ID NO:7).

7. The nucleic acid of Claim 1, further comprising a second nucleic acid encoding a variable region light chain polypeptide comprising an HVR-L1, HVR-L2 and HVR-L3, wherein:

(a) the HVR-L1 sequence is RASQX$_4$X$_5$X$_6$TX$_7$X$_8$A (SEQ ID NOs:8);

(b) the HVR-L2 sequence is SASX$_9$LX$_{10}$S, and (SEQ ID NOs:9);

(c) the HVR-L3 sequence is QQX$_{11}$X$_{12}$X$_{13}$X$_{14}$PX$_{15}$T (SEQ ID NOs:10);

further wherein: X$_4$ is D or V; X$_5$ is V or I; X$_6$ is S or N; X$_7$ is A or F; X$_8$ is V or L; X$_9$ is F or T; X$_{10}$ is Y or A; X$_{11}$ is Y, G, F, or S; X$_{12}$ is L, Y, F or W; X$_{13}$ is Y, N, A, T, G, F or I; X$_{14}$ is H, V, P, T or I; X$_{15}$ is A, W, R, P or T.

8. The nucleic acid of Claim 7 wherein X_4 is D; X_5 is V; X_6 is S; X_7 is A; X_8 is V; X_9 is F; X_{10} is Y; X_{11} is Y; X_{12} is L; X_{13} is Y; X_{14} is H; X_{15} is A.

9. The nucleic acid of Claim 7 further comprising variable region light chain framework sequences juxtaposed between the HVRs according to the formula: (LC-FR1)-(HVR-L1)-(LC-FR2)-(HVR-L2)-(LC-FR3)-(HVR-L3)-(LC-FR4).

10. The nucleic acid of Claim 9 wherein the framework sequences are human.

11. The nucleic acid of Claim 10 wherein the framework sequences are VL kappa I consensus framework.

12. The nucleic acid of Claim 11 wherein one or more of the framework sequences is the following:

LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:13);
LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

13. An isolated nucleic acid encoding a light chain variable region polypeptide that specifically binds to PD-L1 comprising an HVR-L1, HVR-L2 and HVR-L3, wherein:

(a) the HVR-L1 sequence is $RASQX_4X_5X_6TX_7X_8A$ (SEQ ID NOs:8);
(b) the HVR-L2 sequence is $SASX_9LX_{10}S$, and (SEQ ID NOs:9);
(c) the HVR-L3 sequence is $QQX_{11}X_{12}X_{13}X_{14}PX_{15}T$ (SEQ ID NOs:10);

further wherein: X_4 is D or V; X_5 is V or I; X_6 is S or N; X_7 is A or F; X_8 is V or L; X_9 is F or T; X_{10} is Y or A; X_{11} is Y, G, F, or S; X_{12} is L, Y, F or W; X_{13} is Y, N, A, T, G, F or I; X_{14} is H, V, P, T or I; X_{15} is A, W, R, P or T.

14. The nucleic acid of Claim 13 wherein X_4 is D; X_5 is V; X_6 is S; X_7 is A; X_8 is V; X_9 is F; X_{10} is Y; X_{11} is Y; X_{12} is L; X_{13} is Y; X_{14} is H; X_{15} is A.

15. The nucleic acid of Claim 13 further comprising variable region light chain framework sequences juxtaposed between the HVRs according to the formula: (LC-FR1)-(HVR-L1)-(LC-FR2)-(HVR-L2)-(LC-FR3)-(HVR-L3)-(LC-FR4).

16. The nucleic acid of Claim 15 wherein the framework sequences are human.

17. The nucleic acid of Claim 16 wherein the framework sequences are VL kappa I consensus framework.

18. The nucleic acid of Claim 17 wherein one or more of the framework sequences is the following:

LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:13);
LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

19. The nucleic acid of Claim 13, further comprising a second nucleic acid encoding a heavy chain variable region polypeptide comprising an HVR-H1, HVR-H2 and HVR-H3 sequence, wherein:

(a) the HVR-H1 sequence is GFTFSX_1SWIH (SEQ ID NO:1);
(b) the HVR-H2 sequence is AWIX_2PYGGSX_3YYADSVKG (SEQ ID NO:2);
(c) the HVR-H3 sequence is RHWPGGFDY (SEQ ID NO:3);
further wherein: X_1 is D or G; X_2 is S or L; X_3 is T or S.

20. The nucleic acid of Claim 19 wherein X_1 is D; X_2 is S and X_3 is T.

21. The nucleic acid of Claim 19 further comprising variable region heavy chain framework sequences juxtaposed between the HVRs according to the formula: (HC-FR1)-(HVR-H1)-(HC-FR2)-(HVR-H2)-(HC-FR3)-(HVR-H3)-(HC-FR4).

22. The nucleic acid of Claim 21 wherein the framework sequences are human.

23. The nucleic acid of Claim 22 wherein the framework sequences are VH subgroup III consensus framework.

24. The nucleic acid of Claim 23 wherein one or more of the framework sequences is the following:

HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4)
HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5)
HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6)
HC-FR4 is WGQGTLVTVSA (SEQ ID NO:7).

25. An isolated nucleic acid encoding a light chain or a heavy chain variable region sequence of an anti-PD-L1 antibody or antigen binding fragment, wherein:

(a) the heavy chain or antigen binding fragment thereof further comprises and HVR-H1, HVR-H2 and an HVR-H3 sequence having at least 85% sequence identity to GFTFSDSWIH (SEQ ID NO:15), AWISPYGGSTYYADSVKG (SEQ ID NO:16) and RHWPGGFDY (SEQ ID NO:3), respectively, or

(b) the light chain or antigen binding fragment thereof further comprises an HVR-L1, HVR-L2 and an HVR-L3 sequence having at least 85% sequence identity to RASQDVSTAVA (SEQ ID NO:17), SASFLYS (SEQ ID NO:18) and QQYLYHPAT (SEQ ID NO:19), respectively.

26. The nucleic acid of Claim 25, wherein sequence identity is 90%.

27. The nucleic acid of Claim 26, wherein the sequence identity is 95%.

28. The nucleic acid of Claim 25, wherein the anti-PD-L1 antibody further comprises a VL and a VH framework region derived from a human consensus sequence.

29. The nucleic acid of Claim 28, wherein the VH sequence is derived from a Kabat subgroup I, II, or III sequence.

30. The nucleic acid of Claim 29, wherein the VH sequence is derived from Kabat subgroup III.

31. The nucleic acid of Claim 30, further wherein the heavy chain framework sequences are juxtaposed between the HVRs according to the formula: (HC-FR1)-(HVR-H1)-(HC-FR2)-(HVR-H2)-(HC-FR3)-(HVR-H3)-(HC-FR4).

32. The nucleic acid of Claim 31, wherein one or more of the heavy chain framework sequences is the following:

HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4);
HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5);
HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6);
HC-FR4 is WGQGTLVTVSA (SEQ ID NO:7).

33. The nucleic acid of Claim 28, wherein the VL sequence is derived from a Kabat kappa I, II, III or IV subgroup sequence.

34. The nucleic acid of Claim 33, wherein the VL sequence is derived from Kabat kappa I.

35. The nucleic acid of Claim 33, further wherein the encoded variable light chain framework sequences are juxtaposed between the HVRs according to the formula: (LC-FR1)-(HVR-L1)-(LC-FR2)-(HVR-L2)-(LC-FR3)-(HVR-L3)-(LC-FR4).

36. The nucleic acid of Claim 35, wherein one or more of the light chain framework sequences is the following:

LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC, and (SEQ ID NO:13);
LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

37. The nucleic acid of Claim 25, wherein the anti-PD-L1 antibody comprises a constant region derived from a murine antibody.

38. The nucleic acid of Claim 25, wherein the anti-PD-L1 antibody comprises a constant region derived from a human antibody.

39. The nucleic acid of Claim 37, wherein the constant region is IgG2A.

40. The nucleic acid of Claim 38, wherein the constant region is IgG1.

41. The nucleic acid of Claim 40, wherein the encoded antibody has reduced or minimal effector function.

42. The nucleic acid of Claim 41, wherein the minimal effector function results from an effector-less Fc mutation.

43. The nucleic acid of Claim 42, wherein the effector-less Fc mutation is N297A.

44. The nucleic acid of Claim 42, wherein the effector-less Fc mutation is D265A/N297A.

45. An isolated nucleic acid encoding an anti-PD-L1 antibody or antigen binding fragment thereof, wherein the antibody or antibody fragment comprises a heavy chain and a light chain variable region sequence, wherein:

(a) the heavy chain comprises an HVR-H1, HVR-H2 and HVR-H3, wherein further:

(i) the HVR-H1 sequence is GFTFSX$_1$SWIH (SEQ ID NO:1);

(ii) the HVR-H2 sequence is AWIX$_2$PYGGSX$_3$YYADSVKG (SEQ ID NO:2);

(iii) the HVR-H3 sequence is RHWPGGFDY, and (SEQ ID NO:3);

(b) the light chain comprises an HVR-L1, HVR-L2 and HVR-L3, wherein further:

(iv) the HVR-L1 sequence is RASQX$_4$X$_5$X$_6$TX$_7$X$_8$A (SEQ ID NOs:8);

(v) the HVR-L2 sequence is SASX$_9$LX$_{10}$S (SEQ ID NOs:9);

(vi) the HVR-L3 sequence is QQX$_{11}$X$_{12}$X$_{13}$X$_{14}$PX$_{15}$T (SEQ ID NOs:10);

wherein: X$_1$ is D or G; X$_2$ is S or L; X$_3$ is T or S; X$_4$ may be D or V; X$_5$ may be V or I; X$_6$ may be S or N; X$_7$ may be A or F; X$_8$ may be V or L; X$_9$ may be F or T; X$_{10}$ may be Y or A; X$_{11}$ may be Y, G, F, or S; X$_{12}$ may be L, Y, F or W; X$_{13}$ may be Y, N, A, T, G, F or I; X$_{14}$ may be H, V, P, T or I; X$_{15}$ may be A, W, R, P or T.

46. The nucleic acid of Claim 45 wherein X$_1$ is D; X$_2$ is S and X$_3$ is T.

47. The nucleic acid of Claim 45, wherein X$_4$ = D, X$_5$ = V, X$_6$ = S, X$_7$ = A and X$_8$ = V, X$_9$ = F, and X$_{10}$ = Y, X$_{11}$ = Y, X$_{12}$ = L, X$_{13}$ = Y, X$_{14}$ = H and X$_{15}$ = A.

48. The nucleic acid of Claim 45, wherein X$_1$ = D, X$_2$ = S and X$_3$ = T, X$_4$ = D, X$_5$ = V, X$_6$ = S, X$_7$ = A and X$_8$ = V, X$_9$ = F, and X$_{10}$ = Y, X$_{11}$ = Y, X$_{12}$ = L, X$_{13}$ = Y, X$_{14}$ = H and X$_{15}$ = A.

49. The nucleic acid of Claim 46, wherein the encoded variable region heavy chain framework sequences are juxtaposed between the HVRs according to the formula: (HC-FR1)-(HVR-H1)-(HC-FR2)-(HVR-H2)-(HC-FR3)-(HVR-H3)-(HC-FR4).

50. The nucleic acid of claim 49, wherein the framework sequences are human.

51. The nucleic acid of Claim 50 wherein the framework sequences are VH subgroup III consensus framework.

52. The nucleic acid of Claim 51 wherein one or more of the framework sequences is the following:

HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4);
HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5);
HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6);
HC-FR4 is WGQGTLVTVSA (SEQ ID NO:7).

53. The nucleic acid of 47, wherein the encoded variable region light chain framework sequences juxtaposed between the HVRs according to the formula: (LC-FR1)-(HVR-L1)-(LC-FR2)-(HVR-L2)-(LC-FR3)-(HVR-L3)-(LC-FR4).

54. The nucleic acid of Claim 53 wherein the variable region light chain framework sequences are VL kappa I consensus framework.

55. The nucleic acid of Claim 54 wherein one or more of the framework sequences is the following:

LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC, and (SEQ ID NO:13);
LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

56. The nucleic acid of Claim 48 wherein the antibody or antibody fragment comprises:

(a) variable region heavy chain framework sequences juxtaposed between the HVRs according to the formula: (HC-FR1)-(HVR-H1)-(HC-FR2)-(HVR-H2)-(HC-FR3)-(HVR-H3)-(HC-FR4), and

(b) variable region light chain framework sequences juxtaposed between the HVRs according to the formula: (LC-FR1)-(HVR-L1)-(LC-FR2)-(HVR-L2)-(LC-FR3)-(HVR-L3)-(LC-FR4).

wherein the variable heavy chain framework sequences are the following:

(i) HC-FR1 is EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:4);
(ii) HC-FR2 is WVRQAPGKGLEWV (SEQ ID NO:5);
(iii) HC-FR3 is RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR (SEQ ID NO:6);
(iv) HC-FR4 is WGQGTLVTVSA; and (SEQ ID NO:7); and

further wherein the variable light chain framework sequences are the following:

(i) LC-FR1 is DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:11);
(ii) LC-FR2 is WYQQKPGKAPKLLIY (SEQ ID NO:12);
(iii) LC-FR3 is GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:13);
(iv) LC-FR4 is FGQGTKVEIKR (SEQ ID NO:14).

57. The nucleic acid of Claim 56 further comprising a human constant region.

58. The nucleic acid of Claim 57, wherein the constant region is selected from the group consisting of IgG1, IgG2, IgG3 and IgG4.

59. The nucleic acid of Claim 58 wherein the constant region is IgG1.

60. The nucleic acid of Claim 59 having reduced or minimal effector function.

61. The nucleic acid of Claim 60, wherein the minimal effector function results from an effector-less Fc mutation.

62. The nucleic acid of Claim 61, wherein the effector-less Fc mutation is N297A.

63. The nucleic acid of Claim 61, wherein the effector-less Fc mutation is D265A/N297A.

64. The nucleic acid of Claim 60, wherein the minimal effector function results from aglycosylation.

65. The nucleic acid of Claim 56, further comprising a murine constant region.

66. The nucleic acid of Claim 65, wherein the constant region is selected from the group consisting of IgG1, IgG2A, IgG2B and IgG3.

67. The nucleic acid of Claim 66, wherein the constant region is IgG2A.

68. The nucleic acid of Claim 67, which has reduced or minimal effector function.

69. The nucleic acid of Claim 68, wherein the minimal effector function results from an effector-less Fc mutation.

70. The nucleic acid of Claim 69, wherein the effector-less Fc mutation is N297A.

71. The nucleic acid of Claim 69, wherein the effector-less Fc mutation is D265A/N297A.

72. The nucleic acid of Claim 68, wherein the minimal effector function results from aglycosylation.

73. An isolated nucleic acid encoding anti-PD-L1 antibody or antigen binding fragment thereof, wherein the antibody or antibody fragment comprises a heavy chain and light chain variable region sequence, wherein:

(a) the heavy chain comprises the sequence: EVQLVESGGGLVQPGGSLRLS CAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTS KNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSA (SEQ ID NO:20), and

(b) the light chain comprises the sequence: DIQMTQSPSSLSASVGDRVTITC RASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCQQYLYH PATFGQGTKVEIKR (SEQ ID NO:21).

74. The nucleic acid of Claim 73 further comprising a human constant region.

75. The nucleic acid of Claim 74, wherein the constant region is selected from the group consisting of IgG1, IgG2, IgG3 and IgG4.

76. The nucleic acid of Claim 75, wherein the constant region is IgG1.

77. The nucleic acid of Claim 76 having reduced or minimal effector function.

78. The nucleic acid of Claim 77, wherein the minimal effector function results from an effector-less Fc mutation.

79. The nucleic acid of Claim 78, wherein the effector-less Fc mutation is N297A.

80. The nucleic acid of Claim 78, wherein the effector-less Fc mutation is D265A/N297A.

81. The nucleic acid of Claim 77, wherein the minimal effector function results from aglycosylation.

82. A vector comprising the nucleic acid of any of Claims 1-12

83. A vector comprising the nucleic acid of any of Claims 13-24.

84. A vector comprising the nucleic acid of any of Claims 25-44.

85. A vector comprising the nucleic acid of any of Claims 45-72.

86. A vector comprising the nucleic acid of any of Claims 73-81.

87. A host cell comprising the vector of Claim 82.

88. A host cell comprising the vector of Claim 84.

89. A host cell comprising the vector of Claim 85.

90. A host cell comprising the vector of Claim 86.

91. The host cell of Claim 84, which is eukaryotic.

92. The host cell of Claim 91, which is mammalian.

93. The host cell of Claim 92, which is a Chinese Hamster Ovary (CHO) cells.

94. The host cell of Claim 84, which is prokaryotic.

95. The host cell of Claim 94, which is *E. coli.*

96. A process for making an anti-PD-L1 antibody comprising culturing the host cell of Claim 93 under conditions suitable for the expression of the vector encoding the anti-PD-L1 antibody or antigen binding fragment, and recovering the antibody or fragment.