



US 20230042095A1

(19) **United States**(12) **Patent Application Publication**
SEOANE SUAREZ et al.(10) **Pub. No.: US 2023/0042095 A1**(43) **Pub. Date: Feb. 9, 2023**(54) **ANTIBODIES AGAINST LIF AND USES THEREOF**

(60) Provisional application No. 62/467,017, filed on Mar. 3, 2017.

(71) Applicants: **MEDIMMUNE LIMITED**, Cambridge (GB); **FUNDACIO PRIVADA INSTITUT D'INVESTIGACIO ONCOLOGICA DE VALL HEBRON**, Barcelona (ES); **FUNDACIO PRIVADA INSTITUCIO CATALANA DE RECERCA I ESTUDIS AVANCATS**, Barcelona (ES)(30) **Foreign Application Priority Data**

Dec. 19, 2016 (EP) 16382617.5

Oct. 13, 2017 (EP) 17382683.5

Publication Classification(51) **Int. Cl.****C07K 16/24** (2006.01)**A61P 35/00** (2006.01)**A61K 39/395** (2006.01)(52) **U.S. Cl.**CPC **C07K 16/244** (2013.01); **A61P 35/00** (2018.01); **A61K 39/395** (2013.01); **A61K 2039/505** (2013.01)(72) Inventors: **Joan SEOANE SUAREZ**, Barcelona (ES); **Judit ANIDO FOLGUEIRA**, Barcelona (ES); **Johan FRANSSON**, Toronto (CA); **Jean-Philippe JULIEN**, Toronto (CA); **Swetha RAMAN**, Toronto (CA)(21) Appl. No.: **17/808,319**(22) Filed: **Jun. 23, 2022****Related U.S. Application Data**

(62) Division of application No. 16/470,896, filed on Jun. 18, 2019, now Pat. No. 11,390,670, filed as application No. PCT/IB2017/001677 on Dec. 18, 2017.

(57) **ABSTRACT**

Described herein are antibodies that target Leukemia Inhibitory Factor (LIF). Also described herein are uses of these antibodies for the treatment of cancer.

Specification includes a Sequence Listing.

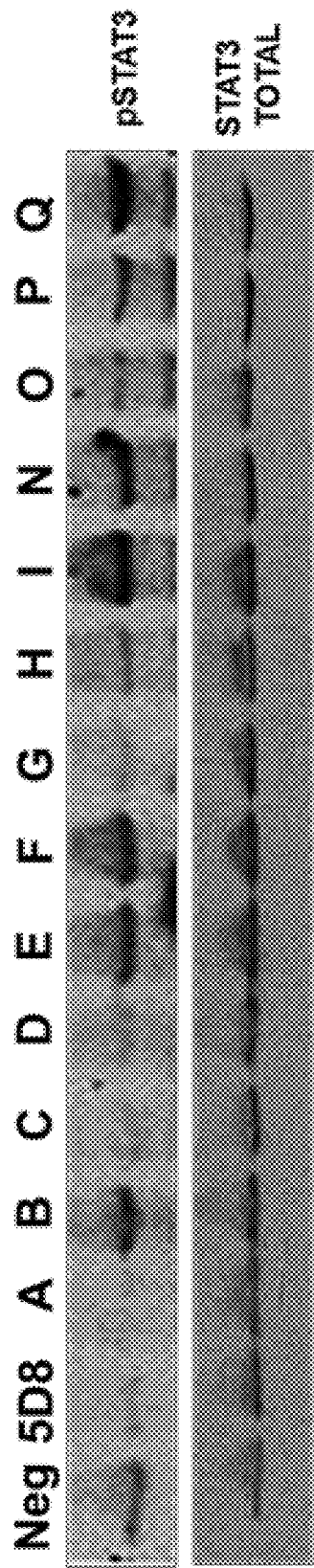


Fig. 1

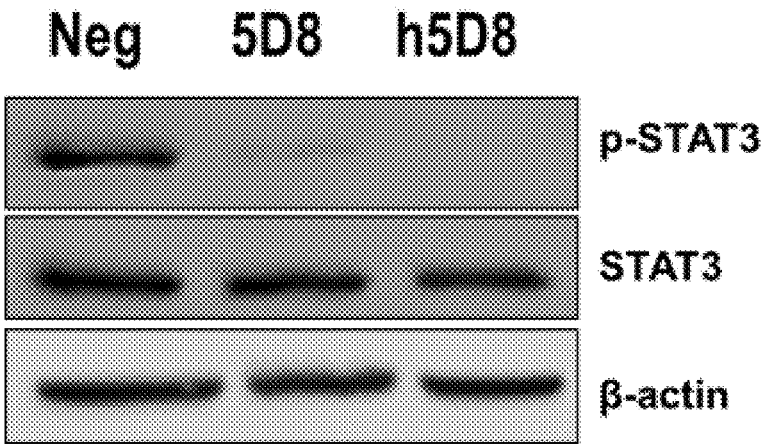


Fig. 2A

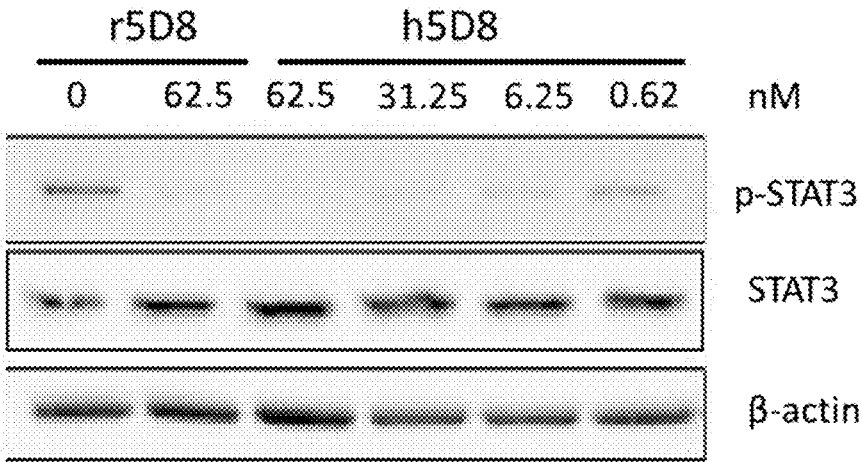


Fig. 2B

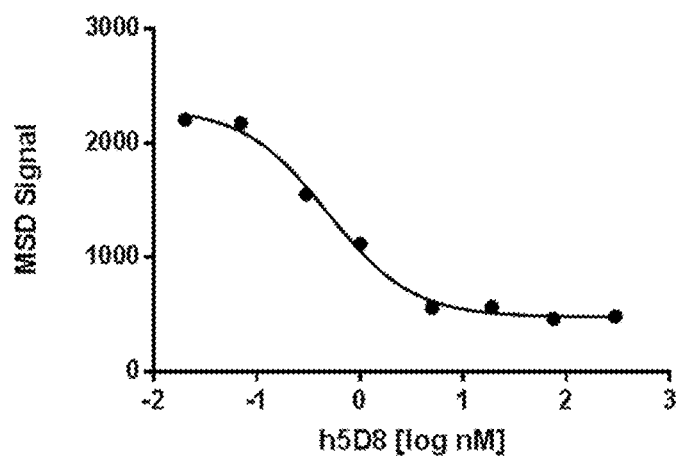


Fig. 3A

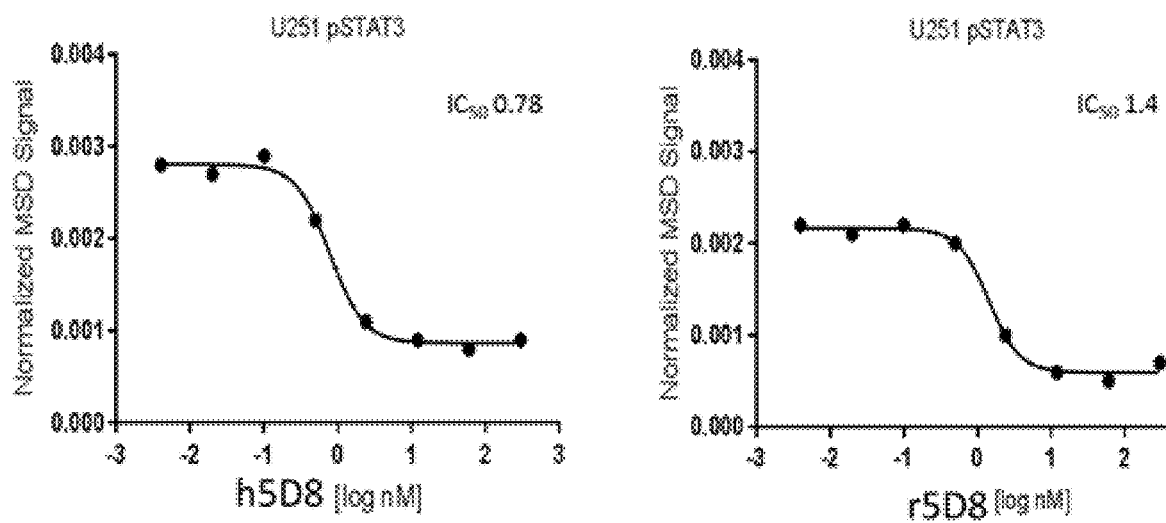


Fig. 3B

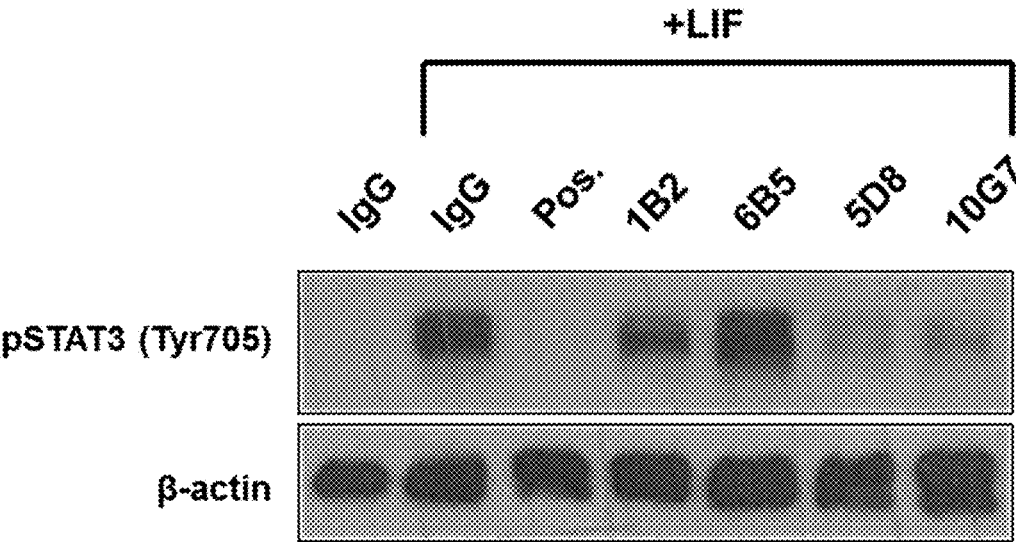


Fig. 4

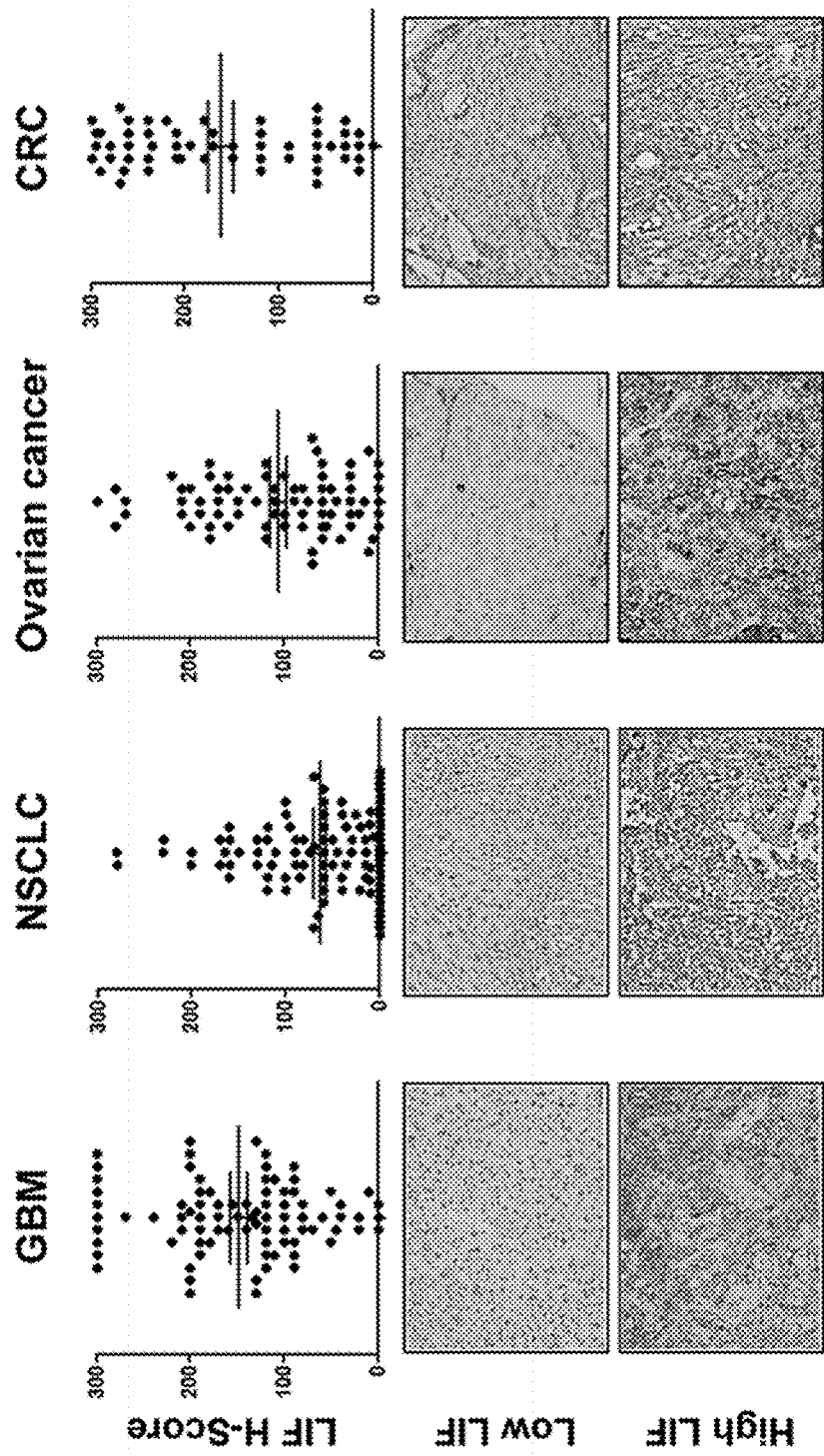


Fig. 5

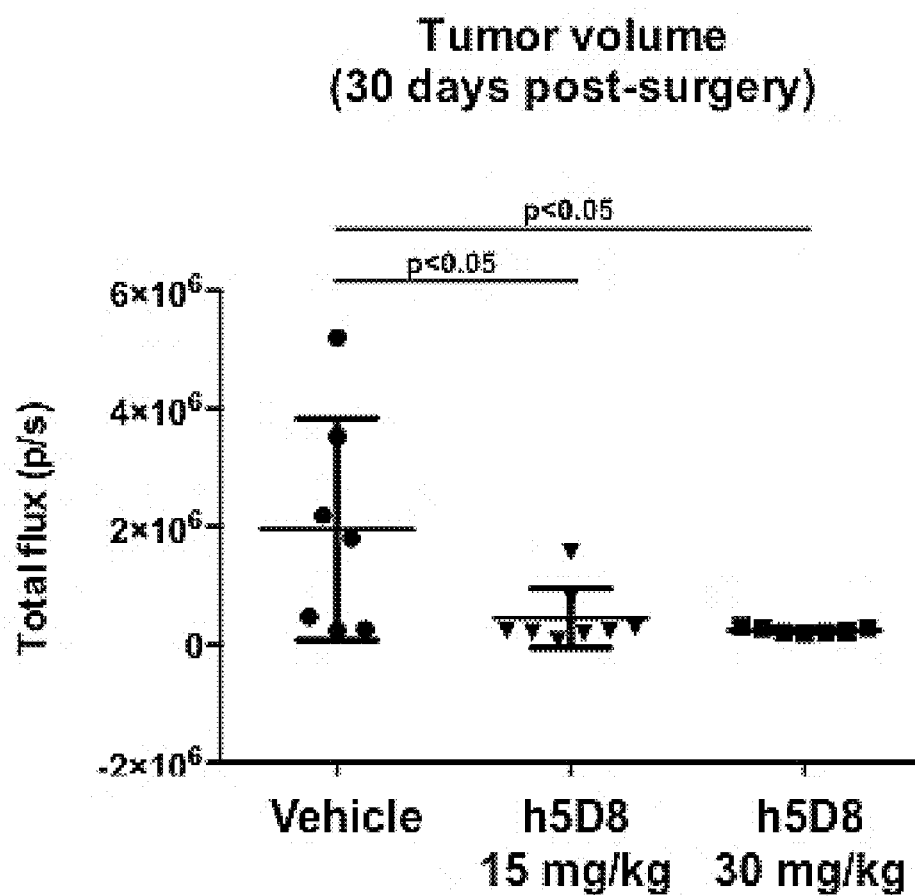


Fig. 6

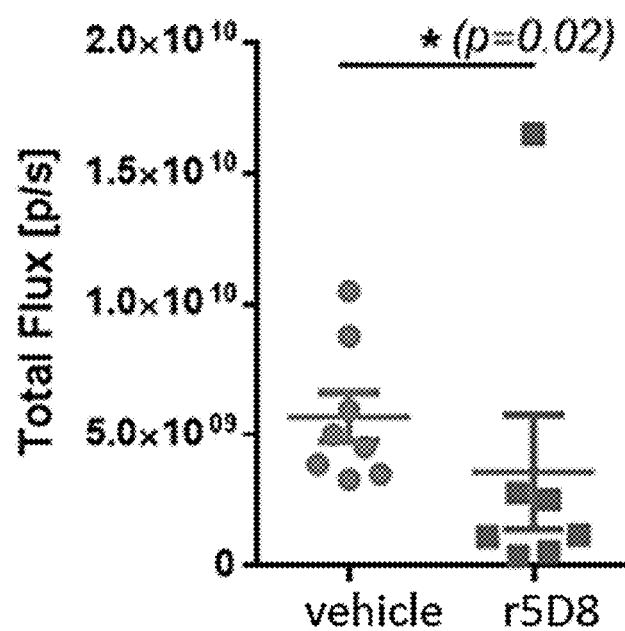


Fig. 7A

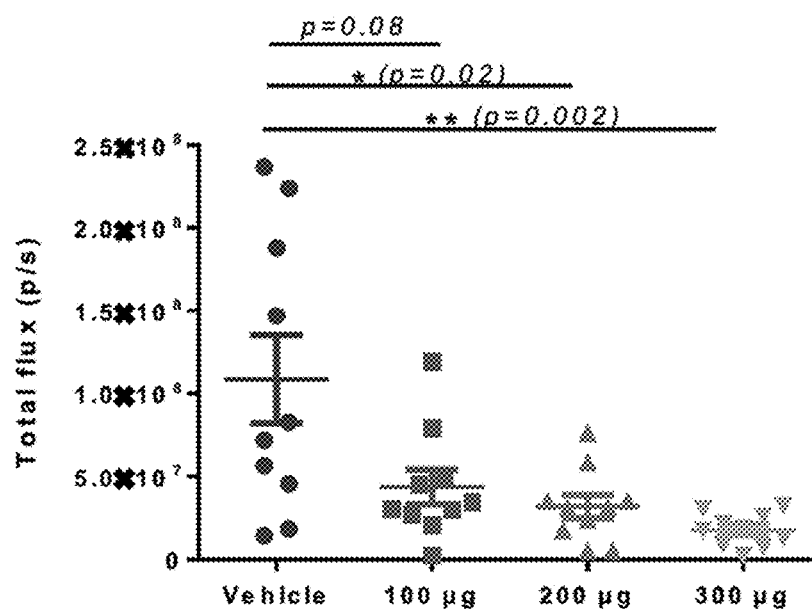


Fig. 7B

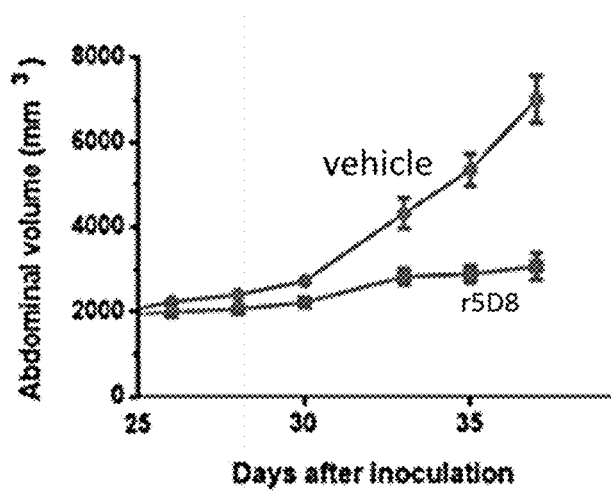


Fig. 8A

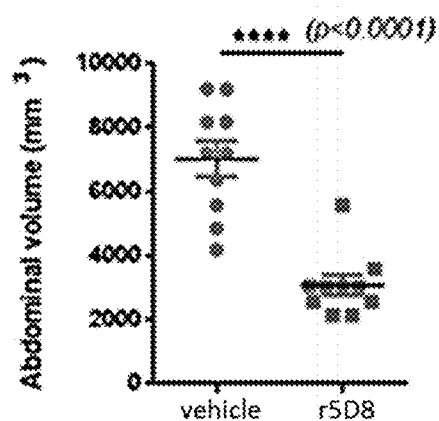


Fig. 8B

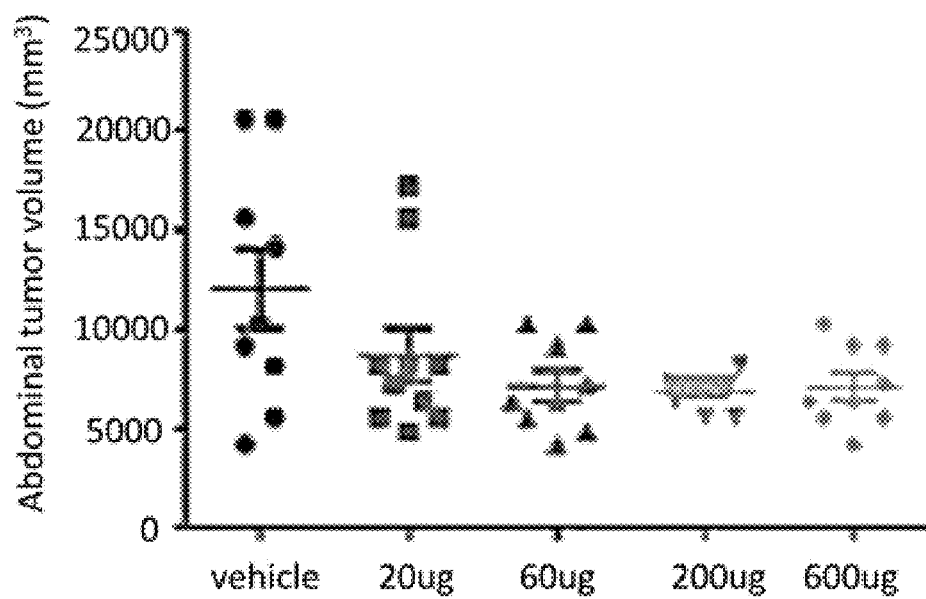


Fig. 8C

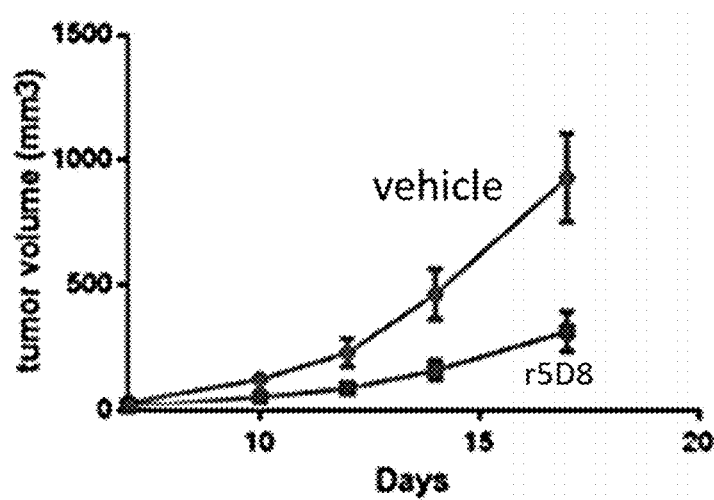


Fig. 9A

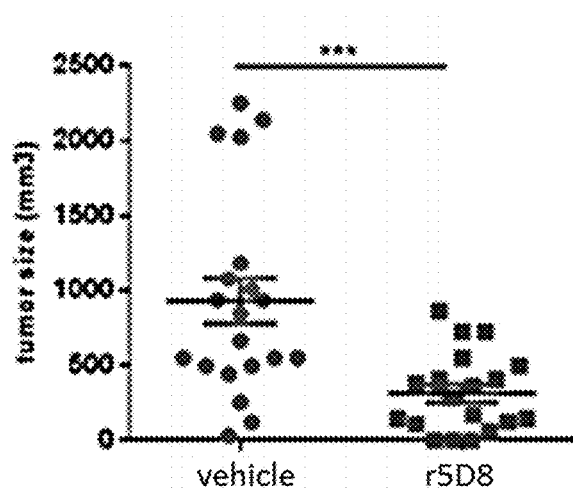


Fig. 9B

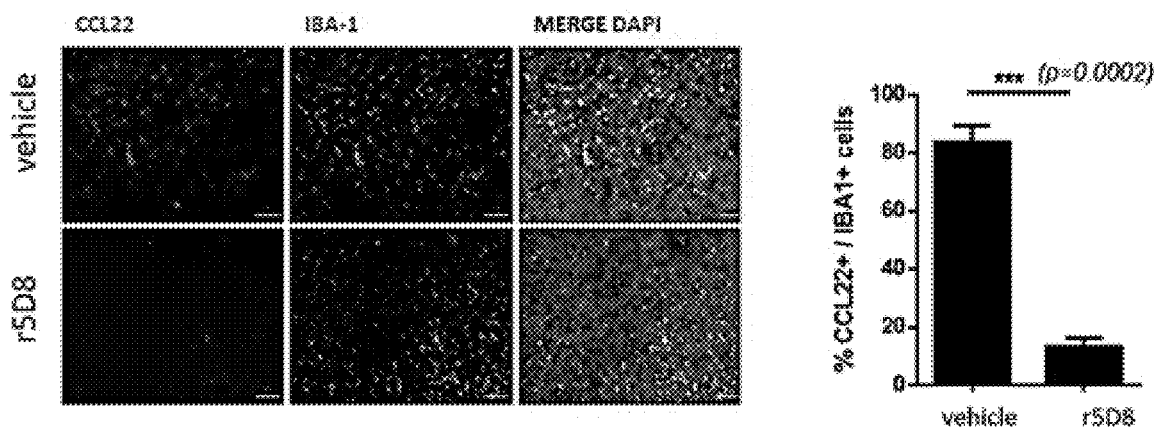


Fig. 10A

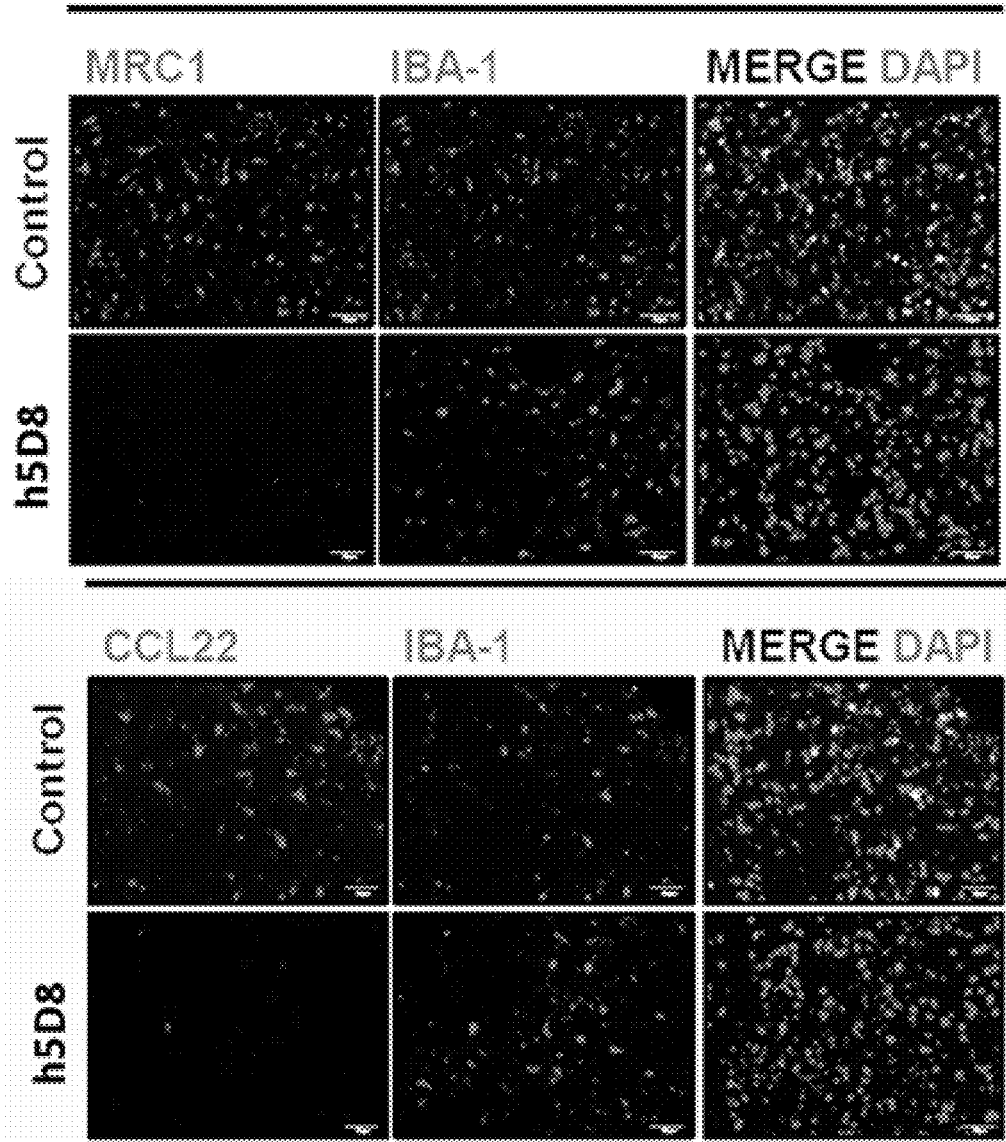


Fig. 10B

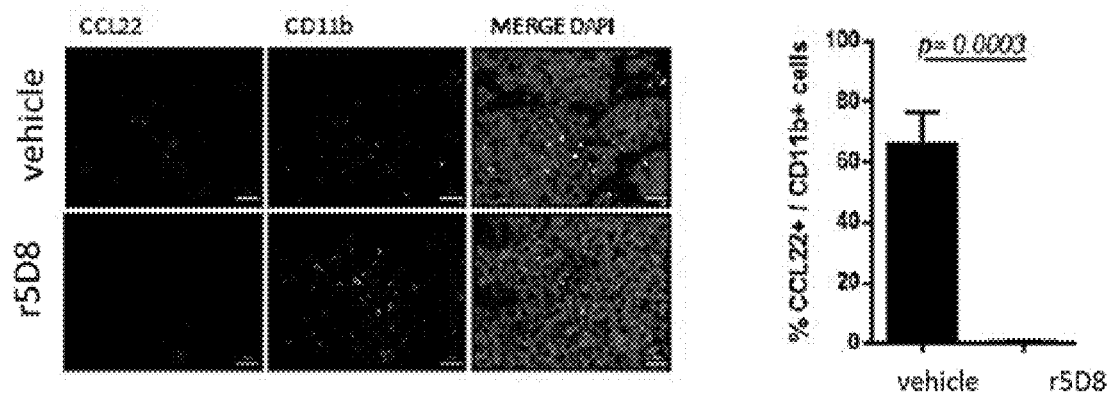


Fig. 10C

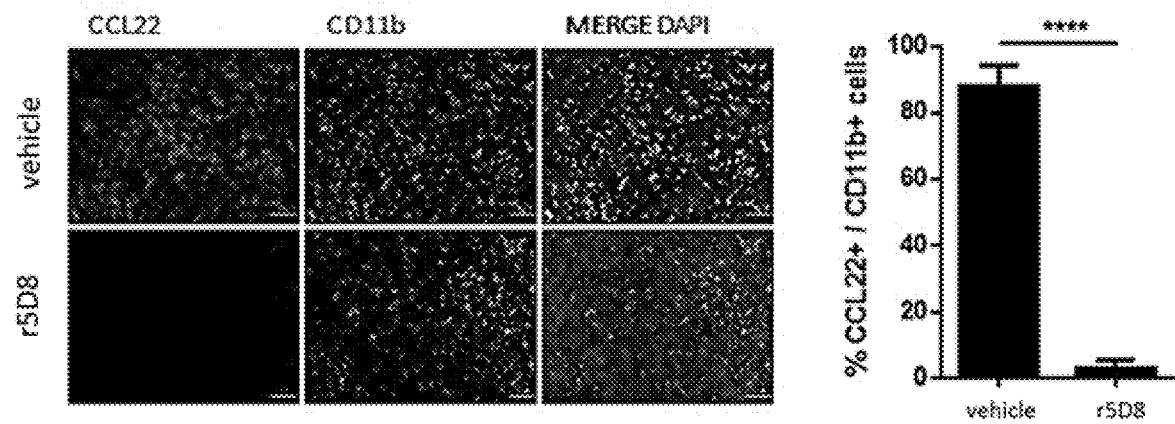


Fig. 10D

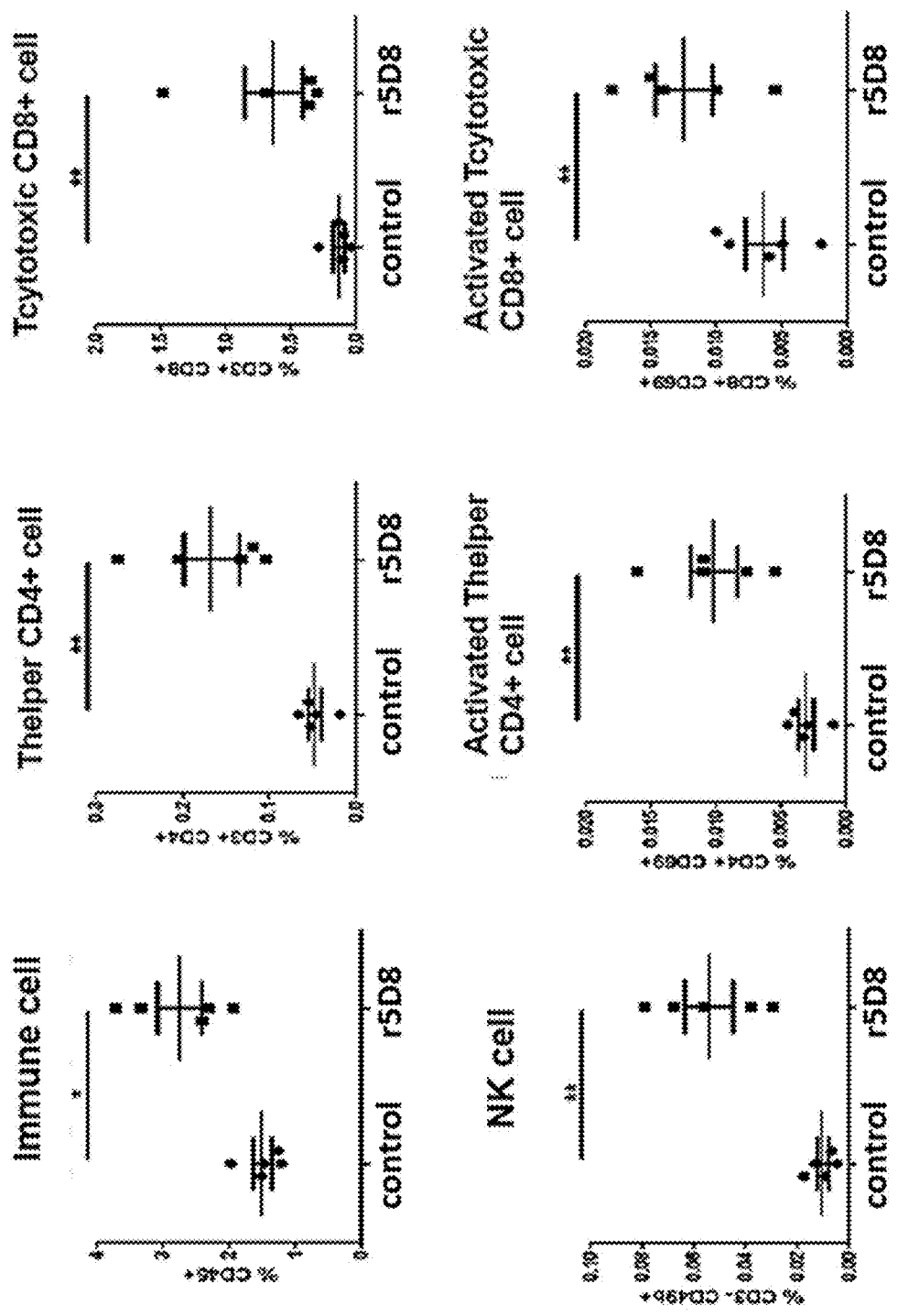


Fig. 11A

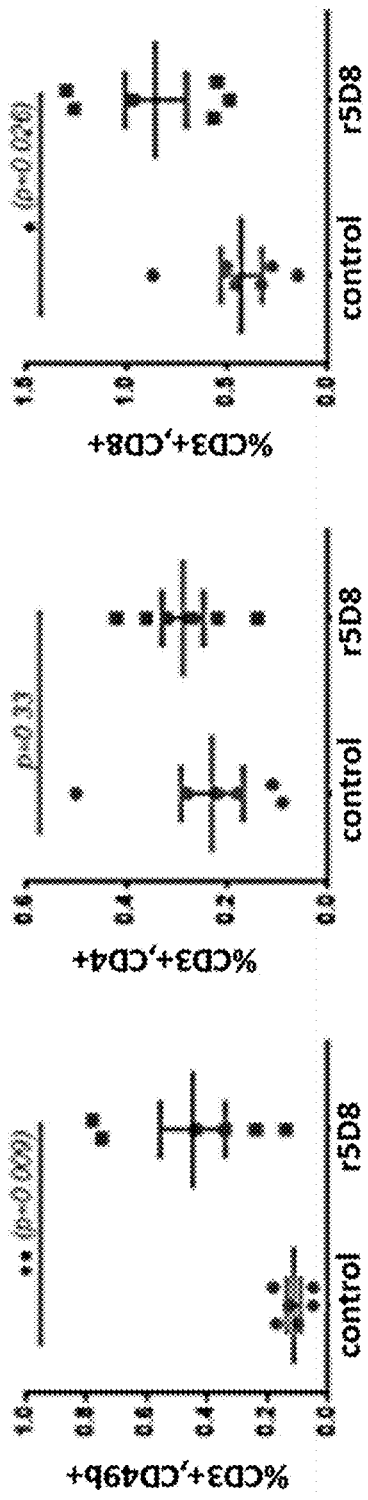


Fig. 11B

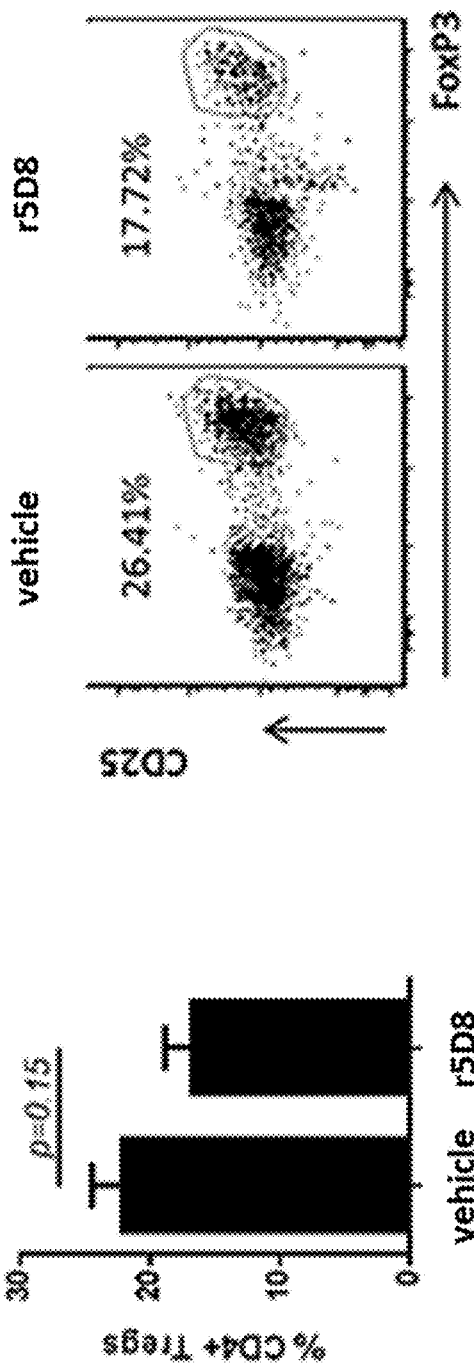


Fig. 11C

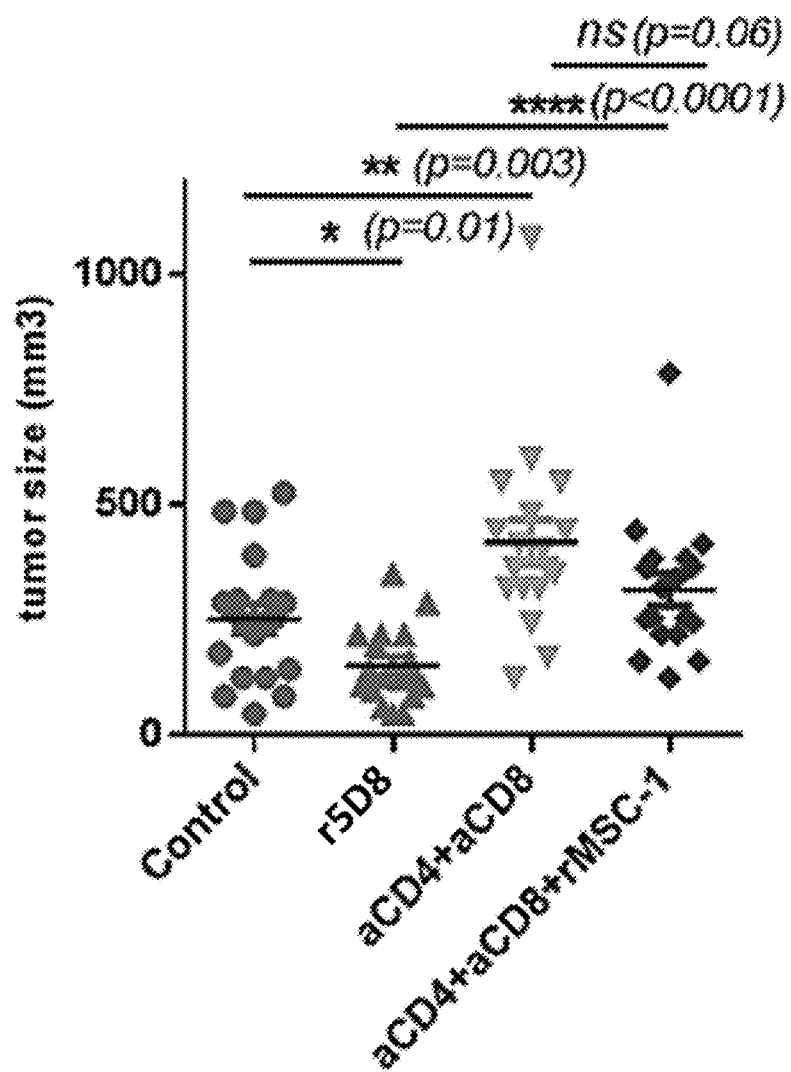


Fig. 12

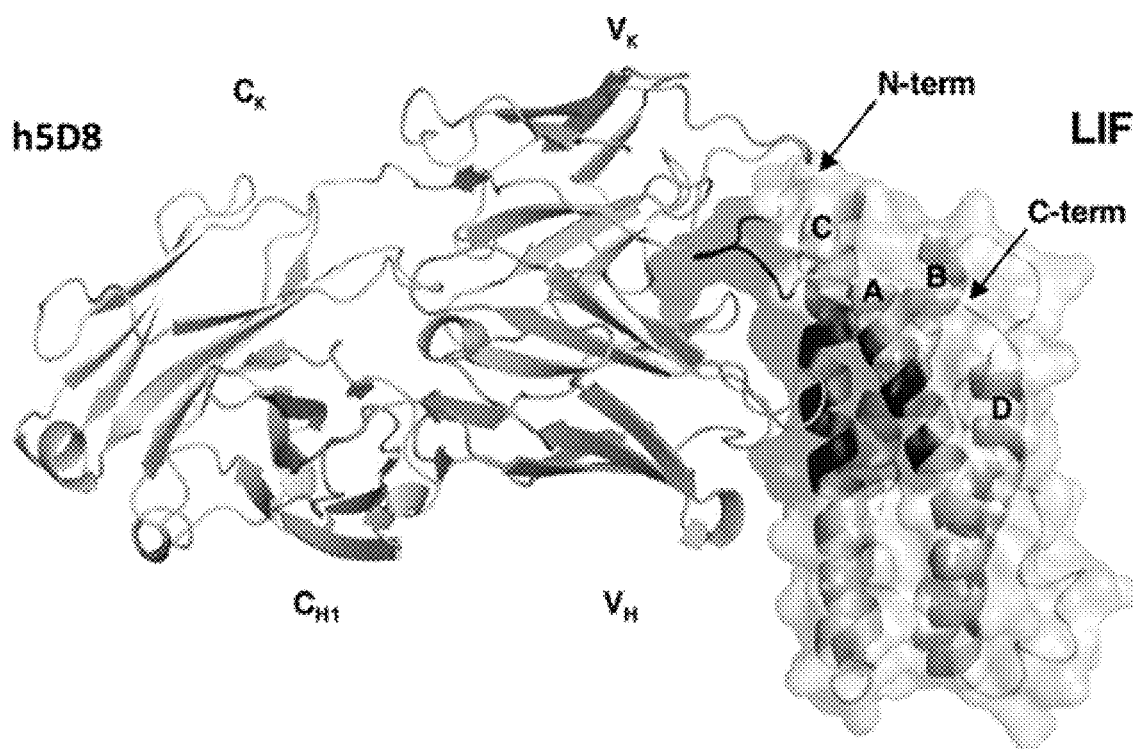


Fig. 13A

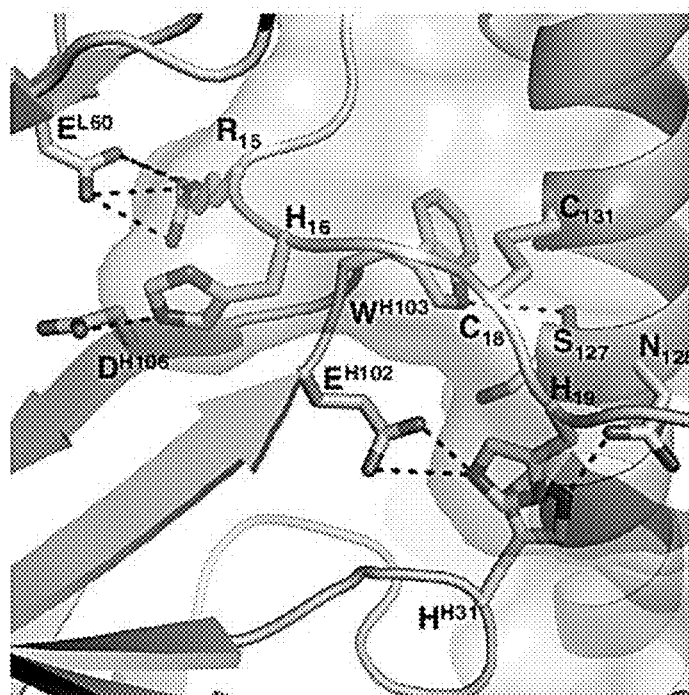


Fig. 13B

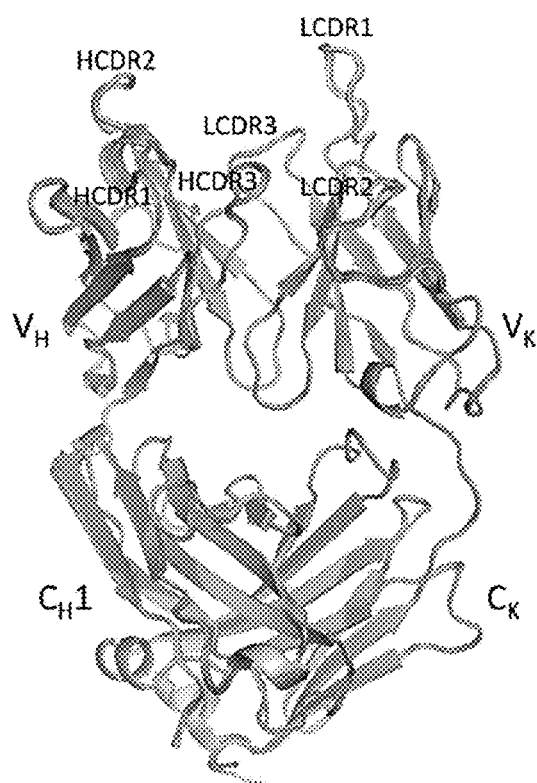


Fig. 14A

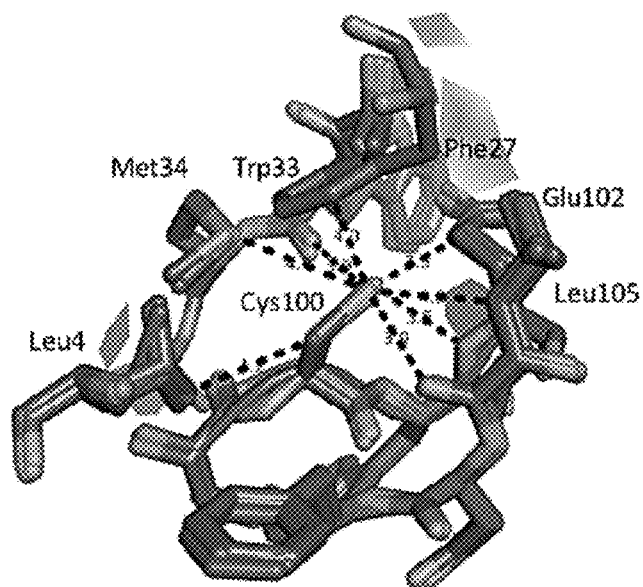
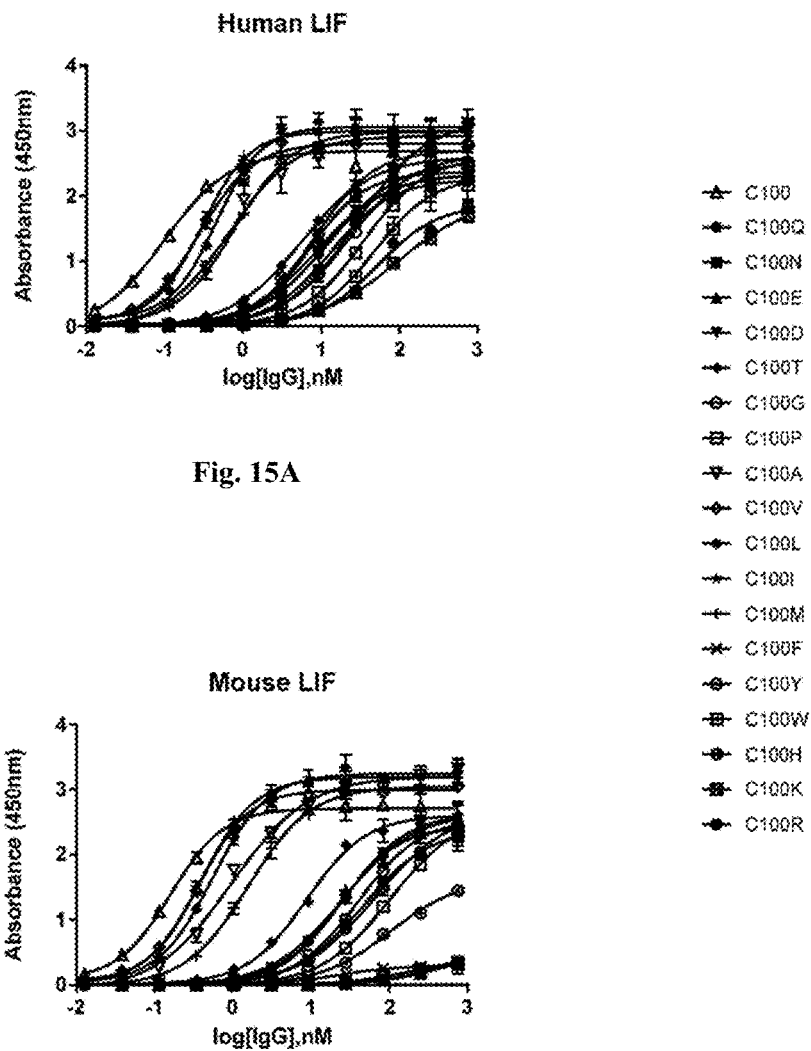


Fig. 14B



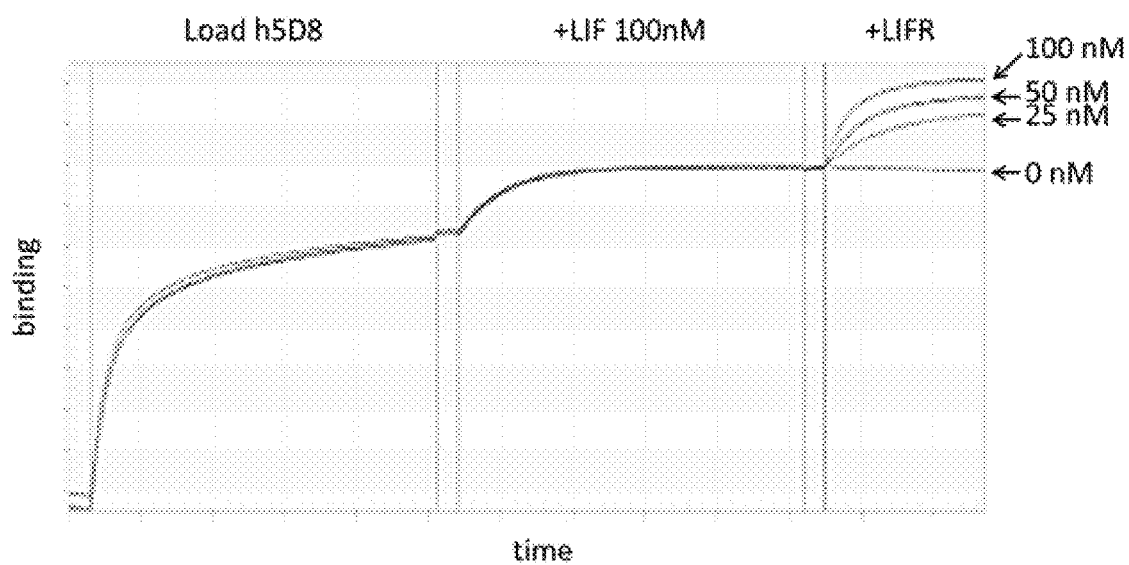


Fig. 16A

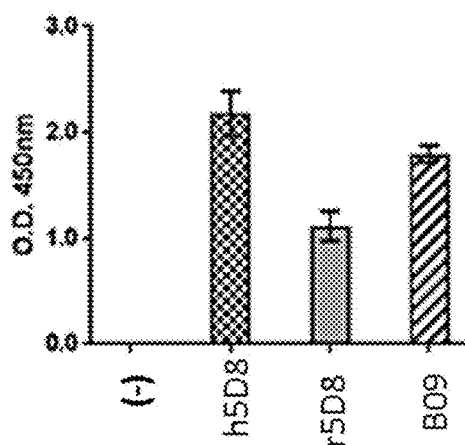


Fig. 16B

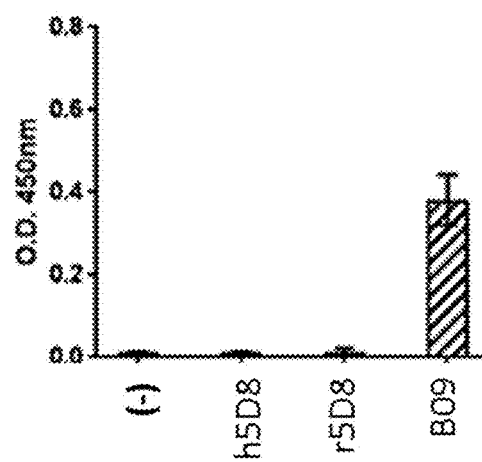


Fig. 16C

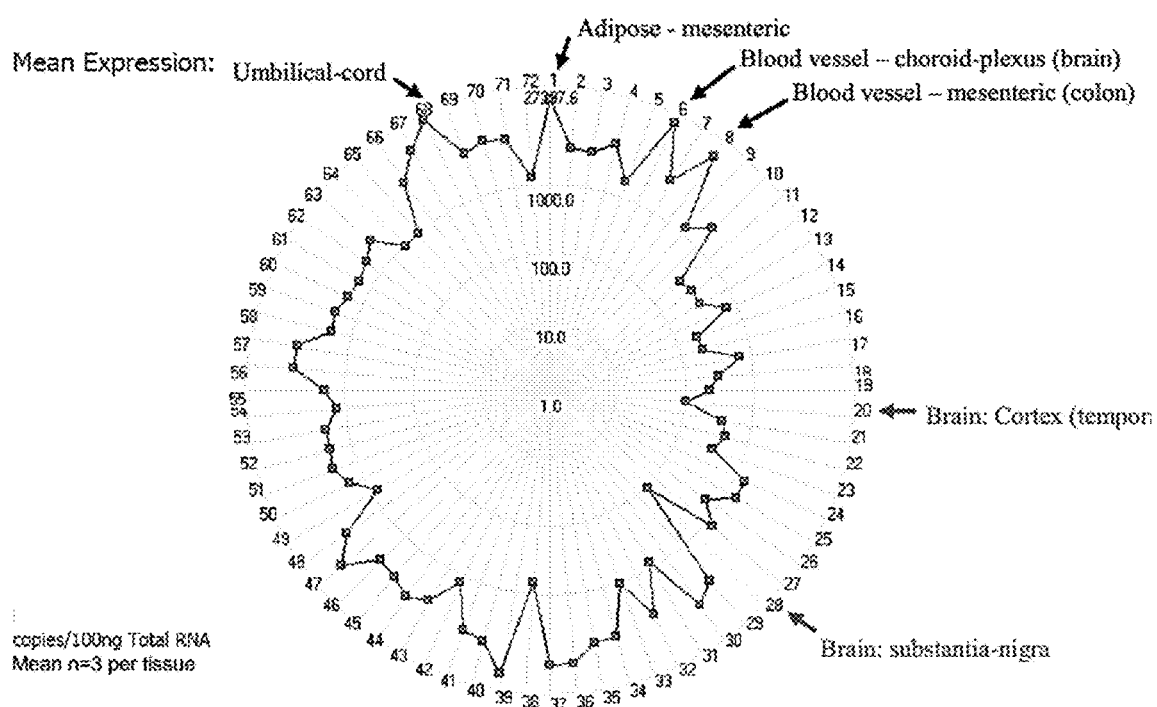


Fig. 17A

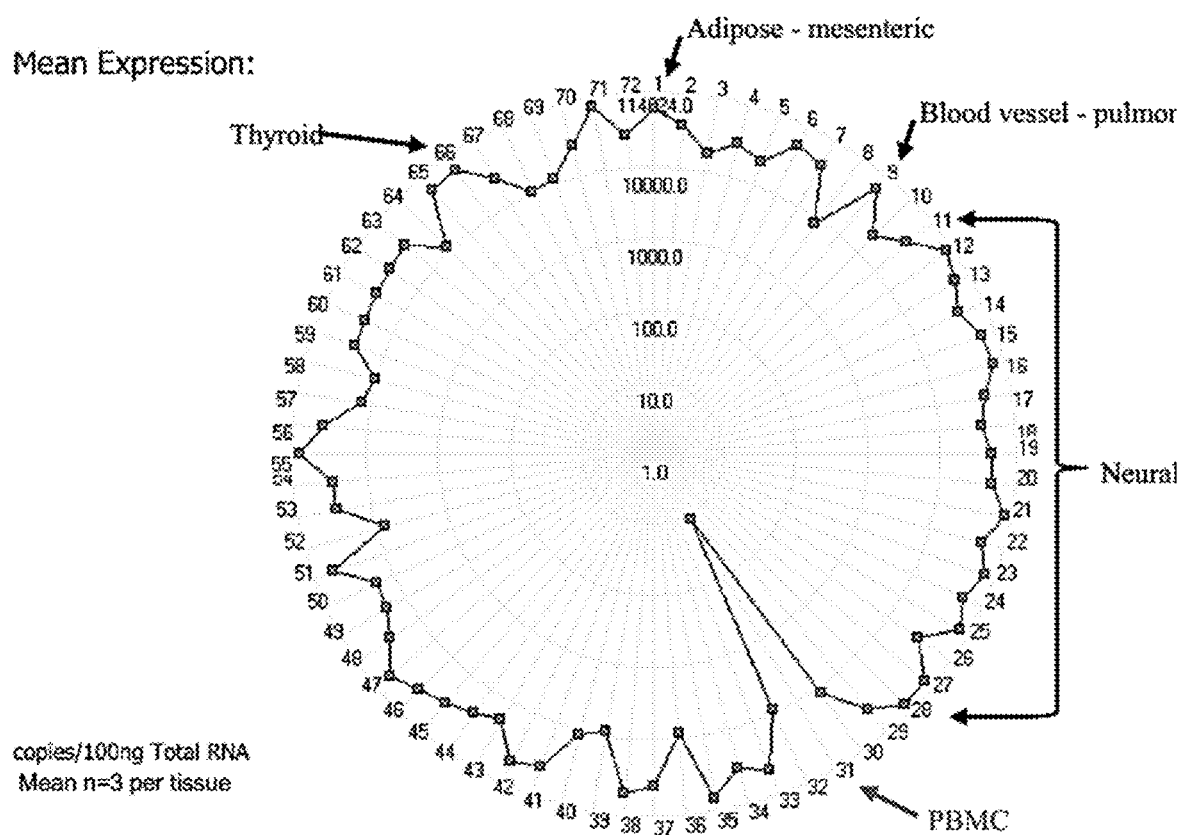


Fig. 17B

ANTIBODIES AGAINST LIF AND USES THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. application Ser. No. 16/470,896 filed Jun. 18, 2019, International Patent Application No. PCT/IB2017/001677 filed on Dec. 18, 2017, U.S. Provisional Patent Application No. 62/467,017 filed on Mar. 3, 2017, European Patent Application No. EP17382683.5 filed on Oct. 13, 2017, and European Patent Application No. EP16382617.5 filed on Dec. 19, 2016 all of which are incorporated by reference herein in their entireties.

BACKGROUND

[0002] Leukemia inhibitory factor (LIF) is an Interleukin 6 (IL-6)-type cytokine that is involved in a variety of biological activities including the inhibition of cell differentiation. Human LIF is a polypeptide of 202 amino acids that exerts biological effects via binding to the cell surface LIF receptor (LIFR or CD118) which heterodimerizes with gp130. This leads to activation of pro-growth signaling pathways such as the mitogen activated protein kinase (MAPK) and the Janus activated kinase (JAK/STAT) pathway. High expression levels and high serum levels of LIF have been demonstrated to be associated with a poor prognosis for many types of cancer.

SUMMARY

[0003] Described herein are novel anti-LIF antibodies that antagonize or block LIF activity. These antibodies are useful for the treatment of cancer. These antibodies can be humanized in order to develop a clinical therapy for cancers that express high levels of LIF, LIF receptor, or exhibit LIF dependent growth. One such antibody described herein exhibits an unexpected improvement in binding affinity and biological effect after the humanization process.

[0004] In one aspect, described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a) a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 1-7 or 33; b) a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 9-13 or 35; c) a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 15-19 or 37; d) a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 21-23 or 39; e) a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 25-27 or 41; and f) a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 29, 30, or 43, wherein the recombinant antibody specifically binds to LIF. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain embodiments, the recombinant antibody comprises at least one framework region derived from a human antibody framework region. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized.

In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody comprises a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 100 picomolar. In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 4 (GFTFSNAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 11 (QIKDKSDNYATYYAESVKG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 17 (TCWEWYLDLF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 7 (SKFMY), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 13 (WIYPGDGDTEYNQKFSE), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 19 (RDYHSSHFAF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 23 (RSSQSLLHNNNGNTYLS), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 27 (QVSNRFS), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 30 (GQGTQYPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 33 (TAGMQ), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 35 (WINTQSGEPQYVDDFRG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 37 (WALYSEYDVMDY), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 39 (KASENVDSYVS), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 41 (GASNRYT), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 43 (GQSYRYPPT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 1 (GFTFSNAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 15 (TCWEWYLDLF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the recombinant antibody comprises one or more of a heavy chain framework 1 (VH-FR1) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a heavy chain framework 2 (VH-FR2) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-51, a light chain framework 1 (VL-FR1) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 52-55, or a light chain framework 2 (VL-FR2) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59.

identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a heavy chain framework 3 (VH-FR3) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, and a heavy chain framework 4 (VH-FR4) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the recombinant antibody comprises one or more of a light chain framework 1 (VL-FR1) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a light chain framework 2 (VL-FR2) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a light chain framework 3 (VL-FR3) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, and a light chain framework 4 (VL-FR4) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the recombinant antibody comprises a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the recombinant antibody comprises a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody comprises a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about

90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody is for use in treating cancer. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, or lung cancer. In certain embodiments, the recombinant antibody is a constituent of a pharmaceutical composition comprising the recombinant antibody and a pharmaceutically acceptable carrier. In certain embodiments, the pharmaceutical composition is formulated for intravenous administration. In certain embodiments, the pharmaceutical composition is formulated for intracerebral administration. In certain embodiments, the pharmaceutical composition is for use in treating cancer. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer.

[0005] In another aspect, described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a) an immunoglobulin heavy chain variable region (VH) sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 71, 72, or 74; and b) an immunoglobulin light chain variable region (VL) sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 75-78. In certain embodiments, the VH sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 72; and the VL sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 76.

[0006] In another aspect, described herein, is a method of treating an individual with cancer comprising administering to the individual a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a) a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 1-7 or 33; b) a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 9-13 or 35; c) a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 15-19 or 37; d) a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 21-23 or 39; e) a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 25-27 or 41; and f) a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 29, 30, or 43, wherein the recombinant antibody specifically binds to LIF. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain embodiments, the recombinant antibody comprises at least one framework region derived from a human antibody framework region. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized. In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody is a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with

a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 100 picomolar. In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 4 (GFTFSNAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 11 (QIKDKSDNYATYYAESVKG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 17 (TCWEWYLDLF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLDSDGHTYLN), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 7 (SKFMY), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 13 (WIYPGDGDTEYNQKFSE), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 19 (RDYHSSHFAY), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 23 (RSSQSLHNNNGNTYLS), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 27 (QVSNRFS), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 30 (GQGTYPPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 33 (TAGMQ), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 35 (WINTQSGEPQYVDDFRG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 37 (WALYSEYDVM DY), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 39 (KASENVDSYVS), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 41 (GASNRYT), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 43 (GQSYRYPPT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 1 (GFTFSNAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 15 (TCWEWDLDF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLDSDGHTYLN), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the recombinant antibody comprises one or more of a heavy chain framework 1 (VH-FR1) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a heavy chain framework 2 (VH-FR2) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a heavy chain framework 3 (VH-FR3) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, and a heavy chain framework 4 (VH-FR4) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino

acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the recombinant antibody comprises one or more of a light chain framework 1 (VL-FR1) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a light chain framework 2 (VL-FR2) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a light chain framework 3 (VL-FR3) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, and a light chain framework 4 (VL-FR4) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the recombinant antibody comprises a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the recombinant antibody comprises a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody comprises a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer. In certain embodiments, the recombinant antibody is administered intravenously. In certain embodiments, the recombinant antibody is administered intracerebrally.

[0007] In another aspect, described herein, is a method of treating an individual with cancer comprising administering to the individual a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a) an immunoglobulin heavy chain variable region (VH) sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 71, 72, or 74; and b) an immunoglobulin light chain variable region (VL) sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 75-78. In certain embodiments, the VH sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 72; and the VL sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 76.

[0008] In another aspect, described herein, is a method of preparing a cancer treatment for treating a subject with cancer comprising admixing a pharmaceutically acceptable carrier and a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising a heavy chain complementarity determining region 1 (VH-CDR1) comprising: a) a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 1-7 or 33; b) a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 9-13 or 35; c) a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 15-19 or 37; d) a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 21-23 or 39; e) a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 25-27 or 41; and f) a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 29, 30, or 43, wherein the recombinant antibody specifically binds to LIF. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain embodiments, the recombinant antibody comprises at least one framework region derived from a human antibody framework region. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized. In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody is a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 100 picomolar. In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 4 (GFTFSNAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 11 (QIKDKSDNYATYYAESVKG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 17 (TCWEWYLDLF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLDSDGHTYLN),

wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 7 (SKFMY), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 13 (WIYPGDGDTEYNQKFSE), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 19 (RDYHSSHFAY), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 23 (RSSQSLHNNNGNTYLS), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 27 (QVSNRFS), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 30 (GQGTQYPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 33 (TAGMQ), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 35 (WINTQSGEPQYVDDFRG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 37 (WALYSEYDVMDY), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 39 (KASENVDSYVS), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 41 (GASNRYT), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 43 (GQSYRYPPT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 1 (GFTFSHAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 15 (TCWEWDLDF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLDSDGHTYLN), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the recombinant antibody comprises one or more of a heavy chain framework 1 (VH-FR1) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a heavy chain framework 2 (VH-FR2) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a heavy chain framework 3 (VH-FR3) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, and a heavy chain framework 4 (VH-FR4) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the recombinant antibody comprises one or more of a light chain framework 1 (VL-FR1) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a light chain framework 2 (VL-FR2) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a light chain framework 3 (VL-FR3) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs:

64-67, and a light chain framework 4 (VL-FR4) region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the recombinant antibody comprises a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the recombinant antibody comprises a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody comprises a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer.

[0009] In another aspect, described herein, is a method of preparing a cancer treatment for treating a subject with cancer comprising admixing a pharmaceutically acceptable carrier and a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a) an immunoglobulin heavy chain variable region (VH) sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 71, 72, or 74; b) and an immunoglobulin light chain variable region (VL) sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 75-78. In certain embodiments, the VH sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ

ID NO: 72; and the VL sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 76.

[0010] In another aspect, described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising at least one complementarity determining region (CDR) of rat origin and at least one immunoglobulin framework region (FR) of human origin, wherein the at least one CDR of rat origin specifically binds to LIF. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain embodiments, the recombinant antibody comprises at least one framework region derived from a human antibody framework region. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized. In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody is a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 100 picomolar. In certain embodiments, the at least one CDR of rat origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 1-3, 9, 10, 15, 16, 21, 22, 25, 26, or 29. In certain embodiments, the at least one CDR of rat origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29. In certain embodiments, the at least one immunoglobulin framework region of human origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 44-70. In certain embodiments, the recombinant antibody comprises a heavy chain CDR1 amino acid sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 amino acid sequence set forth in SEQ ID NO: 9, and a heavy chain CDR3 amino acid sequence set forth in SEQ ID NO: 15. In certain embodiments, the recombinant antibody comprises a light chain CDR1 amino acid sequence set forth in SEQ ID NO: 21, a light chain CDR2 amino acid sequence set forth in SEQ ID NO: 25, and a light chain CDR3 amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the recombinant antibody comprises a heavy chain CDR1 amino acid sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 amino acid sequence set forth in SEQ ID NO: 9, a heavy chain CDR3 amino acid sequence set forth in SEQ ID NO: 15, a light chain CDR1 amino acid sequence set forth in SEQ ID NO: 21, a light chain CDR2 amino acid sequence set forth in SEQ ID NO: 25, and a light chain CDR3 amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the recombinant antibody comprises a heavy chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a heavy chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a heavy chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a heavy chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the recombinant antibody comprises a light chain

FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a light chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a light chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a light chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody comprises a heavy chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a heavy chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a heavy chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a heavy chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a light chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a light chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a light chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a light chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody further comprises a pharmaceutically acceptable carrier. In certain embodiments, the recombinant antibody is formulated for intravenous administration. In certain embodiments, the recombinant antibody is formulated for intracerebral administration. In certain embodiments, the recombinant antibody of is for use in treating cancer. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer.

[0011] In another aspect, described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising an immunoglobulin heavy chain sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 71, 72, or 74; and an immunoglobulin light chain sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 75-78. In certain embodiments, the immunoglobulin heavy chain sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in of SEQ ID NO: 72; and the immunoglobulin light chain sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in of SEQ ID NO: 76.

[0012] In another aspect, described herein, is a method of treating a subject with cancer comprising administering to an individual a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF), wherein the recombinant antibody that specifically binds (LIF) comprises at least one complementarity determining region (CDR) of rat origin and at least one immunoglobulin framework region (FR) of

human origin, wherein the at least one CDR of rat origin specifically binds to LIF. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain embodiments, the recombinant antibody comprises at least one framework region derived from a human antibody framework region. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized. In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody is a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 100 picomolar. In certain embodiments, at least one CDR of rat origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 1-3, 9, 10, 15, 16, 21, 22, 25, 26, or 29. In certain embodiments, the at least one CDR of rat origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 1, 7, 11, 15, 17, and 19. In certain embodiments, the at least one CDR of rat origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29. In certain embodiments, the at least one immunoglobulin framework region of human origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 44-70. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a heavy chain CDR1 amino acid sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 amino acid sequence set forth in SEQ ID NO: 9, and a heavy chain CDR3 amino acid sequence set forth in SEQ ID NO: 15. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a light chain CDR1 amino acid sequence set forth in SEQ ID NO: 21, a light chain CDR2 amino acid sequence set forth in SEQ ID NO: 25, and a light chain CDR3 amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a heavy chain CDR1 amino acid sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 amino acid sequence set forth in SEQ ID NO: 9, a heavy chain CDR3 amino acid sequence set forth in SEQ ID NO: 15, a light chain CDR1 amino acid sequence set forth in SEQ ID NO: 21, a light chain CDR2 amino acid sequence set forth in SEQ ID NO: 25, and a light chain CDR3 amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the recombinant antibody comprises a heavy chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a heavy chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a heavy chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a heavy chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a light chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a light chain FR2 amino acid sequence at least about

80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a light chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a light chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a heavy chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a heavy chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a heavy chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a heavy chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a light chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a light chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a light chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a light chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody is administered intravenously. In certain embodiments, the recombinant antibody is administered intracerebrally. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer.

[0013] In another aspect, described herein, is a method of treating a subject with cancer comprising administering to an individual a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF), wherein the recombinant antibody that specifically binds (LIF) comprises an immunoglobulin heavy chain sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 71, 72, or 74; and an immunoglobulin light chain sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 75-78. In certain embodiments, the immunoglobulin heavy chain sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in of SEQ ID NO: 72; and the immunoglobulin light chain sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in of SEQ ID NO: 76.

[0014] In another aspect, described herein, is a method of preparing a cancer treatment for treating a subject with cancer comprising admixing a pharmaceutically acceptable carrier and a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF), wherein the recombinant antibody that specifically binds (LIF) comprises at least one complementarity determining region (CDR) of rat origin and at least one immunoglobulin framework region (FR) of human origin, wherein the at least one CDR of rat origin specifically binds to LIF. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain

embodiments, the recombinant antibody comprises at least one framework region derived from a human antibody framework region. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized. In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody is a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 100 picomolar. In certain embodiments, the at least one CDR of rat origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 1-3, 9, 10, 15, 16, 21, 22, 25, 26, or 29. In certain embodiments, the at least one CDR of rat origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29. In certain embodiments, the at least one immunoglobulin framework region of human origin comprises an amino acid sequence set forth in any one of SEQ ID NOs: 44-70. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a heavy chain CDR1 amino acid sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 amino acid sequence set forth in SEQ ID NO: 9, and a heavy chain CDR3 amino acid sequence set forth in SEQ ID NO: 15. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a light chain CDR1 amino acid sequence set forth in SEQ ID NO: 21, a light chain CDR2 amino acid sequence set forth in SEQ ID NO: 25, and a light chain CDR3 amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a heavy chain CDR1 amino acid sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 amino acid sequence set forth in SEQ ID NO: 9, a heavy chain CDR3 amino acid sequence set forth in SEQ ID NO: 15, a light chain CDR1 amino acid sequence set forth in SEQ ID NO: 21, a light chain CDR2 amino acid sequence set forth in SEQ ID NO: 25, and a light chain CDR3 amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a heavy chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a heavy chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a heavy chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a heavy chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the recombinant antibody comprises a light chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a light chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a light chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a light chain FR4 amino acid sequence at least about 80%, about

90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the recombinant antibody that specifically binds LIF comprises a heavy chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a heavy chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a heavy chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a heavy chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a light chain FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a light chain FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a light chain FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a light chain FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the pharmaceutically acceptable carrier is suitable for intravenous administration. In certain embodiments, the pharmaceutically acceptable carrier is suitable for intracerebral administration. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer.

[0015] In another aspect, described herein, is a method of preparing a cancer treatment for treating a subject with cancer comprising admixing a pharmaceutically acceptable carrier and a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF), wherein the recombinant antibody that specifically binds (LIF) comprises an immunoglobulin heavy chain sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 71, 72, or 74; and an immunoglobulin light chain sequence with an amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 75-78. In certain embodiments, the immunoglobulin heavy chain sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in of SEQ ID NO: 72; and the immunoglobulin light chain sequence is at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in of SEQ ID NO: 76.

[0016] In another aspect described herein is a recombinant antibody that binds LIF, wherein the antibody comprises: a heavy chain CDR1 amino acid sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 amino acid sequence set forth in SEQ ID NO: 9, a heavy chain CDR3 amino acid sequence set forth in SEQ ID NO: 15, a heavy chain FR1 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 45, a heavy chain FR2 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 49, a heavy chain FR3 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 50,

a heavy chain FR4 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 54, a light chain CDR1 amino acid sequence set forth in SEQ

ID NO: 21, a light chain CDR2 amino acid sequence set forth in SEQ ID NO: 25, a light chain CDR3 amino acid sequence set forth in SEQ ID NO: 29, a light chain FR1 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 57, a light chain FR2 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 61, a light chain FR3 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a light chain FR4 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 68.

[0017] In another aspect described herein is a recombinant antibody that specifically binds LIF, wherein the antibody comprises, a humanized heavy chain variable region at least 90%, 95%, 97%, 98%, or 99% identical to the amino acid set forth in SEQ ID NO: 72, and a humanized light chain variable region at least 90%, 95%, 97%, 98%, or 99% identical to the amino acid set forth in SEQ ID NO: 76. In certain embodiments, the antibody is formulated with a pharmaceutically acceptable diluent, carrier, or excipient to form a pharmaceutical composition.

[0018] In another aspect described herein is a recombinant antibody that specifically binds LIF comprising: a) a heavy chain CDR1 comprising an amino acid sequence set forth in any one of SEQ ID NOs: 1-7 or 33; b) a heavy chain CDR2 comprising an amino acid sequence set forth in any one of SEQ ID NOs: 9-13 or 35; and c) a heavy chain CDR3 comprising an amino acid sequence set forth in any one of SEQ ID NOs: 15-19 or 37, wherein the recombinant antibody specifically binds to LIF. In certain embodiments, the antibody is formulated with a pharmaceutically acceptable diluent, carrier, or excipient to form a pharmaceutical composition.

[0019] In another aspect described herein is a recombinant antibody that specifically binds LIF comprising: a) a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 21-23 or 39; b) a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 25-27 or 41; and c) a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 29, 30, or 43, wherein the recombinant antibody specifically binds to LIF. In certain embodiments, the antibody is formulated with a pharmaceutically acceptable diluent, carrier, or excipient to form a pharmaceutical composition.

[0020] In another aspect described herein is a recombinant antibody that binds LIF, wherein the antibody comprises: a heavy chain variable domain comprising a heavy chain CDR1 amino acid sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 amino acid sequence set forth in SEQ ID NO: 9, and a heavy chain CDR3 amino acid sequence set forth in SEQ ID NO: 15, and a light chain variable domain comprising a light chain CDR1 amino acid sequence set forth in SEQ ID NO: 21, a light chain CDR2 amino acid sequence set forth in SEQ ID NO: 25, and a light chain CDR3 amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the antibody comprises a heavy chain variable region comprising the amino acid sequence set forth in SEQ ID NO: 72. In certain embodiments, the antibody comprises a light chain variable region comprising the amino acid sequence set forth in SEQ ID NO: 76. In certain embodiments, the antibody comprises a heavy chain vari-

able region comprising the amino acid sequence set forth in SEQ ID NO: 72; and a light chain variable region comprising the amino acid sequence set forth in SEQ ID NO: 76. In certain embodiments, the antibody is formulated with a pharmaceutically acceptable diluent, carrier, or excipient to form a pharmaceutical composition.

[0021] In another aspect described herein is a recombinant antibody that specifically binds LIF comprising: a) a light chain comprising an amino acid sequence at least 90%, 95%, 97%, 98%, or 99% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 91-94; and b) a heavy chain comprising an amino acid sequence at least 90%, 95%, 97%, 98%, or 99% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 87-90, wherein the recombinant antibody specifically binds to LIF. In certain embodiments, the light chain has the amino acid sequence set forth in any one of SEQ ID NOs: 91-94; and the heavy chain has the amino acid sequence set forth in any one of SEQ ID NOs: 87-90. In certain embodiments, the light chain has the amino acid sequence set forth in SEQ ID NO: 92; and the heavy chain has the amino acid sequence set forth in SEQ ID NO: 88. In certain embodiments, the antibody is formulated with a pharmaceutically acceptable diluent, carrier, or excipient to form a pharmaceutical composition.

[0022] In another aspect described herein is a recombinant antibody that binds LIF, wherein the antibody comprises: a heavy chain CDR1 having an amino acid sequence at least 90% identical to SEQ ID NO: 1, a heavy chain CDR2 having an amino acid sequence at least 90% identical to SEQ ID NO: 9, a heavy chain CDR3 having an amino acid sequence at least 90% identical to SEQ ID NO: 15, a light chain CDR1 having an amino acid sequence at least 90% identical to SEQ ID NO: 21, a light chain CDR2 having an amino acid sequence at least 90% identical to SEQ ID NO: 25, and a light chain CDR3 having an amino acid sequence at least 90% identical to SEQ ID NO: 29. In certain embodiments, the antibody is formulated with a pharmaceutically acceptable diluent, carrier, or excipient to form a pharmaceutical composition.

[0023] In another aspect herein is a recombinant antibody that binds LIF, wherein the antibody comprises: a heavy chain CDR1 having an amino acid sequence that contains no more than 3, 2 or 1 amino acid substitutions, deletions or insertions as compared to SEQ ID NO: 1 with, a heavy chain CDR2 having an amino acid sequence that contains no more than 3, 2 or 1 amino acid substitutions, deletions or insertions as compared to SEQ ID NO: 9, a heavy chain CDR3 having an amino acid sequence that contains no more than 3, 2, or 1 amino acid substitutions, deletions or insertions as compared to SEQ ID NO: 15, a light chain CDR1 having an amino acid sequence that contains no more than 3, 2 or 1 amino acid substitutions, deletions or insertions as compared to SEQ ID NO: 21, a light chain CDR2 having an amino acid sequence that contains no more than 3, 2 or 1 amino acid substitutions, deletions or insertions as compared to SEQ ID NO: 25, and a light chain CDR3 having an amino acid sequence that contains no more than 3, 2 or 1 amino acid substitutions, deletions or insertions as compared to SEQ ID NO: 29. In certain embodiments, the antibody is formulated with a pharmaceutically acceptable diluent, carrier, or excipient to form a pharmaceutical composition.

[0024] In another aspect described herein is a recombinant antibody that binds LIF and competes with an antibody defined by: a heavy chain CDR1 having an amino acid

sequence set forth in SEQ ID NO: 1, a heavy chain CDR2 having an amino acid sequence set forth in SEQ ID NO: 9, a heavy chain CDR3 having an amino acid sequence set forth in SEQ ID NO: 15, a light chain CDR1 having an amino acid sequence set forth in SEQ ID NO: 21, a light chain CDR2 having an amino acid sequence set forth in SEQ ID NO: 25, and a light chain CDR3 having an amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the antibody is humanized. In certain embodiments, the antibody is formulated with a pharmaceutically acceptable diluent, carrier, or excipient to form a pharmaceutical composition.

[0025] In another aspect described herein is an isolated monoclonal antibody, wherein, when bound to human LIF, the monoclonal antibody binds to at least one of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO:98. In certain embodiments, the monoclonal antibody binds to at least A13. In certain embodiments, the monoclonal antibody binds to at least I14. In certain embodiments, the monoclonal antibody binds to at least R15. In certain embodiments, the monoclonal antibody binds to at least H16. In certain embodiments, the monoclonal antibody binds to at least P17. In certain embodiments, the monoclonal antibody binds to at least C18. In certain embodiments, the monoclonal antibody binds to at least H19. In certain embodiments, the monoclonal antibody binds to at least N20. In certain embodiments, the monoclonal antibody binds to at least Q25. In certain embodiments, the monoclonal antibody binds to at least Q32. In certain embodiments, the monoclonal antibody binds to at least D120. In certain embodiments, the monoclonal antibody binds to at least R123. In certain embodiments, the monoclonal antibody binds to at least S127. In certain embodiments, the monoclonal antibody binds to at least N128. In certain embodiments, the monoclonal antibody binds to at least L130. In certain embodiments, the monoclonal antibody binds to at least C131. In certain embodiments, the monoclonal antibody binds to at least C134. In certain embodiments, the monoclonal antibody binds to at least S135. In certain embodiments, the monoclonal antibody binds to at least H138. In certain embodiments, the monoclonal antibody binds to two distinct alpha helices of human LIF, wherein the two distinct alpha helices are separated by a plurality of amino acids. In certain embodiments, the monoclonal antibody blocks binding of human LIF to human gp130. In certain embodiments, the antibody blocks the biological activity of human LIF in cell culture model. In certain embodiments, the biological activity is LIF-induced STAT3 phosphorylation. In certain embodiments, the antibody is chimeric, humanized, or human. In certain embodiments, a pharmaceutical composition comprises the isolated monoclonal antibody and a pharmaceutically acceptable diluent, carrier, or excipient. In certain embodiments, the pharmaceutical composition is formulated for intravenous injection. In certain embodiments, the isolated monoclonal antibody or the pharmaceutical composition is for use in a method of treating cancer. In certain embodiments, described herein is a method of treating an individual diagnosed with or suspected of having cancer comprising administering to the individual the monoclonal antibody or the pharmaceutical composition.

[0026] In another aspect described herein is an isolated monoclonal antibody, wherein, when bound to human LIF, the monoclonal antibody binds to at least one of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to at least two of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to at least five of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to at least ten of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to two distinct alpha helices of human LIF, wherein the two distinct alpha helices are separated by a plurality of amino acids. In certain embodiments, the monoclonal antibody blocks binding of human LIF to human gp130. In certain embodiments, the antibody blocks the biological activity of human LIF in cell culture model. In certain embodiments, the biological activity is LIF-induced STAT3 phosphorylation. In certain embodiments, the antibody is chimeric, humanized, or human. In certain embodiments, a pharmaceutical composition comprises the isolated monoclonal antibody and a pharmaceutically acceptable diluent, carrier, or excipient. In certain embodiments, the pharmaceutical composition is formulated for intravenous injection. In certain embodiments, the isolated monoclonal antibody or the pharmaceutical composition is for use in a method of treating cancer. In certain embodiments, described herein is a method of treating an individual diagnosed with or suspected of having cancer comprising administering to the individual the monoclonal antibody or the pharmaceutical composition.

[0027] In another aspect described herein is an isolated monoclonal antibody wherein the VH-CDR1 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 1 (GFTFSHAWMH) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VH-CDR2 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VH-CDR3 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 15 (TCWEWDLDF) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VL-CDR1 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 21 (RSSQSLLDSGDGHTYLN) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VL-CDR2 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 25 (SVSNLES) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VL-CDR3 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 29 (MQATHAPPYT) by 0, 1, 2, 3, or 4 amino acid residues, and wherein the monoclonal antibody binds to at least one of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134,

S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to at least two of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to at least five of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to at least ten of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to two distinct alpha helices of human LIF, wherein the two distinct alpha helices are separated by a plurality of amino acids. In certain embodiments, the monoclonal antibody blocks binding of human LIF to human gp130. In certain embodiments, the antibody blocks the biological activity of human LIF in cell culture model. In certain embodiments, the biological activity is LIF-induced STAT3 phosphorylation. In certain embodiments, the antibody is chimeric, humanized, or human. In certain embodiments, a pharmaceutical composition comprises the isolated monoclonal antibody and a pharmaceutically acceptable diluent, carrier, or excipient. In certain embodiments, the pharmaceutical composition is formulated for intravenous injection. In certain embodiments, the isolated monoclonal antibody or the pharmaceutical composition is for use in a method of treating cancer. In certain embodiments, described herein is a method of treating an individual diagnosed with or suspected of having cancer comprising administering to the individual the monoclonal antibody or the pharmaceutical composition.

[0028] In another aspect described herein is an isolated monoclonal antibody wherein the VH-CDR1 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 1 (GFTFSHAWMH) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VH-CDR2 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VH-CDR3 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 95 (TSWEWDLDF) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VL-CDR1 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 21 (RSSQSLLDSGDGHTYLN) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VL-CDR2 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 25 (SVSNLES) by 0, 1, 2, 3, or 4 amino acid residues, wherein the VL-CDR3 comprises an amino acid sequence that differs from that set forth in SEQ ID NO: 29 (MQATHAPPYT) by 0, 1, 2, 3, or 4 amino acid residues, and wherein the monoclonal antibody binds to at least one of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to at least two of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the

monoclonal antibody binds to at least five of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to at least 10 of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO: 98. In certain embodiments, the monoclonal antibody binds to two distinct alpha helices of human LIF, wherein the two distinct alpha helices are separated by a plurality of amino acids. In certain embodiments, the monoclonal antibody blocks binding of human LIF to human gp130. In certain embodiments, the antibody blocks the biological activity of human LIF in cell culture model. In certain embodiments, the biological activity is LIF-induced STAT3 phosphorylation. In certain embodiments, the antibody is chimeric, humanized, or human. In certain embodiments, a pharmaceutical composition comprises the isolated monoclonal antibody and a pharmaceutically acceptable diluent, carrier, or excipient. In certain embodiments, the pharmaceutical composition is formulated for intravenous injection. In certain embodiments, the pharmaceutical composition is formulated for intracerebral injection. In certain embodiments, the isolated monoclonal antibody or the pharmaceutical composition is for use in a method of treating cancer. In certain embodiments, described herein is a method of treating an individual diagnosed with or suspected of having cancer comprising administering to the individual the monoclonal antibody or the pharmaceutical composition.

[0029] In a certain aspect, described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 2; a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 10; a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 15; a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 22; and a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 26; and a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 29.

[0030] In a certain aspect, described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 3; a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 9; a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 16; a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 21; and a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 25; and a light chain

complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 29.

[0031] In a certain aspect, described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 3; a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 10; a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 16; a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 22; and a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 26; and a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 29.

[0032] In a certain aspect described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a) a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 3; b) a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 10; c) a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 16; d) a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 22; e) a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 26; and f) a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 29, wherein the recombinant antibody specifically binds to LIF. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized. In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody comprises a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 100 picomolar. In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 1 (GFTFSHAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 15 (TCWEWDLDF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLLSDGHTYLN), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 1 (GFTFSHAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 9

(QIKAKSDDYATYYAESVKG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 95 (TSWEWDLDF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the recombinant antibody comprises a VH sequence at least about 80% identical to the amino acid sequence set forth in SEQ ID NO: 72; and a VL sequence at least about 80% identical to the amino acid sequence set forth in SEQ ID NO: 76. In certain embodiments, the recombinant antibody comprises VH sequence at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 72; and a VL sequence at least about 90% identical to the amino acid sequence set forth in SEQ ID NO: 76. In certain embodiments, the recombinant antibody blocks binding of human LIF to human gp130. In certain embodiments, the recombinant antibody when bound to LIF, binds to at least one of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO:98. In certain embodiments, the recombinant antibody when bound to LIF, binds all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, H138 of SEQ ID NO:98. In certain embodiments, the recombinant antibody is included in a pharmaceutical composition comprising the recombinant antibody and a pharmaceutically acceptable carrier. In certain embodiments, the recombinant antibody or the pharmaceutical composition is for use in a method of treating cancer. In certain embodiments, a method of treating cancer in an individual comprises administering the recombinant antibody or the pharmaceutical composition to the individual. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer. In certain embodiments, a method of preparing a cancer treatment for treating a subject with cancer comprises admixing a pharmaceutically acceptable carrier and the recombinant antibody.

[0033] In a certain aspect described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a) a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 4-7 or 33; b) a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 11-13 or 35; c) a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 17-19 or 37; d) a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 21-23 or 39; e) a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 25-27 or 41; and f) a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in any one of SEQ ID NOs: 29, 30, or 43; wherein the recombinant antibody

specifically binds to LIF. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized. In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody is a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the -CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 6 (NAWMH), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 12 (IKDKSDNYAT), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 18 (WEWYLDLF), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 22 (QSLLDSDGHTY), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 26 (SVS), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 7 (SKFMY), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 13 (WIYPGDGDTEYNQKFSE), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 19 (RDYHSSHFAY), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 23 (RSSQSLHNNNGNTYLS), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 27 (QVSNRFS), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 30 (GQGTQYPYT). In certain embodiments, the VH-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 33 (TAGMQ), wherein the VH-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 35 (WINTQSGEPQYVDDFRG), wherein the VH-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 37 (WALYSEYDVMDY), wherein the VL-CDR1 comprises an amino acid sequence set forth in SEQ ID NO: 39 (KASENVDSYVS), wherein the VL-CDR2 comprises an amino acid sequence set forth in SEQ ID NO: 41 (GASNRYT), and wherein the VL-CDR3 comprises an amino acid sequence set forth in SEQ ID NO: 43 (GQSYRYPPT). In certain embodiments, the monoclonal antibody blocks binding of human LIF to human gp130. In certain embodiments, the recombinant antibody is included in a pharmaceutical composition comprising the recombinant antibody and a pharmaceutically acceptable carrier. In certain embodiments, the recombinant antibody or the pharmaceutical composition is for use in a method of treating cancer. In certain embodiments, a method of treating cancer in an individual comprises administering the recombinant antibody or the pharmaceutical composition to the individual. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer. In certain embodiments, a method of preparing a cancer treatment for

treating a subject with cancer comprises admixing a pharmaceutically acceptable carrier and the recombinant antibody.

[0034] In a certain aspect described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a) a VH-CDR1 comprising an amino acid sequence set forth in SEQ ID NO: 1 (GFTFSHAWMH); b) a the VH-CDR2 comprising an amino acid sequence set forth in SEQ ID NO: 9 (QIKAKSD-DYATYYAESVKG); c) a VH-CDR3 comprising an amino acid sequence set forth in SEQ ID NO: 15 (TCWEWDLDF), d) a VL-CDR1 comprising an amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLLSDSGHTYLN), e) a VL-CDR2 comprising an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES); and f) a VL-CDR3 comprising an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT); wherein the cysteine residue of SEQ ID NO: 15 is any amino acid except for tyrosine, tryptophan, histidine, lysine or arginine. In certain embodiments, the recombinant antibody binds to glycosylated LIF. In certain embodiments, the recombinant antibody is humanized. In certain embodiments, the recombinant antibody is deimmunized. In certain embodiments, the recombinant antibody comprises two immunoglobulin heavy chains and two immunoglobulin light chains. In certain embodiments, the recombinant antibody is a Fab, F(ab)₂, single-domain antibody, a single chain variable fragment (scFv), or a nanobody. In certain embodiments, the recombinant antibody specifically binds LIF with a dissociation constant (K_D) of less than about 200 picomolar. In certain embodiments, the recombinant antibody blocks binding of human LIF to human gp130. In certain embodiments, the recombinant antibody is included in a pharmaceutical composition comprising the recombinant antibody and a pharmaceutically acceptable carrier. In certain embodiments, the recombinant antibody or the pharmaceutical composition is for use in a method of treating cancer. In certain embodiments, a method of treating cancer in an individual comprises administering the recombinant antibody or the pharmaceutical composition to the individual. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer. In certain embodiments, the cancer comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer. In certain embodiments, a method of preparing a cancer treatment for treating a subject with cancer comprises admixing a pharmaceutically acceptable carrier and the recombinant antibody.

BRIEF DESCRIPTION OF THE DRAWINGS

[0035] FIG. 1 depicts a western blot showing inhibition of LIF-induced STAT3 phosphorylation of different anti-LIF humanized antibodies.

[0036] FIGS. 2A and 2B depicts a western blot showing inhibition of LIF-induced STAT3 phosphorylation humanized and parental 5D8 antibody.

[0037] FIG. 3A shows an IC₅₀ for LIF inhibition in U-251 cells using the h5D8 antibody.

[0038] FIG. 3B shows representative IC₅₀ dose response curves of r5D8 and h5D8-1 inhibition of pSTAT3 under endogenous LIF stimulation conditions. Shown are the representative curves (n=1 h5D8, n=2 r5D8). Refer to Appendix FIG. 2, 3, 4 for all IC₅₀ dose-curves and controls.

[0039] FIG. 4 depicts a western blot showing inhibition of LIF-induced STAT3 phosphorylation of different monoclonal antibodies described in this disclosure.

[0040] FIG. 5 depicts immunohistochemistry staining and quantitation of LIF expression in glioblastoma multiforme (GBM), NSCLC (non-small cell lung carcinoma), ovarian cancer, and colorectal cancer tumors from human patients. Bars represent mean±SEM.

[0041] FIG. 6 is a graph showing an experiment conducted in a mouse model of non-small cell lung cancer using the humanized 5D8 antibody.

[0042] FIG. 7A shows the effect of r5D8 on inhibition of U251 cells in an orthotopic mouse model of GBM quantitation shown at day 26.

[0043] FIG. 7B shows data from mice inoculated with luciferase expressing human U251 GBM cells and then treated with 100, 200 or 300 µg of h5D8 or vehicle twice a week. Tumor size was determined by bioluminescence (Xenogen IVIS Spectrum) on day 7. The graph shows individual tumor measurements with horizontal bars indicating mean±SEM. Statistical significance was calculated using the unpaired non-parametric Mann-Whitney U-test.

[0044] FIG. 8A shows the effect of r5D8 on inhibition of growth of ovarian cancer cells in a syngeneic mouse model.

[0045] FIG. 8B shows the individual measurements of tumors at day 25.

[0046] FIG. 8C illustrates that h5D8 shows a significant reduction in tumor growth when administered at 200 µg/mouse twice weekly (p<0.05). Symbols are mean±SEM, statistical significance compared with vehicle (with unpaired non-parametric Mann-Whitney U-test).

[0047] FIG. 9A shows the effect of r5D8 on inhibition of growth of colorectal cancer cells in a syngeneic mouse model.

[0048] FIG. 9B shows the individual measurements of tumors at day 17.

[0049] FIG. 10A shows reduction of macrophage infiltration to tumor sites in an orthotopic mouse model of GBM with a representative image and quantitation of CCL22+ cells.

[0050] FIG. 10B shows reduction of macrophage infiltration in a human organotypic tissue slice culture model.

[0051] FIG. 10C shows reduction of macrophage infiltration to tumor sites in a syngeneic mouse model of ovarian cancer with a representative image and quantitation of CCL22+ cells.

[0052] FIG. 10D shows reduction of macrophage infiltration to tumor sites in a syngeneic mouse model of colorectal cancer with a representative image and quantitation of CCL22+ cells.

[0053] FIG. 11A shows increases in non-myeloid effector cells in a syngeneic mouse model of ovarian cancer after treatment with r5D8.

[0054] FIG. 11B shows increases in non-myeloid effector cells in a syngeneic mouse model of colorectal cancer after treatment with r5D8.

[0055] FIG. 11C shows decreases in percentage of CD4+ T_{REG} cells in a mouse model of NSCLC cancer after treatment with r5D8.

[0056] FIG. 12 shows data from mice bearing CT26 tumors treated twice weekly with PBS (control) or r5D8 administered intraperitoneally in the presence or absence of anti-CD4 and anti-CD8 depleting antibodies. The graph shows individual tumor measurements at d13 expressed as

mean tumor volume+SEM. Statistical differences between groups was determined by unpaired non-parametric Mann-Whitney U-test. R5D8 inhibited the growth of CT26 tumors (* $p<0.05$). The tumor growth inhibition by r5D8 was significantly reduced in the presence of anti-CD4 and anti-CD8 depleting antibodies (**** $p<0.0001$).

[0057] FIG. 13A illustrates Overview of the co-crystal structure of h5D8 Fab in complex with LIF. The gp130 interacting site is mapped on the surface of LIF (dark shaded)

[0058] FIG. 13B illustrates detailed interactions between LIF and h5D8, showing residues forming salt bridges and h5D8 residues with buried surface areas greater than 100 Å².

[0059] FIG. 14A illustrates superposition of the five h5D8 Fab crystal structures and indicates a high degree of similarity despite being crystallized in different chemical conditions.

[0060] FIG. 14B illustrates an extensive network of van der Waals interactions mediated by unpaired Cys100. This residue is well-ordered, partakes in shaping the conformations of HCDR1 and HCDR3 and is not involved in undesired disulfide scrambling. Distances between residues are shown as dashed lines and labeled.

[0061] FIG. 15A illustrates binding of h5D8 C100 mutants to human LIF by ELISA.

[0062] FIG. 15B illustrates binding of h5D8 C100 mutants to mouse LIF by ELISA.

[0063] FIG. 16A illustrates that h5D8 does not block binding between LIF and LIFR by Octet. Sequential binding of h5D8 to LIF followed by LIFR.

[0064] FIGS. 16B and 16C illustrate ELISA analysis of LIF/mAb complexes binding to immobilized LIFR or gp130. Signals of species-specific peroxidase conjugated anti-IgG antibodies (anti-human for (-) and h5D8, anti-rat for r5d8 and B09) detecting the antibody portion of mAb/LIF complexes binding immobilized LIFR (FIG. 16B) or gp130 (FIG. 16C) coated plates.

[0065] FIGS. 17A and 17B illustrate mRNA expression of LIF (FIG. 16A) or LIFR (FIG. 16B) in 72 different human tissues.

DETAILED DESCRIPTION

Certain Definitions

[0066] Unless otherwise defined, all technical terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. As used in this specification and the appended claims, the singular forms “a,” “an,” and “the” include plural references unless the context clearly dictates otherwise. Any reference to “or” herein is intended to encompass “and/or” unless otherwise stated.

[0067] As used herein, unless otherwise indicated, the term “about” refers to an amount that is near the stated amount, for example by 10%, 5%, or 1%.

[0068] As used herein the terms “individual,” “subject,” and “patient” are used interchangeably and include humans diagnosed with or suspected of being afflicted with a tumor, a cancer or other neoplasm.

[0069] As used herein, unless otherwise indicated, the term “antibody” includes antigen binding fragments of antibodies, i.e. antibody fragments that retain the ability to bind specifically to the antigen bound by the full-length antibody, e.g. fragments that retain one or more CDR regions.

Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies; heavy chain antibodies, single-chain antibody molecules, e.g. single-chain variable region fragments (scFv), nanobodies and multispecific antibodies formed from antibody fragments with separate specificities, such as a bispecific antibody. In certain embodiments, the antibodies are humanized in such a way as to reduce an individual's immune response to the antibody. For example the antibodies may be chimeric, e.g. non-human variable region with human constant region, or CDR grafted, e.g. non-human CDR regions with human constant region and variable region framework sequences. In certain embodiments, antibodies are deimmunized after humanization. Deimmunization involves removing or mutating one or more T-cell epitopes in the constant region of the antibody. In certain embodiments, the antibodies described herein are monoclonal. As used herein a “recombinant antibody” is an antibody that comprises an amino acid sequence derived from two different species or, or two different sources, and includes synthetic molecules, for example, an antibody that comprises a non-human CDR and a human framework or constant region. In certain embodiments, recombinant antibodies of the present invention are produced from a recombinant DNA molecule or synthesized.

[0070] The terms “cancer” and “tumor” relate to the physiological condition in mammals characterized by deregulated cell growth. Cancer is a class of diseases in which a group of cells display uncontrolled growth or unwanted growth. Cancer cells can also spread to other locations, which can lead to the formation of metastases. Spreading of cancer cells in the body can, for example, occur via lymph or blood. Uncontrolled growth, intrusion, and metastasis formation are also termed malignant properties of cancers. These malignant properties differentiate cancers from benign tumors, which typically do not invade or metastasize.

[0071] Percent (%) sequence identity with respect to a reference polypeptide or antibody sequence is the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide or antibody sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are known for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, or Megalign (DNASTAR) software. Appropriate parameters for aligning sequences are able to be determined, including algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc., and the source code has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available from Genentech, Inc., South San Francisco, Calif., or may be compiled from the source code. The ALIGN-2 program should be compiled for use on a UNIX operating system, including digital UNIX

V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0072] In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows: 100 times the fraction X/Y , where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

[0073] The term "epitope" includes any determinant capable of being bound by an antigen binding protein, such as an antibody. An epitope is a region of an antigen that is bound by an antigen binding protein that targets that antigen, and when the antigen is a protein, includes specific amino acids that directly contact the antigen binding protein. Most often, epitopes reside on proteins, but in some instances can reside on other kinds of molecules, such as saccharides or lipids. Epitope determinants can include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl or sulfonyl groups, and can have specific three dimensional structural characteristics, and/or specific charge characteristics. Generally, antibodies specific for a particular target antigen will preferentially recognize an epitope on the target antigen in a complex mixture of proteins and/or macromolecules.

Structural Attributes of the Antibodies Described Herein

[0074] A complementarity determining region ("CDR") is a part of an immunoglobulin (antibody) variable region that is primarily responsible for the antigen binding specificity of the antibody. CDR regions are highly variable from one antibody to the next even when the antibody specifically binds the same target or epitope. A heavy chain variable region comprises three CDR regions, abbreviated VH-CDR1, VH-CDR2, and VH-CDR3; and a light chain variable region comprises three CDR regions, abbreviated VL-CDR1, VL-CDR2, and VL-CDR3. These CDR regions are ordered consecutively in the variable region with the CDR1 being the most N-terminal and the CDR3 being the most C-terminal. Interspersed between the CDRs are framework regions which contribute to the structure and display much less variability than the CDR regions. A heavy chain variable region comprises four framework regions, abbreviated VH-FR1, VH-FR2, VH-FR3, and VH-FR4; and a light chain variable region comprises four framework regions, abbreviated VL-FR1, VL-FR2, VL-FR3, and VL-FR4. Complete full-sized bivalent antibodies comprising two heavy and light chains will comprise: 12 CDRs, with three unique heavy chain CDRs and three unique light chain CDRs; 16 FR regions, with four unique heavy chain FR regions and four unique light chain FR regions. In certain embodiments, the antibodies described herein minimally

comprise three heavy chain CDRs. In certain embodiments, the antibodies described herein minimally comprise three light chain CDRs. In certain embodiments, the antibodies described herein minimally comprise three heavy chain CDRs and three light chain CDRs. The precise amino acid sequence boundaries of a given CDR or FR can be readily determined using any of a number of well-known schemes, including those described by Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. ("Kabat" numbering scheme); Al-Lazikani et al., (1997) *JMB* 273, 927-948 ("Chothia" numbering scheme); MacCallum et al., *J. Mol. Biol.* 262:732-745 (1996), "Antibody-antigen interactions: Contact analysis and binding site topography," ("Contact" numbering scheme); Lefranc M P et al., "IMGT unique numbering for immunoglobulin and T cell receptor variable domains and Ig superfamily V-like domains," *Dev Comp Immunol*, 2003 January; 27(1):55-77 ("IMGT" numbering scheme); and Honegger A and Plückthun A, "Yet another numbering scheme for immunoglobulin variable domains: an automatic modeling and analysis tool," *J Mol Biol*, 2001 Jun. 8; 309(3):657-70, ("Aho" numbering scheme). CDRs are identified herein from variable sequences provided using different numbering systems, herein with the Kabat, the IMGT, the Chothia numbering system, or any combination of the three. The boundaries of a given CDR or FR may vary depending on the scheme used for identification. For example, the Kabat scheme is based on structural alignments, while the Chothia scheme is based on structural information. Numbering for both the Kabat and Chothia schemes is based upon the most common antibody region sequence lengths, with insertions accommodated by insertion letters, for example, "30a," and deletions appearing in some antibodies. The two schemes place certain insertions and deletions ("indels") at different positions, resulting in differential numbering. The Contact scheme is based on analysis of complex crystal structures and is similar in many respects to the Chothia numbering scheme.

[0075] The term "variable region" or "variable domain" refers to the domain of an antibody heavy or light chain that is involved in binding the antibody to antigen. The variable domains of the heavy chain and light chain (VH and VL, respectively) of a native antibody generally have similar structures, with each domain comprising four conserved framework regions (FRs) and three CDRs (See e.g., Kindt et al. *Kuby Immunology*, 6th ed., W.H. Freeman and Co., page 91(2007)). A single VH or VL domain may be sufficient to confer antigen-binding specificity. Furthermore, antibodies that bind a particular antigen may be isolated using a VH or VL domain from an antibody that binds the antigen to screen a library of complementary VL or VH domains, respectively (See e.g., Portolano et al., *J. Immunol.* 150:880-887 (1993); Clarkson et al., *Nature* 352:624-628 (1991)). In certain embodiments, the antibodies described herein comprise variable regions of rat origin. In certain embodiments, the antibodies described herein comprise CDRs of rat origin. In certain embodiments, the antibodies described herein comprise variable regions of mouse origin. In certain embodiments, the antibodies described herein comprise CDRs of mouse origin.

[0076] Alterations (e.g., substitutions) may be made in CDRs, e.g., to improve antibody affinity. Such alterations may be made in CDR encoding codons with a high mutation rate during somatic maturation (See e.g., Chowdhury, *Meth-*

ods *Mol. Biol.* 207:179-196 (2008)), and the resulting variant can be tested for binding affinity. Affinity maturation (e.g., using error-prone PCR, chain shuffling, randomization of CDRs, or oligonucleotide-directed mutagenesis) can be used to improve antibody affinity (See e.g., Hoogenboom et al. in *Methods in Molecular Biology* 178:1-37 (2001)). CDR residues involved in antigen binding may be specifically identified, e.g., using alanine scanning mutagenesis or modeling (See e.g., Cunningham and Wells *Science*, 244:1081-1085 (1989)). CDR-H3 and CDR-L3 in particular are often targeted. Alternatively, or additionally, a crystal structure of an antigen-antibody complex is analyzed to identify contact points between the antibody and antigen. Such contact residues and neighboring residues may be targeted or eliminated as candidates for substitution. Variants may be screened to determine whether they contain the desired properties.

[0077] In certain embodiments, the antibodies described herein comprise a constant region in addition to a variable region. The heavy chain constant region (C_H) comprises four domains abbreviated C_{H1} , C_{H2} , C_{H3} , and C_{H4} , located at the C-terminal end of the full heavy chain polypeptide, C-terminal to the variable region. The light chain constant region (C_L) is much smaller than the C_H and is located at the C-terminal end of the full light chain polypeptide, C-terminal to the variable region. The constant region is highly conserved and comprises different isotypes that are associated with slightly different functions and properties. In certain embodiments, the constant region is dispensable for antibody binding to a target antigen. In certain embodiments, the constant regions of the antibody, both heavy and light chains are dispensable for antibody binding. In certain embodiments, the antibodies described herein lack one or more of a light chain constant region, heavy chain constant region, or both. Most monoclonal antibodies are of an IgG isotype; which is further divided into four subclasses IgG₁, IgG₂, IgG₃, and IgG₄. In certain embodiments, the antibodies described herein comprise any IgG subclass. In certain embodiments, the IgG subclass comprises IgG₁. In certain embodiments, the IgG subclass comprises IgG₂. In certain embodiments, the IgG subclass comprises IgG₃. In certain embodiments, the IgG subclass comprises IgG₄.

[0078] Antibodies comprise a fragment crystallizable region (Fc region) that is responsible for binding to complement and Fc receptors. The Fc region comprises the C_{H2} , C_{H3} , and C_{H4} regions of the antibody molecule. The Fc region of an antibody is responsible for activating complement and antibody dependent cell cytotoxicity (ADCC). The Fc region also contributes to an antibody's serum half-life. In certain embodiments, the Fc region of the antibodies described herein comprise one or more amino acid substitutions that promote complement mediated cell lysis. In certain embodiments, the Fc region of antibodies described herein comprises one or more amino acid substitutions that promote ADCC. In certain embodiments, the Fc region of antibodies described herein comprises one or more amino acid substitutions that reduce complement mediated cell lysis. In certain embodiments, the Fc region of antibodies described herein comprises one or more amino acid substitutions that increase binding of the antibody to an Fc receptor. In certain embodiments, the Fc receptor comprises FcγRI (CD64), FcγRIIA (CD32), FcγRIIIA (CD16a), FcγRIIIB (CD16b), or any combination thereof. In certain embodiments, the Fc region of the antibodies described

herein comprise one or more amino acid substitutions that increase the serum half-life of the antibody. In certain embodiments, the one or more amino acid substitutions that increase the serum half-life of the antibody increase affinity of the antibody to the neonatal Fc receptor (FcRn).

[0079] In some embodiments, the antibodies of this disclosure are variants that possess some but not all effector functions, which make it a desirable candidate for applications in which the half-life of the antibody in vivo is important yet certain effector functions (such as complement and ADCC) are unnecessary or deleterious. In vitro and/or in vivo cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the antibody lacks FcγR binding (hence likely lacking ADCC activity), but retains FcRn binding ability. Non-limiting examples of in vitro assays to assess ADCC activity of a molecule of interest are described in U.S. Pat. Nos. 5,500,362 and 5,821,337. Alternatively, non-radioactive assays methods may be employed (e.g., ACT™ and CytoTox 96® non-radioactive cytotoxicity assays). Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC), monocytes, macrophages, and Natural Killer (NK) cells.

[0080] Antibodies can have increased half-lives and improved binding to the neonatal Fc receptor (FcRn) (See e.g., US 2005/0014934). Such antibodies can comprise an Fc region with one or more substitutions therein which improve binding of the Fc region to FcRn, and include those with substitutions at one or more of Fc region residues: 238, 256, 265, 272, 286, 303, 305, 307, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424 or 434 according to the EU numbering system (See e.g., U.S. Pat. No. 7,371, 826). Other examples of Fc region variants are also contemplated (See e.g., Duncan & Winter, *Nature* 322:738-40 (1988); U.S. Pat. Nos. 5,648,260 and 5,624,821; and WO94/29351).

[0081] Antibodies useful in the clinic are often "humanized" to reduce immunogenicity in human individuals. Humanized antibodies improve safety and efficacy of monoclonal antibody therapy. One common method of humanization is to produce a monoclonal antibody in any suitable animal (e.g., mouse, rat, hamster) and replace the constant region with a human constant region, antibodies engineered in this way are termed "chimeric". Another common method is "CDR grafting" which replaces the non-human V-FRs with human V-FRs. In the CDR grafting method all residues except for the CDR region are of human origin. In certain embodiments, the antibodies described herein are humanized. In certain embodiments, the antibodies described herein are chimeric. In certain embodiments, the antibodies described herein are CDR grafted.

[0082] Humanization generally reduces or has little effect on the overall affinity of the antibody. Described herein are antibodies that unexpectedly possess greater affinity for their target after humanization. In certain embodiments, humanization increases the affinity for the antibody by 10%. In certain embodiments, humanization increases the affinity for the antibody by 25%. In certain embodiments, humanization increases the affinity for the antibody by 35%. In certain embodiments, humanization increases the affinity for the antibody by 50%. In certain embodiments, humanization increases the affinity for the antibody by 60%. In certain embodiments, humanization increases the affinity for the

antibody by 75%. In certain embodiments, humanization increases the affinity for the antibody by 100%. Affinity is suitably measured using surface plasmon resonance (SPR). In certain embodiments, affinity is measured using glycosylated human LIF. In certain embodiments, the glycosylated human LIF is immobilized to the surface of the SPR chip. In certain embodiments, the antibody binds with a K_D of less than about 300 nanomolar, 200 nanomolar, 150 nanomolar, 125 nanomolar, 100 nanomolar, 90 nanomolar, 80 nanomolar, 70 nanomolar, 60 nanomolar, 50 nanomolar, 40 nanomolar, or less.

Novel Antibodies of the Current Disclosure

[0083] The antibodies described herein were generated from rats and mice immunized with DNA encoding human LIF.

[0084] In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 set forth in any one of SEQ ID NOs: 1-7 or 33, a VH-CDR2 set forth in any one of SEQ ID NOs: 9-13 or 35, and a VH-CDR3 set forth in any one of SEQ ID NOs: 15-19 or 37. In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VL-CDR1 set forth in any one of SEQ ID NOs: 21-23 or 39, a VL-CDR2 set forth in SEQ ID NOs: 25-27 or 41, and a VL-CDR3 set forth in any one of SEQ ID NOs: 29, 30, 43. In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 set forth in any one of SEQ ID NOs: 1-7 or 33, a VH-CDR2 set forth in any one of SEQ ID NOs: 9-13 or 35, and a VH-CDR3 set forth in any one of SEQ ID NOs: 15-19 or 37, a VL-CDR1 set forth in any one of SEQ ID NOs: 21-23 or 39, a VL-CDR2 set forth in SEQ ID NOs: 25-27 or 41, and a VL-CDR3 set forth in any one of SEQ ID NOs: 29, 30, 43. In certain embodiments, the antibody specifically binds to human LIF.

[0085] In certain embodiments, the antibody that specifically binds LIF comprises one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprise a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the antibody that specifically binds LIF comprises one or more human light chain framework regions comprising: a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the

amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, or a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the one or more human light chain framework regions comprise a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the one or more human heavy chain framework regions and the one or more human light chain regions comprise a VH-FR1 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence at least about 80%, 90%, or 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least 80%, 90%, or 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least 80%, 90%, or 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the antibody that specifically binds LIF comprises one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprise a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the antibody that specifically binds LIF comprises one or more human light chain framework regions comprising: a VL-FR1 amino acid sequence identical to the amino acid sequence set forth

in any one of SEQ ID NOs: 56-59, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, or a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the one or more human light chain framework regions comprise a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the one or more human heavy chain framework regions and the one or more human light chain regions comprise a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the antibody specifically binds human LIF.

5D8

[0086] The antibodies described herein were generated from rats and mice immunized with DNA encoding human LIF. One such antibody (5D8) was cloned and sequenced and comprises CDRs (using the combination of the Kabat and IMGT CDR numbering methods) with the following amino acid sequences: a VH-CDR1 corresponding to SEQ ID NO: 1 (GFTFSHAWMH), a VH-CDR2 corresponding to SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), a VH-CDR3 corresponding to SEQ ID NO: 15 (TCWEWDLDF), a VL-CDR1 corresponding to SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), a VL-CDR2 corresponding to SEQ ID NO: 25 (SVSNLES), and a VL-CDR3 corresponding to SEQ ID NO: 29 (MQATHAPPYT).

[0087] In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 at least 80% or 90% identical to that set forth in SEQ ID NO: 1 (GFTFSHAWMH), a VH-CDR2 at least 80%, 90%, or 95% identical to that set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), and a VH-CDR3 at least 80% or 90% identical to that set forth in SEQ ID NO: 15 (TCWEWDLDF). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VL-CDR1 at least 80% or 90% identical to that set forth in SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), a VL-CDR2 at least 80% identical to that set forth in SEQ ID NO: 25 (SVSNLES), and a VL-CDR3 at least 80% or 90% identical to that set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 set forth in SEQ ID NO: 1 (GFTFSHAWMH), a VH-CDR2 set forth in

SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), a VH-CDR3 set forth in SEQ ID NO: 15 (TCWEWDLDF), a VL-CDR1 set forth in SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), a VL-CDR2 set forth in SEQ ID NO: 25 (SVSNLES), and a VL-CDR3 set forth in SEQ ID NO: 29 (MQATHAPPYT). Certain conservative amino acid substitutions are envisioned in the amino acid sequences of the CDRs of this disclosure. In certain embodiments, the antibody comprises CDRs that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 by 1, 2, 3, or 4 amino acids. In certain embodiments, the antibody comprises CDRs that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 by 1, 2, 3, or 4 amino acids and does not affect the binding affinity by greater than 10%, 20%, or 30%. In certain embodiments, antibodies that specifically bind LIF comprise one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence at least 90% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprises a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the antibody that specifically binds LIF comprises one or more human light chain framework regions comprising: a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, or a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the one or more human light chain framework regions comprise a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain

embodiments, the one or more human heavy chain framework regions and the one or more human light chain regions comprise all of a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the antibody specifically binds human LIF. In certain embodiments, the antibody that specifically binds LIF comprises one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprise a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the antibody that specifically binds LIF comprises one or more human light chain framework regions comprising: a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, or a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the one or more human light chain framework regions comprise a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the one or more human heavy chain framework regions and the one or more human light chain regions comprise a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2

amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the antibody specifically binds human LIF.

[0088] In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 1 (GFTFSHAWMH), a VH-CDR2 amino acid sequence at least 80%, 90%, or 95% identical to that set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), and a VH-CDR3 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 95 (TSWEWDLDF). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VL-CDR1 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), a VL-CDR2 amino acid sequence at least 80% identical to that set forth in SEQ ID NO: 25 (SVSNLES), and a VL-CDR3 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 amino acid sequence set forth in SEQ ID NO: 1 (GFTFSHAWMH), a VH-CDR2 amino acid sequence set forth in SEQ ID NO: 9 (QIKAKSDDYATYYAESVKG), a VH-CDR3 amino acid sequence set forth in SEQ ID NO: 95 (TSWEWDLDF), a VL-CDR1 amino acid sequence set forth in SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), a VL-CDR2 amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and a VL-CDR3 amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). Certain conservative amino acid substitutions are envisioned in the amino acid sequences of the CDRs of this disclosure. In certain embodiments, the antibody comprises CDRs that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 95, 21, 25, and 29 by 1, 2, 3, or 4 amino acids. In certain embodiments, the antibody comprises CDRs that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 95, 21, 25, and 29 by 1, 2, 3, or 4 amino acids and does not affect the binding affinity by greater than 10%, 20%, or 30%. In certain embodiments, antibodies that specifically bind LIF comprise one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence at least 90% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprises a VH-FR1 amino acid

9; a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 16; a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 21; and a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 25; and a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 29.

[0096] In a certain embodiments, described herein, is a recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF) comprising: a heavy chain complementarity determining region 1 (VH-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 3; a heavy chain complementarity determining region 2 (VH-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 10; a heavy chain complementarity determining region 3 (VH-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 16; a light chain complementarity determining region 1 (VL-CDR1) comprising an amino acid sequence set forth in SEQ ID NO: 22; and a light chain complementarity determining region 2 (VL-CDR2) comprising an amino acid sequence set forth in SEQ ID NO: 26; and a light chain complementarity determining region 3 (VL-CDR3) comprising an amino acid sequence set forth in SEQ ID NO: 29.

10G7

[0097] Another antibody cloned and sequenced from a rat immunization (10G7) comprises CDRs (using the combination of the Kabat and IMGT CDR numbering methods) with the following amino acid sequences: a VH-CDR1 corresponding to SEQ ID NO: 4 (GFTFSNAWMH), a VH-CDR2 corresponding to SEQ ID NO: 11 (QIKDKSDNYATYYAESVKG), a VH-CDR3 corresponding to SEQ ID NO: 17 (TCWEWYLDLF), a VL-CDR1 corresponding to SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), a VL-CDR2 corresponding to SEQ ID NO: 25 (SVSNLES), and a VL-CDR3 corresponding to SEQ ID NO: 29 (MQATHAPPYT).

[0098] In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 comprising an amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 4 (GFTFSNAWMH), a VH-CDR2 comprising an amino acid sequence at least 80%, 90%, or 95% identical to that set forth in SEQ ID NO: 11 (QIKDKSDNYATYYAESVKG), and a VH-CDR3 comprising an amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 17 (TCWEWYLDLF). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VL-CDR1 comprising an amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), a VL-CDR2 comprising an amino acid sequence at least 80% identical to that set forth in SEQ ID NO: 25 (SVSNLES), and a VL-CDR3 comprising an amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 29 (MQATHAPPYT). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 comprising an amino acid sequence set forth in SEQ ID NO: 4 (GFTFSNAWMH), a VH-CDR2 comprising an amino acid sequence set forth in SEQ ID NO: 11 (QIKDKSDNYATYYAESVKG), a VH-CDR3 comprising an amino acid sequence set forth in SEQ ID NO: 17 (TCWEWYLDLF), a VL-CDR1 comprising an amino acid sequence set forth in

SEQ ID NO: 21 (RSSQSLLDSDGHTYLN), a VL-CDR2 comprising an amino acid sequence set forth in SEQ ID NO: 25 (SVSNLES), and a VL-CDR3 comprising an amino acid sequence set forth in SEQ ID NO: 29 (MQATHAPPYT). Certain conservative amino acid substitutions are envisioned in the amino acid sequences of the CDRs of this disclosure. In certain embodiments, the antibody comprises CDR amino acid sequences that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 4, 11, 17, 21, 25, and 29 by 1, 2, 3, or 4 amino acids. In certain embodiments, the antibody comprises CDR amino acid sequences that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 4, 11, 17, 21, 25, and 29 by 1, 2, 3, or 4 amino acids and does not affect the binding affinity by greater than 10%, 20%, or 30%. In certain embodiments, the antibodies that specifically bind LIF comprises one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprise a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the antibodies that specifically bind LIF comprise one or more human light chain framework regions comprising: a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, or a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the one or more human light chain framework regions comprise a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain

embodiments, the one or more human heavy chain framework regions and the one or more human light chain regions comprise all of a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the antibody specifically binds human LIF. In certain embodiments, the antibody that specifically binds LIF comprises one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprise a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the antibody that specifically binds LIF comprises one or more human light chain framework regions comprising: a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, or a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the one or more human light chain framework regions comprise a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the one or more human heavy chain framework regions and the one or more human light chain regions comprise a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2

amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the antibody specifically binds human LIF.

6B5

[0099] Another antibody cloned and sequenced from a rat immunization (6B5) comprises CDRs (using the Kabat numbering method) with the following amino acid sequences: a VH-CDR1 corresponding to SEQ ID NO: 7 (SKFMY), a VH-CDR2 corresponding to SEQ ID NO: 13 (WIYPGDGDTEYNQKFSE), a VH-CDR3 corresponding to SEQ ID NO: 19 (RDYHSSHFAY), a VL-CDR1 corresponding to SEQ ID NO: 23 (RSSQSLHNNNGNTYLS), a VL-CDR2 corresponding to SEQ ID NO: 27 (QVSNRFS), and a VL-CDR3 corresponding to SEQ ID NO: 30 (GQGTQYPYT).

[0100] In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 amino acid sequence at least 80% identical to that set forth in SEQ ID NO: 7 (SKFMY), a VH-CDR2 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 13 (WIYPGDGDTEYNQKFSE), and a VH-CDR3 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 19 (RDYHSSHFAY). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VL-CDR1 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 23 (RSSQSLHNNNGNTYLS), a VL-CDR2 amino acid sequence at least 80% identical to that set forth in SEQ ID NO: 27 (QVSNRFS), and a VL-CDR3 amino acid sequence at least 80% identical to that set forth in SEQ ID NO: 30 (GQGTQYPYT). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 amino acid sequence set forth in SEQ ID NO: 7 (SKFMY), a VH-CDR2 amino acid sequence set forth in SEQ ID NO: 13 (WIYPGDGDTEYNQKFSE), a VH-CDR3 amino acid sequence set forth in SEQ ID NO: 19 (RDYHSSHFAY), a VL-CDR1 amino acid sequence set forth in SEQ ID NO: 23 (RSSQSLHNNNGNTYLS), a VL-CDR2 amino acid sequence set forth in SEQ ID NO: 27 (QVSNRFS), and a VL-CDR3 amino acid sequence set forth in SEQ ID NO: 30 (GQGTQYPYT). Certain conservative amino acid substitutions are envisioned in the amino acid sequences of the CDRs of this disclosure. In certain embodiments, the antibody comprises CDR amino acid sequences that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 7, 13, 19, 23, 27, and 30 by 1, 2, 3, or 4 amino acids. In certain embodiments, the antibody comprises CDR amino acid sequences that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 7, 13, 19, 23, 27, and 30 by 1, 2, 3, or 4 amino acids and does not affect the binding affinity by greater than 10%, 20%, or 30%. In certain embodiments, antibodies that specifically bind LIF comprise one or more human heavy chain framework

Kabat numbering method) with the following amino acid sequences: a VH-CDR1 corresponding to SEQ ID NO: 33 (TAGMQ), a VH-CDR2 corresponding to SEQ ID NO: 35 (WINTQSGEPQYVDDFRG), a VH-CDR3 corresponding to SEQ ID NO: 37 (WALYSEYDVMDY), a VL-CDR1 corresponding to SEQ ID NO: 39 (KASENVDSYVS), a VL-CDR2 corresponding to SEQ ID NO: 41 (GASNRYT), and a VL-CDR3 corresponding to SEQ ID NO: 43 (GQSYRYPPT).

[0102] In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 amino acid sequence at least 80% identical to that set forth in SEQ ID NO: 33 (TAGMQ), a VH-CDR2 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 35 (WINTQSGEPQYVDDFRG), and a VH-CDR3 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 37 (WALYSEYDVMDY). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VL-CDR1 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 39 (KASENVDSYVS), a VL-CDR2 amino acid sequence at least 80% identical set forth in SEQ ID NO: 41 (GASNRYT), and a VL-CDR3 amino acid sequence at least 80% or 90% identical to that set forth in SEQ ID NO: 43 (GQSYRYPPT). In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a VH-CDR1 amino acid sequence set forth in SEQ ID NO: 33 (TAGMQ), a VH-CDR2 amino acid sequence set forth in SEQ ID NO: 35 (WINTQSGEPQYVDDFRG), a VH-CDR3 amino acid sequence set forth in SEQ ID NO: 37 (WALYSEYDVMDY), a VL-CDR1 amino acid sequence set forth in SEQ ID NO: 39 (KASENVDSYVS), a VL-CDR2 amino acid sequence set forth in SEQ ID NO: 41 (GASNRYT), and a VL-CDR3 amino acid sequence set forth in SEQ ID NO: 43 (GQSYRYPPT). Certain conservative amino acid substitutions are envisioned in the amino acid sequences of the CDRs of this disclosure. In certain embodiments, the antibody comprises CDR amino acid sequences that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 39, 41, 43, 33, 35, and 37 by 1, 2, 3, or 4 amino acids. In certain embodiments, the antibody comprises CDR amino acid sequences that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 39, 41, 43, 33, 35, and 37 by 1, 2, 3, or 4 amino acids and does not affect the binding affinity by greater than 10%, 20%, or 30%. In certain embodiments, antibodies that specifically bind LIF comprise one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprise a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the

amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, antibodies that specifically bind LIF comprise one or more human light chain framework regions comprising: a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, or a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the one or more human light chain framework regions comprise a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the one or more human heavy chain framework regions and the one or more human light chain regions comprise all of a VH-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence at least about 80%, about 90%, or about 95% identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the antibody specifically binds human LIF. In certain embodiments, the antibody that specifically binds LIF comprises one or more human heavy chain framework regions comprising: a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 44-47, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 48-49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 50-52, or a VH-FR4 region amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID

NOs: 53-55. In certain embodiments, the one or more human heavy chain framework regions comprise a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 50, and a VH-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 54. In certain embodiments, the antibody that specifically binds LIF comprises one or more human light chain framework regions comprising: a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 56-59, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 60-63, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 64-67, or a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in any one of SEQ ID NOs: 68-70. In certain embodiments, the one or more human light chain framework regions comprise a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the one or more human heavy chain framework regions and the one or more human light chain regions comprise a VH-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 45, a VH-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 49, a VH-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 50, a VH-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 54, a VL-FR1 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 57, a VL-FR2 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 61, a VL-FR3 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 65, and a VL-FR4 amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 68. In certain embodiments, the antibody specifically binds human LIF.

[0103] The antibodies described herein directly bind human LIF. The canonical amino acid sequence of human LIF is given by SEQ ID NO: 98. Those of skill in the art will appreciate that natural variants of SEQ ID NO: 98 are possible amongst the human population that may lead to differences of 1, 2, 3, 4, or 5 amino acids between SEQ ID NO: 98 and LIF expressed by any given human individual. Small changes that arise due to natural variation are not expected to give rise to different binding kinetics or efficacy in treatment of any of the antibodies described herein.

Epitopes Bound by Therapeutically Useful LIF Antibodies

[0104] Described herein is a unique epitope of human LIF that when bound inhibits LIF biological activity (e.g., STAT3 phosphorylation) and inhibits tumor growth in vivo. The epitope described herein consists of two discontinuous stretches of amino acids (from residue 13 to residue 32 and from residue 120 to 138 of human LIF), that are present in two distinct topological domains (alpha helixes A and C) of the human LIF protein. This binding is a combination of

weak (Van der Waals attraction), medium (hydrogen binding), and strong (salt bridge) interactions. In certain embodiments, a contact residue is a residue on LIF that forms a hydrogen bond with a residue on an anti-LIF antibody. In certain embodiments, a contact residue is a residue on LIF that forms a salt bridge with a residue on an anti-LIF antibody. In certain embodiments, a contact residue is a residue on LIF that results in a Van der Waals attraction with and is within at least 5, 4, or 3 angstroms of a residue on an anti-LIF antibody.

[0105] In certain embodiments, described herein is an isolated antibody that binds any one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, or H138 of SEQ ID NO:98. In certain embodiments, described herein is an isolated antibody that binds all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, and H138 of SEQ ID NO:98. In certain embodiments, described herein is an isolated antibody that binds all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, and H138 of SEQ ID NO:98. In certain embodiments, the antibody only binds residues that participate with the antibody in strong or medium interactions. In certain embodiments, the antibody only binds residues that participate with the antibody in strong interactions. In a certain embodiment, the antibody interacts with helix A and C of LIF. In a certain embodiment, the antibody blocks LIF interaction with gp130.

[0106] In certain embodiments, described herein is an antibody comprising CDRs with an amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 that binds any one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, or H138 of SEQ ID NO:98. In certain embodiments, described herein is an antibody comprising CDRs with an amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 that binds to all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, and H138 of SEQ ID NO:98. In certain embodiments, the antibody only binds residues that participate with the antibody in strong or medium interactions. In certain embodiments, the antibody only binds residues that participate with the antibody in strong interactions.

[0107] In certain embodiments, described herein is an antibody comprising CDRs with an amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 that binds any one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, or H138 of SEQ ID NO:98. In certain embodiments, described herein is an antibody comprising CDRs with an amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 that binds to all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120,

R123, S127, N128, L130, C131, C134, S135, and H138 of SEQ ID NO:98. In certain embodiments, the antibody only binds residues that participate with the antibody in strong or medium interactions. In certain embodiments, the antibody only binds residues that participate with the antibody in strong interactions.

[0108] In certain embodiments, described herein is an antibody comprising CDRs that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 by 1, 2, 3, 4, or 5 amino acids and binds any one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, or H138 of SEQ ID NO:98. In certain embodiments, described herein is an antibody comprising CDRs that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 by 1, 2, 3, 4, or 5 amino acids and binds to all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, and H138 of SEQ ID NO:98. In certain embodiments, the antibody only binds residues that participate with the antibody in strong or medium interactions. In certain embodiments, the antibody only binds residues that participate with the antibody in strong interactions.

[0109] In certain embodiments, described herein is an antibody comprising CDRs that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 by 1, 2, 3, 4, or 5 amino acids and binds any one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, or H138 of SEQ ID NO:98. In certain embodiments, described herein is an antibody comprising CDRs that differ from the amino acid sequence set forth in any one of SEQ ID NOs: 1, 9, 15, 21, 25, and 29 by 1, 2, 3, 4, or 5 amino acids and bind to all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, and H138 of SEQ ID NO:98. In certain embodiments, the antibody only binds residues that participate with the antibody in strong or medium interactions. In certain embodiments, the antibody only binds residues that participate with the antibody in strong interactions.

[0110] In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a humanized heavy chain variable region amino acid sequence at least about 80%, about 90%, about 95%, about 97%, about 98%, or about 99% identical to the amino acid sequence set forth in SEQ ID NO:72; and a humanized light chain variable region amino acid sequence at least about 80%, about 90%, about 95%, about 97%, about 98%, or about 99% identical to the amino acid sequence set forth in SEQ ID NO: 76 and binds any one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, or H138 of SEQ ID NO:98. In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a humanized heavy chain variable region amino acid

sequence at least about 80%, about 90%, about 95%, about 97%, about 98%, or about 99% identical to the amino acid sequence set forth in SEQ ID NO:72; and a humanized light chain variable region amino acid sequence at least about 80%, about 90%, about 95%, about 97%, about 98%, or about 99% identical to the amino acid sequence set forth in SEQ ID NO: 76 and binds all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, and H138 of SEQ ID NO:98. In certain embodiments, the antibody only binds residues that participate with the antibody in strong or medium interactions. In certain embodiments, the antibody only binds residues that participate with the antibody in strong interactions.

[0111] In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a humanized heavy chain variable region amino acid sequence at least about 80%, about 90%, about 95%, about 97%, about 98%, or about 99% identical to the amino acid sequence set forth in SEQ ID NO: 96; and a humanized light chain variable region amino acid sequence at least about 80%, about 90%, about 95%, about 97%, about 98%, or about 99% identical to the amino acid sequence set forth in SEQ ID NO: 76 and binds any one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, or H138 of SEQ ID NO:98. In certain embodiments, described herein, is an antibody that specifically binds LIF comprising a humanized heavy chain variable region amino acid sequence at least about 80%, about 90%, about 95%, about 97%, about 98%, or about 99% identical to the amino acid sequence set forth in SEQ ID NO: 96; and a humanized light chain variable region amino acid sequence at least about 80%, about 90%, about 95%, about 97%, about 98%, or about 99% identical to the amino acid sequence set forth in SEQ ID NO: 76 and binds all of the following residues: A13, I14, R15, H16, P17, C18, H19, N20, Q25, Q29, Q32, D120, R123, S127, N128, L130, C131, C134, S135, and H138 of SEQ ID NO:98. In certain embodiments, the antibody only binds residues that participate with the antibody in strong or medium interactions. In certain embodiments, the antibody only binds residues that participate with the antibody in strong interactions.

Therapeutic Indications

[0112] In certain embodiments, the antibodies disclosed herein inhibit LIF signaling in cells. In certain embodiments, the IC_{50} for biological inhibition of the antibody under serum starved conditions in U-251 cells is less than or equal to about 100, 75, 50, 40, 30, 20, 10, 5, or 1 nanomolar. In certain embodiments, the IC_{50} for biological inhibition of the antibody under serum starved conditions in U-251 cells is less than or equal to about 900, 800, 700, 600, 500, 400, 300, 200, or 100 nanomolar.

[0113] In certain embodiments, the antibodies disclosed herein, are useful for treating tumors and cancers that express LIF. In certain embodiments, an individual treated with the antibodies of this disclosure has been selected for treatment as having a LIF positive tumor/cancer. In certain embodiments, the tumor is LIF positive or produces elevated levels of LIF. In certain embodiments, LIF positivity is determined in comparison to a reference value or a set

pathological criteria. In certain embodiments, a LIF positive tumor expresses greater than 2-fold, 3-fold, 5-fold, 10-fold, 100-fold or more LIF than a non-transformed cell from which the tumor is derived. In certain embodiments, the tumor has acquired ectopic expression of LIF. A LIF positive tumor can be determined histologically using, for example, immunohistochemistry with an anti-LIF antibody; by commonly used molecular biology methods such as, for example, mRNA quantitation by real-time PCR or RNA-seq; or protein quantitation, for example, by western blot, flow cytometry, ELISA, or a homogenous protein quantitation assays (e.g., alphaLISA). In certain embodiments, the antibodies can be used to treat patients diagnosed with cancer. In certain embodiments, the cancer comprises one or more cancer stem cells or is one or more cancer stem cells.

[0114] In certain embodiments, the antibodies disclosed herein, are useful for treating tumors in cancers that express the LIF receptor (CD118). A LIF receptor positive tumor can be determined by histopathology or flow cytometry, and, in certain embodiments, comprises a cell that binds a LIF receptor antibody greater than 2x, 3x, 3x, 4x, 5x, 10x or more than an isotype control. In certain embodiments, the tumor has acquired ectopic expression of the LIF receptor. In a certain embodiment, the cancer is a cancer stem cell. In a certain embodiment, a LIF positive tumor or cancer can be determined by immunohistochemistry using anti-LIF an anti-LIF antibody. In a certain embodiment, a LIF positive tumor is determined by IHC analysis with a LIF Level in the top 10%, 20%, 30%, 40%, or top 50% of tumors.

[0115] The antibodies described herein influence numerous outcomes. In a certain embodiment, the antibodies described herein can reduce the presence of M2 macrophages in tumors by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more in a tumor model compared to a control antibody (e.g., isotype control). M2 macrophages can be identified by staining for CCL22 and CD206 in IHC sections or by flow cytometry of tumor infiltrating immune or myeloid cells. In a certain embodiment, the antibodies described herein can reduce the binding of LIF to gp130 tumors by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more when compared to a control antibody (e.g., isotype control). In a certain embodiment, the antibodies described herein can reduce LIF signaling by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more in a LIF responsive cell line compared to a control antibody (e.g., isotype control). LIF signaling can be measured by, for example, western blot for phosphorylated STAT3 (a downstream target of LIF signaling). The antibodies here are also highly specific for LIF compared to other IL-6 family member cytokines. In certain embodiments, the antibodies bind human LIF with an affinity about 10x, about 50x, or about 100x greater than that of any other IL-6 family member cytokine. In certain embodiments, the LIF antibodies do not bind to other IL-6 family member cytokines that are produced in a mammalian system. In certain embodiments, the antibodies do not bind to Oncostatin M that has been produced in a mammalian system.

[0116] In certain embodiments, disclosed herein, are antibodies useful for the treatment of a cancer or tumor. In certain embodiments, the cancer comprises breast, heart, lung, small intestine, colon, spleen, kidney, bladder, head, neck, ovarian, prostate, brain, pancreatic, skin, bone, bone marrow, blood, thymus, uterine, testicular, and liver tumors. In certain embodiments, tumors which can be treated with

the antibodies of the invention comprise adenoma, adenocarcinoma, angiosarcoma, astrocytoma, epithelial carcinoma, germinoma, glioblastoma, glioma, hemangioendothelioma, hemangiosarcoma, hematoma, hepatoblastoma, leukemia, lymphoma, medulloblastoma, melanoma, neuroblastoma, osteosarcoma, retinoblastoma, rhabdomyosarcoma, sarcoma and/or teratoma. In certain embodiments, the tumor/cancer is selected from the group of acral lentiginous melanoma, actinic keratosis, adenocarcinoma, adenoid cystic carcinoma, adenomas, adenocarcinoma, adenosquamous carcinoma, astrocytic tumors, Bartholin gland carcinoma, basal cell carcinoma, bronchial gland carcinoma, capillary carcinoid, carcinoma, carcinosarcoma, cholangiocarcinoma, chondrosarcoma, cystadenoma, endodermal sinus tumor, endometrial hyperplasia, endometrial stromal sarcoma, endometrioid adenocarcinoma, ependymal sarcoma, Swing's sarcoma, focal nodular hyperplasia, gastrinoma, germ line tumors, glioblastoma, glucagonoma, hemangioblastoma, hemangioendothelioma, hemangioma, hepatic adenoma, hepatic adenomatosis, hepatocellular carcinoma, insulinoma, intraepithelial neoplasia, intraepithelial squamous cell neoplasia, invasive squamous cell carcinoma, large cell carcinoma, liposarcoma, lung carcinoma, lymphoblastic leukemia, lymphocytic leukemia, leiomyosarcoma, melanoma, malignant melanoma, malignant mesothelial tumor, nerve sheath tumor, medulloblastoma, medulloepithelioma, mesothelioma, mucoepidermoid carcinoma, myeloid leukemia, neuroblastoma, neuroepithelial adenocarcinoma, nodular melanoma, osteosarcoma, ovarian carcinoma, papillary serous adenocarcinoma, pituitary tumors, plasmacytoma, pseudosarcoma, prostate carcinoma, pulmonary blastoma, renal cell carcinoma, retinoblastoma, rhabdomyosarcoma, sarcoma, serous carcinoma, squamous cell carcinoma, small cell carcinoma, soft tissue carcinoma, somatostatin secreting tumor, squamous carcinoma, squamous cell carcinoma, undifferentiated carcinoma, uveal melanoma, verrucous carcinoma, vagina/vulva carcinoma, VIPoma, and Wilm's tumor. In certain embodiments, the tumor/cancer to be treated with one or more antibodies of the invention comprise brain cancer, head and neck cancer, colorectal carcinoma, acute myeloid leukemia, pre-B-cell acute lymphoblastic leukemia, bladder cancer, astrocytoma, preferably grade II, III or IV astrocytoma, glioblastoma, glioblastoma multiforme, small cell cancer, and non-small cell cancer, preferably non-small cell lung cancer, lung adenocarcinoma, metastatic melanoma, androgen-independent metastatic prostate cancer, androgen-dependent metastatic prostate cancer, prostate adenocarcinoma, and breast cancer, preferably breast ductal cancer, and/or breast carcinoma. In certain embodiments, the cancer treated with the antibodies of this disclosure comprises glioblastoma. In certain embodiments, the cancer treated with one or more antibodies of this disclosure comprises pancreatic cancer. In certain embodiments, the cancer treated with one or more antibodies of this disclosure comprises ovarian cancer. In certain embodiments, the cancer treated with one or more antibodies of this disclosure comprises lung cancer. In certain embodiments, the cancer treated with one or more antibodies of this disclosure comprises prostate cancer. In certain embodiments, the cancer treated with one or more antibodies of this disclosure comprises colon cancer. In certain embodiments, the cancer treated comprises glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer. In a certain embodiment, the cancer is refractory to

other treatment. In a certain embodiment, the cancer treated is relapsed. In a certain embodiment, the cancer is a relapsed/refractory glioblastoma, pancreatic cancer, ovarian cancer, colon cancer, prostate cancer, or lung cancer.

Therapeutic Methods

[0117] In certain embodiments, the antibodies can be administered by any route suitable for the administration of antibody-containing pharmaceutical compositions, such as, for example, subcutaneous, intraperitoneal, intravenous, intramuscular, intratumoral, or intracerebral, etc. In certain embodiments, the antibodies are administered intravenously. In certain embodiments, the antibodies are administered on a suitable dosage schedule, for example, weekly, twice weekly, monthly, twice monthly, etc. In certain embodiments, the antibodies are administered once every three weeks. The antibodies can be administered in any therapeutically effective amount. In certain embodiments, the therapeutically acceptable amount is between about 0.1 mg/kg and about 50 mg/kg. In certain embodiments, the therapeutically acceptable amount is between about 1 mg/kg and about 40 mg/kg. In certain embodiments, the therapeutically acceptable amount is between about 5 mg/kg and about 30 mg/kg.

Additional Therapeutic Agents

[0118] In certain embodiments, the antibodies can be administered with or during treatment with an additional therapeutic agent. In certain embodiments, the therapeutic agent comprises a recombinant protein or monoclonal antibody. In certain embodiments, the recombinant protein or monoclonal antibody comprises Etaracizumab (Abegrin), Tacatuzumab tetraxetan, Bevacizumab (Avastin), Labetuzumab, Cetuximab (Erbix), Obinutuzumab (Gazyva), Trastuzumab (Herceptin), Clivatuzumab, Trastuzumab emtansine (Kadcyla), Ramucirumab, Rituximab (MabThera, Rituxan), Gemtuzumab ozogamicin (Mylotarg), Pertuzumab (Omnitarg), Girentuximab (Rencarex), or Nimotuzumab (Theracim, Theraloc). In certain embodiments, the monoclonal antibody comprises an immunomodulatory that targets a checkpoint inhibitor, for example PD-1 or CTLA-4. In certain embodiments, the immunomodulator comprises Nivolumab, Ipilimumab, Atezolizumab, or Pembrolizumab. In certain embodiments, the additional therapeutic agent is a chemotherapeutic agent. In certain embodiments, the chemotherapeutic agent is an alkylating agent (e.g., cyclophosphamide, ifosfamide, chlorambucil, busulfan, melphalan, mechlorethamine, uramustine, thiotepa, nitrosoureas, or temozolomide), an anthracycline (e.g., doxorubicin, adriamycin, daunorubicin, epirubicin, or mitoxantrone), a cytoskeletal disruptor (e.g., paclitaxel or docetaxel), a histone deacetylase inhibitor (e.g., vorinostat or romidepsin), an inhibitor of topoisomerase (e.g., irinotecan, topotecan, amsacrine, etoposide, or teniposide), a kinase inhibitor (e.g., bortezomib, erlotinib, gefitinib, imatinib, vemurafenib, or vismodegib), a nucleoside analog or precursor analog (e.g., azacitidine, azathioprine, capecitabine, cytarabine, fluorouracil, gemcitabine, hydroxyurea, mercaptopurine, methotrexate, or thioguanine), a peptide antibiotic (e.g., actinomycin or bleomycin), a platinum-based agent (e.g., cisplatin, oxaloplatin, or carboplatin), or a plant alkaloid (e.g., vincristine, vinblastine, vinorelbine, vindesine, podophyllotoxin, paclitaxel, or doc-

etaxel). In some embodiments, the chemotherapeutic agent is a nucleoside analog. In some embodiments, the chemotherapeutic agent is gemcitabine. In certain embodiments, the additional therapeutic agent is radiation therapy.

Pharmaceutically Acceptable Carriers

[0119] In certain embodiments, the antibodies of the current disclosure are administered suspended in a sterile solution. In certain embodiments, the solution comprises a physiologically appropriate salt concentration (e.g., NaCl). In certain embodiments, the solution comprises between about 0.6% and 1.2% NaCl. In certain embodiments, the solution comprises between about 0.7% and 1.1% NaCl. In certain embodiments, the solution comprises between about 0.8% and 1.0% NaCl. In certain embodiments, a highly concentrated stock solution of antibody may be diluted in about 0.9% NaCl. In certain embodiments, the solution comprises about 0.9% NaCl. In certain embodiments, the solution further comprises one or more of: buffers, for example, acetate, citrate, histidine, succinate, phosphate, bicarbonate and hydroxymethylaminomethane (Tris); surfactants, for example, polysorbate 80 (Tween 80), polysorbate 20 (Tween 20), polysorbate and poloxamer 188; polyol/disaccharide/polysaccharides, for example, glucose, dextrose, mannose, mannitol, sorbitol, sucrose, trehalose, and dextran 40; amino acids, for example, histidine, glycine or arginine; antioxidants, for example, ascorbic acid, methionine; and chelating agents, for example, EGTA or EDTA. In certain embodiments, the antibodies of the current disclosure are shipped/stored lyophilized and reconstituted before administration. In certain embodiments, lyophilized antibody formulations comprise a bulking agent such as, mannitol, sorbitol, sucrose, trehalose, and dextran 40. In a certain embodiment, anti-LIF antibodies of this disclosure can be shipped and stored as a concentrated stock solution to be diluted at the treatment site of use. In certain embodiments, the stock solution comprises about 25 mM histidine, about 6% sucrose, about 0.01% polysorbate, and about 20 mg/mL of anti-LIF antibody.

EXAMPLES

[0120] The following illustrative examples are representative of embodiments of the software applications, systems, and methods described herein and are not meant to be limiting in any way.

Example 1—Generation of Rat Antibodies Specific for LIF

[0121] A cDNA encoding amino acids 23-202 of human LIF was cloned into expression plasmids (Aldevron GmbH, Freiburg, Germany). Groups of laboratory rats (Wistar) were immunized by intradermal application of DNA-coated gold-particles using a hand-held device for particle-bombardment ("gene gun"). Cell surface expression on transiently transfected HEK cells was confirmed with anti-tag antibodies recognizing a tag added to the N-terminus of the LIF protein. Serum samples were collected after a series of immunizations and tested in flow cytometry on HEK cells transiently transfected with the aforementioned expression plasmids. Antibody-producing cells were isolated and fused with mouse myeloma cells (Ag8) according to standard procedures. Hybridomas producing antibodies specific for LIF were identified by screening in a flow cytometry assay as

described above. Cell pellets of positive hybridoma cells were prepared using an RNA protection agent (RNAlater, cat. #AM7020 by ThermoFisher Scientific) and further processed for sequencing of the variable domains of the antibodies.

Example 2—Generation of Mouse Antibodies
Specific for LIF

[0122] A cDNA encoding amino acids 23-202 of human LIF was cloned into expression plasmids (Aldevron GmbH, Freiburg, Germany). Groups of laboratory mice (NMRI) were immunized by intradermal application of DNA-coated gold-particles using a hand-held device for particle-bombardment (“gene gun”). Cell surface expression on transiently transfected HEK cells was confirmed with anti-tag antibodies recognizing a tag added to the N-terminus of the LIF protein. Serum samples were collected after a series of immunizations and tested in flow cytometry on HEK cells transiently transfected with the aforementioned expression plasmids. Antibody-producing cells were isolated and fused with mouse myeloma cells (Ag8) according to standard procedures. Hybridomas producing antibodies specific for LIF were identified by screening in a flow cytometry assay as described above. Cell pellets of positive hybridoma cells were prepared using an RNA protection agent (RNAlater, cat. #AM7020 by ThermoFisher Scientific) and further processed for sequencing of the variable domains of the antibodies.

Example 3—Humanization of Rat Antibodies
Specific for LIF

[0123] One clone from the rat immunization (5D8) was chosen for subsequent humanization. Humanization was conducted using standard CDR grafting methods. The heavy chain and light chain regions were cloned from the 5D8 hybridoma using standard molecular cloning techniques and sequenced by the Sanger method. A BLAST search was then conducted against human heavy chain and light chain variable sequences and 4 sequences from each were chosen as acceptor frameworks for humanization. These acceptor frameworks were deimmunized to remove T cell response epitopes. The heavy chain and light chain CDR1, CDR2 and CDR3 of 5D8 were cloned into the 4 different heavy chain acceptor frameworks (H1 to H4), and 4 different light chain frameworks (L1 to L4). Then all 16 different antibodies were tested for: expression in CHO-S cells (Selexis); inhibition of LIF-induced STAT3 phosphorylation; and binding affinity by Surface Plasmon Resonance (SPR). These experiments are summarized in Table 1.

TABLE 1

Summary of 5D8 humanization			
Heavy chain light chain combination	Inhibition of LIF-induced pSTAT3 from FIG. 1	Affinity by SPR K_{D1} (pM)	Expression (ug/mL)
H0L0	+++	133 ± 46	393
H1L1	–	N/A	627
H1L2	+++	55 ± 23	260
H1L3	+++	54 ± 31	70
H1L4	–	N/A	560
H2L1	–	N/A	369
H2L2	+++	52 ± 22	392

TABLE 1-continued

Summary of 5D8 humanization			
Heavy chain light chain combination	Inhibition of LIF-induced pSTAT3 from FIG. 1	Affinity by SPR K_{D1} (pM)	Expression (ug/mL)
H2L3	++	136 ± 19	185
H2L4	–	N/A	78
H3L1	N/A	N/A	No expression
H3L2	N/A	N/A	No expression
H3L3	N/A	N/A	No expression
H3L4	N/A	N/A	No expression
H4L1	–	N/A	259
H4L2	++	913 ± 308	308
H4L3	+		252
H4L4	–	N/A	186

N/A = Not attempted;
H0L0 = chimeric antibody with full rat heavy and light chain variable regions

[0124] The expression performance of the transfected cells was compared in Erlenmeyer flasks (seeding 3×10⁵ cells/mL, 200 mL culture volume) within fed-batch cultivation after 10 days of cell culture. At this point cells were harvested and the secreted antibody purified using a Protein A column and then quantitated. All humanized antibodies expressed except those using the H3 heavy chain.

[0125] Inhibition of LIF-induced STAT3 phosphorylation at tyrosine 705 was determined by western blot. U251 glioma cells were plated in 6-well plates at a density of 100,000 cells/well. Cells were cultured in complete medium for 24 hours before any treatment and after that, cells were serum starved for 8 hours. After that, cells with the indicated antibodies over night at a concentration of 10 µg/mL. After treatment, proteins were obtained in radio-immunoprecipitation assay (RIPA) lysis buffer containing phosphatase and protease inhibitors, quantified (BCA-protein assay, Thermo Fisher Scientific) and used in western blot. For western blot, membranes were blocked for 1 hour in 5% non-fat dried milk—TBST and incubated with the primary antibody over night (p-STAT3, catalog #9145, Cell Signaling or STAT3, catalog #9132, Cell Signaling) or 30 minutes (β-actin-peroxidase, catalog #A3854, Sigma-Aldrich). Membranes were then washed with TBST, incubated with secondary and washed again. Proteins were detected by chemiluminescence (SuperSignal Substrate, catalog #34076, Thermo Fisher Scientific). These results are shown in FIG. 1. The darker the pSTAT3 band the less inhibition is present. Inhibition was high in lanes labeled 5D8 (non humanized rat), A (H0L0), C (H1L2), D (H1L3), and G (H2L2); inhibition was moderate in H (H2L3), O (H4L2), and P (H4L3); inhibition was absent in B (H1L1), E (H1L4), F (H2L1), I (H2L4), N (H4L1) and Q (H4L4).

[0126] Antibodies that exhibited inhibition of LIF-induced STAT3 phosphorylation were then analyzed by SPR to determine binding affinity. Briefly, binding of the A (H0L0), C (H1L2), D (H1L3), and G (H2L2), H (H2L3) and O (H4L2) humanized antibodies to amine coupled hLIF was observed using a Biacore™ 2002 Instrument. Kinetic constants and affinities were determined by mathematical sensorgram fitting (Langmuir interaction model [A+B=AB]) of all sensorgrams generated on all sensor chip surfaces at six ligand concentrations. The best fitted curves (minimal Chi2) of each concentration were used for calculation of kinetic constants and affinities. See Table 1.

[0127] Since the experimental setup used bivalent antibodies as analytes, best fitted sensorgrams, were also analyzed on basis of a bivalent analyte fitting model [A+B=AB; AB+B=AB₂] in order to obtain a more detailed insight into the target binding mechanism of the humanized antibodies. Kinetic sensorgram analysis using a bivalent fitting model [A+B=AB; AB+B=AB₂] confirmed the relative affinity ranking of the mAb samples.

[0128] The humanized 5D8 comprising H2 and L2 was selected for more in-depth analysis due to its high binding affinity and high yield from batch culture.

Example 4—Humanization of Clone 5D8 Improves Binding to LIF

[0129] We selected the H2L2 clone (h5D8) for further analysis and compared binding by SPR to the parental rat 5D8 (r5D8) and a mouse clone 1B2. The 1B2 antibody is a previously disclosed mouse anti-LIF antibody previously deposited at the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ ACC3054) and was included for comparison purposes. Recombinant human LIF, purified from *E. coli* and HEK-293 cells, respectively, were used as ligands. The LIF from human or *E. coli* sources was covalently coupled to the surface of Biacore optical sensor chips using amine coupling chemistry, and binding affinities were calculated from the kinetic constants.

Materials and Methods

[0130] Human LIF from *E. coli* was obtained from Millipore, reference LIF 1010; human LIF from HEK-293 cells was obtained from ACRO Biosystems, reference LIF-H521b. LIF was coupled to the sensor chips using the Biacore Amine Coupling Kit (BR-1000-50; GE-Healthcare, Uppsala). Samples were run on a Biacore™ 2002 Instrument using CM5 optical sensor chips (BR-1000-12; GE-Healthcare, Uppsala). Biacore HBS-EP buffer was used during the machine runs (BR-1001-88; GE-Healthcare, Uppsala). Kinetic analysis of binding sensorgrams was performed using BIAevaluation 4.1 software. Kinetic constants and affinities were determined by mathematical sensorgram fitting (Langmuir interaction model [A+B=AB]) of all sensorgrams generated on all sensor chip surfaces at increasing analyte concentrations. Sensorgrams were also analyzed on the basis of a bivalent analyte sensorgram fitting model [A+B=AB; AB+B=AB₂], including component analysis, in order to generate an estimate on the bivalent contribution to the determined Langmuir antibody—target affinities (e.g., avidity contribution). The best fitted curves (minimal Chi²) of each concentration were used for calculation of kinetic constants and affinities. Summaries of these affinity experiments are shown in Table 2 (human LIF made in *E. coli*) and Table 3 (human LIF made in HEK 293 cells).

TABLE 2		
Improved binding of 5D8 after humanization		
hLIF (<i>E. coli</i>)	K _D [pM]	
	Langmuir 1:1 sensorgram fitting	Bivalent analyte fitting
Mouse 1B2	400 ± 210	1500 ± 200
r5D8 (Rat)	130 ± 30	780 ± 130
h5D8 (humanized)	26 ± 14	82 ± 25

TABLE 3		
Improved binding of 5D8 after humanization		
hLIF (HEK 293)	K _D [pM]	
	Langmuir 1:1 sensorgram fitting	Bivalent analyte fitting
Mouse 1B2	320 ± 150	3900 ± 900
r5D8 (rat)	135 ± 100	410 ± 360
h5D8 (humanized)	13 ± 6	63 ± 30

[0131] The Langmuir 1:1 sensorgram fitting model from this set of experiments indicates that the humanized 5D8 (h5D8) antibody bound with ~10-25 times higher affinity to human LIF than mouse 1B2 and r5D8.

[0132] Next, the h5D8 antibody was tested against LIF of multiple species by SPR. h5D8 SPR binding kinetics were performed for recombinant LIF analytes derived from different species and expression systems: human LIF (*E. coli*, HEK293 cells); mouse LIF (*E. coli*, CHO cells); rat LIF (*E. coli*); cynomolgus monkey LIF (yeast, HEK293 cells).

Materials and Methods

[0133] The h5D8 antibody was immobilized to the sensor chip surface by non covalent, Fc specific capturing. Recombinant, Ig(Fc) specific *S. aureus* Protein A/G was used as capturing agent, allowing sterically uniform and flexible presentation of the anti-LIF antibody to the LIF analytes. Sources of the LIF analytes are as follows: Human LIF (from *E. coli*; Millipore reference LIF 1050); Human LIF (from HEK cells ACRO Biosystems LIF-H521); Mouse LIF (*E. coli*; Millipore Cat. No NF-LIF2010); Mouse LIF (from CHO cells; ReproKine Catalog #RCP09056); Monkey LIF (yeast Kingfisher Biotech Catalog #RP1074Y); Monkey LIF produced in HEK-293 cell. Overall h5D8 exhibited binding to LIF from several species. A summary of this affinity experiment is shown in Table 4.

TABLE 4			
Broad species reactivity of humanized 5D8			
Analyte	Langmuir 1:1 sensorgram fitting		
	mean K _a (1/Ms)[10 ⁵]	mean K _d (1/S) [10 ⁻³]	mean K _D [pM]
Human LIF (<i>E.coli</i>)	8.5 ± 0.7	7.2 ± 0.7	86 ± 9
Human LIF (HEK-293)	5.5 ± 0.02	3.1 ± 0.7	56 ± 13
Mouse LIF (<i>E. coli</i>)	21.4 ± 3.7	5.7 ± 1.0	27 ± 6
Mouse LIF(CHO cells)	6.5 ± 0.7	1.1 ± 0.3	17 ± 4
Cyno Monkey LIF (yeast)	6.3 ± 0.8	5.4 ± 0.7	89 ± 10
Cyno Monkey LIF (HEK-293)	2.4 ± 0.2	3.3 ± 0.3	134 ± 6

Example 5—Humanized Clone 5D8 Inhibits LIF-Induced Phosphorylation of STAT3 In Vitro

[0134] To determine the biological activity of h5D8, the humanized and parental versions were tested in a cell culture model of LIF activation. FIG. 2A shows that the humanized clone exhibited increased inhibition of STAT3 phosphorylation (Tyr 705) when a glioma cell line was incubated with human LIF. FIG. 2B shows an experiment with the same set up of FIG. 2A repeated with different dilutions of the h5D8 antibody.

Methods

[0135] U251 glioma cells were plated in 6-well plates at a density of 150,000 cells/well. Cells were cultured in complete medium for 24 hours before any treatment. After that, cells were treated over night or not (control cells) with r5D8 anti-LIF antibody or h5D8 anti-LIF antibody at a concentration of 10 µg/ml.

[0136] After treatment, proteins were obtained in radio-immunoprecipitation assay (RIPA) lysis buffer containing phosphatase and protease inhibitors, quantified (BCA-protein assay, Thermo Fisher Scientific) and used in western blot. For western blot, membranes were blocked for 1 hour in 5% non-fatty milk—TBST and incubated with the primary antibody overnight (p-STAT3, catalog #9145, Cell Signaling or STAT3, catalog #9132, Cell Signaling) or 30 minutes (β-actin-peroxidase, catalog #A3854, Sigma-Aldrich). Membranes were then washed with TBST, incubated with secondary antibody if necessary, and washed again. Proteins were detected by chemiluminescence (SuperSignal Substrate, catalog #34076, Thermo Fisher Scientific).

Example 6—IC₅₀ Value of h5D8 Antibody Treatment on Endogenous Levels of LIF in U-251 Cells

[0137] We also determined an IC₅₀ of as low as 490 picomolar (FIG. 3A) for biological inhibition for h5D8 under serum starved conditions in U-251 cells. See representative results FIGS. 3A and 3B and Table 5.

TABLE 5

Cell Line Tissue	Cell Line Name	Treatment	IC ₅₀ (nM)				IC ₉₀ (nM)	JAK inhibition (%)
Endogenous LIF Condition			n = 1	n = 2	Mean	SD	Mean	Mean
GBM	U251	h5D8	0.78	0.54	0.66	0.12	4.1	84%
		r5D8	1.6	1.5	1.4	0.15	8.5	86%
			1.2	1.4				

Methods

[0138] The U-251 cells were seeded at 600,000 cells per 6 cm plate (per condition). Cells were treated with h5D8 in corresponding concentration (titration) overnight at 37° C., under serum starvation (0.1% FBS). As a positive control for pSTAT3, recombinant LIF (R&D #7734-LF/CF) was used to stimulate the cells at 1.79 nM for 10 min at 37° C. As a negative control of pSTAT3, the JAK I inhibitor (Calbiochem #420099) was used at 1 µM for 30 min at 37° C. Cells were then harvested on ice for lysates following the Meso Scale Discovery Multi-Spot Assay System Total STAT3 (Cat #K150SND-2) and Phospho-STAT3 (Tyr705) (Cat #K150SVD-2) kits' protocol, to measure protein levels detectable by the MSD Meso Sector 5600.

Example 7—Additional Antibodies that Specifically Bind to Human LIF

[0139] Other rat antibody clones (10G7 and 6B5) that specifically bind human LIF were identified and a summary of their binding characteristics are shown below in Table 6, clone 1B2 served as a comparison.

Methods

[0140] Kinetic real time binding analysis was performed for anti-LIF mAbs 1B2, 10G7 and 6B5, immobilized on the

surface of CM5 optical sensor chips, applying recombinant LIF target proteins [human LIF (*E. coli*); Millipore Cat. No. LIF 1010 and human LIF (HEK293 cells); ACRO Biosystems Cat. No. LIF-H521b] as analytes.

[0141] Kinetic constants and affinities were obtained by mathematical sensorgram fitting using a Langmuir 1:1 binding model applying global (simultaneous fitting of sensorgram sets) as well as single curve fitting algorithms. Plausibility of global fits was assessed by kobs analysis.

TABLE 6

Affinity measurements of additional anti-LIF antibodies				
Langmuir 1:1 sensorgram fitting				
Analyte	clone	mean K _a (1/Ms)	mean K _d (1/S)	mean K _D [nM]
Human LIF (<i>E. coli</i>)	1B2	1.1 ± 0.4E5	1.1 ± 0.3E-3	9.7 ± 1.4
Human LIF (HEK-293)	1B2	2.0 ± 0.04E6	1.4 ± 0.2E-3	0.7 ± 0.03
Human LIF (<i>E. coli</i>)	10G7	7.9 ± 5.8E4	6.0 ± 2.3E-4	12.6 ± 9.5
Human LIF (HEK-293)	10G7	3.6 ± 1.75E5	3.1 ± 0.5E-4	1.1 ± 0.6
Human LIF (<i>E. coli</i>)	6B5	N/A	N/A	N/A

TABLE 6-continued

Affinity measurements of additional anti-LIF antibodies				
Langmuir 1:1 sensorgram fitting				
Analyte	clone	mean K _a (1/Ms)	mean K _d (1/S)	mean K _D [nM]
Human LIF (HEK-293)	6B5	3.6 ± 1.7E5	3.1 ± 0.5E-4	62 ± 6

Example 8—Additional Anti LIF Antibodies Inhibit LIF-Induced Phosphorylation of STAT3 In Vitro

[0142] Additional clones were tested for their ability to inhibit LIF-induced phosphorylation of STAT3 in cell culture. As shown in FIG. 4 clones 10G7 and the previously detailed r5D8 exhibited high inhibition of LIF-induced STAT3 phosphorylation, compared to the 1B2 clone. Anti-LIF polyclonal anti-sera (pos.) was included as a positive control While 6B5 exhibited no inhibition, this may be explained by a possible lack of 6B5 binding to non-glycosylated LIF which was used in this experiment.

Methods

[0143] Patient derived glioma cells were plated in 6-well plates at a density of 150,000 cells/well. Cells were cultured in GBM medium that consisted of Neurobasal medium (Life Technologies) supplemented with B27 (Life Technologies), penicillin/streptomycin and growth factors (20 ng/ml EGF and 20 ng/ml FGF-2 [PeproTech]) for 24 hours before any treatment. The following day, cells were treated or not with recombinant LIF produced in *E. coli* or a mix of recombinant LIF plus the indicated antibodies for 15 minutes (final concentration of 10 µg/ml for the antibodies and 20 ng/ml of recombinant LIF). After treatment, proteins were obtained in radio-immunoprecipitation assay (RIPA) lysis buffer containing phosphatase and protease inhibitors, quantified (BCA-protein assay, Thermo Fisher Scientific) and used in western blot. For western blot, membranes were blocked for 1 hour in 5% non-fatty milk—TBST and incubated with the primary antibody overnight (p-STAT3, catalog #9145, Cell Signaling) or 30 minutes (β-actin-peroxidase, catalog #A3854, Sigma-Aldrich). Membranes were then washed with TBST, incubated with secondary antibody if necessary, and washed again. Proteins were detected by chemiluminescence (SuperSignal Substrate, catalog #34076, Thermo Fisher Scientific).

Example 9—LIF is Highly Overexpressed Across Multiple Tumor Types

[0144] Immunohistochemistry was conducted on multiple human tumor types to determine the degree of LIF expression. As shown in FIG. 5 LIF is highly expressed in glioblastoma multiforme (GBM), non-small cell lung cancer (NSCLC), ovarian cancer, and colorectal cancer (CRC).

Example 10—Humanized Clone h5D8 Inhibits Tumor Growth in a Mouse Model of Non-Small Cell Lung Carcinoma

[0145] To determine the ability of the humanized 5D8 clone to inhibit a LIF positive cancer in vivo this antibody was tested in a mouse model of non-small cell lung carcinoma (NSCLC). FIG. 6 shows reduced tumor growth in mice treated with this antibody compared to a vehicle negative control.

Methods

[0146] The murine non-small cell lung cancer (NSCLC) cell line KLN205 with high LIF levels was stably infected with lentivirus expressing the firefly luciferase gene for in vivo bioluminescence monitoring. To develop the mouse model, 5×10^5 KLN205 non-small cell lung cancer (NSCLC) cells were orthotopically implanted into the left lung of 8-week-old immunocompetent syngeneic DBA/2 mice by intercostal puncture. Mice were treated with a control vehicle or with 15 mg/kg or 30 mg/kg of the h5D8 antibody intraperitoneally twice a week and tumor growth was monitored by bioluminescence. For the bioluminescence imaging, mice received an intraperitoneal injection of 0.2 mL of 15 mg/mL D-luciferin under 1-2% inhaled isoflurane anesthesia. The bioluminescence signals were monitored using the IVIS system 2000 series (Xenogen Corp., Alameda, Calif., USA) consisting of a highly sensitive cooled CCD camera. Living Image software (Xenogen Corp.) was used to grid the imaging data and integrate the total bioluminescence signals in each boxed region. Data were analyzed using the total photon flux emission (photons/second) in the regions of interest (ROI). The results demonstrate that

treatment with the h5D8 antibody promote tumor regression. Data are presented as mean±SEM.

Example 11—h5D8 Inhibits Tumor Growth in a Mouse Model of Glioblastoma Multiforme

[0147] In an orthotopic GBM tumor model using a luciferase expressing human cell line U251, r5D8 significantly reduced tumor volumes in mice administered 300 µg r5D8 and h5D8 by intraperitoneal (IP) injection twice a week. Results of this study are shown in FIG. 7A (quantitation at day 26 post treatment). This experiment was also conducted using humanized h5D8 mice treated with 200 µg or 300 µg showed a statistically significant reduction in tumor after 7 days of treatment.

Methods

[0148] U251 cells stably expressing luciferase were harvested, washed in PBS, centrifuged at 400 g for 5 min, resuspended in PBS and counted with an automated cell counter (Countess, Invitrogen). Cells were kept on ice to maintain optimal viability. Mice were anaesthetized with intraperitoneal administration of Ketamine (Ketalar50®)/Xylazine (Rompún®) (75 mg/kg and 10 mg/kg respectively). Each mouse was carefully placed in the stereotactic device and immobilized. Hair from the head was removed with depilatory cream, and the head skin was cut with a scalpel to expose the skull. A small incision was carefully made with a drill in the coordinates 1.8 mm lateral and 1 mm anterior to the Lambda. 5 µL of cells were inoculated using a Hamilton 30G syringe into the right corpus striatum, at 2.5 mm of depth. Head incision was closed with Hystoacryl tissue adhesive (Braun) and mice were injected with subcutaneous analgesic Meloxicam (Metacam®) (1 mg/kg). The final cell number implanted into each mouse was 3×10^5 .

[0149] Mice were treated twice a week with h5D8 administered intraperitoneally. Treatment was initiated on day 0, immediately after tumor cell inoculation. Mice received a total of 2 doses of h5D8 or vehicle control.

[0150] Body weight and tumor volume: Body weight was measured 2 times/week and tumor growth was quantified by bioluminescence on day 7 (Xenogen IVIS Spectrum). To quantify bioluminescence activity in vivo, mice were anaesthetized using isoflurane, and injected intraperitoneally with luciferin substrate (PerkinElmer) (167 µg/kg).

[0151] Tumor size as determined by bioluminescence (Xenogen IVIS Spectrum) was evaluated at day 7. The individual tumor measurements and mean±SEM for each treatment group were calculated. Statistical significance was determined by the unpaired non-parametric Mann-Whitney U-test.

Example 12—h5D8 Inhibits Tumor Growth in a Mouse Model of Ovarian Cancer

[0152] The efficacy of r5D8 was evaluated in two other syngeneic tumor models. In the ovarian orthotopic tumor model ID8, IP administration of 300 µg r5D8 twice weekly significantly inhibited tumor growth as measured by abdominal volume (FIGS. 8A and 8B). Results in FIG. 8C show that h5D8 also reduced tumor volume at a dose of 200 µg and above.

Methods

[0153] ID8 cells were cultured in Dulbecco's Modified Eagle Medium (DMEM) (Gibco, Invitrogen), supplemented with 10% Fetal Bovine Serum (FBS) (Gibco, Invitrogen), 40 U/mL Penicillin and 40 µg/mL Streptomycin (PenStrep) (Gibco, Invitrogen) and 0.25 µg/mL Plasmocin (Invivogen). [0154] The ID8 cells were harvested, washed in PBS, centrifuged at 400 g for 5 min and resuspended in PBS. Cells were kept on ice to maintain optimal viability and 200 µL of the cell suspension was injected intraperitoneally with a 27G needle. The final cell number implanted into mice was 5×10⁶. [0155] Mice were treated twice weekly with h5D8 administered ip at different doses as indicated. Body weights were measured 2 times/week and tumor progression was monitored by measuring abdominal girth using a caliper (Fisher Scientific).

Example 13—r5D8 Inhibits Tumor Growth in a Mouse Model of Colorectal Cancer

[0156] In mice with subcutaneous colon CT26 tumors, r5D8 (administered 300 µg IP twice weekly) significantly inhibited tumor growth (FIGS. 9A and 9B).

Methods

[0157] CT26 cells were cultured in Roswell Park Memorial Institute medium (RPMI [Gibco, Invitrogen]), supplemented with 10% Fetal Bovine Serum (FBS), 40 U/mL penicillin and 40 µg/mL streptomycin (PenStrep) and 0.25 µg/mL Plasmocin. [0158] CT26 cells (8×10⁵) were trypsinized, rinsed with PBS, centrifuged at 400 g for 5 minutes and resuspended in 100 µL PBS. Cells were kept on ice to avoid cell death. The CT26 cells were administered to mice via subcutaneous injection using a 27G needle. [0159] 300 µg r5D8, or vehicle control, was administered to the mice via intraperitoneal injection (IP) twice weekly from day 3 post CT26 cell implant. [0160] Body weight and tumor volumes were measured three times per week. Tumor volume was measured using a caliper (Fisher Scientific).

Example 14—r5D8 Reduces Inflammatory Infiltration in Tumor Models

[0161] In the U251 GBM orthotopic model, expression of CCL22, a marker of M2 polarized macrophages, was significantly decreased in tumors treated with r5D8 as shown in FIG. 10A. This finding was also confirmed in a physiologically relevant organotypic tissue slice culture model using h5D8 in which three patient samples showed a significant decrease in CCL22 and CD206 (MRC1) expression (also a marker of M2 macrophages) after treatment with as shown in FIG. 10B (compare upper left, control, to lower right, treated, for both MRC1 and CCL22). Furthermore, r5D8 also decreased CCL22⁺M2 macrophages in syngeneic ID8 (FIG. 10C) and CT26 (FIG. 10D) tumors in immunocompetent mice.

Example 15—r5D8 Increases Non-Myeloid Effector Cells

[0162] To investigate additional immune mechanisms, the effect of r5D8 on T cells and other non-myeloid immune

effector cells within the tumor microenvironment were evaluated. In the ovarian orthotopic ID8 syngeneic model, r5D8 treatment resulted in an increase in intratumoral NK cells and an increase in total and activated CD4⁺ and CD8⁺ T cells as shown in FIG. 11A. Similarly, in the colon syngeneic CT26 tumor model, r5D8 increased intratumoral NK cells, increased CD4⁺ and CD8⁺ T cells and trended to decrease CD4⁺CD25⁺FoxP3⁺ T-reg cells as shown in FIG. 11B. A trend for a decrease in CD4⁺CD25⁺FoxP3⁺ T-reg cells was also observed in the syngeneic orthotopic KLN205 tumor model following r5D8 treatment as shown in FIG. 11C. Consistent with a requirement for T cells to mediate efficacy, depletion of CD4⁺ and CD8⁺ T cells in the CT26 model inhibited the anti-tumor efficacy of r5D8 as shown in FIG. 12.

Methods for T Cell Depletion

[0163] CT26 cells were cultured in RPMI culture medium (Gibco, Invitrogen), supplemented with 10% Fetal Bovine Serum (FBS [Gibco, Invitrogen]), 40 U/mL penicillin and 40 µg/mL streptomycin (PenStrep [Gibco, Invitrogen]) and 0.25 µg/mL Plasmocin (Invivogen). CT26 cells (5×10⁵) were collected, rinsed with PBS, centrifuged at 400 g for 5 minutes and resuspended in 100 µL PBS. Cells were kept on ice to avoid cell death. The CT26 cells were administered in both flanks to mice via subcutaneous injection using a 27G syringe. Mice were treated twice weekly with r5D8 administered intraperitoneally as indicated in the study design. Vehicle control (PBS), rat r5D8, and/or anti-CD4 and anti-CD8 was administered to the mice via intraperitoneal injection (IP) twice weekly as stated in the study design. All antibody treatments were administered concomitantly.

Example 16—Crystal Structure of h5D8 in Complex with Human LIF

[0164] The crystal structure of h5D8 was solved to a resolution of 3.1 angstroms in order to determine the epitope on LIF that h5D8 was bound to and to determine residues of h5D8 that participate in binding. The co-crystal structure revealed that the N-terminal loop of LIF is centrally positioned between the light and heavy chain variable regions of h5D8 (FIG. 13A). In addition, h5D8 interacts with residues on helix A and C of LIF, thereby forming a discontinuous and conformational epitope. Binding is driven by several salt-bridges, H-bonds and Van der Waals interactions (Table 7, FIG. 13B). The h5D8 epitope of LIF spans the region of interaction with gp130. See Boulanger, M. J., Bankovich, A. J., Kortemme, T., Baker, D. & Garcia, K. C. Convergent mechanisms for recognition of divergent cytokines by the shared signaling receptor gp130. Molecular cell 12, 577-589 (2003). The results are summarized below in Table 7 and depicted in FIG. 13.

TABLE 7

Summary of X-Ray crystal structure for h5D8 in complex with human LIF		
LIF Residue (epitope)	Interaction type	h5D8 Residue (paratope, Kabat numbering)
Ala13	VDW	L-Tyr49, L-Asn53
Ile14-O	HB	L-Ser50-OG
Ile	VDW	L-His30, L-Tyr32, L-Tyr49, L-Ser50 H-Trp97

TABLE 7-continued

Summary of X-Ray crystal structure for h5D8 in complex with human LIF		
LIF Residue (epitope)	Interaction type	h5D8 Residue (paratope, Kabat numbering)
Arg15-NE	SB	L-Glu55-OE1, L-Glu55-OE2
Arg15-NH1	SB	L-Glu55-OE1, L-Glu55-OE2
Arg15-NH2	SB	L-Glu55-OE1, L-Glu55-OE2
Arg15-O	HB	L-Asn34-ND2
Arg15	VDW	L-Asn34, L-Leu46, L-Tyr49, L-Glu55, L-Ser56 H-Glu96, H-Trp97, H-Asp98, H-Leu99, H-Asp101
His16-NE2	SB	H-Asp101-OD2
His16	VDW	L-Tyr32, L-Asn34, L-Met89 H-Trp95, H-Glu96, H-Trp97, H-Asp101
Pro17	VDW	L-Tyr32, L-Ala91
Cys18	VDW	H-Trp97 L-Tyr32
His19-NE2	SB	H-Trp33, H-Trp97
His19	VDW	H-Glu96-OE1, H-Glu96-OE2
Asn20-OD1	HB	H-His31, H-Trp33, H-Glu96
Asn20-ND2	HB	H-Lys52-NZ
Asn20	VDW	H-Asp53-OD1
Gln25-NE2	HB	H-Trp33, H-Lys52, H-Asp53
Gln25	VDW	H-Asp53-OD2
Gln29	VDW	H-His31, H-Ser52C, H-Asp53
Gln32	VDW	H-His31
Asp120-OD2	HB	H-Lys52B
Asp120	VDW	H-Ser30-OG
Arg123-NE	HB	H-Thr28, H-Ser30
Arg123	VDW	H-Thr28-OG
Gly124	VDW	H-Thr28
Leu125	VDW	H-His31
Ser127-OG	HB	H-His31
Ser127-O	HB	H-Asp98-OD2
Ser127	VDW	H-Trp97-NE1
Asn128-OD1	HB	H-His31, H-Trp97, H-Asp98
Asn128	VDW	H-His31-NE2
Leu130	VDW	H-His31
Cys131	VDW	H-Trp97
Cys134	VDW	H-Trp97
Ser135-O	HB	L-His30-NE2
Ser135	VDW	L-His30
His138	VDW	L-His30

VDW, van der Waals low energy binding;
HB, hydrogen bond (medium energy binding);
SB, salt bridge (high energy binding)

Methods

[0165] LIF was transiently expressed in HEK 293S (Gnt I^{-/-}) cells and purified using Ni-NTA affinity chromatography, followed by gel-filtration chromatography in 20 mM Tris pH 8.0 and 150 mM NaCl. The recombinant h5D8 Fab was transiently expressed in HEK 293F cells and purified using KappaSelect affinity chromatography, followed by cation exchange chromatography. Purified h5D8 Fab and LIF were mixed at a 1:2.5 molar ratio and incubated at room temperature for 30 min prior to deglycosylation using EndoH. Gel-filtration chromatography was subsequently used to purify the complex. The complex was concentrated to 20 mg/mL and set up for crystallization trials using sparse matrix screens. Crystals formed at 4° C. in a condition containing 19% (v/v) isopropanol, 19% (w/v) PEG 4000, 5% (v/v) glycerol, 0.095 M sodium citrate pH 5.6. The crystal diffracted to a resolution of 3.1 Å at the 08ID-1 beamline at the Canadian Light Source (CLS). Data were collected, processed and scaled using XDS as per Kabsch et

al. Xds. *Acta crystallographica. Section D, Biological crystallography* 66, 125-132 (2010). Structures were determined by molecular replacement using Phaser as per McCoy et al. Phaser crystallographic software. *J Appl Crystallogr* 40, 658-674 (2007). Several iterations of model building and refinement were performed using Coot and phenix.refine until the structures converged to an acceptable R_{work} and R_{free}. See Emsley et al. Features and development of Coot. *Acta crystallographica. Section D, Biological crystallography* 66, 486-501 (2010); and Adams, et al. PHENIX: a comprehensive Python-based system for macromolecular structure solution. *Acta crystallographica. Section D, Biological crystallography* 66, 213-221 (2010) respectively. The figures were generated in PyMOL (The PyMOL Molecular Graphics System, Version 2.0 Schrödinger, LLC).

Example 17—h5D8 has High Specificity for LIF

[0166] We sought to test binding of h5D8 to other LIF family members to determine the binding specificity. Using Octet96 analysis h5D8 binding to human LIF is approximately 100-fold greater than binding to LIFs highest homology IL-6 family member Oncostatin M (OSM) when both proteins are produced in *E. coli*. When both proteins are produced in a mammalian system h5D8 exhibits no binding to OSM. Data are summarized in Table 8.

TABLE 8

Summary of h5D8 Affinity Measurements for Cytokines as Measured by Octet			
	K _D [M]	k _{on} [1/Ms]	k _{dis} [1/s]
h5D8 + huLIF (<i>E. coli</i>)	4.3E-10 +/- -2.0E-11	3.1E+05 +/- -3.1E+03	1.3E-04 +/- -5.8E-06
h5D8 + huLIF (mammalian)	1.3E-09 +/- -7.2E-11	1.2E+05 +/- -1.3E+03	1.5E-04 +/- -8.5E-06
h5D8 + huOSM (<i>E. coli</i>)	3.6E-08 +/- -1.4E-09	8.5E+04 +/- -3.1E+03	3.1E-03 +/- -4.1E-05
h5D8 + huOSM (mammalian)	ND	ND	ND
h5D8 + huIL-6 (<i>E. coli</i>)	ND	ND	ND

ND = no binding

Methods

[0167] Octet Binding Experiments: Reagents were used and prepared as per manufacturer's provided manual. A Basic Kinetics Experiment was performed using Octet Data Acquisition software ver. 9.0.0.26 as follows: Setup of sensors/program: i) Equilibration (60 seconds); ii) Loading (15 seconds); iii) Baseline (60 seconds); iv) Association (180 seconds); and v) Dissociation (600 seconds)

[0168] Octet Affinity of h5D8 for cytokines: A Basic Kinetics Experiment was performed using Octet Data Acquisition software ver. 9.0.0.26 as follows: Amine Reactive 2nd Generation Biosensors (AR2G) were hydrated for a minimum of 15 minutes in water. Amine conjugation of h5D8 to the biosensors was performed according to ForteBio Technical Note 26 (please see References) using the Amine Coupling Second Generation Kit. Dip steps were as performed at 30° C., 1000 rpm as follows: i) 60 seconds Equilibration in water; ii) 300 seconds Activation in 20 mM ECD, 10 mM sulfo-NHS in water; iii) 600 second Immobilization of 10 µg/ml h5D8 in 10 mM Sodium Acetate, pH

6.0; iv) 300 seconds Quench in 1M Ethanolamine, pH 8.5; v) 120 seconds Baseline in water. Kinetics experiments were then performed with the following Dip and Read steps at 30° C., 1000 rpm: vi) 60 seconds Baseline in 1× kinetics buffer; vii) 180 seconds Association of appropriate serial dilutions of a cytokine in 1× kinetics buffer; viii) 300 seconds Dissociation in 1× kinetics buffer; ix) Three Regeneration/Neutralization cycles alternating between 10 mM glycine pH 2.0 and 1× kinetics buffer respectively (5 seconds in each for 3 cycles). Following regeneration, the biosensors were reused for subsequent binding analyses.

[0169] Human recombinant LIF produced from mammalian cells was from ACROBiosystems (LIF-H521b); human recombinant OSM produced in mammalian cells was from R & D (8475-OM/CF); and human recombinant OSM produced in *E. coli* cells was from R & D (295-OM-050/CF).

Example 18—Crystal Structure of h5D8 Fab

[0170] Five crystal structures of the h5D8 Fab under a wide spectrum of chemical conditions were determined. The high resolutions of these structures indicate that the conformations of CDR residues are associated with minor flexibility, and are highly similar in different chemical environments. A unique feature of this antibody is the presence of a non-canonical cysteine in position 100 of the variable heavy region. Structure analysis shows that the cysteine is unpaired and largely inaccessible to the solvent.

[0171] H5D8 Fab was obtained by papain digestion of its IgG, followed by purification using standard affinity, ion exchange and size chromatography techniques. Crystals were obtained using vapor diffusion methods and allowed to determine five crystal structures ranging between 1.65 Å to 2.0 Å in resolution. All structures were solved in the same crystallographic space group and with similar unit cell dimensions (P212121, a~53.8 Å, b~66.5 Å, c~143.3 Å), despite crystallization conditions ranging across five different pH levels: 5.6, 6.0, 6.5, 7.5 and 8.5. As such, these crystal structures allow for comparison of the three-dimensional disposition of h5D8 Fab unimpeded by crystal packing artefacts and across a wide spectrum of chemical conditions.

[0172] Electron density was observed for all complementarity determining region (CDR) residues, which were subsequently modeled. Noticeably, LCDR1 and HCDR2 adopted elongated conformations that together with shallow LCDR3 and HCDR3 regions formed a binding groove at the center of the paratope (FIG. 14A). The five structures were highly similar across all residues, with all-atoms root mean square deviations ranging between 0.197 Å and 0.327 Å (FIG. 14A). These results indicated that the conformations of CDR residues were maintained in various chemical environments, including pH levels ranging between 5.6 and 8.5 and ionic strengths ranging between 150 mM and 1 M. Analysis of the electrostatic surface of the h5D8 paratope revealed that positively and negatively charged regions equally contributed to hydrophilic properties, with no prevalent hydrophobic patches. h5D8 has the uncommon feature of a non-canonical cysteine at the base of HCDR3 (Cys100). In all five structures, this free cysteine is ordered and does not form any disulfide scrambles. Additionally, it is not modified by the addition of Cys (cysteinylation) or glutathione (glutathiolation) and makes van der Waals interactions (3.5-4.3 Å distances) with main chain and side chain atoms of Leu4, Phe27, Trp33, Met34, Glu102 and Leu105 of

the heavy chain (FIG. 14B). Finally, Cys100 is a predominantly buried structural residue that appears to be involved in mediating the conformations of CDR1 and HCDR3. It is thus unlikely to have reactivity with other cysteines, as observed by a homogeneous disposition of this region in our five crystal structures.

Methods

[0173] H5D8-1 IgG was obtained from Catalent Biologics and was formulated in 25 mM histidine, 6% sucrose, 0.01% polysorbate 80, at pH 6.0. The formulated IgG was extensively buffer-exchanged into PBS using a 10K MWCO concentrator (Millipore) prior to digestion with 1:100 microgram papain (Sigma) for 1 hour at 37° C. in PBS, 1.25 mM EDTA, 10 mM cysteine. The papain-digested IgG was flown through a Protein A column (GE Healthcare) using an AKTA Start chromatography system (GE Healthcare). The Protein A flow-through, which contained the h5D8 Fab was recovered and buffer-exchanged into 20 mM sodium acetate, pH 5.6 using a 10K MWCO concentrator (Millipore). The resulting sample was loaded onto a Mono S cation exchange column (GE Healthcare) using an AKTA Pure chromatography system (GE Healthcare). Elution with a gradient of 1 M potassium chloride resulted in a predominant h5D8 Fab peak that was recovered, concentrated and purified to size homogeneity using a Superdex 200 Increase gel filtration column (GE Healthcare) in 20 mM Tris-HCl, 150 mM sodium chloride, at pH 8.0. The high purity of the h5D8 Fab was confirmed by SDS-PAGE under reducing and non-reducing conditions.

[0174] Purified h5D8 Fab was concentrated to 25 mg/mL using a 10K MWCO concentrator (Millipore). An Oryx 4 dispenser (Douglas Instruments) was used to set up vapor diffusion crystallization experiments with sparse matrix 96-conditions commercial screens JCSG TOP96 (Rigaku Reagents) and MCSG-1 (Anatrace) at 20° C. Crystals were obtained and harvested after four days in the following five crystallization conditions: 1) 0.085 M sodium citrate, 25.5% (w/v) PEG 4000, 0.17 M ammonium acetate, 15% (v/v) glycerol, pH 5.6; 2) 0.1 M MES, 20% (w/v) PEG 6000, 1 M lithium chloride, pH 6.0; 3) 0.1 M MES, 20% (w/v) PEG 4000, 0.6 M sodium chloride, pH 6.5; 4) 0.085 M sodium HEPES, 17% (w/v) PEG 4000, 8.5% (v/v) 2-propanol, 15% (v/v) glycerol, pH 7.5; and 5) 0.08 M Tris, 24% (w/v) PEG 4000, 0.16 M magnesium chloride, 20% (v/v) glycerol, pH 8.5. Prior to flash-freezing in liquid nitrogen, mother liquors containing the crystals were supplemented with 5-15% (v/v) glycerol or 10% (v/v) ethylene glycol, as required. Crystals were subjected to X-ray synchrotron radiation at the Advanced Photon Source, beamline 23-ID-D (Chicago, Ill.) and diffraction patterns were recorded on a Pilatus3 6M detector. Data were processed using XDS and structures were determined by molecular replacement using Phaser. Refinement was carried out in PHENIX with iterative model building in Coot. Figures were generated in PyMOL. All software were accessed through SBGrid.

Example 19—Mutations at Cysteine 100 of h5D8 Preserve Binding

[0175] Analysis of h5D8 revealed a free cysteine residue at position 100 (C100) in the variable region of the heavy chain. H5D8 variants were generated by substituting C100 with each naturally occurring amino acid in order to char-

acterize binding to and affinity for human and mouse LIF. Binding was characterized using ELISA and Octet assay. Results are summarized in Table 9. ELISA EC50 curves are shown in FIG. 15 (FIG. 15A human LIF and FIG. 15B Mouse LIF).

TABLE 9

Summary of affinities determined by Octet assay and EC50 determined by ELISA				
Mutation	Affinity/ k_D (M)		Binding EC50 (nM)	
	human LIF	mouse LIF	human LIF	mouse LIF
C100	<1.0E-12 ± 2.252E-11	9.946E-11 ± 8.272E-12	0.09878	0.1605
C100S	8.311E-10 ± 5.886E-11	2.793E-09 ± 5.925E-11	n.d.	n.d.
C100Q	3.87E-09 ± 1.55E-10	2.84E-09 ± 4.85E-11	10.18	26.33
C100N	5.59E-09 ± 1.01E-10	6.68E-09 ± 9.8E-11	13.18	45.87
C100E	2.67E-09 ± 4.64E-11	4.1E-09 ± 7.56E-11	7.179	25.3
C100D	2.02E-09 ± 8.08E-11	6.49E-09 ± 7.16E-11	11.89	22.88
C100T	4.36E-10 ± 2.1E-11	1.02E-09 ± 1.77E-11	5.575	8.753
C100G	2.49E-09 ± 4.2E-11	3.33E-09 ± 5.42E-11	21.94	40.17
C100P	2.74E-10 ± 2.97E-10	<1.0E-12 ± 7.64E-10	34.44	101.9
C100A	<1.0E-12 ± 2.713E-11	<1.0E-12 ± 1.512E-11	0.6705	0.9532
C100V	<1.0E-12 ± 1.805E-11	<1.0E-12 ± 8.086E-12	0.2785	0.3647
C100L	<1.0E-12 ± 1.963E-11	1.998E-10 ± 1.055E-11	0.454	0.547
C100I	<1.0E-12 ± 1.424E-11	3.361E-11 ± 7.545E-12	0.299	0.3916
C100M	1.155E-09 ± 3.400E-11	2.676E-09 ± 2.449E-11	0.7852	1.563
C100F	4.376E-09 ± 1.127E-10	1.147E-08 ± 9.099E-11	8.932	21.53
C100Y	1.444E-08 ± 1.159E-09	2.514E-08 ± 2.047E-09	n.d.	n.d.
C100W	2.508E-08 ± 7.036E-09	4.819E-08 ± 4.388E-09	n.d.	n.d.
C100H	1.304E-10 ± 1.416E-10	4.284E-09 ± 1.231E-10	8.254	n.d.
C100K	7.477E-08 ± 1.581E-09	6.053E-08 ± 2.589E-09	n.d.	n.d.
C100R	1.455E-07 ± 6.964E-09	5.142E-08 ± 3.247E-09	n.d.	n.d.

Methods

[0176] ELISA: Binding of h5D8 C100 variants to human and mouse LIF was determined by ELISA. Recombinant human or mouse LIF protein was coated on Maxisorp 384-well plates at 1 ug/mL overnight at 4° C. Plates were blocked with 1× blocking buffer for 2 hours at room temperature. Titrations of each h5D8 C100 variants were added and allowed to bind for 1 hour at room temperature. Plates were washed three times with PBS+0.05% Tween-20. HRP-conjugated anti-human IgG was added and allowed to bind for 30 min at room temperature. Plates were washed three times with PBS+0.05% Tween-20 and developed using 1×TMB substrate. The reaction was stopped with 1M HCl and absorbance at 450 nm was measured. Generation of figures and non-linear regression analysis was performed using Graphpad Prism.

[0177] Octet RED96: The affinity of h5D8 C100 variants to human and mouse LIF was determined by BLI using the Octet RED96 system. h5D8 C100 variants were loaded onto Anti-Human Fc biosensors at 7.5 ug/mL following a 30 second baseline in 1× kinetics buffer. Titrations of human or mouse LIF protein were associated to the loaded biosensors for 90 seconds and allowed to dissociate in 1× kinetics buffer for 300 seconds. KDs were calculated by the data analysis software using a 1:1 global fit model.

Example 20—h5D8 Blocks Binding of LIF to Gp130 In Vitro

[0178] To determine whether h5D8 prevented LIF from binding to LIFR, a molecular binding assay using the Octet RED 96 platform was performed. H5D8 was loaded onto AHC biosensors by anti-human Fc capture. Then, the biosensors were dipped in LIF and, as expected, association was observed (FIG. 16A, middle third). Subsequently, the biosensors were dipped in different concentrations of LIFR. A dose-dependent association was observed (FIG. 16A, right third). The control experiment demonstrated that this association was LIF-specific (not shown), and not due to a non-specific interaction of LIFR with h5D8 or with the biosensors.

[0179] To further characterize the binding of h5D8 and LIF, a series of ELISA binding experiments was conducted. H5D8 and LIF were pre-incubated and were then introduced to plates coated with either recombinant human LIFR (hLIFR) or gp130. The lack of binding between the h5D8/LIF complex and the coated substrate would indicate that h5D8 in some way disrupted the binding of LIF to the receptor. Additionally, control antibodies that either did not bind LIF (isotype control, indicated by (-)) or that bind LIF at known binding sites (B09 does not compete with either gp130 or LIFR for LIF binding; r5D8 is the rat parental version of h5D8) were also used. The ELISA results demonstrated that the h5D8/LIF complex was able to bind hLIFR (as was r5D8/LIF complex), indicating that these antibodies did not prevent the LIF/LIFR association (FIG. 16A). In contrast, the h5D8/LIF complex (and a r5D8/LIF complex) was not able to bind recombinant human gp130 (FIG. 16B). This indicates that the gp130 binding site of LIF was affected when LIF was bound to h5D8.

Example 21—LIF and LIFR Expression in Human Tissues

[0180] Quantitative real-time PCR was performed on many different types of human tissue in order to determine expression levels of LIF and LIFR. The mean expression levels shown in FIGS. 17A and 17B are given as copies per 100 ng of total RNA. Most tissues expressed at least 100 copies per 100 ng of total RNA. LIF mRNA expression was highest in human adipose tissue (mesenteric-ileum [1]), blood-vessel tissue (choroid-plexus [6] and mesenteric [8]) and umbilical cord [68] tissue and lowest in brain tissue (cortex [20] and substantia-nigra [28]). LIFR mRNA expression was highest in human adipose tissue (mesenteric-ileum [1]), blood vessel tissue (pulmonary [9]), brain tissue [11-28] and thyroid [66] tissue and was lowest in PBMCs [31]. LIF and LIFR mRNA expression levels in cynomolgus tissues were similar to those observed in human tissues, wherein LIF expression was high in adipose tissue and LIFR expression was high in adipose tissue and low in PBMCs (data not shown).

The tissue numbering for FIG. 17A and FIG. 17B is: 1—adipose (mesenteric-ileum); 2—adrenal gland; 3—bladder; 4—bladder (trigone); 5—blood-vessel (cerebral: middle-cerebral-artery); 6—blood vessel (choroid-plexus); 7—blood vessel (coronary artery); 8—blood vessel (mesenteric (colon)); 9—blood vessel (pulmonary); 10—blood vessel (renal); 11—brain (amygdala); 12—brain (caudate); 13—brain (cerebellum); 14 brain—(cortex: cingulate-anterior); 15—brain (cortex: cingulate-posterior); 16—brain (cortex: frontal-lateral); 17—brain (cortex: frontal-medial); 18—brain (cortex: occipital); 19—brain (cortex: parietal); 20—brain (cortex: temporal); 21—brain (dorsal-raphenucleus); 22—brain (hippocampus); 23—brain (hypothalamus: anterior); 24—brain (hypothalamus: posterior); 25—brain (locus coeruleus); 26—brain (medulla oblongata); 27—brain (nucleus accumbens); 28—brain (substantia nigra); 29—breast; 30—caecum; 31-peripheral blood mononuclear cell (PBMCs); 32—colon; 33—dorsal root ganglia (DRG); 34—duodenum; 35—fallopian tube; 36—gallbladder; 37—heart (left atrium); 38—heart (left ventricle); 39—ileum; 40—jejunum; 41—kidney (cortex); 42—kidney (medulla); 43—kidney (pelvis); 44—liver (parenchyma); 45—liver (bronchus: primary); 46—liver (bronchus: tertiary); 47—lung (parenchyma); 48—lymph gland (tonsil); 49—muscle (skeletal); 50—esophagus; 51—ovary;

52—pancreas; 53—pineal gland; 54—pituitary gland; 55—placenta; 56—prostate; 57—rectum; 58—skin (fore-skin); 59—spinal cord; 60—spleen (parenchyma); 61—stomach (antrum); 62—stomach (body); 63—stomach (fundus); 64—stomach (pyloric canal); 65—testis; 66—thyroid gland; 67—trachea; 68—umbilical cord; 69—ureter; 70—uterus (cervix); 71—uterus (myometrium); and 72—vas deferens.

[0181] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention.

[0182] All publications, patent applications, issued patents, and other documents referred to in this specification are herein incorporated by reference as if each individual publication, patent application, issued patent, or other document was specifically and individually indicated to be incorporated by reference in its entirety. Definitions that are contained in text incorporated by reference are excluded to the extent that they contradict definitions in this disclosure.

SEQUENCES		
SEQ ID NO	Sequence	
1	GFTFSAWMH	
2	GFTFSHAW	
3	HAWMH	
4	GFTFSNAWMH	
5	GFTFSNAW	
6	NAWMH	
7	SKPMY	
8	SNFIH	
9	QIKAKSDDYATYYAESVKG	
10	IKAKSDDYAT	
11	QIKDKSDNYATYYAESVKG	
12	IKDKSDNYAT	
13	WIYPGDGDTEYNQKFSE	
14	WIYPGDGDIEYNQKFIG	
15	TCWEWDLDF	
16	WEWDLDF	
17	TCWEWYLDF	
18	WEWYLDF	
19	RDYHSSHFAY	
20	HYSSMDA	
21	RSSQSLDSDGHTYLN	

- continued

SEQUENCES		
SEQ ID NO	Sequence	
22	QSLDSDGHTY	
23	RSSQSLHNGNTYLS	
24	RSSQSLVHNGNTFLS	
25	SVSNLES	
26	SYS	
27	QVSNRFS	
28	KVSNRFS	
29	MQATHAPPYT	
30	GQGTQYPYT	
31	GQGTQYPFT	
32	SGYYWN	
33	TAGMQ	
34	CISYDGRNNYNPSLKN	
35	WINTQSGEPQYVDDFRG	
36	RYRYNYGSYYAVDY	
37	WALYSEYDVMDY	
38	RASENIDGYLE	
39	KASENYDSYVS	
40	AATLLAD	
41	GASNRYT	
42	QHYYNTPLT	
43	GQSYRYPPT	
44	EVQLVESGGGLVKPGGSLKLSCAAS	
45	QVQLQESGGGLVKPGGSLRLSCAAS	
46	EVQLVESGGGVVQPGRSRLRLSCAAS	
47	EVQLMESGGGLVKPGGSLRLSCATS	
48	WVRQAPGKGLEWVA	
49	WVRQAPGKGLEWVG	
50	RFTISRDDSKNTLYLQMNSLKTEDTAVYYC	
51	RFSISRDNAKNSLYLQMNSLRVEDTVVYYC	
52	RFTISRDDSKSTLFLQMNNLKTEDTAVYYC	
53	WGQGTLLTVSS	
54	WGQGTMTVTVSS	
55	WGQGTTVTVSS	
56	DVVMTQSPLSLPVTLGQPASISC	
57	DIVMTQTPLSSPVTLGQPASISC	

- continued

SEQUENCES		
SEQ ID NO	Sequence	
58	DIVMTQTPLSLSVTPGQPASISC	
59	DVVMTQSPLSQPVTLGQPASISC	
60	WFQQRPGQSPRRLIY	
61	WLQQRPGQPPRLLIY	
62	WLLQKPGQPPQLLIY	
63	WLQQRPGQSPRRLIY	
64	GVPDRFSGSGGTDFTLKISRVEADVGLYYC	
65	GVPDRFSGSGAGTDFTLKISRVEADVGVYYC	
66	GVPNRFSGSGGTDFTLKISRVEADVGLYYC	
67	GVPDRFNGSGGTDFTLISRVEADVGVYYC	
68	FGQGTKLEIK	
69	FGGGTKVEIK	
70	FGQGTKVEIK	
71	EVQLVESGGGLVKPGGSLRLSCAASGFTFSHAWMHWRQAPGKLEWVAQIKAKSDDYATYYAE SVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTCWEWDLDFWGQGLTVTVSS	
72	QVQLQESGGGLVKPGGSLRLSCAASGFTFSHAWMHWRQAPGKLEWVGQIKAKSDDYATYYAE SVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTCWEWDLDFWGQGMVTVSS	
73	EVQLVESGGGVQPGRSLRLSCAASGFTFSHAWMHWRQAPGKLEWVAQIKAKSDDYATYYAE SVKGRFISRDNAKNSLYLQMNSLRVEDTVVYYCTCWEWDLDFWGQGTTVTVSS	
74	EVQLMESGGGLVKPGGSLRLSCATSGFTFSHAWMHWRQAPGKLEWVGQIKAKSDDYATYYAE SVKGRFTISRDDSKSTFLQMNNLKTEDTAVYYCTCWEWDLDFWGQGLTVTVSS	
75	DVVMTQSPLSLPVTLGQPASISCRSSQSLDSDGHTYLNWLFQQRPGQSPRRLIYSVSNLESGVP DRFSGSGSGTDFTLKISRVEADVGLYYCMQATHAPPYTFGQGTKLEIK	
76	DIVMTQTPLSSPVTLGQPASISCRSSQSLDSDGHTYLNWLFQQRPGQPPRLLIYSVSNLESGVP DRFSGSGAGTDFTLKISRVEADVGVYYCMQATHAPPYTFGQGTKLEIK	
77	DIVMTQTPLSLSVTPGQPASISCRSSQSLDSDGHTYLNWLLQKPGQPPQLLIYSVSNLESGVP NRFSGSGSGTDFTLKISRVEADVGLYYCMQATHAPPYTFGGGTKVEIK	
78	DVVMTQSPLSQPVTLGQPASISCRSSQSLDSDGHTYLNWLFQQRPGQSPRRLIYSVSNLESGVP DRFNGSGSGTDFTLISRVEADVGVYYCMQATHAPPYTFGQGTKVEIK	
79	MGWTLVFLFLLSVTAGVHSEVQLVESGGGLVKPGGSLRLSCAASGFTFSHAWMHWRQAPGKGL EWVAQIKAKSDDYATYYAESVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTCWEWDLDFWG QGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFPSCSVM HEALHNHYTQKSLSLSPGK	
80	MGWTLVFLFLLSVTAGVHSQVQLQESGGGLVKPGGSLRLSCAASGFTFSHAWMHWRQAPGKGL EWVGQIKAKSDDYATYYAESVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTCWEWDLDFWG QGLTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFPSCSVM HEALHNHYTQKSLSLSPGK	
81	MGWTLVFLFLLSVTAGVHSEVQLVESGGGVQPGRSLRLSCAASGFTFSHAWMHWRQAPGKGL EWVAQIKAKSDDYATYYAESVKGRFISRDNAKNSLYLQMNSLRVEDTVVYYCTCWEWDLDFWG QGLTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPELLG	

- continued

SEQUENCES	
SEQ ID NO	Sequence
	GPSVFLFPPKPKDTLMISRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
82	MGWTLVFLFLLSVTAGVHSEVQLMESGGGLVKPGGSLRLSCATSGFTFSHAWMHWRQAPGKGL EWVGQIKAKSDDYATYYAESVKGRFTISRDDSKSTFLQMNNLKTEDTAVYYCTCWEWDLDFWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
83	MVSSAQFLGLLLCFQGTTRCDVMTQSPSLSPVTLGQPASISCRSSQSLDSDGHTYLNWFQOR PGQSPRRLIYSVSNLESGVDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQATHAPPYTFGGGT KLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
84	MVSSAQFLGLLLCFQGTTRCDIVMTQTPLSLSPVTLGQPASISCRSSQSLDSDGHTYLNWLQOR PGQSPRRLIYSVSNLESGVDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQATHAPPYTFGGGT KLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
85	MVSSAQFLGLLLCFQGTTRCDIVMTQTPLSLSPVTPGQPASISCRSSQSLDSDGHTYLNWLQK PGQPPQLLIYSVSNLESGVDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQATHAPPYTFGGGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
86	MVSSAQFLGLLLCFQGTTRCDVMTQSPSLSPVTLGQPASISCRSSQSLDSDGHTYLNWLQOR PGQSPRRLIYSVSNLESGVDRFSGSGSGTDFTLISRVEAEDVGLYYCMQATHAPPYTFGGGT KVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
87	EVQLVESGGGLVKPGGSLKLSCAASGFTFSHAWMHWRQAPGKGLEWVAQIKAKSDDYATYYAE SVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTCWEWDLDFWGQGTTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
88	QVQLQESGGGLVKPGGSLRLSCAASGFTFSHAWMHWRQAPGKGLEWVQGIKAKSDDYATYYAE SVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTCWEWDLDFWGQGTMTVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
89	EVQLVESGGGVVQGRSLRLSCAASGFTFSHAWMHWRQAPGKGLEWVAQIKAKSDDYATYYAE SVKGRFTISRDNKNSLYLQMNSLRVEDTVVYYCTCWEWDLDFWGQGTMTVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
90	EVQLMESGGGLVKPGGSLRLSCATSGFTFSHAWMHWRQAPGKGLEWVQGIKAKSDDYATYYAE SVKGRFTISRDDSKSTFLQMNNLKTEDTAVYYCTCWEWDLDFWGQGTTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
91	DVMTQSPSLSPVTLGQPASISCRSSQSLDSDGHTYLNWFQORPGQSPRRLIYSVSNLESGV DRFSGSGSGTDFTLKISRVEAEDVGLYYCMQATHAPPYTFGGGT KLEIKRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC

- continued

SEQUENCES		
SEQ ID NO	Sequence	
92	DIVMTQTPLSSPVTLGQPASISCRSSQSLLSDSGHTYLNWLQQRPGQPPRLLIYSVSNLESGVP DRFSGSGAGTDFTLTKISRVEAEDVGVIYCMQATHAPPYTFGGGKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC	
93	DIVMTQTPLSLSVTPGQPASISCRSSQSLLSDSGHTYLNWLLQKPGQPQLLIYSVSNLESGVP NRFSGSGAGTDFTLTKISRVEAEDVGVIYCMQATHAPPYTFGGGKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC	
94	DVVMTQSPLSQPVTLGQPASISCRSSQSLLSDSGHTYLNWLQQRPGQSPRLLIYSVSNLESGVP DRFSGSGAGTDFTLTKISRVEAEDVGVIYCMQATHAPPYTFGGGKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC	
95	TSWEWDLDF	
96	QVQLQESGGGLVKPGGSLRLSCAASGFTFSHAWMHWRQAPGKGLEWVGQIKAKSDDYATYYAE SVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSWEWDLDFWGQGTMTVSS	
97	QVQLQESGGGLVKPGGSLRLSCAASGFTFSHAWMHWRQAPGKGLEWVGQIKAKSDDYATYYAE SVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTSWEWDLDFWGQGTMTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK	
98	SPLPITPVNATCAIRPHCHNNLMNQIRSQLAQLNGSANALFILYYTAQGEPPFNNLDKLCGPNV TDFPPPHANGTEKAKLVLELYRIVVYLGTSLGNIIRDQKILNPSALSLHSLNATADILRGLLSN VLCRLCSKYHVGHVDTYGPDTSGKDVFPKKKLGQQLLGKYGKQIIAVLAQAF	

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 98

<210> SEQ ID NO 1
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 1

Gly Phe Thr Phe Ser His Ala Trp Met His
1 5 10

<210> SEQ ID NO 2
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 2

Gly Phe Thr Phe Ser His Ala Trp
1 5

<210> SEQ ID NO 3

-continued

<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 3

His Ala Trp Met His
1 5

<210> SEQ ID NO 4
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 4

Gly Phe Thr Phe Ser Asn Ala Trp Met His
1 5 10

<210> SEQ ID NO 5
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 5

Gly Phe Thr Phe Ser Asn Ala Trp
1 5

<210> SEQ ID NO 6
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 6

Asn Ala Trp Met His
1 5

<210> SEQ ID NO 7
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 7

Ser Lys Phe Met Tyr
1 5

<210> SEQ ID NO 8
<211> LENGTH: 5

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 8

Ser Asn Phe Ile His
1 5

<210> SEQ ID NO 9
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 9

Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> SEQ ID NO 10
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 10

Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr
1 5 10

<210> SEQ ID NO 11
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 11

Gln Ile Lys Asp Lys Ser Asp Asn Tyr Ala Thr Tyr Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> SEQ ID NO 12
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 12

Ile Lys Asp Lys Ser Asp Asn Tyr Ala Thr
1 5 10

-continued

<210> SEQ ID NO 13
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 13

Trp Ile Tyr Pro Gly Asp Gly Asp Thr Glu Tyr Asn Gln Lys Phe Ser
1 5 10 15

Glu

<210> SEQ ID NO 14
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 14

Trp Ile Tyr Pro Gly Asp Gly Asp Ile Glu Tyr Asn Gln Lys Phe Ile
1 5 10 15

Gly

<210> SEQ ID NO 15
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 15

Thr Cys Trp Glu Trp Asp Leu Asp Phe
1 5

<210> SEQ ID NO 16
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 16

Trp Glu Trp Asp Leu Asp Phe
1 5

<210> SEQ ID NO 17
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 17

-continued

Thr Cys Trp Glu Trp Tyr Leu Asp Phe
1 5

<210> SEQ ID NO 18
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 18

Trp Glu Trp Tyr Leu Asp Phe
1 5

<210> SEQ ID NO 19
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 19

Arg Asp Tyr His Ser Ser His Phe Ala Tyr
1 5 10

<210> SEQ ID NO 20
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 20

His Tyr Ser Ser Ser Met Asp Ala
1 5

<210> SEQ ID NO 21
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 21

Arg Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly His Thr Tyr Leu Asn
1 5 10 15

<210> SEQ ID NO 22
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 22

Gln Ser Leu Leu Asp Ser Asp Gly His Thr Tyr

-continued

1	5	10
---	---	----

<210> SEQ ID NO 23
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 23

Arg Ser Ser Gln Ser Leu Leu His Asn Asn Gly Asn Thr Tyr Leu Ser
1 5 10 15

<210> SEQ ID NO 24
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 24

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Phe Leu Ser
1 5 10 15

<210> SEQ ID NO 25
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 25

Ser Val Ser Asn Leu Glu Ser
1 5

<210> SEQ ID NO 26
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 26

Ser Val Ser
1

<210> SEQ ID NO 27
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 27

Gln Val Ser Asn Arg Phe Ser
1 5

-continued

<210> SEQ ID NO 28
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 28

Lys Val Ser Asn Arg Phe Ser
1 5

<210> SEQ ID NO 29
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 29

Met Gln Ala Thr His Ala Pro Pro Tyr Thr
1 5 10

<210> SEQ ID NO 30
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 30

Gly Gln Gly Thr Gln Tyr Pro Tyr Thr
1 5

<210> SEQ ID NO 31
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 31

Gly Gln Gly Thr Gln Tyr Pro Phe Thr
1 5

<210> SEQ ID NO 32
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 32

Ser Gly Tyr Tyr Trp Asn
1 5

-continued

<210> SEQ ID NO 33
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 33

Thr Ala Gly Met Gln
1 5

<210> SEQ ID NO 34
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 34

Cys Ile Ser Tyr Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu Lys Asn
1 5 10 15

<210> SEQ ID NO 35
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 35

Trp Ile Asn Thr Gln Ser Gly Glu Pro Gln Tyr Val Asp Asp Phe Arg
1 5 10 15

Gly

<210> SEQ ID NO 36
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 36

Arg Tyr Arg Tyr Tyr Asn Tyr Gly Ser Tyr Tyr Ala Val Asp Tyr
1 5 10 15

<210> SEQ ID NO 37
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 37

Trp Ala Leu Tyr Ser Glu Tyr Asp Val Met Asp Tyr
1 5 10

-continued

<210> SEQ ID NO 38
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 38

Arg Ala Ser Glu Asn Ile Asp Gly Tyr Leu Glu
1 5 10

<210> SEQ ID NO 39
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 39

Lys Ala Ser Glu Asn Val Asp Ser Tyr Val Ser
1 5 10

<210> SEQ ID NO 40
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 40

Ala Ala Thr Leu Leu Ala Asp
1 5

<210> SEQ ID NO 41
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 41

Gly Ala Ser Asn Arg Tyr Thr
1 5

<210> SEQ ID NO 42
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 42

Gln His Tyr Tyr Asn Thr Pro Leu Thr
1 5

-continued

<210> SEQ ID NO 43
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 43

Gly Gln Ser Tyr Arg Tyr Pro Pro Thr
1 5

<210> SEQ ID NO 44
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 44

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser
20 25

<210> SEQ ID NO 45
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 45

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> SEQ ID NO 46
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 46

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> SEQ ID NO 47
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source

-continued

<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 47

Glu Val Gln Leu Met Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Thr Ser
20 25

<210> SEQ ID NO 48

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: source

<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 48

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> SEQ ID NO 49

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: source

<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 49

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
1 5 10

<210> SEQ ID NO 50

<211> LENGTH: 30

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: source

<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 50

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> SEQ ID NO 51

<211> LENGTH: 30

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: source

<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 51

Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Arg Val Glu Asp Thr Val Val Tyr Tyr Cys
20 25 30

-continued

<210> SEQ ID NO 52
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 52

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Phe Leu Gln
1 5 10 15
Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> SEQ ID NO 53
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 53

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> SEQ ID NO 54
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 54

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> SEQ ID NO 55
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 55

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> SEQ ID NO 56
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 56

-continued

Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly
1				5					10					15	

Gln	Pro	Ala	Ser	Ile	Ser	Cys
				20		

<210> SEQ ID NO 57
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 57

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Ser	Pro	Val	Thr	Leu	Gly
1				5					10					15	

Gln	Pro	Ala	Ser	Ile	Ser	Cys
				20		

<210> SEQ ID NO 58
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 58

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Thr	Pro	Gly
1				5					10					15	

Gln	Pro	Ala	Ser	Ile	Ser	Cys
				20		

<210> SEQ ID NO 59
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 59

Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Gln	Pro	Val	Thr	Leu	Gly
1				5					10					15	

Gln	Pro	Ala	Ser	Ile	Ser	Cys
				20		

<210> SEQ ID NO 60
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 60

Trp	Phe	Gln	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Arg	Arg	Leu	Ile	Tyr
1				5					10					15

-continued

<210> SEQ ID NO 61
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 61

Trp Leu Gln Gln Arg Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> SEQ ID NO 62
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 62

Trp Leu Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> SEQ ID NO 63
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 63

Trp Leu Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
1 5 10 15

<210> SEQ ID NO 64
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 64

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys
20 25 30

<210> SEQ ID NO 65
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 65

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr
1 5 10 15

-continued

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> SEQ ID NO 66
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 66

Gly Val Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys
20 25 30

<210> SEQ ID NO 67
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 67

Gly Val Pro Asp Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Ser Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> SEQ ID NO 68
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 68

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> SEQ ID NO 69
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 69

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> SEQ ID NO 70
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic peptide"

<400> SEQUENCE: 70

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> SEQ ID NO 71
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 71

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Ala
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 72
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 72

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Ala
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly Gln Gly Thr

-continued

100	105	110
Met Val Thr Val Ser Ser		
115		
<210> SEQ ID NO 73		
<211> LENGTH: 118		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<221> NAME/KEY: source		
<223> OTHER INFORMATION: /note="Description of Artificial Sequence: Synthetic polypeptide"		
<400> SEQUENCE: 73		
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg		
1 5 10 15		
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Ala		
20 25 30		
Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35 40 45		
Ala Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr Tyr Ala Glu		
50 55 60		
Ser Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser		
65 70 75 80		
Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Val Val Tyr		
85 90 95		
Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly Gln Gly Thr		
100 105 110		
Thr Val Thr Val Ser Ser		
115		
<210> SEQ ID NO 74		
<211> LENGTH: 118		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<221> NAME/KEY: source		
<223> OTHER INFORMATION: /note="Description of Artificial Sequence: Synthetic polypeptide"		
<400> SEQUENCE: 74		
Glu Val Gln Leu Met Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly		
1 5 10 15		
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser His Ala		
20 25 30		
Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35 40 45		
Gly Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr Tyr Ala Glu		
50 55 60		
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr		
65 70 75 80		
Leu Phe Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr		
85 90 95		
Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly Gln Gly Thr		
100 105 110		
Leu Val Thr Val Ser Ser		
115		

-continued

<210> SEQ ID NO 75
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 75

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30
Asp Gly His Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45
Pro Arg Arg Leu Ile Tyr Ser Val Ser Asn Leu Glu Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Ala
85 90 95
Thr His Ala Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> SEQ ID NO 76
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 76

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30
Asp Gly His Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45
Pro Arg Leu Leu Ile Tyr Ser Val Ser Asn Leu Glu Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95
Thr His Ala Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> SEQ ID NO 77
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 77

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30
Asp Gly His Thr Tyr Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Pro
35 40 45
Pro Gln Leu Leu Ile Tyr Ser Val Ser Asn Leu Glu Ser Gly Val Pro
50 55 60
Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Ala
85 90 95
Thr His Ala Pro Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> SEQ ID NO 78
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 78

Asp Val Val Met Thr Gln Ser Pro Leu Ser Gln Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30
Asp Gly His Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45
Pro Arg Arg Leu Ile Tyr Ser Val Ser Asn Leu Glu Ser Gly Val Pro
50 55 60
Asp Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95
Thr His Ala Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> SEQ ID NO 79
<211> LENGTH: 467
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 79

Met 1	Gly	Trp	Thr	Leu 5	Val	Phe	Leu	Phe	Leu 10	Leu	Ser	Val	Thr	Ala 15	Gly
Val	His	Ser	Glu 20	Val	Gln	Leu	Val	Glu 25	Ser	Gly	Gly	Gly	Leu 30	Val	Lys
Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser 40	Cys	Ala	Ala	Ser	Gly 45	Phe	Thr	Phe
Ser	His	Ala	Trp	Met	His	Trp 55	Val	Arg	Gln	Ala	Pro 60	Gly	Lys	Gly	Leu
Glu 65	Trp	Val	Ala	Gln	Ile 70	Lys	Ala	Lys	Ser	Asp 75	Asp	Tyr	Ala	Thr	Tyr 80
Tyr	Ala	Glu	Ser	Val 85	Lys	Gly	Arg	Phe	Thr 90	Ile	Ser	Arg	Asp	Asp 95	Ser
Lys	Asn	Thr	Leu 100	Tyr	Leu	Gln	Met	Asn 105	Ser	Leu	Lys	Thr	Glu 110	Asp	Thr
Ala	Val	Tyr	Tyr	Cys	Thr	Cys	Trp 120	Glu	Trp	Asp	Leu	Asp 125	Phe	Trp	Gly
Gln	Gly	Thr	Leu	Val	Thr	Val 135	Ser	Ser	Ala	Ser	Thr 140	Lys	Gly	Pro	Ser
Val 145	Phe	Pro	Leu	Ala	Pro 150	Ser	Ser	Lys	Ser	Thr 155	Ser	Gly	Gly	Thr	Ala 160
Ala	Leu	Gly	Cys	Leu 165	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr 175	Val
Ser	Trp	Asn	Ser	Gly 180	Ala	Leu	Thr	Ser 185	Gly	Val	His	Thr 190	Phe	Pro	Ala
Val	Leu	Gln	Ser	Ser 195	Gly	Leu	Tyr 200	Ser	Leu	Ser	Ser	Val 205	Val	Thr	Val
Pro	Ser	Ser	Ser	Leu 210	Gly	Thr 215	Gln	Thr	Tyr	Ile	Cys 220	Asn	Val	Asn	His
Lys 225	Pro	Ser	Asn	Thr	Lys 230	Val	Asp	Lys	Lys	Val 235	Glu	Pro	Lys	Ser	Cys 240
Asp	Lys	Thr	His	Thr 245	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu 255	Gly
Gly	Pro	Ser	Val	Phe 260	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr 270	Leu	Met
Ile	Ser	Arg	Thr	Pro 275	Glu	Val	Thr 280	Cys	Val	Val	Val	Asp 285	Val	Ser	His
Glu	Asp 290	Pro	Glu	Val	Lys	Phe 295	Asn	Trp	Tyr	Val	Asp 300	Gly	Val	Glu	Val
His 305	Asn	Ala	Lys	Thr	Lys 310	Pro	Arg	Glu	Glu	Gln 315	Tyr	Asn	Ser	Thr	Tyr 320
Arg	Val	Val	Ser	Val 325	Leu	Thr	Val	Leu	His	Gln 330	Asp	Trp	Leu	Asn 335	Gly
Lys	Glu	Tyr	Lys	Cys 340	Lys	Val	Ser	Asn 345	Lys	Ala	Leu	Pro	Ala 350	Pro	Ile
Glu	Lys	Thr	Ile	Ser 355	Lys	Ala	Lys	Gly 360	Gln	Pro	Arg	Glu 365	Pro	Gln	Val
Tyr	Thr 370	Leu	Pro	Pro	Ser	Arg 375	Asp	Glu	Leu	Thr	Lys 380	Asn	Gln	Val	Ser
Leu 385	Thr	Cys	Leu	Val	Lys 390	Gly	Phe	Tyr	Pro	Ser	Asp 395	Ile	Ala	Val	Glu 400

-continued

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Pro Gly Lys
 465
 <210> SEQ ID NO 80
 <211> LENGTH: 467
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: source
 <223> OTHER INFORMATION: /note="Description of Artificial Sequence:
 Synthetic polypeptide"
 <400> SEQUENCE: 80
 Met Gly Trp Thr Leu Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys
 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser His Ala Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Gly Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr
 65 70 75 80
 Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85 90 95
 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
 100 105 110
 Ala Val Tyr Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly
 115 120 125
 Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 130 135 140
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 145 150 155 160
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 165 170 175
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 180 185 190
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 195 200 205
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 210 215 220
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 225 230 235 240
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 245 250 255
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

-continued

260	265	270
Ile Ser Arg Thr Pro Glu Val	Thr Cys Val Val Val	Asp Val Ser His
275	280	285
Glu Asp Pro Glu Val Lys Phe	Asn Trp Tyr Val Asp	Gly Val Glu Val
290	295	300
His Asn Ala Lys Thr Lys Pro	Arg Glu Glu Gln Tyr Asn	Ser Thr Tyr
305	310	315
Arg Val Val Ser Val Leu Thr	Val Leu His Gln Asp Trp	Leu Asn Gly
325	330	335
Lys Glu Tyr Lys Cys Lys Val	Ser Asn Lys Ala Leu Pro	Ala Pro Ile
340	345	350
Glu Lys Thr Ile Ser Lys Ala	Lys Gly Gln Pro Arg Glu	Pro Gln Val
355	360	365
Tyr Thr Leu Pro Pro Ser Arg	Asp Glu Leu Thr Lys Asn	Gln Val Ser
370	375	380
Leu Thr Cys Leu Val Lys Gly	Phe Tyr Pro Ser Asp Ile	Ala Val Glu
385	390	395
Trp Glu Ser Asn Gly Gln Pro	Glu Asn Asn Tyr Lys Thr	Thr Pro Pro
405	410	415
Val Leu Asp Ser Asp Gly Ser	Phe Phe Leu Tyr Ser Lys	Leu Thr Val
420	425	430
Asp Lys Ser Arg Trp Gln Gln	Gly Asn Val Phe Ser Cys	Ser Val Met
435	440	445
His Glu Ala Leu His Asn His	Tyr Thr Gln Lys Ser Leu	Ser Leu Ser
450	455	460
Pro Gly Lys		
465		

<210> SEQ ID NO 81
 <211> LENGTH: 467
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: source
 <223> OTHER INFORMATION: /note="Description of Artificial Sequence:
 Synthetic polypeptide"

<400> SEQUENCE: 81

Met Gly Trp Thr Leu Val Phe	Leu Phe Leu Leu Ser Val	Thr Ala Gly
1	5	10
Val His Ser Glu Val Gln Leu	Val Glu Ser Gly Gly Gly	Val Val Gln
20	25	30
Pro Gly Arg Ser Leu Arg Leu	Ser Cys Ala Ala Ser Gly	Phe Thr Phe
35	40	45
Ser His Ala Trp Met His Trp	Val Arg Gln Ala Pro Gly	Lys Gly Leu
50	55	60
Glu Trp Val Ala Gln Ile Lys	Ala Lys Ser Asp Asp Tyr	Ala Thr Tyr
65	70	75
Tyr Ala Glu Ser Val Lys Gly	Arg Phe Ser Ile Ser Arg	Asp Asn Ala
85	90	95
Lys Asn Ser Leu Tyr Leu Gln	Met Asn Ser Leu Arg Val	Glu Asp Thr
100	105	110
Val Val Tyr Tyr Cys Thr Cys	Trp Glu Trp Asp Leu Asp	Phe Trp Gly
115	120	125

-continued

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 130 135 140
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 145 150 155 160
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 165 170 175
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 180 185 190
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 195 200 205
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 210 215 220
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 225 230 235 240
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 245 250 255
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 275 280 285
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 305 310 315 320
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 340 345 350
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Pro Gly Lys
 465

<210> SEQ ID NO 82

<211> LENGTH: 467

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: source

 <223> OTHER INFORMATION: /note="Description of Artificial Sequence:
 Synthetic polypeptide"

-continued

<400> SEQUENCE: 82

```

Met Gly Trp Thr Leu Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
 1          5          10          15

Val His Ser Glu Val Gln Leu Met Glu Ser Gly Gly Gly Leu Val Lys
 20          25          30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe
 35          40          45

Ser His Ala Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50          55          60

Glu Trp Val Gly Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr
 65          70          75          80

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85          90          95

Lys Ser Thr Leu Phe Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
100          105          110

Ala Val Tyr Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly
115          120          125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130          135          140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145          150          155          160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165          170          175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180          185          190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195          200          205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210          215          220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225          230          235          240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245          250          255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260          265          270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275          280          285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290          295          300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305          310          315          320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325          330          335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340          345          350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355          360          365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370          375          380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

```

-continued

385		390		395		400									
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
			405						410					415	
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
		420						425					430		
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
		435						440				445			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	450				455						460				
Pro	Gly	Lys													
465															

<210> SEQ ID NO 83
 <211> LENGTH: 240
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: source
 <223> OTHER INFORMATION: /note="Description of Artificial Sequence:
 Synthetic polypeptide"

<400> SEQUENCE: 83

Met	Val	Ser	Ser	Ala	Gln	Phe	Leu	Gly	Leu	Leu	Leu	Cys	Phe	Gln
1				5				10					15	
Gly	Thr	Arg	Cys	Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu
		20					25					30		Pro
Val	Thr	Leu	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln
		35				40					45			Ser
Leu	Leu	Asp	Ser	Asp	Gly	His	Thr	Tyr	Leu	Asn	Trp	Phe	Gln	Gln
	50				55						60			Arg
Pro	Gly	Gln	Ser	Pro	Arg	Arg	Leu	Ile	Tyr	Ser	Val	Ser	Asn	Leu
	65				70				75					80
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
			85					90					95	Phe
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Leu	Tyr
		100					105						110	Tyr
Cys	Met	Gln	Ala	Thr	His	Ala	Pro	Pro	Tyr	Thr	Phe	Gly	Gln	Gly
		115				120						125		Thr
Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile
	130				135						140			Phe
Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val
	145				150				155					Cys
Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys
		165						170					175	Val
Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu
		180					185						190	Gln
Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu
		195					200					205		Ser
Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr
	210					215					220			His
Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu
	225				230					235				Cys

<210> SEQ ID NO 84

-continued

<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 84

Met Val Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
1 5 10 15
Gly Thr Arg Cys Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro
20 25 30
Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45
Leu Leu Asp Ser Asp Gly His Thr Tyr Leu Asn Trp Leu Gln Gln Arg
50 55 60
Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Ser Val Ser Asn Leu Glu
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe
85 90 95
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Met Gln Ala Thr His Ala Pro Pro Tyr Thr Phe Gly Gln Gly Thr
115 120 125
Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
130 135 140
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
145 150 155 160
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
165 170 175
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
180 185 190
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
195 200 205
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
210 215 220
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235 240

<210> SEQ ID NO 85
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 85

Met Val Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
1 5 10 15
Gly Thr Arg Cys Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser
20 25 30
Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

-continued

```

Leu Leu Asp Ser Asp Gly His Thr Tyr Leu Asn Trp Leu Leu Gln Lys
 50          55          60

Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr Ser Val Ser Asn Leu Glu
65          70          75          80

Ser Gly Val Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
          85          90          95

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr
          100          105          110

Cys Met Gln Ala Thr His Ala Pro Pro Tyr Thr Phe Gly Gly Gly Thr
          115          120          125

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
          130          135          140

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
          145          150          155          160

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
          165          170          175

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
          180          185          190

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
          195          200          205

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
          210          215          220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
          225          230          235          240

<210> SEQ ID NO 86
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
        Synthetic polypeptide"

<400> SEQUENCE: 86

Met Val Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln
1          5          10          15

Gly Thr Arg Cys Asp Val Val Met Thr Gln Ser Pro Leu Ser Gln Pro
          20          25          30

Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
          35          40          45

Leu Leu Asp Ser Asp Gly His Thr Tyr Leu Asn Trp Leu Gln Gln Arg
          50          55          60

Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr Ser Val Ser Asn Leu Glu
          65          70          75          80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
          85          90          95

Thr Leu Ser Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
          100          105          110

Cys Met Gln Ala Thr His Ala Pro Pro Tyr Thr Phe Gly Gln Gly Thr
          115          120          125

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
          130          135          140

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys

```

-continued

145	150	155	160
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val	165	170	175
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln	180	185	190
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser	195	200	205
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His	210	215	220
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	225	230	235
			240

<210> SEQ ID NO 87
 <211> LENGTH: 448
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: source
 <223> OTHER INFORMATION: /note="Description of Artificial Sequence:
 Synthetic polypeptide"

<400> SEQUENCE: 87

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly	1	5	10	15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Ala	20	25	30	
Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45	
Ala Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr Tyr Ala Glu	50	55	60	
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr	65	70	75	80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr	85	90	95	
Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly Gln Gly Thr	100	105	110	
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro	115	120	125	
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly	130	135	140	
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn	145	150	155	160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln	165	170	175	
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser	180	185	190	
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser	195	200	205	
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr	210	215	220	
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser	225	230	235	240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg	245	250	255	

-continued

<400> SEQUENCE: 88

Gln 1	Val	Gln	Leu 5	Gln	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Lys	Pro	Gly 15	Gly
Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Phe	Thr	Phe	Ser 30	His	Ala
Trp	Met	His 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val
Gly	Gln 50	Ile	Lys	Ala	Lys	Ser 55	Asp	Asp	Tyr	Ala	Thr 60	Tyr	Tyr	Ala	Glu
Ser 65	Val	Lys	Gly	Arg	Phe 70	Thr	Ile	Ser	Arg	Asp 75	Asp	Ser	Lys	Asn	Thr 80
Leu	Tyr	Leu	Gln	Met 85	Asn	Ser	Leu	Lys	Thr 90	Glu	Asp	Thr	Ala	Val 95	Tyr
Tyr	Cys	Thr 100	Cys	Trp	Glu	Trp	Asp	Leu 105	Asp	Phe	Trp	Gly	Gln 110	Gly	Thr
Met	Val	Thr 115	Val	Ser	Ser	Ala	Ser 120	Thr	Lys	Gly	Pro	Ser 125	Val	Phe	Pro
Leu 130	Ala	Pro	Ser	Ser	Lys	Ser 135	Thr	Ser	Gly	Gly	Thr 140	Ala	Ala	Leu	Gly

-continued

```

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                      150                      155                      160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                      165                      170                      175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
                      180                      185                      190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195                      200                      205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210                      215                      220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                      230                      235                      240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                      245                      250                      255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
                      260                      265                      270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275                      280                      285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290                      295                      300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                      310                      315                      320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                      325                      330                      335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
                      340                      345                      350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
                      355                      360                      365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370                      375                      380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                      390                      395                      400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                      405                      410                      415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
                      420                      425                      430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435                      440                      445

<210> SEQ ID NO 89
<211> LENGTH: 448
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
        Synthetic polypeptide"

<400> SEQUENCE: 89

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1                      5                      10                      15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Ala
20                      25                      30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

```

-continued

35	40	45
Ala Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr Tyr Ala Glu		
50	55	60
Ser Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser		
65	70	75 80
Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Val Val Tyr		
	85	90 95
Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly Gln Gly Thr		
	100	105 110
Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
	115	120 125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly		
	130	135 140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
145	150	155 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
	165	170 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser		
	180	185 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser		
	195	200 205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr		
	210	215 220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser		
225	230	235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
	245	250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro		
	260	265 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
	275	280 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val		
	290	295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr		
305	310	315 320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr		
	325	330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu		
	340	345 350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys		
	355	360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser		
	370	375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp		
385	390	395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser		
	405	410 415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala		
	420	425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
	435	440 445

-continued

<210> SEQ ID NO 90
<211> LENGTH: 448
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 90

Glu Val Gln Leu Met Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser His Ala
20 25 30
Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Gln Ile Lys Ala Lys Ser Asp Asp Tyr Ala Thr Tyr Tyr Ala Glu
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80
Leu Phe Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Thr Cys Trp Glu Trp Asp Leu Asp Phe Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

-continued

```

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
      340                      345                      350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
      355                      360                      365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
      370                      375                      380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
      385                      390                      395                      400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
      405                      410                      415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
      420                      425                      430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
      435                      440                      445

<210> SEQ ID NO 91
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
      Synthetic polypeptide"

<400> SEQUENCE: 91

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1      5      10      15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
      20      25      30

Asp Gly His Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
      35      40      45

Pro Arg Arg Leu Ile Tyr Ser Val Ser Asn Leu Glu Ser Gly Val Pro
      50      55      60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
      65      70      75      80

Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Ala
      85      90      95

Thr His Ala Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
      100     105     110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
      115     120     125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
      130     135     140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
      145     150     155     160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
      165     170     175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
      180     185     190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
      195     200     205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      210     215     220

```

-continued

<210> SEQ ID NO 92
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 92

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30
Asp Gly His Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45
Pro Arg Leu Leu Ile Tyr Ser Val Ser Asn Leu Glu Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95
Thr His Ala Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> SEQ ID NO 93
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
Synthetic polypeptide"

<400> SEQUENCE: 93

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30
Asp Gly His Thr Tyr Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Pro
35 40 45
Pro Gln Leu Leu Ile Tyr Ser Val Ser Asn Leu Glu Ser Gly Val Pro
50 55 60

-continued

```

Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65          70          75          80

Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Ala
85          90          95

Thr His Ala Pro Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100         105         110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115         120         125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130         135         140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145         150         155         160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165         170         175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180         185         190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195         200         205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210         215         220

```

```

<210> SEQ ID NO 94
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
        Synthetic polypeptide"

```

```

<400> SEQUENCE: 94

```

```

Asp Val Val Met Thr Gln Ser Pro Leu Ser Gln Pro Val Thr Leu Gly
1          5          10          15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
20         25         30

Asp Gly His Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35         40         45

Pro Arg Arg Leu Ile Tyr Ser Val Ser Asn Leu Glu Ser Gly Val Pro
50         55         60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile
65          70          75          80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85          90          95

Thr His Ala Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100         105         110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115         120         125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130         135         140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145         150         155         160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165         170         175

```

-continued

Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr
			180					185					190		

Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
		195					200					205			

Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys
	210					215					220

<210> SEQ ID NO 95
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: source
 <223> OTHER INFORMATION: /note="Description of Artificial Sequence:
 Synthetic peptide"

<400> SEQUENCE: 95

Thr	Ser	Trp	Glu	Trp	Asp	Leu	Asp	Phe
1				5				

<210> SEQ ID NO 96
 <211> LENGTH: 118
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: source
 <223> OTHER INFORMATION: /note="Description of Artificial Sequence:
 Synthetic polypeptide"

<400> SEQUENCE: 96

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
1			5					10					15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	His	Ala
		20						25					30		

Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Gly	Gln	Ile	Lys	Ala	Lys	Ser	Asp	Asp	Tyr	Ala	Thr	Tyr	Tyr	Ala	Glu
	50					55					60				

Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr
	65				70					75				80	

Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr
			85						90					95	

Tyr	Cys	Thr	Ser	Trp	Glu	Trp	Asp	Leu	Asp	Phe	Trp	Gly	Gln	Gly	Thr
			100					105					110		

Met	Val	Thr	Val	Ser	Ser
			115		

<210> SEQ ID NO 97
 <211> LENGTH: 448
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: source
 <223> OTHER INFORMATION: /note="Description of Artificial Sequence:
 Synthetic polypeptide"

<400> SEQUENCE: 97

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
1			5					10					15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	His	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

-continued

20						25						30					
Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
	35						40					45					
Gly	Gln	Ile	Lys	Ala	Lys	Ser	Asp	Asp	Tyr	Ala	Thr	Tyr	Tyr	Ala	Glu		
	50					55					60						
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr		
65					70					75				80			
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr		
				85					90					95			
Tyr	Cys	Thr	Ser	Trp	Glu	Trp	Asp	Leu	Asp	Phe	Trp	Gly	Gln	Gly	Thr		
			100					105					110				
Met	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro		
			115					120				125					
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly		
	130					135					140						
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn		
145					150					155					160		
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln		
				165					170					175			
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser		
			180					185					190				
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser		
	195					200						205					
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr		
	210					215					220						
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser		
225					230					235					240		
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
				245					250					255			
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro		
			260					265					270				
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
		275					280					285					
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val		
	290					295					300						
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
305					310					315					320		
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr		
				325					330					335			
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu		
			340					345					350				
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys		
			355				360						365				
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
	370					375						380					
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp		
385					390					395					400		
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser		
				405					410					415			
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		
			420					425					430				

-continued

```

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    435                440                445

<210> SEQ ID NO 98
<211> LENGTH: 180
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: source
<223> OTHER INFORMATION: /note="Description of Artificial Sequence:
        Synthetic polypeptide"

<400> SEQUENCE: 98

Ser Pro Leu Pro Ile Thr Pro Val Asn Ala Thr Cys Ala Ile Arg His
1          5          10          15

Pro Cys His Asn Asn Leu Met Asn Gln Ile Arg Ser Gln Leu Ala Gln
          20          25          30

Leu Asn Gly Ser Ala Asn Ala Leu Phe Ile Leu Tyr Tyr Thr Ala Gln
          35          40          45

Gly Glu Pro Phe Pro Asn Asn Leu Asp Lys Leu Cys Gly Pro Asn Val
          50          55          60

Thr Asp Phe Pro Pro Phe His Ala Asn Gly Thr Glu Lys Ala Lys Leu
65          70          75          80

Val Glu Leu Tyr Arg Ile Val Val Tyr Leu Gly Thr Ser Leu Gly Asn
          85          90          95

Ile Thr Arg Asp Gln Lys Ile Leu Asn Pro Ser Ala Leu Ser Leu His
          100         105         110

Ser Lys Leu Asn Ala Thr Ala Asp Ile Leu Arg Gly Leu Leu Ser Asn
          115         120         125

Val Leu Cys Arg Leu Cys Ser Lys Tyr His Val Gly His Val Asp Val
          130         135         140

Thr Tyr Gly Pro Asp Thr Ser Gly Lys Asp Val Phe Gln Lys Lys Lys
145         150         155         160

Leu Gly Cys Gln Leu Leu Gly Lys Tyr Lys Gln Ile Ile Ala Val Leu
          165         170         175

Ala Gln Ala Phe
          180

```

What is claimed is:

1.-286. (canceled)

287. A recombinant antibody that specifically binds Leukemia Inhibitory Factor (LIF), the antibody comprising a heavy chain variable region with an amino acid sequence set forth in SEQ ID NO: 72, and a light chain variable region with an amino acid sequence set forth in SEQ ID NO: 76.

288. The recombinant antibody of claim **287**, wherein the recombinant antibody binds to glycosylated LIF.

289. The recombinant antibody of claim **287**, wherein the recombinant antibody is humanized.

290. The recombinant antibody of claim **287**, wherein the recombinant antibody is deimmunized.

291. The recombinant antibody of claim **287**, wherein the recombinant antibody comprises two heavy chains and two light chains.

292. The recombinant antibody of claim **287**, wherein the recombinant antibody is an IgG antibody.

* * * * *