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(54) **Method for inhibiting bone resorption**

Verfahren zur Hemmung von Knochenresorption

Procédé d'inhibition de la résorption osseuse

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Description

TECHNICAL FIELD OF THE INVENTION

5 **[0001]** The invention generally relates to methods of using sclerostin binding agents to modulate bone density.

BACKGROUND OF THE INVENTION

10 **[0002]** Loss of bone mineral content can be caused by a wide variety of conditions and may result in significant medical problems. For example, osteoporosis is a debilitating disease in humans and is characterized by marked decreases in skeletal bone mass and mineral density, structural deterioration of bone, including degradation of bone microarchitecture and corresponding increases in bone fragility (i.e., decreases in bone strength), and susceptibility to fracture in afflicted individuals. Osteoporosis in humans is generally preceded by clinical osteopenia, a condition found in approximately 25 million people in the United States. Another 7-8 million patients in the United States have been diagnosed with clinical osteoporosis. The frequency of osteoporosis in the human population increases with age. Among Caucasians, osteoporosis is predominant in women who, in the United States, comprise 80% of the osteoporosis patient pool. The increased fragility and susceptibility to fracture of skeletal bone in the aged is aggravated by the greater risk of accidental falls in this population. Fractured hips, wrists, and vertebrae are among the most common injuries associated with osteoporosis. Hip fractures in particular are extremely uncomfortable and expensive for the patient, and for women, correlate with high rates of mortality and morbidity.

20 **[0003]** The following documents are acknowledged:

- 25 • an Amgen press release of 19 September 2006 which is concerned with the presentation of Denosumab and Sclerostin Antibody Data at the American Society for Bone and Mineral Research Annual Meeting; the Data Suggesting the Potential for Targeting the Key Proteins, RANK Ligand and Sclerostin, for Bone Loss Conditions;
- 30 • Li et al (2007) J Bone Mineral Research, 22, Supplement 1: S36, which is concerned with treatment with an anti-sclerostin antibody increasing bone mass by stimulating bone formation with increasing bone resorption in aged male rats;
- Padhi et al (2007) J Bone Mineral Research, 22: Supplement: S37, which is concerned with anti-sclerostin antibody increases markers of bone formation in healthy postmenopausal women; and
- 35 • Padhi et al (2007) Oasis Abstract, which is concerned with anti-sclerostin antibody increasing markers of bone formation in healthy postmenopausal women.

SUMMARY OF THE INVENTION

40 **[0004]** The invention is directed to methods of using a sclerostin inhibitor for inhibiting bone resorption in humans. The method comprises administering to a human an amount of sclerostin inhibitor that is effective to reduce the level of a marker of bone resorption and optionally increase the level of a marker of bone formation. In some embodiments, bone resorption is inhibited and bone formation is increased for at least about 7 days, 2 weeks, 3 weeks, 4 weeks, 1 month, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 2 months, 3 months or longer. In related embodiments, the invention provides a method of increasing bone mineral density or treating a bone-related disorder. The invention further provides a method of ameliorating the effects of an osteoclast-related disorder. The method comprises administering to a human a sclerostin inhibitor that reduces the level of a marker of bone resorption compared to bone marker levels absent treatment. The sclerostin inhibitor also increases the level of a marker of bone formation by at least about 10% compared to bone marker levels absent treatment. The sclerostin inhibitor can be administered via a single dose or in multiple doses. For example, the sclerostin inhibitor can be administered in a short-term therapy regimen to, e.g., increase bone formation, and/or can be administered long-term to prevent loss of bone mineral density in a maintenance therapeutic regimen.

50 **[0005]** In any of the methods disclosed herein, the level of one or more markers of bone resorption is reduced by at least about 5%, 10%, 15%, 20%, 30%, 40%, 50% or more for at least 2 weeks, 3 weeks, 30 days, 1 month, 6 weeks, 2 months or longer, compared to pre-treatment levels or normal levels for that patient population. By way of non-limiting example, the level of the marker of bone resorption by 3 weeks after treatment is decreased by, e.g., at least about 20% compared to pre-treatment levels or normal levels for that patient population. In any of the preceding methods, the level of the marker of bone formation is increased by at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 100% or more for at least about 2 weeks, 3 weeks, 30 days, 1 month, 6 weeks, 2 months or longer, compared to pre-treatment levels or normal levels for that patient population. By

way of non-limiting example, the level of the marker of bone formation by 3 weeks after treatment is increased by, e.g., at least about 20% compared to pre-treatment levels or normal levels for that patient population. In one exemplary embodiment, the marker of bone resorption is serum level of C-telopeptide of type I collagen (CTX). In other exemplary embodiments, the marker of bone formation is bone-specific alkaline phosphatase (BSAP), osteocalcin (OstCa), and/or N-terminal extension of procollagen type 1 (P1NP).

[0006] The invention also provides a method of treating a bone-related disorder, wherein the method comprises administering to a human one or more amounts of a sclerostin inhibitor effective to increase bone mineral density for the total body (e.g., head, trunk, arms, and legs) or at the hip (e.g., total hip and/or femoral neck), spine (e.g., lumbar spine), wrist, finger, shin bone and/or heel by about 1%, about 2%, about 3%, about 4%, about 5%, about 6%, about 8%, about 10%, about 12%, about 15%, about 18%, about 20%, about 25%, or 30% or more. In some embodiments, the bone mineral density of the human before treatment is characteristic of osteoporosis or osteopenia, and one or more doses of sclerostin inhibitor are administered in an amount and for a time effective to improve bone mineral density such that the bone mineral density is no longer characteristic of osteoporosis and/or osteopenia. For example, one or more doses may be administered for an initial time period to increase bone mineral density to within 2.5, or one, standard deviations of the density normal for a young adult (i.e., a T-score ≥ -2.5 or a T-score ≥ -1 , as defined below). In exemplary embodiments, the initial time period is about 3 months or less, 6 months or less, 9 months or less, 1 year or less, 18 months or less, or longer. The method may further comprise subsequently administering one or more amounts of a sclerostin inhibitor effective to maintain bone mineral density, optionally for a maintenance time period of at least about 6 months, 1 year, 2 years or longer (e.g., over the life-time of the subject).

[0007] The invention further provides a method of treating a bone-related disorder in a human by administering one or more doses between about 0.1 to about 20 mg/kg, or about 0.1 to about 12 mg/kg, or about 0.5 to about 12 mg/kg, or about 1 to about 10 mg/kg, or about 1 to about 8 mg/kg, or about 2 to about 8 mg/kg, or about 3 to about 8 mg/kg. In some embodiments, doses may be administered at an interval of about once 2 weeks or longer, once every month or longer, or once every 2 months or longer, or once every 3 months or longer, or once every 4 months or longer, or once every 5 months or longer, or once every 6 months or longer, or once every 9 months or longer, or once every year or longer. The sclerostin inhibitor may be used in the preparation of a medicament for administration using any of the dosing and timing regimens described herein. Optionally, the sclerostin inhibitor is presented in a container, such as a single dose or multidose vial, containing a dose of sclerostin inhibitor for administration (e.g., about 70 to about 450 mg of sclerostin inhibitor). In one exemplary embodiment, a vial may contain about 70 mg or 75 mg of sclerostin inhibitor, e.g. anti-sclerostin antibody, and would be suitable for administering a single dose of about 1 mg/kg. In other embodiments, a vial may contain about 140 mg or 150 mg; or about 210 mg or 220 mg or 250 mg; or about 280 mg or 290 mg or 300 mg; or about 350 mg or 360 mg; or about 420 mg or 430 mg or 440 mg or 450 mg of sclerostin inhibitor, e.g., anti-sclerostin antibody.

[0008] Additionally, the invention provides a method of treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia, a human in which treatment with a parathyroid hormone or analog thereof is contraindicated, or a human in which treatment with a bisphosphonate is contraindicated. The method comprises administering to the human an amount of a sclerostin inhibitor effective to increase the level of a marker of bone formation and/or reduce the level of a marker of bone resorption, without resulting in hypocalcemia or hypercalcemia (e.g., clinically-significant hypocalcemia or hypercalcemia).

[0009] The invention also provides a method of monitoring anti-sclerostin therapy, i.e., the physiological response to a sclerostin inhibitor. The method comprises the steps of administering one or more doses of a sclerostin inhibitor, and detecting the level of one or more markers of bone resorption, wherein a reduction of at least about 5%, about 10%, about 15%, about 20%, about 30%, about 40%, about 50% or more in the level of a marker of bone resorption, compared to pre-treatment levels or normal levels for that patient population, is indicative of effective treatment. The method optionally further comprises the step of detecting the level of one or more markers of bone formation, wherein an increase of at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or about 100% in the level of a marker of bone formation, compared to pre-treatment levels or normal levels for that patient population, is indicative of effective treatment. In certain embodiments, the increase in bone formation marker levels is about 20%. The method may further comprise the step of adjusting the dose of a sclerostin inhibitor to a different amount, e.g., higher if the change in bone resorption and/or bone formation is less than desired, or lower if the change in bone resorption and/or bone formation is more than desired.

[0010] In a different aspect, the invention provides selected sclerostin inhibitors that reduce the level of a marker of bone resorption by at least about 5%, about 10%, about 15%, about 20%, about 30%, about 40%, about 50% or more and increase the level of a marker of bone formation by at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 100%, or more, for at least about 1 week, about 2 weeks, about 1 month, about 6 weeks, about 2 months, about 10 weeks, or about 3 months. In a related aspect, the invention provides a method of selecting such sclerostin inhibitors by administering a candidate sclerostin inhibitor to an animal and selecting a candidate sclerostin inhibitor that changes the level of a marker of bone resorption and/or formation to

the desired extent.

[0011] In any of the preceding methods or embodiments of the invention, the sclerostin inhibitor may be a sclerostin binding agent. The use of sclerostin binding agents disclosed in U.S. Patent Publication No. 20070110747, e.g., in any of the methods disclosed herein or for preparation of medicaments for administration according to any of the methods disclosed herein, is specifically contemplated. In this regard, the invention includes use of a sclerostin binding agent in preparation of a medicament for inhibiting bone resorption in an amount from about 1 mg/kg to about 10 mg/kg, wherein the amount is effective to reduce serum level of C-telopeptide of type I collagen (CTX) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins. The invention also includes use of a sclerostin binding agent in preparation of a medicament for increasing bone mineral density in an amount from about 1 mg/kg to about 10 mg/kg, wherein the amount is effective to (a) reduce serum level of CTX by at least 20% compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and (b) increase serum level of a bone formation marker selected from the group consisting of serum level of bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of procollagen type 1 (PINP), and serum level of osteocalcin (OstCa), by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins.

[0012] The invention further includes use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg for a first period of time, wherein the amount is effective to increase bone mineral density at the hip, spine, wrist, finger, shin bone and/or heel by at least about 3%, followed by an amount of from about 1 mg/kg to about 10 mg/kg for a second period of time effective to maintain bone mineral density. Use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia in an amount from about 1 mg/kg to about 10 mg/kg, also is contemplated, as well as use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in (a) a human in which treatment with a parathyroid hormone or analog thereof is contraindicated or (b) a human in which treatment with bisphosphonate is contraindicated.

[0013] The invention also includes containers comprising anti-sclerostin antibody or fragment thereof. In one embodiment, the container comprises anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or fragment thereof in an amount effective to (a) reduce serum level of C-telopeptide of type I collagen (CTX) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and (b) increase serum level bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of procollagen type 1 (PINP), or serum level of osteocalcin (OstCa) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins. Alternatively or in addition, the container comprises an amount of anti-sclerostin antibody from about 70 mg to about 450 mg. The invention further provides a container comprising anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or fragment thereof for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg every two or four weeks. In addition, the invention provides a container comprising anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or fragment thereof for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg for a period of about 3 months.

BRIEF DESCRIPTION OF THE FIGURES

[0014]

Figure 1 is a graph of percent change of N-terminal extension of procollagen type 1 (P1NP) levels compared to baseline and placebo P1NP levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

Figure 2 is a graph of percent change of bone-specific alkaline phosphatase (BSAP) levels compared to baseline and placebo BSAP levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

Figure 3 is a graph of percent change of osteocalcin levels compared to baseline and placebo osteocalcin levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

Figure 4 is a graph of percent change of serum C-terminal telopeptide of type 1 collagen (CTX) levels compared to baseline and placebo serum CTX levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

Figure 5 are graphs of percent change of osteocalcin, BSAP, P1NP, and CTX levels compared to baseline and placebo levels versus time (day) post-administration of a single dose of 5 mg/kg or 10 mg/kg of sclerostin binding

agent in healthy, postmenopausal women.

Figure 6 is a graph of percent change of serum calcium levels compared to baseline and placebo serum calcium levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

Figure 7 are graphs of percent change of bone mineral density compared to baseline and placebo versus time (day) post-administration of various single doses of sclerostin binding agent in healthy, postmenopausal women.

DETAILED DESCRIPTION OF THE INVENTION

[0015] The invention is predicated, at least in part, on the surprising discovery that blocking or inhibiting the biological activity of human sclerostin triggers multiple physiological responses linked to increased bone mineral density (BMD), including significant inhibition of bone resorption. Most currently available therapies only inhibit bone resorption without increasing bone formation. Some currently available therapies for disorders associated with reduced BMD only increase bone formation without significantly reducing bone resorption. For example, when bone formation is triggered by some current drugs, bone resorption may also increase (albeit potentially at a lower rate than before therapy). In contrast, agents that interfere with sclerostin activity both enhance bone formation *and* reduce bone resorption. In other words, sclerostin inhibitors "uncouple" bone formation and bone resorption to more effectively build bone. The materials and methods of the invention are superior to existing therapies whose therapeutic efficacy is limited and which are accompanied by potentially serious adverse side effects.

[0016] In this regard, the invention provides a method of inhibiting bone resorption, e.g., bone resorption mediated by osteoclasts, bone cells that dissolve bone mineral matrices. The invention further provides a method of ameliorating the effects of an osteoclast-related disorder, i.e., a disorder caused by abnormally increased osteoclast activity that, in some embodiments, manifests as abnormally high bone resorption. The inventive method comprises administering to a human an amount of sclerostin binding agent that reduces the level of a marker of bone resorption and, optionally, increases the level of a marker of bone formation.

[0017] Activity of a sclerostin inhibitor, e.g., a sclerostin binding agent, (further described below) may be measured in a variety of ways. Sclerostin binding agent-mediated increases in bone mineral content or bone density may be measured using single- and dual-energy X-ray absorptometry, ultrasound, computed tomography, radiography, and magnetic resonance imaging. The amount of bone mass may also be calculated from body weights or by using other methods (see Guinness-Hey, *Metab. Bone Dis. Relat. Res.*, 5:177-181 (1984)). Animals and particular animal models are used in the art for testing the effect of the pharmaceutical compositions and methods on, for example, parameters of bone loss, bone resorption, bone formation, bone strength, or bone mineralization that mimic conditions of human disease such as osteoporosis and osteopenia. Examples of such models include the ovariectomized rat model (Kalu, *Bone and Mineral*, 15:175-192 (1991); Frost and Jee, *Bone and Mineral*, 18:227-236 (1992); and Jee and Yao, *J. Musculoskel. Neuron. Interact.*, 1:193-207 (2001)). The methods for measuring sclerostin binding agent activity described herein also may be used to determine the efficacy of other sclerostin inhibitors.

[0018] In humans, bone mineral density can be determined clinically using dual x-ray absorptiometry (DXA) of, for example, the hip and spine. Other techniques include quantitative computed tomography (QCT), ultrasonography, single-energy x-ray absorptiometry (SXA), and radiographic absorptiometry. Common central skeletal sites for measurement include the spine and hip; peripheral sites include the forearm, finger, wrist and heel. Except for ultrasonography, the American Medical Association notes that BMD techniques typically involve the use of x-rays and are based on the principle that attenuation of the radiation depends on thickness and composition of the tissues in the radiation path. All techniques involve the comparison of results to a normative database.

[0019] Alternatively, a physiological response to one or more sclerostin binding agents can be gauged by monitoring bone marker levels. Bone markers are products created during the bone remodeling process and are released by bone, osteoblasts, and/or osteoclasts. Fluctuations in bone resorption and/or bone formation "marker" levels imply changes in bone remodeling/modeling. The International Osteoporosis Foundation (IOF) recommends using bone markers to monitor bone density therapies (see, e.g., Delmas et al., *Osteoporos Int.*, Suppl. 6:S2-17 (2000)). Markers indicative of bone resorption (or osteoclast activity) include, for example, C-telopeptide (e.g., C-terminal telopeptide of type 1 collagen (CTX) or serum cross-linked C-telopeptide), N-telopeptide (N-terminal telopeptide of type 1 collagen (NTX)), deoxypyridinoline (DPD), pyridinoline, urinary hydroxyproline, galactosyl hydroxylysine, and tartrate-resistant acid phosphatase (e.g., serum tartrate-resistant acid phosphatase isoform 5b). Bone formation/mineralization markers include, but are not limited to, bone-specific alkaline phosphatase (BSAP), peptides released from N- and C-terminal extension of type I procollagen (P1NP, PICP), and osteocalcin (OstCa). Several kits are commercially-available to detect and quantify markers in clinical samples, such as urine and blood.

[0020] Upon administration, the sclerostin binding agent preferably reduces the level of one or more markers of bone

resorption, such as the serum level of C-telopeptide of type I collagen (CTX). Accordingly, the invention further provides a method of monitoring anti-sclerostin therapy, i.e., the physiological response to a sclerostin binding agent or other sclerostin inhibitor. The method comprises administering a sclerostin binding agent, then measuring the level of one or more markers of bone resorption. In addition, the method can comprise measuring the level of one or more markers of bone formation before administration of a sclerostin binding agent. The level of bone resorption marker during and/or after treatment with the sclerostin binding agent may be compared to a pre-treatment level, or alternatively may be compared to a standard range typical of that patient population. One of ordinary skill in the art can readily determine a suitable standard range by testing a representative number of patients of like age, gender, disease level, and/or other characteristics of the patient population. The level of bone resorption marker can be reduced by at least about 5% (e.g., about 10%, about 20%, or about 30%) by a single dose of sclerostin binding agent. In some embodiments, the dose of sclerostin binding agent reduces the level of bone resorption marker at least about 40% (e.g., about 50%, about 60%, or about 70%) compared to the level of the bone resorption marker prior to administering the sclerostin binding agent. In addition, the bone resorption marker level may be reduced for at least about 3 days (e.g., about 7 days, about 2 weeks, about 3 weeks, about 1 month, about 5 weeks, about 6 weeks, about 7 weeks, about 2 months, about 9 weeks, about 10 weeks, about 11 weeks, or about 3 months) after administration of a single dose of the sclerostin binding agent.

[0021] In addition to decreasing the level of bone resorption markers, the amount of sclerostin binding agent administered to a patient also can increase the level of one or more markers of bone formation, such as the serum level of BSAP, the serum level of P1NP, and/or the serum level of OstCa. A single dose of sclerostin binding agent can increase the level of a bone formation marker by, for example, at least about 5% (e.g., about 10%, about 20%, or about 30%). In some embodiments, the dose of sclerostin binding agent elevates the level of a bone formation marker at least about 40% (e.g., about 50%, about 60%, or about 70%). In other embodiments, the dose of sclerostin binding agent increases the level of one or more bone formation markers by at least about 75% (e.g., about 80%, about 90%, about 100%, or about 110%). In yet other embodiments, the dose of sclerostin binding agent increases the level of a bone formation marker by at least about 120% (e.g., about 130%, about 140%, about 150%, about 160% or about 170%). In alternative embodiments, the sclerostin binding agent increases the level of bone formation marker by least about 180% (e.g., about 190% or about 200%). Bone formation marker levels ideally remain elevated (compared to bone formation marker levels pre-treatment or to a standard range typical of that patient population) for at least about 3 days (e.g., about 7 days, about 2 weeks, about 3 weeks, about 1 month, about 5 weeks, about 6 weeks, about 7 weeks, about 2 months, about 9 weeks, about 10 weeks, about 11 weeks, or about 3 months) after administration of a single dose of the sclerostin binding agent.

[0022] The invention also provides a method of increasing bone mineral density (BMD), wherein an amount of sclerostin binding agent that (a) reduces the level of a marker of bone resorption and (b) increases the level of a marker of bone formation is administered to a human. BMD generally correlates with skeletal fragility and osteoporosis. Typically, BMD is can be measured "total body" (e.g., head, trunk, arms, and legs) or at the hip (e.g., total hip and/or femoral neck), spine (e.g., lumbar spine), wrist, finger, shin bone and/or heel. In osteoporosis diagnosis, a patient's BMD is compared to the peak density of a 30-year old healthy adult (i.e., a "young adult"), creating the so-called "T-score." A patient's BMD also may be compared to an "age-matched" bone density (see, e.g., World Health Organization Scientific Group on the Prevention and Management of Osteoporosis, "Prevention and management of osteoporosis: report of a WHO scientific group." WHO Technical Report Series; 921, Geneva, Switzerland (2000)). The difference between a patient's BMD and that of a healthy, young adult is conventionally referred to in terms of the multiple of a "standard deviation," which typically equals about 10% to about 12% decrease in bone density. The World Health Organization proposed four diagnostic categories based on BMD T-scores. A BMD value within 1 standard deviation of the young adult reference mean ($T\text{-score} \geq -1$) is "normal." Low bone mass (osteopenia) is indicated by a BMD value more than 1 standard deviation below the young adult mean, but less than 2 standard deviations ($T\text{-score} < -1$ and > -2.5). A T-score of more than 2.5 standard deviations below the norm supports a diagnosis of osteoporosis. If a patient additionally suffers from one or more fragility fractures, the patient qualifies as having severe osteoporosis.

[0023] The sclerostin inhibitor, e.g., a sclerostin binding agent, may be administered to a patient to improve bone mineral density regardless of the patient's T-score. The sclerostin binding agent may be administered at a dose and for a time period effective to increase BMD in the patient by at least about 1% (about 2%, about 3%, about 4%, about 5%, or about 6%). In some embodiments, BMD is increased by at least about 8% (e.g., at least about 10%, about 12%, about 15%, or about 18%). In other embodiments, BMD is increased by the sclerostin binding agent at least about 20% (e.g., at least about 22%, about 25%, or about 28%) at the hip, spine, wrist, finger, shin bone, and/or heel. In yet other embodiments, BMD is increased at least about 30% (e.g., at least about 32%, about 35%, about 38%, or about 40%). In other words, the BMD can be increased to the range of about 1 to about 2.5 standard deviations (preferably a range of about 0 to about 1 standard deviations) below the normal BMD of a healthy young adult.

[0024] Alterations in bone remodeling can lead to fluctuations in mineral concentrations throughout the body. Bone is one of the principal regulators of calcium levels in the bloodstream. Osteoclast-mediated bone resorption releases stored calcium into the systemic circulation, while osteoblast-mediated bone formation removes calcium from circulation to incorporate into bone tissue. In normal bone remodeling, these processes cycle to maintain healthy, strong bone and

maintain free calcium levels at about 8.5 mg/dL to about 10.5 mg/dL (e.g., about 2.2 mmol/L to about 2.6 mmol/L). Bone disorders, other illnesses, and even certain therapies can disrupt systemic calcium levels with dire consequences. Hypercalcemia is associated with high levels of calcium in the blood (e.g., greater than 12 mg/dL or 3 mmol/L). Extraordinarily high calcium levels leads to, for example, fatigue, confusion, constipation, decreased appetite, frequent urination, heart problems, and bone pain. Hypocalcemia is an electrolyte imbalance indicated by an abnormally low level of calcium in the blood (e.g., less than about 9 mg/dL or 2.2 mmol/L). Calcium levels of < 7.5 mg/dL (< 1.87 mmol/L) or less are considered severe hypocalcemia and may be accompanied by clinical symptoms.

[0025] Common symptoms of hypocalcemia include nerve and muscle spasms and cramps, numbness, tingling in the extremities, confusion, and heart irregularities. Extreme variations in system calcium can lead to coma and death.

[0026] Several ailments and pharmaceutical therapies alter system calcium levels. Hypercalcemia and hypocalcemia can result from, for example, chronic kidney disease, renal failure, primary or secondary hyperparathyroidism, pseudo-hyperparathyroidism, hypoparathyroidism, pseudohypoparathyroidism, magnesium depletion, alcoholism, bisphosphonate therapy, severe hypermagnesemia, vitamin D deficiency, hyperphosphatemia, acute pancreatitis, hungry bone syndrome, chelation, osteoblastic metastases, sepsis, surgery, chemotherapy, neoplasia syndrome, familial hypocalciuric hypercalcemia, sarcoidosis, tuberculosis, berylliosis, histoplasmosis, Candidiasis, Coccidioidomycosis, histiocytosis X, Hodgkin's or Non-Hodgkin's lymphoma, Crohn's disease, Wegener's granulomatosis, leukemia, pneumonia, silicone-induced granulomas, immobilization, or drug therapy, such as administration of thiazide diuretics, lithium, estrogens, fluorides, glucose, and insulin. In addition, serum calcium fluctuations are a side effect of many existing bone-related therapies, such as bisphosphonate and parathyroid hormone therapy. Because of the potentially life-threatening consequences of calcium imbalance, patients susceptible to hypocalcemia or hypercalcemia may need to forego certain therapy options.

[0027] Remarkably, sclerostin inhibitors, e.g., sclerostin binding agents, have been shown to promote bone formation and inhibit (or slow) bone resorption with minimal fluctuations in systemic calcium levels (e.g., calcium levels fluctuate 10% or less from baseline serum calcium levels). Accordingly, the materials and method of the invention are particularly advantageous in treating patients that are susceptible or sensitive to unstable calcium levels. The amount of sclerostin binding agent administered to a human in the context of this aspect of the invention is an amount that does not result in hypocalcemia or hypercalcemia (e.g., clinically-significant hypocalcemia or hypercalcemia). In addition, the invention provides a method of treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia or a human in which treatment with bisphosphonate, a parathyroid hormone, or parathyroid hormone analog is contraindicated. The method comprises administering to the human an amount of a sclerostin binding agent effective to increase the level of a marker of bone formation, such as serum levels of BSAP, P1NP, and/or OstCa and/or reduce the level of a marker of bone resorption, such as CTX.

[0028] The inventive method is useful for treating or preventing bone-related disorders, such as bone-related disorders associated with abnormal osteoblast or osteoclast activity. Indeed, the sclerostin inhibitor (e.g., sclerostin binding agent) can be administered to a human suffering from a bone related disorder selected from the group consisting of achondroplasia, cleidocranial dysostosis, enchondromatosis, fibrous dysplasia, Gaucher's Disease, hypophosphatemic rickets, Marfan's syndrome, multiple hereditary exotoses, neurofibromatosis, osteogenesis imperfecta, osteopetrosis, osteopoikilosis, sclerotic lesions, pseudoarthrosis, pyogenic osteomyelitis, periodontal disease, anti-epileptic drug induced bone loss, primary and secondary hyperparathyroidism, familial hyperparathyroidism syndromes, weightlessness induced bone loss, osteoporosis in men, postmenopausal bone loss, osteoarthritis, renal osteodystrophy, infiltrative disorders of bone, oral bone loss, osteonecrosis of the jaw, juvenile Paget's disease, melorheostosis, metabolic bone diseases, mastocytosis, sickle cell anemia/disease, organ transplant related bone loss, kidney transplant related bone loss, systemic lupus erythematosus, ankylosing spondylitis, epilepsy, juvenile arthritides, thalassemia, mucopolysaccharidoses, Fabry Disease, Turner Syndrome, Down Syndrome, Klinefelter Syndrome, leprosy, Perthe's Disease, adolescent idiopathic scoliosis, infantile onset multi-system inflammatory disease, Winchester Syndrome, Menkes Disease, Wilson's Disease, ischemic bone disease (such as Legg-Calve-Perthes disease and regional migratory osteoporosis), anemic states, conditions caused by steroids, glucocorticoid-induced bone loss, heparin-induced bone loss, bone marrow disorders, scurvy, malnutrition, calcium deficiency, osteoporosis, osteopenia, alcoholism, chronic liver disease, postmenopausal state, chronic inflammatory conditions, rheumatoid arthritis, inflammatory bowel disease, ulcerative colitis, inflammatory colitis, Crohn's disease, oligomenorrhea, amenorrhea, pregnancy, diabetes mellitus, hyperthyroidism, thyroid disorders, parathyroid disorders, Cushing's disease, acromegaly, hypogonadism, immobilization or disuse, reflex sympathetic dystrophy syndrome, regional osteoporosis, osteomalacia, bone loss associated with joint replacement, HIV associated bone loss, bone loss associated with loss of growth hormone, bone loss associated with cystic fibrosis, chemotherapy-associated bone loss, tumor-induced bone loss, cancer-related bone loss, hormone ablative bone loss, multiple myeloma, drug-induced bone loss, anorexia nervosa, disease-associated facial bone loss, disease-associated cranial bone loss, disease-associated bone loss of the jaw, disease-associated bone loss of the skull, bone loss associated with aging, facial bone loss associated with aging, cranial bone loss associated with aging, jaw bone loss associated with aging, skull bone loss associated with aging, and bone loss associated with space travel.

[0029] The inventive method need not cure the patient of the disorder or completely protect against the onset of a bone-related disorder to achieve a beneficial biological response. The method may be used prophylactically, meaning to protect, in whole or in part, against a bone-related disorder or symptom thereof. The method also may be used therapeutically to ameliorate, in whole or in part, a bone-related disorder or symptom thereof, or to protect, in whole or in part, against further progression of a bone-related disorder or symptom thereof. Indeed, the materials and methods of the invention are particularly useful for increasing bone mineral density and maintaining the increased BMD over a period of time. In this regard, the invention provides a method of treating a bone-related disorder, which method comprises (a) administering one or more amounts of a sclerostin binding agent effective to increase BMD measured for the total body (e.g., head, trunk, arms, and legs) or at the hip (e.g., total hip and/or femoral neck), spine (e.g., lumbar spine), wrist, finger, shin bone and/or heel by about 1%, about 2%, about 3%, about 6%, about 8%, about 10%, about 12%, about 15%, about 18%, about 20%, about 25%, or 30% or more. One or more administrations of a pharmaceutical composition comprising the sclerostin binding agent may be carried out over a therapeutic period of, for example, about 1 month to about 12 months (e.g., about 2 months, about 3 months, about 4 months, about 5 months, about 6 months, about 7 months, about 8 months, about 9 months, about 10 months, or about 11 months). The method further includes (b) subsequently administering one or more amounts of a sclerostin binding agent effective to maintain bone mineral density. By "maintain bone mineral density" is meant that the increased BMD resulting from step (a) does not fall more than about 1% to about 5% over the course of step (b) (e.g., about 6 months, about 9 months about 1 year, about 18 months, about 2 years, or over the course of the patient's life). It will be appreciated that a patient can require alternate treatment phases for increasing bone density and maintaining bone density.

[0030] The sclerostin binding agent is preferably administered to a patient in a physiologically-acceptable (e.g., pharmaceutical) composition, which can include carrier, excipients, or diluents. It will be appreciated that the sclerostin binding agents described herein may be used in the preparation of a medicament for administration using any of the dosage and timing regimens disclosed herein. Pharmaceutical compositions and methods of treatment are disclosed in U.S. Patent Publication No. 20050106683. "Physiologically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. In addition, the composition administered to a subject may contain more than one sclerostin inhibitor (e.g., a sclerostin binding agent and a synthetic chemical sclerostin inhibitor) or a sclerostin inhibitor in combination with one or more therapeutics having different mechanisms of action.

[0031] The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including e.g., subcutaneous, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art and discussed in U.S. Patent Publication No. 20070110747. For example, in certain circumstances, it will be desirable to deliver a pharmaceutical composition comprising a sclerostin binding agent subcutaneously, parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U.S. Patent Nos. 5,543,158; 5,641,515; and 5,399,363. Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U.S. Patent No. 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists.

[0032] In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous, and intraperitoneal administration. For example, one dose may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion (see, for example, Remington's Pharmaceutical Sciences, 15th ed., Mack Pub. Co., Easton, PA, pp. 1035-1038 and 1570-1580). Some variation in dosage and frequency of administration may occur depending on the condition of the subject being treated; age, height, weight, and overall health of the patient; and the existence of any side effects. In addition, a pharmaceutical composition comprising a sclerostin binding agent may be placed within containers (e.g., vials), along with packaging material that provides instructions regarding the use of such pharmaceutical compositions. Generally, such instructions will include a tangible expression describing the reagent concentration, as well as within certain embodiments, relative amounts of excipient ingredients or diluents (e.g., water, saline or PBS) that may be necessary to reconstitute the pharmaceutical composition.

[0033] The sclerostin binding agent is administered in an amount that reduces the level of a bone resorption marker and/or increases the level of a bone formation marker and/or increases bone density. The dose of sclerostin binding agent administered may range from about 0.5 mg/kg to about 20 mg/kg (e.g., 12 mg/kg) of body weight. For example, the dose of sclerostin binding agent may range from about 1 mg/kg to about 10 mg/kg (e.g., about 2 mg/kg or about 9 mg/kg), about 1 mg/kg to about 3 mg/kg, or about 3 mg/kg to about 8 mg/kg (e.g., about 4 mg/kg, 5 mg/kg, 6 mg/kg, or 7 mg/kg).

[0034] In addition, it may be advantageous to administer multiple doses of a sclerostin binding agent or space out the administration of doses, depending on the therapeutic regimen selected for a particular patient. The sclerostin binding

agent can be administered periodically over a time period of one year or less (e.g., 9 months or less, 6 months or less, or 3 months or less). In this regard, the sclerostin binding agent can be administered to the human once every about 7 days, or 2 weeks, or 3 weeks, or 1 month, or 5 weeks, or 6 weeks, or 7 weeks, or 2 months, or 9 weeks, or 10 weeks, or 11 weeks, or 3 months, or 13 weeks, or 14 weeks, or 15 weeks, or 4 months, or 17 weeks, or 18 weeks, or 19 weeks, or 5 months, or 21 weeks, or 22 weeks, or 23 weeks, or 6 months, or 12 months.

[0035] The inventive method comprises administering an amount of a "sclerostin inhibitor." As used herein, the term "sclerostin inhibitor" means any molecule that inhibits the biological activity of sclerostin on bone, as measured by changes to bone mineralization, bone density, effect on osteoblasts and/or osteoclasts, markers of bone formation, markers of bone resorption, markers of osteoblast activity, and/or markers of osteoclast activity. Such inhibitors may act by binding to sclerostin or its receptor or binding partner. Inhibitors in this category include "sclerostin binding agents," such as, e.g., antibodies or peptide-based molecules. "Sclerostin inhibitors" also refers to small organic chemical compounds, optionally of less than about 1000 Daltons in molecular weight that bind sclerostin and inhibit its activity. Inhibitors may alternatively act by inhibiting expression of sclerostin. Inhibitors in this category include polynucleotides or oligonucleotides that bind to sclerostin DNA or mRNA and inhibit sclerostin expression, including an antisense oligonucleotide, inhibitory RNA, DNA enzyme, ribozyme, an aptamer or pharmaceutically acceptable salts thereof that inhibit the expression of sclerostin.

[0036] A "sclerostin binding agent" specifically binds to sclerostin or portions thereof to block or impair binding of human sclerostin to one or more ligands. Sclerostin, the product of the SOST gene, is absent in sclerosteosis, a skeletal disease characterized by bone overgrowth and strong dense bones (Brunkow et al., *Am. J. Hum. Genet.*, 68:577-589 (2001); Balemans et al., *Hum. Mol. Genet.*, 10:537-543 (2001)). The amino acid sequence of human sclerostin is reported by Brunkow et al. and is disclosed in U.S. Patent Publication No. 20070110747 as SEQ ID NO: 1. Recombinant human sclerostin/SOST is commercially available from R&D Systems (Minneapolis, Minn., USA; 2006 Catalog #1406-ST-025). Additionally, recombinant mouse sclerostin/SOST is commercially available from R&D Systems (Minneapolis, Minn., USA; 2006 Catalog #1589-ST-025). Research grade sclerostin-binding monoclonal antibodies are commercially available from R&D Systems (Minneapolis, Minn., USA; mouse monoclonal: 2006 Catalog # MAB1406; rat monoclonal: 2006 Catalog # MAB1589). U.S. Patent Nos. 6,395,511 and 6,803,453, and U.S. Patent Publication Nos. 20040009535 and 20050106683 refer to anti-sclerostin antibodies generally. Examples of sclerostin binding agents suitable for use in the context of the invention also are described in U.S. Patent Publication Nos. 20070110747 and 20070072797. Additional information regarding materials and methods for generating sclerostin binding agents can be found in U.S. Patent Publication No. 20040158045.

[0037] The sclerostin binding agent of the invention preferably is an antibody. The term "antibody" refers to an intact antibody, or a binding fragment thereof. An antibody may comprise a complete antibody molecule (including polyclonal, monoclonal, chimeric, humanized, or human versions having full length heavy and/or light chains), or comprise an antigen binding fragment thereof. Antibody fragments include F(ab')₂, Fab, Fab', Fv, Fc, and Fd fragments, and can be incorporated into single domain antibodies, single-chain antibodies, maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv (see, e.g., Hollinger and Hudson, *Nature Biotechnology*, 23(9):1126-1136 (2005)). Antibody polypeptides, including fibronectin polypeptide monobodies, also are disclosed in U.S. Patent No. 6,703,199. Other antibody polypeptides are disclosed in U.S. Patent Publication No. 20050238646. Anti-sclerostin antibodies may bind to sclerostin of SEQ NO: 1, or a naturally occurring variant thereof, with an affinity of less than or equal to 1×10^{-7} M, less than or equal to 1×10^{-8} M, less than or equal to 1×10^{-9} M, less than or equal to 1×10^{-1} M, less than or equal to 1×10^{-11} M, or less than or equal to 1×10^{-12} M. Affinity may be determined by an affinity ELISA assay. In certain embodiments, affinity may be determined by a BIAcore assay. In certain embodiments, affinity may be determined by a kinetic method. In certain embodiments, affinity may be determined by an equilibrium/solution method.

[0038] An antibody fragment may be any synthetic or genetically engineered protein. For example, antibody fragments include isolated fragments consisting of the light chain variable region, "Fv" fragments consisting of the variable regions of the heavy and light chains, recombinant single chain polypeptide molecules in which light and heavy variable regions are connected by a peptide linker (scFv proteins).

[0039] Another form of an antibody fragment is a peptide comprising one or more complementarity determining regions (CDRs) of an antibody. CDRs (also termed "minimal recognition units" or "hypervariable region") can be obtained by constructing polynucleotides that encode the CDR of interest. Such polynucleotides are prepared, for example, by using the polymerase chain reaction to synthesize the variable region using mRNA of antibody-producing cells as a template (see, for example, Larrick et al., *Methods: A Companion to Methods in Enzymology*, 2:106 (1991); Courtenay-Luck, "Genetic Manipulation of Monoclonal Antibodies," in *Monoclonal Antibodies Production, Engineering and Clinical Application*, Ritter et al. (eds.), page 166, Cambridge University Press (1995); and Ward et al., "Genetic Manipulation and Expression of Antibodies," in *Monoclonal Antibodies: Principles and Applications*, Birch et al., (eds.), page 137, Wiley-Liss, Inc. (1995)).

[0040] In one embodiment of the invention, the sclerostin binding agent cross-blocks the binding of at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13,

Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 (all of which are described in U.S. Patent Publication No. 20070110747) to sclerostin. Alternatively or in addition, the sclerostin binding agent is cross-blocked from binding to sclerostin by at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 (all of which are described in U.S. Patent Publication No. 20070110747). The terms "cross-block," "cross-blocked," and "cross-blocking" are used interchangeably herein to mean the ability of an antibody or other binding agent to interfere with the binding of other antibodies or binding agents to sclerostin. The extent to which an antibody or other binding agent is able to interfere with the binding of another to sclerostin, and therefore whether it can be said to cross-block, can be determined using competition binding assays. In some aspects of the invention, a cross-blocking antibody or fragment thereof reduces sclerostin binding of a reference antibody between about 40% and about 100%, such as about 60% and about 100%, specifically between 70% and 100%, and more specifically between 80% and 100%. A particularly suitable quantitative assay for detecting cross-blocking uses a Biacore machine which measures the extent of interactions using surface plasmon resonance technology. Another suitable quantitative cross-blocking assay uses an ELISA-based approach to measure competition between antibodies or other binding agents in terms of their binding to sclerostin.

[0041] Suitable sclerostin binding agents include antibodies and portions thereof described in U.S. Patent Publication No. 20070110747, such as one or more of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 as specifically disclosed therein. At least one of the regions of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 may have at least one amino acid substitution, provided that the binding agent retains the binding specificity of the non-substituted CDR. The non-CDR portion of the binding agent may be a non-protein molecule, wherein the binding agent cross-blocks the binding of an antibody disclosed herein to sclerostin and/or neutralizes sclerostin. The non-CDR portion of the binding agent may be a non-protein molecule in which the binding agent exhibits a similar binding pattern to human sclerostin peptides in a human sclerostin peptide epitope competition binding assay as that exhibited by at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 (all of which are described in U.S. Patent Publication No. 20070110747), and/or neutralizes sclerostin. The non-CDR portion of the binding agent may be composed of amino acids, wherein the binding agent is a recombinant binding protein or a synthetic peptide, and the recombinant binding protein cross-blocks the binding of an antibody to sclerostin and/or neutralizes sclerostin. The non-CDR portion of the binding agent may be composed of amino acids, wherein the binding agent is a recombinant binding protein, and the recombinant binding protein exhibits a similar binding pattern to human sclerostin peptides in the human sclerostin peptide epitope competition binding assay (described in U.S. Patent Publication No. 20070110747) as that exhibited by at least one of the antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 (described in U.S. Patent Publication No. 20070110747), and/or neutralizes sclerostin. Preferably, the sclerostin binding agent is Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, or Ab-24 of U.S. Patent Publication No. 20070110747.

[0042] In addition, the sclerostin binding agent can comprise at least one CDR sequence having at least 75% identity (e.g., 100% identity) to a CDR selected from SEQ ID NOs: 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 78, 79, 80, 81, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 351, 352, 353, 358, 359, and 360 disclosed in U.S. Patent Publication No. 20070110747. Preferably, the sclerostin binding agent comprises at least one CDR sequence having at least 75% identity to a CDR selected from SEQ ID NOs: 245, 246, 247, 78, 79, 80, 269, 270, 271, 239, 240, and 24, all of which is described in U.S. Patent Publication No. 20070110747. As described in U.S. Patent Publication No. 20070110747, the sclerostin binding agent can comprise: a) CDR sequences of SEQ ID NOs:54, 55, and 56 and CDR sequences of SEQ ID NOs:51, 52, and 53; b) CDR sequences of SEQ ID NOs:60, 61, and 62 and CDR sequences of SEQ ID NOs:57, 58, and 59; c) CDR sequences of SEQ ID NOs:48, 49, and 50 and CDR sequences of SEQ ID NOs:45, 46, and 47; d) CDR sequences of SEQ ID NOs:42, 43, and 44 and CDR sequences of SEQ ID NOs:39, 40, and 41; e) CDR sequences of SEQ ID NOs:275, 276, and 277 and CDR sequences of SEQ ID NOs:287, 288, and 289; f) CDR sequences of SEQ ID NOs:278, 279, and 280 and CDR sequences of SEQ ID NOs:290, 291, and 292; g) CDR sequences of SEQ ID NOs:78, 79, and 80 and CDR sequences of SEQ ID NOs: 245, 246, and 247; h) CDR sequences of SEQ ID NOs:81, 99, and 100 and CDR sequences of SEQ ID NOs:248, 249, and 250; i) CDR sequences of SEQ ID NOs:101, 102, and 103 and CDR sequences of SEQ ID NOs:251, 252, and 253; j) CDR sequences of SEQ ID NOs:104, 105, and 106 and CDR sequences of SEQ ID NOs:254, 255, and 256; k) CDR sequences of SEQ ID NOs:107, 108, and 109 and CDR sequences of SEQ ID NOs:257, 258, and 259; l) CDR sequences of SEQ ID NOs:110, 111, and 112 and CDR sequences of SEQ ID NOs:260, 261, and 262; m) CDR sequences of SEQ ID NOs:281, 282, and 283 and CDR sequences of SEQ ID NOs:293, 294, and 295; n) CDR sequences of SEQ ID NOs: 113, 114,

and 115 and CDR sequences of SEQ ID NOs:263, 264, and 265; o) CDR sequences of SEQ NOs:284, 285, and 286 and CDR sequences of SEQ ID NOs:296, 297, and 298; p) CDR sequences of SEQ ID NOs:116, 237, and 238 and CDR sequences of SEQ ID NOs:266, 267, and 268; q) CDR sequences of SEQ ID NOs:239, 240, and 241 and CDR sequences of SEQ ID NOs:269, 270, and 271; r) CDR sequences of SEQ ID NOs:242, 243, and 244 and CDR sequences of SEQ ID NOs:272, 273, and 274; or s) CDR sequences of SEQ ID NOs:351, 352, and 353 and CDR sequences of SEQ ID NOs:358, 359, and 360.

[0043] The sclerostin binding agent also can comprise at least one CDR sequence having at least 75% identity to a CDR selected from CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 wherein CDR-H1 has the sequence given in SEQ ID NO: 245 or SEQ ID NO: 269, CDR-H2 has the sequence given in SEQ ID NO: 246 or SEQ ID NO: 270, CDR-H3 has the sequence given in SEQ NO: 247 or SEQ ID NO: 271, CDR-L1 has the sequence given in SEQ ID NO: 78 or SEQ ID NO: 239, CDR-L2 has the sequence given in SEQ ID NO: 79 or SEQ ID NO: 240 and CDR-L3 has the sequence given in SEQ ID NO: 80 or SEQ ID NO 241, all of which is described in U.S. Patent Publication No. 20070110747.

[0044] Alternatively, the sclerostin binding agent can have a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 137 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 245, 246, and 247, respectively, and a light chain comprising CDR's L1, L2 and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 133 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 78, 79, and 80, respectively (as described in U.S. Patent Publication No. 20070110747).

[0045] The sclerostin binding agent may have a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 145 or 392 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 245, 246, and 247, respectively, and a light chain comprising CDR's L1, L2, and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 141 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 78, 79, and 80, respectively (as described in U.S. Patent Publication No. 20070110747).

[0046] The sclerostin binding agent may have a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 335 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 269, 270, and 271, respectively, and a light chain comprising CDR's L1, L2, and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 334 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 239, 240, and 241, respectively (as described in U.S. Patent Publication No. 20070110747).

[0047] Alternatively, the sclerostin binding agent has a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 331 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 269, 270, and 271, respectively, and a light chain comprising CDR's L1, L2, and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 330 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 239, 240, and 241, respectively (as described in U.S. Patent Publication No. 20070110747).

[0048] The sclerostin binding agent may have a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 345 or 396 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 269, 270, and 271, respectively, and a light chain comprising CDR's L1, L2, and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 341 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 239, 240, and 241, respectively (as described in U.S. Patent Publication No. 20070110747).

[0049] Alternatively, the sclerostin binding agent has a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 137, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 133; or a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 145 or 392, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 141; or a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 335, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 334; or a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 331, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 330; or a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 345 or 396, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 341 (as described in U.S. Patent Publication No. 20070110747).

[0050] Sclerostin binding agents for use in the inventive method preferably modulate sclerostin function in the cell-based assay described in U.S. Patent Publication No. 20070110747 and/or the *in vivo* assay described in U.S. Patent Publication No. 20070110747 and/or bind to one or more of the epitopes described in U.S. Patent Publication No. 20070110747 and/or cross-block the binding of one of the antibodies described in U.S. Patent Publication No. 20070110747 and/or are cross-blocked from binding sclerostin by one of the antibodies described in U.S. Patent Publication No. 20070110747.

[0051] Alternatively, the inventive method can comprise administering a sclerostin inhibitor other than a sclerostin

binding agent described herein. Such agents can act directly or indirectly on SOST or sclerostin, Sclerostin inhibitors contemplated for use in the inventive method include those described in U.S. Patent Publication No. 20030229041. For example, agents useful for modulating SOST expression and sclerostin activity include, but are not limited to, steroids (such as those corresponding to Formula 1 of U.S. Patent Publication No. 20030229041), alkaloids, teipenoids, peptoids, and synthetic chemicals. In some embodiments, the SOST antagonist or agonist can bind to a glucocorticoid receptor. For example, dexamethasone tends to abolish the stimulatory effect of BMP-4 and BMP-6 on SOST expression. Other chemical entities including glucocorticoid analogs, bile salts (such as those corresponding to Formula 3 of U.S. Patent Publication No. 20030229041), and prostaglandins (such as those corresponding to Formula 2 of U.S. Patent Publication No. 20030229041) also modulate the effects of bone morphogenetic proteins on SOST expression, and are contemplated for use in the inventive method.

[0052] The sclerostin inhibitor may also be other small molecule therapeutics that act directly or indirectly on SOST or sclerostin to decrease the level of at least one bone resorptive marker and/or increase the level of at least one bone formation marker *in vivo*. The term "small molecule" includes a compound or molecular complex, either synthetic, naturally derived, or partially synthetic, and which preferably has a molecular weight of less than 5,000 Daltons (e.g., between about 100 and 1,500 Daltons). Agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including spatially addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the "one-bead one-compound" library method, and synthetic library methods using affinity chromatography selection (see, e.g., Lam, *Anticancer Drug Des.*, 12:145 (1997) and U.S. Patent Nos. 5,738,996; 5,807,683; and 7,261,892). Methods of developing and screening sclerostin inhibitors are further described in U.S. Patent Publication No. 20030229041.

[0053] Sclerostin expression inhibitors that may be used according to the methods of the invention include inhibitor oligonucleotides or polynucleotides, including pharmaceutically acceptable salts thereof, e.g., sodium salts. Nonlimiting examples include: antisense oligonucleotides (Eckstein, *Antisense Nucleic Acid Drug Dev.*, 10: 117-121 (2000); Croke, *Methods Enzymol.*, 313: 3-45 (2000); Guvalcova et al., *J. Biol. Chem.*, 270: 2620-2627 (1995); Manoharan, *Biochim. Biophys. Acta*, 1489: 117-130 (1999); Baker et al., *J. Biol. Chem.*, 272: 11994-12000 (1997); Kurreck, *Eur. J. Biochem.*, 270: 1628-1644 (2003); Sieralcowska et al., *Proc. Natl. Acad. Sci. USA*, 93: 12840-12844 (1996); Marwick, *J. Am. Med. Assoc.*, 280: 871 (1998); Tomita and Morishita, *Curr. Pharm. Des.*, 10: 797-803 (2004); Gleave and Monia, *Nat. Rev. Cancer*, 5: 468-479 (2005) and Patil, *AAPS J.*, 7: E61-E77 (2005)), triplex oligonucleotides (Francois et al., *Nucleic Acids Res.*, 16: 11431-11440 (1988) and Moser and Dervan, *Science*, 238: 645-650 (1987)), ribozymes/deoxyribozymes (DNAzymes) (Kruger et al., *Tetrahymena. Cell*, 31: 147-157 (1982); Uhlenbeck, *Nature*, 328: 596-600 (1987); Sigurdsson and Eckstein, *Trends Biotechnol.*, 13: 286-289 (1995); Kumar et al., *Gene Ther.*, 12: 1486-1493 (2005); Breaker and Joyce, *Chem. Biol.*, 1: 223-229 (1994); Khachigian, *Curr. Pharm. Biotechnol.*, 5: 337-339 (2004); Khachigian, *Biochem. Pharmacol.*, 68: 1023-1025 (2004) and Trulzsch and Wood, *J. Neurochem.*, 88: 257-265 (2004)), small-interfering RNAs/siRNAs (Fire et al., *Nature*, 391: 806-811 (1998); Montgomery et al., *Proc. Natl. Acad. Sci. U.S.A.*, 95: 15502-15507 (1998); Cullen, *Nat. Immunol.*, 3: 597-599 (2002); Hannon, *Nature*, 418: 244-251 (2002); Bernstein et al., *Nature*, 409: 363-366 (2001); Nykanen et al., *Cell*, 107: 309-321 (2001); Gilmore et al., *J. Drug Target.*, 12: 315-340 (2004); Reynolds et al., *Nat. Biotechnol.*, 22: 326-330 (2004); Soutschek et al., *Nature*, 432: 173-178 (2004); Ralph et al., *Nat. Med.*, 11: 429-433 (2005); Xia et al., *Nat. Med.*, 10: 816-820 (2004) and Miller et al., *Nucleic Acids Res.*, 32: 661-668 (2004)), aptamers (Ellington and Szostak, *Nature*, 346: 818-822 (1990); Doudna et al., *Proc. Natl. Acad. Sci. U.S.A.*, 92: 2355-2359 (1995); Tuerk and Gold, *Science*, 249: 505-510 (1990); White et al., *Mol. Ther.*, 4: 567-573 (2001); Rusconi et al., *Nature*, 419: 90-94 (2002); Nimjee et al., *Mol. Ther.*, 14: 408-415 (2006); Gragoudas et al., *N. Engl. J. Med.*, 351: 3805-2816 (2004); Vinorel, *Curr. Opin. Mol. Ther.*, 5: 673-679 (2003) and Kourlas and Schiller et al., *Clin. Ther.*, 28: 36-44 (2006)) or decoy oligonucleotides (Morishita et al., *Proc. Natl. Acad. Sci. U.S.A.*, 92: 5855-5859 (1995); Alexander et al., *J. Am. Med. Assoc.*, 294: 2446-2454 (2005); Mann and Dzau, *J. Clin. Invest.*, 106: 1071-1075 (2000) and Nimjee et al., *Annu. Rev. Med.*, 56: 555-583 (2005)). Commercial providers such as Ambion Inc. (Austin, TX), Dharmacon Inc. (Lafayette, CO), InvivoGen (San Diego, CA), and Molecular Research Laboratories, LLC (Herndon, VA) generate custom siRNA molecules. In addition, commercial kits are available to produce custom siRNA molecules, such as SILENCER™ siRNA Construction Kit (Ambion Inc., Austin, TX) or psiRNA System (InvivoGen, San Diego, CA).

[0054] Inhibitory oligonucleotides which are stable, have a high resistance to nucleases, possess suitable pharmacokinetics to allow them to traffic to target tissue site at non-toxic doses, and have the ability to cross through plasma membranes are contemplated for use as a therapeutic. Inhibitory oligonucleotides may be complementary to the coding portion of a target gene, 3' or 5' untranslated regions, or intronic sequences in a gene, or alternatively coding or intron sequences in the target mRNA. Intron sequences are generally less conserved and thus may provide greater specificity. In one embodiment, the inhibitory oligonucleotide inhibits expression of a gene product of one species but not its homologue in another species; in other embodiments, the inhibitory oligonucleotide inhibits expression of a gene in two species, e.g. human and primate, or human and murine.

[0055] The constitutive expression of antisense oligonucleotides in cells has been shown to inhibit gene expression, possibly via the blockage of translation or prevention of splicing. In certain embodiments, the inhibitory oligonucleotide

is capable of hybridizing to at least 8, 9, 10, 11, or 12 consecutive bases of the sclerostin gene or mRNA (or the reverse strand thereof) under moderate or high stringency conditions. Suitable inhibitory oligonucleotides may be single stranded and contain a segment, e.g. at least 12, 15 or 18 bases in length, that is sufficiently complementary to, and specific for, an mRNA or DNA molecule such that it hybridizes to the mRNA or DNA molecule and inhibits transcription, splicing or translation. Generally complementarity over a length of less than 30 bases is more than sufficient.

[0056] Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short nucleic acids (e.g., 10 to 50 nucleotides) and at least about 60°C for longer nucleic acids (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30% to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50°C to 55°C. Exemplary moderate stringency conditions include hybridization in 40% to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55°C to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60°C to 65°C. Duration of hybridization is generally less than about 24 hours, usually about 4 hours to about 12 hours.

[0057] In some cases, depending on the length of the complementary region, one, two or more mismatches may be tolerated without affecting inhibitory function. In certain embodiments, the inhibitory oligonucleotide is an antisense oligonucleotide, an inhibitory RNA (including siRNA or RNAi, or shRNA), a DNA enzyme, a ribozyme (optionally a hammerhead ribozyme), an aptamer, or pharmaceutically acceptable salts thereof. In one embodiment, the oligonucleotide is complementary to at least 10 bases of the nucleotide sequence encoding SEQ ID NO: 1 of U.S. Patent Publication No. 20040158045. In one embodiment, the oligonucleotide targets the nucleotides located in the vicinity of the 3' untranslated region of the sclerostin mRNA.

[0058] The specific sequence utilized in design of the oligonucleotides may be any contiguous sequence of nucleotides contained within the expressed gene message of the target. Factors that govern a target site for the inhibitory oligonucleotide sequence include the length of the oligonucleotide, binding affinity, and accessibility of the target sequence. Sequences may be screened *in vitro* for potency of their inhibitory activity by measuring inhibition of target protein translation and target related phenotype, e.g., inhibition of cell proliferation in cells in culture. In general it is known that most regions of the RNA (5' and 3' untranslated regions, AUG initiation, coding, splice junctions and introns) can be targeted using antisense oligonucleotides. Programs and algorithms, known in the art, may be used to select appropriate target sequences. In addition, optimal sequences may be selected utilizing programs designed to predict the secondary structure of a specified single stranded nucleic acid sequence and allowing selection of those sequences likely to occur in exposed single stranded regions of a folded mRNA. Methods and compositions for designing appropriate oligonucleotides may be found, for example, in U.S. Patent No. 6,251,588.

[0059] Phosphorothioate antisense oligonucleotides may be used. Modifications of the phosphodiester linkage as well as of the heterocycle or the sugar may provide an increase in efficiency. Phosphorothioate is used to modify the phosphodiester linkage. An N3'-P5' phosphoramidate linkage has been described as stabilizing oligonucleotides to nucleases and increasing the binding to RNA. Peptide nucleic acid (PNA) linkage is a complete replacement of the ribose and phosphodiester backbone and is stable to nucleases, increases the binding affinity to RNA, and does not allow cleavage by RNAse H. Its basic structure is also amenable to modifications that may allow its optimization as an antisense component. With respect to modifications of the heterocycle, certain heterocycle modifications have proven to augment antisense effects without interfering with RNAse H activity. An example of such modification is C-5 thiazole modification. Finally, modification of the sugar may also be considered. 2'-O-propyl and 2'-methoxyethoxy ribose modifications stabilize oligonucleotides to nucleases in cell culture and *in vivo*.

[0060] Most mRNAs have been shown to contain a number of secondary and tertiary structures. Secondary structural elements in RNA are formed largely by Watson-Crick type interactions between different regions of the same RNA molecule. Important secondary structural elements include intramolecular double stranded regions, hairpin loops, bulges in duplex RNA and internal loops. Tertiary structural elements are formed when secondary structural elements come in contact with each other or with single stranded regions to produce a more complex three dimensional structure. A number of researchers have measured the binding energies of a large number of RNA duplex structures and have derived a set of rules which can be used to predict the secondary structure of RNA (see, e.g., Jaeger et al., Proc. Natl. Acad. Sci. USA, 86:7706 (1989); and Turner et al., Annu. Rev. Biophys. Biophys. Chem. 17:167 (1988)). The rules are useful in identification of RNA structural elements and, in particular, for identifying single stranded RNA regions which may represent segments of the mRNA to target for siRNA, ribozyme, or antisense technologies.

[0061] Short interfering (si) RNA technology (also known as RNAi) generally involves degradation of an mRNA of a particular sequence induced by double-stranded RNA (dsRNA) that is homologous to that sequence, thereby "interfering" with expression of the corresponding gene. Any selected gene may be repressed by introducing a dsRNA which corresponds to all or a substantial part of the mRNA for that gene. It appears that when a long dsRNA is expressed, it is initially processed by a ribonuclease III into shorter dsRNA oligonucleotides of as few as 21 to 22 base pairs in length.

Accordingly, siRNA may be affected by introduction or expression of relatively short homologous dsRNAs. Exemplary siRNAs have sense and antisense strands of about 21 nucleotides that form approximately 19 nucleotides of double stranded RNA with overhangs of two nucleotides at each 3' end. Indeed the use of relatively short homologous dsRNAs may have certain advantages.

5 **[0062]** Mammalian cells have at least two pathways that are affected by double-stranded RNA (dsRNA). In the sequence-specific siRNA pathway, the initiating dsRNA is first broken into short interfering RNAs, as described above. Short interfering RNAs are thought to provide the sequence information that allows a specific messenger RNA to be targeted for degradation. In contrast, the nonspecific pathway is triggered by dsRNA of any sequence, as long as it is at least about 30 base pairs in length.

10 **[0063]** The nonspecific effects occur because dsRNA activates two enzymes: PKR, which in its active form phosphorylates the translation initiation factor eIF2 to shut down all protein synthesis, and 2', 5' oligoadenylate synthetase (2', 5'-AS), which synthesizes a molecule that activates RNase L, a nonspecific enzyme that targets all mRNAs. The nonspecific pathway may represent a host response to stress or viral infection, and, in general, the effects of the nonspecific pathway are preferably minimized. Significantly, longer dsRNAs appear to be required to induce the nonspecific pathway and, accordingly, dsRNAs shorter than about 30 base pairs are contemplated to effect gene repression by RNAi (see Hunter et al., J. Biol. Chem., 250: 409-17 (1975); Manche et al., Mol. Cell. Biol. 12: 5239-48 (1992); Minks et al., J. Biol. Chem., 254: 10180-3 (1979); and Elbashir et al., Nature, 411: 494-8 (2001)).

15 **[0064]** siRNA has proven to be an effective means of decreasing gene expression in a variety of cell types. siRNA typically decreases expression of a gene to lower levels than that achieved using antisense techniques, and frequently eliminates expression entirely (see Bass, Nature, 411: 428-9 (2001)). In mammalian cells, siRNAs are effective at concentrations that are several orders of magnitude below the concentrations typically used in antisense experiments (Elbashir et al., Nature, 411:494-8 (2001)).

20 **[0065]** The double stranded oligonucleotides used to effect RNAi are preferably less than 30 base pairs in length, for example, about 25, 24, 23, 22, 21, 20, 19, 18, or 17 base pairs or less in length, and contain a segment sufficiently complementary to the target mRNA to allow hybridization to the target mRNA. Optionally the dsRNA oligonucleotides may include 3' overhang ends. Exemplary 2-nucleotide 3' overhangs may be composed of ribonucleotide residues of any type and may even be composed of 2'-deoxythymidine residues, which lowers the cost of RNA synthesis and may enhance nuclease resistance of siRNAs in the cell culture medium and within transfected cells (see Elbashi et al., *supra*). Exemplary dsRNAs may be synthesized chemically or produced *in vitro* or *in vivo* using appropriate expression vectors (see, e.g., Elbashir et al., Genes Dev., 15:188-200 (2001)). Longer RNAs may be transcribed from promoters, such as T7 RNA polymerase promoters, known in the art.

25 **[0066]** Longer dsRNAs of 50, 75, 100, or even 500 base pairs or more also may be utilized in certain embodiments of the invention. Exemplary concentrations of dsRNAs for effecting RNAi are about 0.05 nM, 0.1 nM, 0.5 nM, 1.0 nM, 1.5 nM, 25 nM, or 100 nM, although other concentrations may be utilized depending upon the nature of the cells treated, the gene target and other factors readily discernable to the skilled artisan.

30 **[0067]** Further compositions, methods and applications of siRNA technology are provided in U.S. Patent Nos. 6,278,039; 5,723,750; and 5,244,805.

35 **[0068]** Compared to siRNA, shRNA offers advantages in silencing longevity and delivery options. See, e.g., Hannon et al., Nature, 431:371-378 (2004) for review. Vectors that produce shRNAs, which are processed intracellularly into short duplex RNAs having siRNA-like properties have been reported (Brummelkamp et al., Science, 296: 550-553 (2000); Paddison et al., Genes Dev., 16: 948-958 (2002)). Such vectors provide a renewable source of a gene-silencing reagent that can mediate persistent gene silencing after stable integration of the vector into the host-cell genome. Furthermore, the core silencing 'hairpin' cassette can be readily inserted into retroviral, lentiviral, or adenoviral vectors, facilitating delivery of shRNAs into a broad range of cell types (Brummelkamp et al., Cancer Cell, 2:243-247 (2002); Dirac et al., J. Biol. Chem., 278:11731-11734 (2003); Michiels et al., Nat. Biotechnol., 20:1154-1157 (2002); Stegmeie et al., Proc. Natl. Acad. Sci. USA, 102:13212-13217 (2005); Khvorova et al., Cell, 115:209-216 (2003)) in any of the innumerable ways that have been devised for delivery of DNA constructs that allow ectopic mRNA expression.

40 **[0069]** A hairpin can be organized in either a left-handed hairpin (i.e., 5'-antisense-loop-sense-3') or a right-handed hairpin (i.e., 5'-sense-loop-antisense-3'). The siRNA may also contain overhangs at either the 5' or 3' end of either the sense strand or the antisense strand, depending upon the organization of the hairpin. Preferably, if there are any overhangs, they are on the 3' end of the hairpin and comprise between 1 to 6 bases. The overhangs can be unmodified, or can contain one or more specificity or stabilizing modifications, such as a halogen or O-alkyl modification of the 2' position, or internucleotide modifications such as phosphorothioate, phosphorodithioate, or methylphosphonate modifications. The overhangs can be ribonucleic acid, deoxyribonucleic acid, or a combination of ribonucleic acid and deoxyribonucleic acid.

45 **[0070]** Additionally, a hairpin can further comprise a phosphate group on the 5'-most nucleotide. The phosphorylation of the 5'-most nucleotide refers to the presence of one or more phosphate groups attached to the 5' carbon of the sugar moiety of the 5'-terminal nucleotide. Preferably, there is only one phosphate group on the 5' end of the region that will

form the antisense strand following Dicer processing. In one exemplary embodiment, a right-handed hairpin can include a 5' end (i.e., the free 5' end of the sense region) that does not have a 5' phosphate group, or can have the 5' carbon of the free 5'-most nucleotide of the sense region being modified in such a way that prevents phosphorylation. This can be achieved by a variety of methods including, but not limited to, addition of a phosphorylation blocking group (e.g., a 5'-O-alkyl group), or elimination of the 5'-OH functional group (e.g., the 5'-most nucleotide is a 5'-deoxy nucleotide). In cases where the hairpin is a left-handed hairpin, preferably the 5' carbon position of the 5'-most nucleotide is phosphorylated.

[0071] Hairpins that have stem lengths longer than 26 base pairs can be processed by Dicer such that some portions are not part of the resulting siRNA that facilitates mRNA degradation. Accordingly the first region, which may comprise sense nucleotides, and the second region, which may comprise antisense nucleotides, may also contain a stretch of nucleotides that are complementary (or at least substantially complementary to each other), but are or are not the same as or complementary to the target mRNA. While the stem of the shRNA can be composed of complementary or partially complementary antisense and sense strands exclusive of overhangs, the shRNA can also include the following: (1) the portion of the molecule that is distal to the eventual Dicer cut site contains a region that is substantially complementary/homologous to the target mRNA; and (2) the region of the stem that is proximal to the Dicer cut site (i.e., the region adjacent to the loop) is unrelated or only partially related (e.g., complementary/homologous) to the target mRNA. The nucleotide content of this second region can be chosen based on a number of parameters including but not limited to thermodynamic traits or profiles.

[0072] Modified shRNAs can retain the modifications in the post-Dicer processed duplex. In exemplary embodiments, in cases in which the hairpin is a right handed hairpin (e.g., 5'-S-loop-AS-3') containing 2-6 nucleotide overhangs on the 3' end of the molecule, 2'-O-methyl modifications can be added to nucleotides at position 2, positions 1 and 2, or positions 1, 2, and 3 at the 5' end of the hairpin. Also, Dicer processing of hairpins with this configuration can retain the 5' end of the sense strand intact, thus preserving the pattern of chemical modification in the post-Dicer processed duplex. Presence of a 3' overhang in this configuration can be particularly advantageous since blunt ended molecules containing the prescribed modification pattern can be further processed by Dicer in such a way that the nucleotides carrying the 2' modifications are removed. In cases where the 3' overhang is present/retained, the resulting duplex carrying the sense-modified nucleotides can have highly favorable traits with respect to silencing specificity and functionality. Examples of exemplary modification patterns are described in detail in U.S. Patent Publication No. 20050223427 and International Patent Publication Nos. WO 2004/090105 and WO 2005/078094.

[0073] shRNA may comprise sequences that were selected at random, or according to any rational design selection procedure. For example, rational design algorithms are described in International Patent Publication No. WO 2004/045543 and U.S. Patent Publication No. 20050255487. Additionally, it may be desirable to select sequences in whole or in part based on average internal stability profiles ("AISPs") or regional internal stability profiles ("RISPs") that may facilitate access or processing by cellular machinery.

[0074] Ribozymes are enzymatic RNA molecules capable of catalyzing specific cleavage of mRNA, thus preventing translation. (For a review, see Rossi, *Current Biology*, 4:469-471 (1994)). The mechanism of ribozymes action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage event. The ribozyme molecules preferably include (1) one or more sequences complementary to a target mRNA, and (2) the well known catalytic sequence responsible for mRNA cleavage or a functionally equivalent sequence (see, e.g., U.S. Patent No. 5,093,246).

[0075] While ribozymes that cleave mRNA at site-specific recognition sequences can be used to destroy target mRNAs, hammerhead ribozymes may alternatively be used. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. Preferably, the target mRNA has the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, *Nature*, 334:585-591 (1988); and International Patent Publication No. WO 89/05852.

[0076] Gene targeting ribozymes may contain a hybridizing region complementary to two regions of a target mRNA, each of which is at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleotides (but which need not both be the same length).

[0077] Hammerhead ribozyme sequences can be embedded in a stable RNA such as a transfer RNA (tRNA) to increase cleavage *efficiency in vivo* (Perriman et al., *Proc. Natl. Acad. Sci. USA*, 92:6175-79 (1995); de Feyter and Gaudron, *Methods in Molecular Biology*, Vol. 74, Chapter 43, "Expressing Ribozymes in Plants," Turner, P. C. (ed.), Humana Press Inc., Totowa, N.J.). In particular, RNA polymerase III-mediated expression of tRNA fusion ribozymes are well known in the art (see Kawasaki et al., *Nature*, 393:284-9 (1998); Kuwabara et al., *Nature Biotechnol.*, 16:961-5 (1998); and Kuwabara et al., *Mol. Cell*, 2:617-27 (1998); Koseki et al., *J. Virol.*, 73:1868-77 (1999); Kuwabara et al., *Proc. Natl. Acad. Sci. USA*, 96:1886-91 (1999); Tanabe et al., *Nature*, 406:473-4 (2000)). There are typically a number of potential hammerhead ribozyme cleavage sites within a given target cDNA sequence. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target mRNA- to increase efficiency

and minimize the intracellular accumulation of non-functional mRNA transcripts. Furthermore, the use of any cleavage recognition site located in the target sequence encoding different portions of the target mRNA would allow the selective targeting of one or the other target genes.

5 [0078] Ribozymes for use in the inventive method also include RNA endoribonucleases ("Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described in Zaug et al., Science, 224:574-578 (1984); Zaug, et al., Science, 231:470-475 (1986); Zaug et al., Nature, 324:429-433 (1986); International Patent Publication No. WO 88/04300; and Been et al., Cell, 47:207-216 (1986)). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. In one embodiment, the inventive method employs those 10 Cech-type Ribozymes which target eight base-pair active site sequences that are present in a target gene or nucleic acid sequence.

[0079] Ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and can be chemically synthesized or produced through an expression vector. Because ribozymes, unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency. Additionally, in certain embodiments, a ribozyme 15 may be designed by first identifying a sequence portion sufficient to cause effective knockdown by RNAi. Portions of the same sequence may then be incorporated into a ribozyme.

[0080] Alternatively, target gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the gene (i.e., the promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See generally Helene, C., Anticancer Drug Des., 6:569-84 (1991); 20 Helene et al., Ann. N.Y. Acad. Sci., 660:27-36 (1992); and Maher, L. J., Bioassays, 14:807-15 (1992)).

[0081] Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription are preferably single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides should promote triple 25 helix formation via Hoogsteen base pairing rules, which generally require sizable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, containing a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in CGC triplets across the three strands in the triplex.

30 [0082] Alternatively, the target sequences that can be targeted for triple helix formation may be increased by creating a so-called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizable stretch of either purines or pyrimidines to be present on one strand of a duplex.

[0083] Alternatively, DNA enzymes may be used to inhibit expression of target gene, such as the sclerostin gene. 35 DNA enzymes incorporate some of the mechanistic features of both antisense and ribozyme technologies. DNA enzymes are designed so that they recognize a particular target nucleic acid sequence, much like an antisense oligonucleotide. They are, however, also catalytic and specifically cleave the target nucleic acid.

[0084] DNA enzymes include two basic types identified by Santoro and Joyce (see, for example, U.S. Patent No. 6,110,462). The 10-23 DNA enzyme comprises a loop structure which connect two arms. The two arms provide specificity 40 by recognizing the particular target nucleic acid sequence while the loop structure provides catalytic function under physiological conditions.

[0085] Preferably, the unique or substantially unique sequence is a G/C rich segment of approximately 18 to 22 nucleotides. High G/C content helps insure a stronger interaction between the DNA enzyme and the target sequence. The specific antisense recognition sequence that will target the enzyme to the message may be divided between the 45 two arms of the DNA enzyme.

[0086] Methods of making and administering DNA enzymes can be found, for example, in U.S. Patent No. 6,110,462. Additionally, one of skill in the art will recognize that, like antisense oligonucleotide, DNA enzymes can be optionally modified to improve stability and improve resistance to degradation.

[0087] Inhibitory oligonucleotides can be administered directly or delivered to cells by transformation or transfection 50 via a vector, including viral vectors or plasmids, into which has been placed DNA encoding the inhibitory oligonucleotide with the appropriate regulatory sequences, including a promoter, to result in expression of the inhibitory oligonucleotide in the desired cell. Known methods include standard transient transfection, stable transfection and delivery using viruses ranging from retroviruses to adenoviruses. Delivery of nucleic acid inhibitors by replicating or replication-deficient vectors is contemplated. Expression can also be driven by either constitutive or inducible promoter systems (Paddison et al., 55 Methods Mol. Biol., 265:85-100 (2004)). In other embodiments, expression may be under the control of tissue or development-specific promoters.

[0088] For example, vectors may be introduced by transfection using carrier compositions such as Lipofectamine 2000 (Life Technologies) or Oligofectamine (Life Technologies). Transfection efficiency may be checked using fluorescence

microscopy for mammalian cell lines after co-transfection of hGFP-encoding pAD3 (Kehlenback et al., J. Cell Biol., 141:863-74 (1998)).

[0089] The delivery route will be the one that provides the best inhibitory effect as measured according to the criteria described above. Delivery mediated by cationic liposomes, delivery by retroviral vectors and direct delivery are efficient.

[0090] The effectiveness of the inhibitory oligonucleotide may be assessed by any of a number of assays, including reverse transcriptase polymerase chain reaction or Northern blot analysis to determine the level of existing human sclerostin mRNA, or Western blot analysis using antibodies which recognize the human sclerostin protein, after sufficient time for turnover of the endogenous pool after new protein synthesis is repressed.

[0091] The invention is further described in the following example. The example serves only to illustrate the invention and are not intended to limit the scope of the invention in any way.

EXAMPLE

[0092] This example describes *in vivo* studies wherein a sclerostin binding agent reduced the level of a marker of bone resorption and increased the level of one or more markers of bone formation.

[0093] A single-center, randomized, double-blind, placebo-controlled, ascending single-dose study in healthy men and postmenopausal women was conducted. Approximately 72 subjects enrolled in one of six dose cohorts. For cohorts 1, 2, 3a, 4, 5 and 6a, eight healthy postmenopausal women were randomized to receive a sclerostin binding agent or placebo via subcutaneous injection in a 3:1 ratio at dose levels of 0.1 mg/kg, 0.3 mg/kg, 1 mg/kg, 3 mg/kg, 5 mg/kg, or 10 mg/kg, respectively. In cohorts 3b and 6b, 8 healthy males received the sclerostin binding agent or a placebo intravenously and subcutaneously in a 3:3:1:1 ratio (sclerostin binding agent intravenously: sclerostin binding agent subcutaneously: placebo intravenously: placebo subcutaneously) at a dose level of 1 mg/kg or 10 mg/kg (reduced to 5 mg/kg), respectively. For cohorts 3c and 6c, four healthy postmenopausal women were randomized to receive the sclerostin binding agent or placebo intravenously in a 3:1 ratio at a dose level of 1 mg/kg or 10 mg/kg (reduced to 5 mg/kg), respectively.

[0094] The anti-sclerostin therapy was monitored by measuring the levels of bone resorption markers and bone formation markers prior to administration, then at least every week for 12 weeks post-administration. P1NP and BSAP levels were monitored following a single-dose subcutaneous administration of sclerostin binding agent in healthy, postmenopausal women (see Figures 1 and 2). Subjects dosed at 0.1 mg/kg and 0.3 mg/kg enjoyed the least elevation of P1NP or BSAP levels (e.g., levels increased less than 20%).

[0095] P1NP levels in subjects given 1 mg/kg increased approximately 20% by Day 10 and gradually tapered off to baseline around Day 56, while BSAP levels peaked at Day 14 at about 30% above baseline. P1NP and BSAP levels in subjects given 3 mg/kg peaked at Day 21 at approximately 100% (P1NP) and 60% (BSAP) increase from baseline, and returned to baseline about Day 56. In subjects administered 5 mg/kg, the level of P1NP rose to about 140% above baseline at Day 14 post-administration, and remained elevated at Day 77. In other words, the level of P1NP increased about 140% by two weeks post-treatment. BSAP rose to about 115% above baseline and remained elevated at Day 84. Similarly, administration of 10 mg/kg triggered a 180% increase in P1NP levels at about Day 28. P1NP levels remained elevated throughout the monitoring period. Subjects administered 10 mg/kg demonstrated a peak increase of BSAP levels at Day 21 (125% baseline for 3 weeks post-administration), which also remained elevated at Day 84. The results of the study are illustrated in Figures 1 and 2.

[0096] Osteocalcin also was monitored following a single-dose, subcutaneous administration of sclerostin binding agent in healthy, postmenopausal women (see Figure 3). Subjects given less than 1 mg/kg experienced little elevation of Osteocalcin. Osteocalcin levels fluctuated in patients administered 1 mg/kg, peaking at about 30% above baseline at Days 21 and 35. Osteocalcin levels peaked at about 100% above baseline at Day 21 in subjects administered 3 mg/kg, and levels remained elevated until about Day 56. Likewise, administration of 5 mg/kg sclerostin binding agent resulted in a 140% increase in osteocalcin levels at day 28, which levels remained at Day 84. Subjects dosed at 10 mg/kg demonstrated a peak osteocalcin level of about 180% above baseline at Day 35. Osteocalcin levels remained elevated above baseline until at least about Day 77.

[0097] Levels of the bone resorptive marker sCTX also were monitored (see Figure 4). Subjects administered placebo and 0.1 mg/kg demonstrated modest decreases in sCTX levels (e.g., less than 20%). Administration of 0.3 mg/kg of sclerostin binding agent reduced sCTX levels by about 20% by Day 21 (i.e., sCTX levels were reduced about 20% by two weeks after treatment). Levels fluctuated in subjects dosed at 1 mg/kg but reached about 30% below baseline at Days 10, 28, and 49. Levels in subjects administered 3 mg/kg, 5 mg/kg, and 10 mg/kg fell lowest at Day 14 to about 35%, 55%, and 55% below baseline, respectively, and levels remained below baseline when monitored thereafter. A comparison of the levels of all monitored biomarkers is provided in Figure 5.

[0098] Serum ionized calcium levels were monitored following a single, subcutaneous dose of sclerostin binding agent in healthy, postmenopausal women (see Figure 6). Remarkably, ionized calcium levels did not fluctuate dramatically at any dosage. Indeed, all subjects (including those receiving placebo) experienced a modest transient decrease in serum

ionized calcium of approximately 5% during the monitoring period.

[0099] Finally, bone mineral density was measured in the spine and hip of healthy, postmenopausal women receiving 1 mg/kg, 3 mg/kg, 5 mg/kg, or 10 mg/kg sclerostin binding agent (see Figure 7). Significant increases in BMD were observed in the spine, for example, at Days 28, 56, and 84, particularly in patients receiving 5 mg/kg and 10 mg/kg. BMD in the hip increased less than that of the spine, but BMD was elevated at Day 56 in patients administered 3 mg/kg, 5 mg/kg, and 10 mg/kg. BMD was further elevated at Day 84 in patients dosed at 5 mg/kg and 10 mg/kg.

[0100] This example illustrates the ability of the inventive method to reduce levels of a marker of bone resorption, elevate levels of markers of bone formation, and increase bone mineral density without dramatic alterations in serum calcium. The therapeutic effect of a single dose of sclerostin binding agent is long-lived, with increased bone formation marker levels and decreased bone resorptive marker levels continuing to be observed at 84 days (12 weeks) post treatment. Furthermore, data described herein suggests that the therapeutic efficacy of the invention have significant advantages compared to other treatments by "uncoupling" bone formation and bone resorption to maximize bone formation and mineralization *in vivo*.

[0101] NUMBERED FURTHER ASPECTS, Not part of the claimed subject-matter unless thus claimed.

(1) A method for inhibiting bone resorption in a subject, the method comprising administering to the subject a sclerostin binding agent in an amount from about 1 mg/kg to about 10 mg/kg, wherein the amount is effective to reduce serum level of C-telopeptide of type I collagen (CTX) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and wherein bone resorption is inhibited.

(2) The method of (1), wherein the amount of sclerostin binding agent increases a marker of bone formation selected from the group consisting of serum level of bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of procollagen type 1 (PINP), and serum level of osteocalcin (OstCa), by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins.

(3) The method of (1), wherein the amount of sclerostin binding agent does not result in hypocalcemia or hypercalcemia.

(4) A method for increasing bone mineral density in a subject, the method comprising administering to the subject a sclerostin binding agent in an amount from about 1 mg/kg to about 10 mg/kg, wherein the amount is effective to (a) reduce serum level of CTX by at least 20% compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and (b) increase serum level of a bone formation marker selected from the group consisting of serum level of bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of procollagen type 1 (PINP), and serum level of osteocalcin (OstCa), by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and wherein bone mineral density is increased.

(5) The method of (4), wherein hip, spine, wrist, finger, shin bone and/or heel bone mineral density is increased by at least about 1%.

(6) The method of (5), wherein bone mineral density in the spine is increased by at least about 1%.

(7) The method of (4), wherein bone mineral density is increased to the range of about 1 to 2.5 standard deviations below the normal bone mineral density of a healthy young adult.

(8) The method of (4), wherein bone mineral density is increased to the range of about 0 to 1 standard deviations below the normal bone mineral density of a healthy young adult.

(9) A method for treating a bone-related disorder in a subject, the method comprising

(a) administering to the subject a sclerostin binding agent in an amount from about 1 mg/kg to about 10 mg/kg for a first period of time, wherein the amount is effective to increase bone mineral density at the hip, spine, wrist, finger, shin bone and/or heel by at least about 3%, and

(b) administering to the subject a sclerostin binding agent in an amount of from about 1 mg/kg to about 10 mg/kg for a second period of time effective to maintain bone mineral density.

(10) The method of (9), wherein the first period of time is 3 months or less.

(11) The method of claim (9), wherein the second period of time is at least 6 months.

(12) The method of claim (9), wherein bone mineral density in the spine is increased by at least about 3%.

(13) A method of treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia, the method comprising administering to the human a sclerostin binding agent in a therapeutically effective amount from about 1 mg/kg to about 10 mg/kg.

(14) The method of (13), wherein the hypocalcemia or hypercalcemia results from chronic kidney disease, renal failure, primary or secondary hyperparathyroidism, pseudohyperparathyroidism, hypoparathyroidism, pseudohypoparathyroidism, magnesium depletion, severe hypermagnesemia, vitamin D deficiency, hyperphosphatemia,

acute pancreatitis, hungry bone syndrome, chelation, osteoblastic metastases, sepsis, surgery, chemotherapy, neoplasia syndrome, hypoparathyroidism, familial hypocalciuric hypercalcemia, sarcoidosis, tuberculosis, berylliosis, histoplasmosis, Candidiasis, Coccidioidomycosis, histiocytosis X, Hodgkin's or Non-Hodgkin's lymphoma, Crohn's disease, Wegener's granulomatosis, pneumonia, silicone-induced granulomas, administration of thiazide diuretics or lithium, or immobilization.

(15) A method of treating a bone-related disorder in (a) a human in which treatment with a parathyroid hormone or analog thereof is contraindicated or (b) a human in which treatment with bisphosphonate is contraindicated, the method comprising administering to the human a therapeutically effective amount of a sclerostin binding agent from about 1 mg/kg to about 10 mg/kg.

(16) The method any one of (1) to (15), wherein an amount of sclerostin binding agent is administered to the subject once every two weeks.

(17) The method of any one of (1) to (15), wherein an amount of sclerostin binding agent is administered to the subject once a month.

(18) The method of any one of (1) to (17), where the sclerostin binding agent cross-blocks the binding of at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 to sclerostin.

(19) The method of any one of (1) to (18), wherein the sclerostin binding agent is cross-blocked from binding to sclerostin by at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24.

(20) The method of any one of (1) to (17), wherein the sclerostin binding agent is an antibody or fragment thereof that demonstrates a binding affinity for sclerostin of SEQ ID NO: 1 of less than or equal to 1×10^{-7} M.

(21) The method of (20), wherein the antibody or fragment thereof comprises:

a) CDR sequences of SEQ ID NOs:54, 55, and 56 and CDR sequences of SEQ ID NOs:51, 52, and 53; b) CDR sequences of SEQ ID NOs:60, 61, and 62 and CDR sequences of SEQ ID NOs:57, 58, and 59; c) CDR sequences of SEQ ID NOs:48, 49, and 50 and CDR sequences of SEQ ID NOs:45, 46, and 47; d) CDR sequences of SEQ ID NOs:42, 43, and 44 and CDR sequences of SEQ ID NOs:39, 40, and 41; e) CDR sequences of SEQ ID NOs:275, 276, and 277 and CDR sequences of SEQ ID NOs:287, 288, and 289; f) CDR sequences of SEQ ID NOs:278, 279, and 280 and CDR sequences of SEQ ID NOs:290, 291, and 292; g) CDR sequences of SEQ ID NOs:78, 79, and 80 and CDR sequences of SEQ ID NOs: 245, 246, and 247; h) CDR sequences of SEQ ID NOs:81, 99, and 100 and CDR sequences of SEQ ID NOs:248, 249, and 250; i) CDR sequences of SEQ ID NOs:101, 102, and 103 and CDR sequences of SEQ ID NOs:251, 252, and 253; j) CDR sequences of SEQ ID NOs:104, 105, and 106 and CDR sequences of SEQ ID NOs:254, 255, and 256; k) CDR sequences of SEQ ID NOs:107, 108, and 109 and CDR sequences of SEQ ID NOs:257, 258, and 259; l) CDR sequences of SEQ ID NOs:110, 111, and 112 and CDR sequences of SEQ ID NOs:260, 261, and 262; m) CDR sequences of SEQ ID NOs:281, 282, and 283 and CDR sequences of SEQ ID NOs:293, 294, and 295; n) CDR sequences of SEQ ID NOs:113, 114, and 115 and CDR sequences of SEQ ID NOs:263, 264, and 265; o) CDR sequences of SEQ ID NOs:284, 285, and 286 and CDR sequences of SEQ ID NOs:296, 297, and 298; p) CDR sequences of SEQ ID NOs: 116, 237, and 238 and CDR sequences of SEQ ID NOs:266, 267, and 268; q) CDR sequences of SEQ ID NOs:239, 240, and 241 and CDR sequences of SEQ ID NOs:269, 270, and 271; r) CDR sequences of SEQ ID NOs:242, 243, and 244 and CDR sequences of SEQ ID NOs:272, 273, and 274; or s) CDR sequences of SEQ ID NOs:351, 352, and 353 and CDR sequences of SEQ ID NOs:358, 359, and 360.

(22) The method of (21), wherein the antibody or fragment thereof comprises CDRH-1, CDR-H2, CDR-H3, CDR-L1 CDR-L2 and CDR-L3 wherein (a) CDR-H1 is SEQ ID NO:245, CDR-H2 is SEQ ID NO:246, CDR-H3 is SEQ ID NO:247, CDR-L1 is SEQ ID NO:78, CDR-L2 is SEQ ID NO:79 and CDR-L3 is SEQ ID NO:80; or (b) CDR-H1 is SEQ ID NO:269, CDR-H2 is SEQ ID NO:270, CDR-H3 is SEQ ID NO:271, CDR-L1 is SEQ ID NO:239, CDR-L2 is SEQ ID NO:240 and CDR-L3 is SEQ ID NO:241.

(23) The method of any one of (20) to (22), wherein the antibody is a human antibody, a humanized antibody, a monoclonal antibody, or a chimeric antibody.

(24) Use of a sclerostin binding agent in preparation of a medicament for inhibiting bone resorption in an amount from about 1 mg/kg to about 10 mg/kg, wherein the amount is effective to reduce serum level of C-telopeptide of type I collagen (CTX) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins.

(25) The use of (24), wherein the amount of sclerostin binding agent increases a marker of bone formation selected from the group consisting of serum level of bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of procollagen type 1 (PINP), and serum level of osteocalcin (OstCa), by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins.

(26) The use of (24) or (25), wherein the amount of sclerostin binding agent does not result in hypocalcemia or hypercalcemia.

(27) Use of a sclerostin binding agent in preparation of a medicament for increasing bone mineral density in an amount from about 1 mg/kg to about 10 mg/kg, wherein the amount is effective to (a) reduce serum level of CTX by at least 20% compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and (b) increase serum level of a bone formation marker selected from the group consisting of serum level of bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of procollagen type 1 (PINP), and serum level of osteocalcin (OstCa), by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins.

(28) The use of (27), wherein hip, spine, wrist, finger, shin bone and/or heel bone mineral density is increased by at least about 1%.

(29) The use of (28), wherein bone mineral density in the spine is increased by at least about 1%.

(30) The use of any one of (27) to (29), wherein bone mineral density is increased to the range of about 1 to 2.5 standard deviations below the normal bone mineral density of a healthy young adult.

(31) The use of any one of (27) to (29), wherein bone mineral density is increased to the range of about 0 to 1 standard deviations below the normal bone mineral density of a healthy young adult.

(32) Use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg for a first period of time, wherein the amount is effective to increase bone mineral density at the hip, spine, wrist, finger, shin bone and/or heel by at least about 3%, followed by an amount of from about 1 mg/kg to about 10 mg/kg for a second period of time effective to maintain bone mineral density.

(33) The use of (32), wherein the first period of time is 3 months or less.

(34) The use of (32) or (33), wherein the second period of time is at least 6 months.

(35) The use of any one of (32) to (34), wherein bone mineral density in the spine is increased by at least about 3%.

(36) Use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia in an amount from about 1 mg/kg to about 10 mg/kg.

(37) The use of (36), wherein the hypocalcemia or hypercalcemia results from chronic kidney disease, renal failure, primary or secondary hyperparathyroidism, pseudohyperparathyroidism, hypoparathyroidism, pseudohypoparathyroidism, magnesium depletion, severe hypermagnesemia, vitamin D deficiency, hyperphosphatemia, acute pancreatitis, hungry bone syndrome, chelation, osteoblastic metastases, sepsis, surgery, chemotherapy, neoplasia syndrome, hypoparathyroidism, familial hypocalciuric hypercalcemia, sarcoidosis, tuberculosis, berylliosis, histoplasmosis, Candidiasis, Coccidioidomycosis, histiocytosis X, Hodgkin's or Non-Hodgkin's lymphoma, Crohn's disease, Wegener's granulomatosis, pneumonia, silicone-induced granulomas, administration of thiazide diuretics or lithium, or immobilization.

(38) Use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in (a) a human in which treatment with a parathyroid hormone or analog thereof is contraindicated or (b) a human in which treatment with bisphosphonate is contraindicated.

(39) The use of any one of (32) to (38) in which the bone-related disorder is selected from the group consisting of achondroplasia, cleidocranial dysostosis, enchondromatosis, fibrous dysplasia, Gaucher's Disease, hypophosphatemic rickets, Marfan's syndrome, multiple hereditary exotoses, neurofibromatosis, osteogenesis imperfecta, osteopetrosis, osteopoikilosis, sclerotic lesions, pseudoarthrosis, pyogenic osteomyelitis, periodontal disease, anti-epileptic drug induced bone loss, primary and secondary hyperparathyroidism, familial hyperparathyroidism syndromes, weightlessness induced bone loss, osteoporosis in men, postmenopausal bone loss, osteoarthritis, renal osteodystrophy, infiltrative disorders of bone, oral bone loss, osteonecrosis of the jaw, juvenile Paget's disease, melorheostosis, metabolic bone diseases, mastocytosis, sickle cell anemia/disease, organ transplant related bone loss, kidney transplant related bone loss, systemic lupus erythematosus, ankylosing spondylitis, epilepsy, juvenile arthritides, thalassemia, mucopolysaccharidoses, Fabry Disease, Turner Syndrome, Down Syndrome, Klinefelter Syndrome, leprosy, Perthes' Disease, adolescent idiopathic scoliosis, infantile onset multi-system inflammatory disease, Winchester Syndrome, Menkes Disease, Wilson's Disease, ischemic bone disease (such as Legg-Calve-Perthes disease, regional migratory osteoporosis), anemic states, conditions caused by steroids, glucocorticoid-induced bone loss, heparin-induced bone loss, bone marrow disorders, scurvy, malnutrition, calcium deficiency, osteoporosis, osteopenia, alcoholism, chronic liver disease, postmenopausal state, chronic inflammatory conditions, rheumatoid arthritis, inflammatory bowel disease, ulcerative colitis, inflammatory colitis, Crohn's disease, oligomenorrhea, amenorrhea, pregnancy, diabetes mellitus, hyperthyroidism, thyroid disorders, parathyroid disorders, Cushing's disease, acromegaly, hypogonadism, immobilization or disuse, reflex sympathetic dystrophy syndrome, regional osteoporosis, osteomalacia, bone loss associated with joint replacement, HIV associated bone loss, bone loss associated with loss of growth hormone, bone loss associated with cystic fibrosis, chemotherapy associated bone loss, tumor induced bone loss, cancer-related bone loss, hormone ablative bone loss, multiple myeloma, drug-induced bone loss, anorexia nervosa, disease associated facial bone loss, disease associated cranial bone loss,

disease associated bone loss of the jaw, disease associated bone loss of the skull, bone loss associated with aging, facial bone loss associated with aging, cranial bone loss associated with aging, jaw bone loss associated with aging, skull bone loss associated with aging, and bone loss associated with space travel.

(40) The use of any one of (24) to (39), where the sclerostin binding agent cross-blocks the binding of at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 to sclerostin.

(41) The use of any one of (24) to (39), wherein the sclerostin binding agent is cross-blocked from binding to sclerostin by at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24.

(42) The use of any one of (24) to (39), wherein the sclerostin binding agent is an antibody or fragment thereof that demonstrates a binding affinity for sclerostin of SEQ ID NO: 1 of less than or equal to 1×10^{-7} M.

(43) The use of (42), wherein the antibody or fragment thereof comprises: a) CDR sequences of SEQ ID NOs:54, 55, and 56 and CDR sequences of SEQ ID NOs:51, 52, and 53; b) CDR sequences of SEQ ID NOs:60, 61, and 62 and CDR sequences of SEQ ID NOs:57, 58, and 59; c) CDR sequences of SEQ ID NOs:48, 49, and 50 and CDR sequences of SEQ ID NOs:45, 46, and 47; d) CDR sequences of SEQ ID NOs:42, 43, and 44 and CDR sequences of SEQ ID NOs:39, 40, and 41; e) CDR sequences of SEQ ID NOs:275, 276, and 277 and CDR sequences of SEQ ID NOs:287, 288, and 289; f) CDR sequences of SEQ ID NOs:278, 279, and 280 and CDR sequences of SEQ ID NOs:290, 291, and 292; g) CDR sequences of SEQ ID NOs:78, 79, and 80 and CDR sequences of SEQ ID NOs:245, 246, and 247; h) CDR sequences of SEQ ID NOs:81, 99, and 100 and CDR sequences of SEQ ID NOs:248, 249, and 250; i) CDR sequences of SEQ ID NOs:101, 102, and 103 and CDR sequences of SEQ ID NOs:251, 252, and 253; j) CDR sequences of SEQ ID NOs:104, 105, and 106 and CDR sequences of SEQ ID NOs:254, 255, and 256; k) CDR sequences of SEQ ID NOs:107, 108, and 109 and CDR sequences of SEQ ID NOs:257, 258, and 259; l) CDR sequences of SEQ ID NOs:110, 111, and 112 and CDR sequences of SEQ ID NOs:260, 261, and 262; m) CDR sequences of SEQ ID NOs:281, 282, and 283 and CDR sequences of SEQ ID NOs:293, 294, and 295; n) CDR sequences of SEQ ID NOs:113, 114, and 115 and CDR sequences of SEQ ID NOs:263, 264, and 265; o) CDR sequences of SEQ ID NOs:284, 285, and 286 and CDR sequences of SEQ ID NOs:296, 297, and 298; p) CDR sequences of SEQ ID NOs:116, 237, and 238 and CDR sequences of SEQ ID NOs:266, 267, and 268; q) CDR sequences of SEQ ID NOs:239, 240, and 241 and CDR sequences of SEQ ID NOs:269, 270, and 271; r) CDR sequences of SEQ ID NOs:242, 243, and 244 and CDR sequences of SEQ ID NOs:272, 273, and 274; or s) CDR sequences of SEQ ID NOs:351, 352, and 353 and CDR sequences of SEQ ID NOs:358, 359, and 360.

(44) The use of (43), wherein the antibody or fragment thereof comprises CDRH-1, CDR-H2, CDR-H3, CDR-L1 CDR-L2 and CDR-L3 wherein (a) CDR-H1 is SEQ ID NO:245, CDR-H2 is SEQ ID NO:246, CDR-H3 is SEQ ID NO:247, CDR-L1 is SEQ ID NO:78, CDR-L2 is SEQ ID NO:79 and CDR-L3 is SEQ ID NO:80; or (b) CDR-H1 is SEQ ID NO:269, CDR-H2 is SEQ ID NO:270, CDR-H3 is SEQ ID NO:271, CDR-L1 is SEQ ID NO:239, CDR-L2 is SEQ ID NO:240 and CDR-L3 is SEQ ID NO:241.

(45) The use of any one of (42) to (44), wherein the antibody is a human antibody, a humanized antibody, a monoclonal antibody, or a chimeric antibody.

(46) A container comprising anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or fragment thereof in an amount effective to (a) reduce serum level of C-telopeptide of type I collagen (CTX) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and (b) increase serum level bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of procollagen type 1 (PINP), or serum level of osteocalcin (OstCa) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins.

(47) A container comprising an amount of anti-sclerostin antibody from about 70 mg to about 450 mg.

(48) A container comprising anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or fragment thereof for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg every two or four weeks.

(49) A container comprising anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or fragment thereof for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg for a period of about 3 months.

SEQUENCE LISTING

[0102]

<110> Amgen Inc. Padhi, et al.

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

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

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Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
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 Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
 275 280 285
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 Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
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 Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
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 Ser Pro Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
 325 330 335
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 Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu
 340 345 350
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 Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
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 Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
 370 375 380
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 Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
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40	ttcatctaca gcaagctcaa tgtgcagaag agcaactggg aggcaggaaa tactttcacc	1260
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10	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
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15	Thr	Asp	His	Tyr	Met	Ser	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu
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20	Glu	Trp	Ile	Gly	Asp	Ile	Asn	Pro	Tyr	Ser	Gly	Glu	Thr	Thr	Tyr	Asn
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25	Gln	Lys	Phe	Lys	Gly	Thr	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser
30																
35																
40																
45																
50																
55																

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				85					90					95		
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50	Gly	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	Glu	Val	Ser	Ser	Val	Phe
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				260					265					270		
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			275					280					285			
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		290					295					300				
70	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu
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				325						330					335	
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Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
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 Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
 370 375 380
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 385 390 395 400
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 Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
 405 410 415
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 Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
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Val Ser Leu Gly Leu Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
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45

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Gly Ile Pro Ala Arg Phe Ser Gly Asn Gly Ser Gly Thr Asp Phe Thr
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Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Val Thr Tyr Tyr Cys
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Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
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Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
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Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
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Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
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30 <400> 19

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 20 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
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 30 Ala Arg Ser His Tyr Tyr Phe Asp Gly Arg Val Pro Trp Asp Ala Met
 35 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr
 40 Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
 45 Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
 50 Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
 55

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Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
 180 185 190
 5 Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
 195 200 205
 10 Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
 210 215 220
 Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
 225 230 235 240
 15 Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
 245 250 255
 20 Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
 260 265 270
 Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
 275 280 285
 25 Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
 290 295 300
 30 Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
 325 330 335
 35 Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
 340 345 350
 40 Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
 355 360 365
 45 Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
 370 375 380
 Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
 385 390 395 400
 50 Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys
 405 410 415
 55 Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
 420 425 430

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Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 435 440 445

5 Lys

<210> 20
 <211> 1350
 10 <212> DNA
 <213> Mus musculus

<400> 20

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20 catgggaaga gccttgaatg gattggagat attaatcctt tcaacgggtg tactacctac 180

aaccagaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240

atgcagctca acagcctgac atctgacgac tctgcagtct attactgtgc aagatcccat 300

25 tattacttcg atggtagagt cccttgggat gctatggact actggggtca aggaacctca 360

gtcaccgtct cctcagccaa aacgacaccc ccatctgtct atccactggc ccctggatct 420

gctgcccaaa ctaactccat ggtgaccctg ggatgcctgg tcaagggcta tttccctgag 480

30 ccagtgcagc tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac cttcccagct 540

gtcctgcagt ctgacctcta cactctgagc agctcagtga ctgtcccctc cagcacctgg 600

35 cccagcgaga ccgtcacctg caacggtgcc caccgggcca gcagcaccaa ggtggacaag 660

aaaattgtgc ccagggattg tggttgtaag ccttgcatat gtacagtccc agaagtatca 720

tctgtcttca tcttcccccc aaagcccaag gatgtgctca ccattactct gactcctaag 780

40 gtcacgtgtg ttgtggtaga catcagcaag gatgatcccc aggtccagtt cagctggttt 840

gtagatgatg tggaggtgca cacagctcag acgcaacccc gggaggagca gttcaacagc 900

actttccgct cagtccagtga acttcccata atgcaccagg actgggtcaa tggcaaggag 960

45 ttcaaatgca gggccaacag tgcagctttc cctgccccca tcgagaaaac catctccaaa 1020

accaaaggca gaccgaaggc tccacaggtg tacaccattc cacctcccaa ggagcagatg 1080

50 gccaaggata aagtccagtct gacctgcattg ataacagact tcttccctga agacattact 1140

gtggagtggc agtggaatgg gcagccagcg gagaactaca agaactca gccatcatg 1200

gacacagatg gctcttactt catctacagc aagctcaatg tgcagaagag caactgggag 1260

55 gcaggaaata ctttcacctg ctctgtgtta catgagggcc tgcacaacca ccatactgag 1320

aagagcctct cccactctcc tggtaaatga 1350

<210> 21
<211> 468
<212> PRT
<213> Mus musculus

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<400> 21

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40

45

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55

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

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Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
 260 265 270
 5 Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
 275 280 285
 10 Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
 290 295 300
 15 Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
 305 310 315 320
 Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
 325 330 335
 20 Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
 340 345 350
 25 Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
 355 360 365
 30 Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
 370 375 380
 Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
 385 390 395 400
 35 Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
 405 410 415
 40 Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn
 420 425 430
 45 Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
 435 440 445
 Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
 450 455 460
 50 Ser Pro Gly Lys
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<210> 22

<211> 1407

55 <212> DNA

<213> Mus musculus

<400> 22

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tgtaaggctt ctggatacac attcactgac tgctacatga actgggtgaa gcagagccat 180

gggaagagcc ttgaatggat tggagatatt aatcctttca acggtggtac tacctacaac 240

10 cagaagttca agggcaaggc cacattgact gtagacaaat cctccagcac agcctacatg 300

cagctcaaca gcctgacatc tgacgactct gcagtctatt actgtgcaag atccccattat 360

tacttcgatg gtagagtccc ttgggatgct atggactact ggggtcaagg aacctcagtc 420

15 accgtctcct cagccaaaac gacacccccca tctgtctatc cactggcccc tggatctgct 480

gcccuaacta actccatggt gaccctggga tgccctggtca agggctatth ccctgagcca 540

20 gtgacagtga cctggaactc tggatccctg tccagcgggtg tgcacacctt cccagctgtc 600

ctgcagtctg acctctacac tctgagcagc tcagtgactg tcccctccag cacctggccc 660

agcgagaccg tcacctgcaa cgttgcccac ccggccagca gcaccaaggt ggacaagaaa 720

25 attgtgcccga gggattgtgg ttgtaagcct tgcatatgta cagtcccaga agtatcatct 780

gtcttcatct tccccccaaa gcccuaaggat gtgctcacca ttactctgac tcctaaggtc 840

acgtgtgttg tggtagacat cagcaaggat gatcccagag tccagttcag ctggtttgta 900

30 gatgatgtgg aggtgcacac agctcagacg caacccccggg aggagcagtt caacagcact 960

ttccgctcag tcagtgaact tcccattcatg caccaggact ggctcaatgg caaggagttc 1020

35 aatgcaggg tcaacagtgc agctttccct gcccccatcg agaaaacat ctccaaaacc 1080

aaaggcagac cgaaggctcc acaggtgtac accattccac ctcccuaagga gcagatggcc 1140

aaggataaag tcagtctgac ctgcatgata acagacttct tccctgaaga cattactgtg 1200

40 gagtggcagt ggaatgggca gccagcggag aactacaaga aactcagcc catcatggac 1260

acagatggct cttacttcat ctacagcaag ctcaatgtgc agaagagcaa ctgggaggca 1320

ggaaatactt tcacctgctc tgtgttacat gagggcctgc acaaccacca tactgagaag 1380

45 agcctctccc actctcctgg taaatga 1407

<210> 23

<211> 217

50 <212> PRT

<213> Rabbit-Mouse Chimera

<400> 23

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Ala Gln Val Leu Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
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5 Gly Thr Val Thr Ile Asn Cys Gln Ser Ser Gln Ser Val Tyr Asp Asn
 20 25 30

10 Asn Trp Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
 35 40 45

Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser Gly Val Pro Ser Arg Phe
 50 55 60

15 Ser Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Gly Val
 65 70 75 80

20 Gln Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gly Ala Tyr Asn Asp
 85 90 95

25 Val Ile Tyr Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys Arg Thr
 100 105 110

Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu
 115 120 125

30 Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro
 130 135 140

35 Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn
 145 150 155 160

40 Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr
 165 170 175

Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His
 180 185 190

45 Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile
 195 200 205

50 Val Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 24

<211> 654

55 <212> DNA

<213> Rabbit-Mouse Chimera

<400> 24

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5	aaaccagggc agcctcccaa gctcctgatt tatgatgcat ccgatctggc atctggggtc	180
	ccatcgcggt tcagtggcag tggatctggg acacagttca ctctcaccat cagcggcgtg	240
	cagtgtgccg atgctgccac ttactactgt caaggcgctt ataatgatgt tatttatgct	300
10	ttcggcggag ggaccgaggt ggtggtcaaa cgtacggatg ctgcaccaac tgtatccatc	360
	ttcccaccat ccagtgagca gttaacatct ggaggtgcct cagtcgtgtg cttcttgaac	420
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20	ggcgtcctga acagttggac tgatcaggac agcaaagaca gcacctacag catgagcagc	540
	accctcacgt tgaccaagga cgagtatgaa cgacataaca gctatacctg tgaggccact	600
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	<212> PRT	
	<213> Rabbit-Mouse Chimera	
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	<400> 25	
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Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

5 Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Pro Ala Ser
20 25 30

10 Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
35 40 45

15 Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala Trp Phe Gln Gln Lys Pro
50 55 60

20 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser
65 70 75 80

25 Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Thr
85 90 95

30 Leu Thr Ile Ser Gly Val Gln Cys Ala Asp Ala Ala Thr Tyr Tyr Cys
100 105 110

35 Gln Gly Ala Tyr Asn Asp Val Ile Tyr Ala Phe Gly Gly Gly Thr Glu
115 120 125

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

45 Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe
145 150 155 160

50 Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp
165 170 175

55 Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp
180 185 190

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

Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys
210 215 220

Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230 235

<210> 26
<211> 720

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<212> DNA
 <213> Rabbit-Mouse Chimera

<400> 26

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 10 gtcaccatca attgccagtc cagtcagagt gtttatgata acaactggtt agcctggttt 180
 cagcagaaac cagggcagcc tcccaagctc ctgatttatg atgcatccga tctggcatct 240
 ggggtcccat cgcggttcag tggcagtgga tctgggacac agttcactct caccatcagc 300
 15 ggcgtgcagt gtgccgatgc tgccacttac tactgtcaag gcgcttataa tgatgttatt 360
 tatgctttcg gcggagggac cgaggtggtg gtcaaacgta cggatgctgc accaactgta 420
 20 tccatcttcc caccatccag tgagcagtta acatctggag gtgcctcagt cgtgtgcttc 480
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 caaaatggcg tcctgaacag ttggactgat caggacagca aagacagcac ctacagcatg 600
 25 agcagcacc ctcacgttgac caaggacgag tatgaacgac ataacagcta tacctgtgag 660
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<220>
 <223> Synthetic Polypeptide

<220>
 <221> MISC_FEATURE
 <223> Humanized Antibody

<400> 27

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 Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser Ser Tyr Trp
 20 25 30

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55

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Met Asn Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Ile Gly
35 40 45

5 Thr Ile Asp Ser Gly Gly Arg Thr Asp Tyr Ala Ser Trp Ala Lys Gly
50 55 60

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

15 Ser Leu Thr Thr Gly Asp Thr Ala Arg Tyr Phe Cys Ala Arg Asn Trp
85 90 95

Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
100 105 110

20 Lys Gly Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
115 120 125

25 Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
130 135 140

30 Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
145 150 155 160

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
165 170 175

35 Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
180 185 190

40 Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
195 200 205

45 Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
210 215 220

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
225 230 235 240

50 Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
245 250 255

Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
260 265 270

55 Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
275 280 285

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Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
 290 295 300

5 Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
 305 310 315 320

10 Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
 325 330 335

15 Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
 340 345 350

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
 355 360 365

20 Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
 370 375 380

25 Asn Thr Asn Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
 385 390 395 400

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
 405 410 415

30 Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 420 425 430

35 Lys

<210> 28

<211> 1302

<212> DNA

40 <213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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<221> misc_feature

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<400> 28

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 20 tccagcacct ggcccagcga gaccgtcacc tgcaacgttg cccacccggc cagcagcacc 600
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 25 ctgactccta aggtcacgtg tgttgtggta gacatcagca aggatgatcc cgaggtccag 780
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45 <210> 29
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 <212> PRT
 <213> Artificial Sequence

50 <220>
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 <223> Humanized Antibody

55 <400> 29

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5 Val His Cys Gln Ser Leu Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20 25 30

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

15 Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu
50 55 60

20

25

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Trp Ile Gly Thr Ile Asp Ser Gly Gly Arg Thr Asp Tyr Ala Ser Trp
65 70 75 80

5 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Met Asp Leu
85 90 95

10 Lys Met Thr Ser Leu Thr Thr Gly Asp Thr Ala Arg Tyr Phe Cys Ala
100 105 110

Arg Asn Trp Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

15 Ala Ser Thr Lys Gly Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
130 135 140

20 Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
145 150 155 160

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
165 170 175

25 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
180 185 190

30 Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
195 200 205

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
210 215 220

35 Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
225 230 235 240

40 Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
245 250 255

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
260 265 270

45 Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
275 280 285

50 Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
290 295 300

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
305 310 315 320

55 Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro

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5	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln
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10	Val	Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val
			355					360					365			
15	Ser	Leu	Thr	Cys	Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val
		370					375					380				
20	Glu	Trp	Gln	Trp	Asn	Gly	Gln	Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln
	385					390					395					400
25	Pro	Ile	Met	Asn	Thr	Asn	Gly	Ser	Tyr	Phe	Val	Tyr	Ser	Lys	Leu	Asn
				405						410					415	
30	Val	Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val
				420					425					430		
35	Leu	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Glu	Lys	Ser	Leu	Ser	His
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40	Ser	Pro	Gly	Lys												
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50 <400> 30

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5	acagcctctg gattctccct cagtagttat tggatgaact ggggccgcca ggctccaggg	180
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 15 Ser Ser Val Ser Phe Val Asp Trp Phe Gln Gln Lys Pro Gly Thr Ser
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 25 Ala Arg Phe Ser Gly Gly Gly Ser Gly Thr Ser His Ser Leu Thr Ile
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 35 Ser Thr Tyr Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
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 45 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
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 50 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
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 55 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
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 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
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 10 Gly Met Gly Val Gly Trp Ile Arg His Pro Ser Gly Lys Asn Leu Glu
 15 Trp Leu Ala His Ile Trp Trp Asp Asp Val Lys Arg Tyr Asn Pro Val
 20 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn Ser Gln Val
 25 Phe Leu Lys Ile Ala Asn Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
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 35 Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser Ala Lys Thr
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Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
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5 Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
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10 Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
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Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
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15 Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
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20 Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
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Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
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40 Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
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Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
325 330 335

45 Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
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Asn Pro Val Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn
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Ser Gln Val Phe Leu Lys Ile Ala Asn Val Asp Thr Ala Asp Thr Ala
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Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser
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Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
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Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
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Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
 45 180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 195 200 205

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Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser
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20 Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

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

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Ser Ser Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
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 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 130 135 140
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 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
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 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
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 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
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 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
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 20 Gln Asp Lys Ala Ile Met Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
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 5 Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
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 10 Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
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 15 Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
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 20 Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
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 25 Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
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 30 Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
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 35 Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
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 40 Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
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 45 Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
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 Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
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 Lys Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
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 Glu Trp Ile Gly Arg Leu Asp Pro Glu Asp Gly Glu Ser Asp Tyr Ala
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 35 Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg
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 55 Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe
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Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr
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 20 acgttgacca aggacgagta tgaacgacat aacagctata cctgtgaggc cactcacaag 600
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<211> 237

<212> PRT

<213> Mus musculus

<400> 127

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 35 Val Ile Leu Ser Ser Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Leu
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Met Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Val Ser
35 40 45

5 Ser Thr Ile Ser Ser Asn His Leu His Trp Phe Gln Gln Lys Ser Asp
50 55 60

10 Thr Ser Pro Lys Pro Trp Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
65 70 75 80

15 Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
85 90 95

20 Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
100 105 110

25 Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
115 120 125

30 Leu Arg Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser
130 135 140

35 Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn
145 150 155 160

40 Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser
165 170 175

45 Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys
180 185 190

50 Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu
195 200 205

55 Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser
210 215 220

Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
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<210> 128
<211> 714
<212> DNA
<213> Mus musculus

<400> 128

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30 <210> 129
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<400> 129

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 5 Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
 180 185 190
 Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
 10 195 200 205
 Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
 210 215 220
 15 Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
 225 230 235 240
 Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
 20 245 250 255
 Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
 260 265 270
 25 Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
 275 280 285
 Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
 30 290 295 300
 Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 35 Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
 40 340 345 350
 Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
 355 360 365
 45 Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
 370 375 380
 Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
 50 385 390 395 400
 Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys
 405 410 415
 55 Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu

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5 Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
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Lys

10 <210> 130
<211> 1350
<212> DNA
<213> Mus musculus

15 <400> 130

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	gattatttcc acgatggtag ctctactgg tacttcgatg tctggggcgc agggaccaca	360
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	ccagtgcagc tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac cttcccagct	540
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 5 20 25 30
 Pro Gly Ala Leu Val Lys Leu Ser Cys Thr Ala Ser Asp Phe Asn Ile
 10 35 40 45
 Lys Asp Phe Tyr Leu His Trp Met Arg Gln Arg Pro Glu Gln Gly Leu
 15 50 55 60
 Asp Trp Ile Gly Arg Ile Asp Pro Glu Asn Gly Asp Thr Leu Tyr Asp
 65 70 75 80
 Pro Lys Phe Gln Asp Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Asn
 20 85 90 95
 Thr Ala Tyr Leu Gln Leu Ser Gly Leu Thr Ser Glu Thr Thr Ala Val
 25 100 105 110
 Tyr Tyr Cys Ser Arg Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr
 30 115 120 125
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Ile Thr Val Ser Ser
 130 135 140
 Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
 35 145 150 155 160
 Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
 40 165 170 175
 Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 195 200 205
 Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
 210 215 220
 Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 225 230 235 240

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Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
245 250 255

5
Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
260 265 270

10
Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
275 280 285

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Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
290 295 300

20
Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
305 310 315 320

25
Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
325 330 335

30
Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
340 345 350

35
Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
355 360 365

40
Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
370 375 380

45
Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
385 390 395 400

50
Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
405 410 415

55
Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn
420 425 430

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
435 440 445

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
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Ser Pro Gly Lys
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<210> 132
<211> 1407

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<212> DNA
<213> Mus musculus

<400> 132

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10 tgcacagctt ctgacttcaa cattaagac ttctatctac actggatgag gcagcggcct 180
gaacagggcc tggactggat tggaaggatt gatcctgaga atggtgatac tttatatgac 240
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<210> 133
<211> 214
<212> PRT
<213> Mus musculus

<400> 133

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 5 Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 10 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
 35 40 45
 15 Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 20 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr Asn Leu Glu Gln
 65 70 75 80
 25 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90
 30 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
 100 105 110
 35 Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
 115 120 125
 40 Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
 130 135 140
 45 Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
 145 150 155 160
 50 Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
 165 170 175
 55 Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
 180 185 190
 60 Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
 195 200 205
 65 Phe Asn Arg Asn Glu Cys
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<210> 134

<211> 645

55 <212> DNA

<213> Mus musculus

<400> 134

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 15 cccaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480
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 25 <212> PRT
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<400> 135

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

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<210> 136
 <211> 705
 <212> DNA
 <213> Mus musculus

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<400> 136

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<210> 137
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 <212> PRT
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<400> 137

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 Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Thr Leu Glu Trp Ile
 35 40 45

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Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe
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5 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 65 70 75 80

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

10 Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
 100 105 110

15 Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro
 115 120 125

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
 130 135 140

20 Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
 145 150 155 160

25 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
 165 170 175

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
 180 185 190

30 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 195 200 205

35 His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 210 215 220

40 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 225 230 235 240

Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 245 250 255

45 Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 260 265 270

50 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
 275 280 285

Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
 290 295 300

55 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys

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	<211> 466	
	<212> PRT	
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50	<400> 139	
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Met Gly Trp Ser Trp Thr Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
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 20 25 30

10 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

15 Thr Asp Tyr Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Thr Leu
 50 55 60

Glu Trp Ile Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn
 65 70 75 80

20 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr
 85 90 95

25 Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

30 Tyr Tyr Cys Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr
 115 120 125

Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
 130 135 140

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45

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Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
 145 150 155 160
 5 Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
 165 170 175
 10 Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
 180 185 190
 15 His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
 195 200 205
 20 Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
 210 215 220
 25 Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
 225 230 235 240
 30 Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
 245 250 255
 35 Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile
 260 265 270
 40 Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp
 275 280 285
 45 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
 290 295 300
 50 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 305 310 315 320
 55 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 60 Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
 340 345 350
 65 Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
 355 360 365
 70 Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu
 370 375 380
 75 Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp
 385 390 395 400

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Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
405 410 415

5 Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
420 425 430

10 Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
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15 Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
450 455 460

Gly Lys
465

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<212> DNA
<213> Mus musculus

25 <400> 140

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 5 tgcaaggctt ctggatatac attcactgac tacaacatgc actgggtgaa gcagaaccaa 180
 ggaaagacc tagagtggat aggagaaatt aatcctaaca gtggtggtgc tggctacaac 240
 cagaagttca agggcaaggc cacattgact gtagacaagt cctccaccac agcctacatg 300
 10 gagctccgca gcctgacatc tgaggactct gcagtctatt actgtgcaag attgggctac 360
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 30 gtggaggtgc acacagctca gacgcaacc cgggaggagc agttcaacag cactttccgc 960
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 35 agaccgaagg ctccacaggt gtacaccatt ccacctcca aggagcagat ggccaaggat 1140
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 40 cagtggaatg ggcagccagc ggagaactac aagaacactc agcccatcat ggacacagat 1260
 ggctcttact tcatctacag caagctcaat gtgcagaaga gcaactggga ggcaggaaat 1320
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 50 <212> PRT
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55 <220>
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 <223> Humanized Antibody Sequence

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<400> 141

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10 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
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15 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

20 Tyr Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

25 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

30 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85 90 95

35 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

40 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

45 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

50 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

55 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

60 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

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

70 Phe Asn Arg Gly Glu Cys
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<210> 142
 <211> 642
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<220>

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ggcaaagcac ctaaactcct catttactat acatcaagac tcctctccgg cgttccatca 180
15 cgattctcag gctccggctc cggcacagat ttcacactca ctatttcctc cctccaacca 240
gaagattttg caacctatta ctgtcaacaa ggcgatacac tcccatacac attcggcggc 300
ggcacaaaag ttgaaattaa acgtacggtg gctgcacat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
25 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
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<210> 143

<211> 236

<212> PRT

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<223> Humanized Antibody Sequence

<400> 143

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20 25 30

10 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

15 Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu Leu Ser Gly Val
65 70 75 80

20 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

25 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100 105 110

Gly Asp Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125

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

35 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145 150 155 160

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

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

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

50 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210 215 220

55 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<210> 144

<211> 708

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<212> DNA
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gtaaccataa catgtagagc atctcaagat atttccaact atttgaattg gtaccaacaa 180
20 aaaccggca aagcacctaa actcctcatt tactatacat caagactcct ctccggcggt 240
ccatcacgat tctcaggctc cggctccggc acagatttca cactcactat ttctccctc 300
caaccagaag attttgcaac ctattactgt caacaaggcg atacactccc atacacattc 360
25 ggcggcggca caaaagttga aattaaacgt acgggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540
30 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
35 cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

40 <210> 145
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	Met	Glu	Leu	Arg	Ser 85	Leu	Arg	Ser	Asp	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys
10	Ala	Arg	Leu	Gly 100	Tyr	Asp	Asp	Ile	Tyr 105	Asp	Asp	Trp	Tyr	Phe 110	Asp	Val
	Trp	Gly	Gln 115	Gly	Thr	Thr	Val	Thr	Val 120	Ser	Ser	Ala	Ser 125	Thr	Lys	Gly
15	Pro	Ser 130	Val	Phe	Pro	Leu	Ala 135	Pro	Cys	Ser	Arg	Ser 140	Thr	Ser	Glu	Ser
20	Thr 145	Ala	Ala	Leu	Gly	Cys 150	Leu	Val	Lys	Asp	Tyr 155	Phe	Pro	Glu	Pro	Val 160
	Thr	Val	Ser	Trp	Asn 165	Ser	Gly	Ala	Leu	Thr 170	Ser	Gly	Val	His	Thr 175	Phe
25	Pro	Ala	Val 180	Leu	Gln	Ser	Ser	Gly	Leu 185	Tyr	Ser	Leu	Ser 190	Ser	Val	Val
30	Thr	Val 195	Pro	Ser	Ser	Asn	Phe	Gly 200	Thr	Gln	Thr	Tyr 205	Thr	Cys	Asn	Val
	Asp	His 210	Lys	Pro	Ser	Asn	Thr 215	Lys	Val	Asp	Lys	Thr 220	Val	Glu	Arg	Lys
35	Cys 225	Cys	Val	Glu	Cys	Pro 230	Pro	Cys	Pro	Ala	Pro 235	Pro	Val	Ala	Gly	Pro 240
40	Ser	Val	Phe	Leu	Phe 245	Pro	Pro	Lys	Pro	Lys 250	Asp	Thr	Leu	Met	Ile 255	Ser
	Arg	Thr	Pro	Glu 260	Val	Thr	Cys	Val	Val 265	Val	Asp	Val	Ser	His 270	Glu	Asp
45	Pro	Glu 275	Val	Gln	Phe	Asn	Trp	Tyr 280	Val	Asp	Gly	Val 285	Glu	Val	His	Asn
50	Ala	Lys 290	Thr	Lys	Pro	Arg	Glu 295	Glu	Gln	Phe	Asn	Ser 300	Thr	Phe	Arg	Val
	Val	Ser	Val	Leu	Thr	Val 310	Val	His	Gln	Asp	Trp 315	Leu	Asn	Gly	Lys	Glu 320
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Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 5
 Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 10
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 15
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 20
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
 385 390 395 400
 25
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415
 30
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
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 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445
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 Lys

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 <400> 146

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	tcttgtaaag caagcggata tacatttaca gattacaaca tgcattgggt aagacaagcg	120
5	ccaggacaag gattggaatg gatggggcga attaaccccta atagtggagg agcaggctac	180
	aatcaaaaat tcaaagggag agttacaatg acaacagaca caagcacttc aacagcatat	240
10	atggaactgc gatcacttag aagcgacgat acagctgtat actattgctc acgacttggg	300
	tatgatgata tatatgatga ctgggtatttc gatgtttggg gccagggaac aacagttacc	360
	gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcgccctg ctccaggagc	420
15	acctccgaga gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg	480
	acggtgtcgt ggaactcagg cgctctgacc agcggcgtgc acaccttccc agctgtccta	540
20	cagtcctcag gactctactc cctcagcagc gtgggtgaccg tgcctccag caacttcggc	600
	accagacct acacctgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca	660
	gttgagcgca aatggtgtgt cgagtgccca ccgtgccccag caccacctgt ggaggaccg	720
25	tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctccc gaccctgag	780
	gtcacgtgcg tgggtggtgga cgtgagccac gaagacccc aggtccagtt caactggtac	840
	gtggacggcg tggaggtgca taatgccaa acaaagccac gggaggagca gttcaacagc	900
30	acgttccgtg tggtcagcgt cctcacctgt gtgcaccagg actggctgaa cggcaaggag	960
	tacaagtgca aggtctcaa caaaggcctc ccagccccca tcgagaaaac catctccaaa	1020
35	accaaagggc agccccgaga accacaggtg tacaccctgc ccccatccc ggaggagatg	1080
	accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc	1140
	gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccagctg	1200
40	gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag	1260
	caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag	1320
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Ala His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

15
Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

20

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

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5	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	
				340					345					350			
10	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	
			355					360					365				
15	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	
		370					375					380					
20	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	
	385					390					395					400	
25	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	
					405					410					415		
30	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	
				420					425					430			
35	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	
			435					440					445				
40	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	
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45	Ser	Pro	Gly	Lys													
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 5 tgtaaagcaa gcggatatac atttacagat tacaacatgc attgggtaag acaagcgcca 180
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 10 gaactgcatg cacttagaag cgacgatata gctgtatact attgagcagc acttgggtat 360
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 30 gacggcgtgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcagc 960
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<210> 149
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 5 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
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 10 Leu Asn Trp Phe Gln Gln Lys Pro Asp Gly Thr Leu Lys Leu Leu Ile
 35 40 45
 Phe Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 15 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80
 20 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala
 100 105 110
 Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
 115 120 125
 30
 Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
 130 135 140
 35 Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
 145 150 155 160
 40 Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
 165 170 175
 45 Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
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 Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
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55 <210> 150
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 <212> DNA
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<400> 150

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 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540
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25 <211> 234

<212> PRT

<213> Mus musculus

30 <400> 151

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Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
 20 25 30
 5
 Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
 35 40 45
 10
 Ile Ser Asn Tyr Leu Asn Trp Phe Gln Gln Lys Pro Asp Gly Thr Leu
 50 55 60
 15
 Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
 65 70 75 80
 20
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
 85 90 95
 25
 Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp
 100 105 110
 30
 Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg Arg
 115 120 125
 35
 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 130 135 140
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 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 145 150 155 160
 45
 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 165 170 175
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 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 180 185 190
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 Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
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 His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
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 Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
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<210> 152

<211> 705

55 <212> DNA

<213> Mus musculus

<400> 152

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	gggaccaagc tggaaataag acgggctgat gctgcaccaa ctgtatccat cttcccacca	420
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	ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca	660
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Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
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5 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
165 170 175

10 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
180 185 190

15 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
195 200 205

20 His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
210 215 220

25 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
225 230 235 240

30 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
245 250 255

35 Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
260 265 270

40 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
275 280 285

45 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
290 295 300

50 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
305 310 315 320

55 Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

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

65 Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
355 360 365

70 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
370 375 380

75 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
385 390 395 400

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Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
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5 Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
420 425 430

10 His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
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<210> 154

<211> 1344

<212> DNA

15 <213> Mus musculus

<400> 154

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5	caaggaaaga gcctagagtg gataggagaa attaatccta acagtgggtg tagtggctac	180
	aacccaaaagt tcaaaggcaa ggccacattg actgtagaca agtcttccag cacagcctac	240
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	tacgatggca gctacgagga ctggtacttc gatgtctggg gcgcagggac cacggtcacc	360
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	gatggctctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga	1260
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 5 Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys
 20 25 30
 10 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 15 Thr Asp Tyr Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Ser Leu
 50 55 60
 20 Glu Trp Ile Gly Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn
 65 70 75 80
 25 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
 85 90 95
 30 Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 35 Tyr Tyr Cys Ala Arg Leu Val Tyr Asp Gly Ser Tyr Glu Asp Trp Tyr
 115 120 125
 40 Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
 130 135 140
 45 Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
 145 150 155 160
 50 Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
 165 170 175
 55 Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
 180 185 190
 His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
 195 200 205
 Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
 210 215 220
 Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val

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<210> 156
 <211> 1401
 <212> DNA
 <213> Mus musculus

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<400> 156

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 15 ggaaagagcc tagagtggat aggagaaatt aatcctaaca gtggtggtag tggctacaac 240
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 gagctccgca gcctgacatc tgaggactct gcagtctatt actgtgcaag attggtctac 360
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 25 gtgacctgga actctggatc cctgtccagc ggtgtgcaca ccttcccagc tgcctgcag 600
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 accgtcacct gcaacgttgc ccaccgggc agcagcacca aggtggacaa gaaaattgtg 720
 30 cccagggatt gtggttgtaa gccttgcata tgtacagtcc cagaagtatc atctgtcttc 780
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 35 gttgtggtag acatcagcaa ggatgatccc gaggtccagt tcagctggtt tgtagatgat 900
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<210> 157
 <211> 214
 <212> PRT
 <213> Mus musculus

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<400> 157

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10 Asp Arg Val Thr Ile Cys Cys Arg Ala Ser Gln Val Ile Thr Asn Tyr
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15 Leu Tyr Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
35 40 45

20 Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

25 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

30 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85 90 95

35 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
100 105 110

40 Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
115 120 125

45 Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
130 135 140

50 Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145 150 155 160

55 Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
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<210> 158

<211> 642

EP 2 556 841 B9

<212> DNA
 <213> Mus musculus

<400> 158

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 10 gatggaactt ttaaactcct gatctactac acatcaagat tacactcagg agtcccatca 180
 aggttcagtg gcagtgggtc tggaacagat tattctctca ccattagcaa cctggaacag 240

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 gaagatattg ccacttactt ttgccaacag ggtgatacgc ttccgtacac gttcggaggg 300
 20 gggaccaagc tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 360
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 25 cccaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480
 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540
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<210> 159
 <211> 234
 <212> PRT
 <213> Mus musculus

<400> 159

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

15 Ile Thr Asn Tyr Leu Tyr Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe
50 55 60

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
65 70 75 80

20 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
85 90 95

25 Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp
100 105 110

30 Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
130 135 140

35 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160

40 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175

45 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205

50 His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
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55 Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
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<210> 160

<211> 702

EP 2 556 841 B9

<212> DNA
 <213> Mus musculus

<400> 160

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 aggttcagtg gcagtgggtc tggaacagat tattctctca ccattagcaa cctggaacag 300
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<210> 161
 <211> 447
 <212> PRT
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<400> 161

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 Asn Met His Trp Met Lys Gln Asn Gln Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 50
 55

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Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Gln Phe
 50 55 60

5 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
 65 70 75 80

10 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Leu Gly Tyr Val Gly Asn Tyr Glu Asp Trp Tyr Phe Asp Val
 100 105 110

15 Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro
 115 120 125

20 Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
 130 135 140

25 Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
 145 150 155 160

Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
 165 170 175

30 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
 180 185 190

35 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 195 200 205

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 210 215 220

40 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 225 230 235 240

45 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 245 250 255

Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 260 265 270

50 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
 275 280 285

55 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
 290 295 300

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Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
 305 310 315 320

5

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

10

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

15

Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
 355 360 365

20

Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
 370 375 380

25

Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
 385 390 395 400

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Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
 405 410 415

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Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
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His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
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<210> 162
 <211> 1341
 <212> DNA
 <213> Mus musculus

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<400> 162

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	tggcagtgga atgggcagcc agcggagaac tacaagaaca ctgagcccat catggacaca	1200
	gatggctctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga	1260
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 Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys
 20 25 30
 10
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 15
 Thr Asp Tyr Asn Met His Trp Met Lys Gln Asn Gln Gly Lys Ser Leu
 50 55 60
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 Glu Trp Ile Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn
 65 70 75 80
 25
 Gln Gln Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg
 85 90 95
 30
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 35
 Tyr Tyr Cys Ala Arg Leu Gly Tyr Val Gly Asn Tyr Glu Asp Trp Tyr
 115 120 125
 40
 Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
 45
 50
 55

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5	Thr 145	Thr	Pro	Pro	Ser	Val 150	Tyr	Pro	Leu	Ala	Pro 155	Gly	Ser	Ala	Ala	Gln 160
10	Thr	Asn	Ser	Met	Val 165	Thr	Leu	Gly	Cys	Leu 170	Val	Lys	Gly	Tyr	Phe 175	Pro
15	Glu	Pro	Val	Thr	Val 180	Thr	Trp	Asn	Ser	Gly 185	Ser	Leu	Ser	Ser	Gly	Val 190
20	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp 200	Leu	Tyr	Thr	Leu	Ser	Ser 205
25	Ser	Val	Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys 210
30	Asn	Val	Ala	His	Pro	Ala 230	Ser	Ser	Thr	Lys	Val 235	Asp	Lys	Lys	Ile	Val 240
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40	Ser	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro 265	Lys	Asp	Val	Leu	Thr	Ile 270
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50	Asp	Pro	Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His 290
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60	Ser	Val	Ser	Glu	Leu	Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys 310
65	Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu 315
70	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr 320
75	Thr	Ile	Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu 325
80	Thr	Cys	Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	Trp 330
85						390					395					400

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	Gln	Trp	Asn	Gly	Gln	Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro	Ile
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5	Met	Asp	Thr	Asp	Gly	Ser	Tyr	Phe	Ile	Tyr	Ser	Lys	Leu	Asn	Val	Gln
				420					425					430		
10	Lys	Ser	Asn	Trp	Glu	Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu	His
			435					440					445			
15	Glu	Gly	Leu	His	Asn	His	His	Thr	Glu	Lys	Ser	Leu	Ser	His	Ser	Pro
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<210> 165

<211> 214

<212> PRT

50 <213> Mus musculus

<400> 165

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 20 25 30
 10 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
 35 40 45
 15 Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 20 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr Asn Leu Glu Gln
 65 70 75 80
 25 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 30 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
 100 105 110
 35 Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
 115 120 125
 40 Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
 130 135 140
 45 Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
 145 150 155 160
 50 Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
 165 170 175
 55 Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
 180 185 190
 60 Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
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 65 Phe Asn Arg Asn Glu Cys
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<210> 166

<211> 645

55 <212> DNA

<213> Mus musculus

<400> 166

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 aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttaciaa cctggagcaa 240
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 10 gggaccaaac tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 360
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 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcagc 540
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<210> 167

<211> 234

<212> PRT

25 <213> Mus musculus

<400> 167

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 Ala Ser Leu Gly Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp
 40 35 40 45
 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe
 50 55 60
 45 Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser
 65 70 75 80

50

55

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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr
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 5
 Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp
 100 105 110
 10
 Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125
 15
 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 130 135 140
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 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 145 150 155 160
 25
 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 165 170 175
 30
 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 180 185 190
 Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
 195 200 205
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<210> 168

<211> 705

<212> DNA

<213> Mus musculus

<400> 168

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 5 atcagttgca gggcaagtca agacattagc aattatttaa actggtatca gcagaaacca 180
 gatggaactt ttaaactcct tatcttctac acatcaagat tactctcagg agtcccatca 240
 aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttacia cctggagcaa 300
 10 gaagattttg ccacttactt ttgccaacag ggagatacgc ttccgtacac tttcggaggg 360
 gggaccaaac tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 420
 15 tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 480
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 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcagc 600
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 <211> 447
 <212> PRT
 <213> Mus musculus
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 <400> 169

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 5 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 10 Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Thr Leu Asp Trp Ile
 15 Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe
 20 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 25 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 30 Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
 35 Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro
 40 Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
 45 Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
 50 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
 55 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
 60 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
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His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 210 215 220
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 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 225 230 235 240
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 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 245 250 255
 Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 260 265 270
 15
 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
 275 280 285
 20
 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
 290 295 300
 25
 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
 305 310 315 320
 30
 Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
 340 345 350
 35
 Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
 355 360 365
 40
 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
 370 375 380
 45
 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
 385 390 395 400
 Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
 405 410 415
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 Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
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 His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

<210> 170
 <211> 1344

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<212> DNA
 <213> Mus musculus

<400> 170

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 10 caaggaaaga ccctagactg gataggagaa attaatccta acagtgggtg tgctggctac 180
 aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccac cacagcctac 240
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50 <210> 171
 <211> 466
 <212> PRT
 <213> Mus musculus

55 <400> 171

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 5 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 10 Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
 340 345 350
 15 Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
 355 360 365
 Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu
 370 375 380
 20 Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp
 385 390 395 400
 25 Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
 405 410 415
 Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
 420 425 430
 30 Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
 435 440 445
 35 Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
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 40 Gly Lys
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<210> 172

<211> 1401

<212> DNA

45 <213> Mus musculus

<400> 172

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<210> 173

<211> 214

50 <212> PRT

<213> Mus musculus

<400> 173

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 10 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
 35 40 45
 15 Phe Tyr Thr Ser Arg Leu Phe Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 20 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr Asn Leu Glu Gln
 65 70 75 80
 25 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 30 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala
 100 105 110
 35 Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
 115 120 125
 40 Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
 130 135 140
 45 Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
 145 150 155 160
 50 Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
 165 170 175
 55 Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
 180 185 190
 60 Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
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<210> 174

<211> 642

55 <212> DNA

<213> Mus musculus

<400> 174

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<210> 175

<211> 234

<212> PRT

25 <213> Mus musculus

<400> 175

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10 Ala Ser Leu Gly Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp
 35 40 45

15 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe
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Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu Phe Ser Gly Val Pro Ser
 65 70 75 80

20 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr
 85 90 95

25 Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp
 100 105 110

30 Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 130 135 140

35 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 145 150 155 160

40 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 165 170 175

45 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 180 185 190

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
 195 200 205

50 His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
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55 Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
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<210> 176

<211> 702

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<212> DNA
 <213> Mus musculus

<400> 176

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 10 atcagttgca gggcaagtca agacattagc aattatthaa attggtatca gcagaaacca 180
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 aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttacia cctggagcaa 300
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 gggaccaagg tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 420
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 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 600
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 <212> PRT
 <213> Mus musculus

<400> 177

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1 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Thr
 5 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 10 Asn Met His Trp Val Lys Gln Thr Gln Gly Lys Thr Leu Glu Trp Ile
 15 Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe
 20 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 25 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 30 Ala Lys Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
 35
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Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Ala
115 120 125

5 Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser
130 135 140

10 Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
145 150 155 160

15 Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Asp Val His Thr Phe
165 170 175

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

20 Val Thr Thr Trp Pro Ser Gln Thr Ile Thr Cys Asn Val Ala His Pro
195 200 205

25 Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Ser Pro
210 215 220

Thr His Lys Pro Cys Pro Pro Cys Pro Ala Pro Asn Leu Leu Gly Gly
225 230 235 240

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

35 Ser Leu Ser Pro Met Val Thr Cys Val Val Val Asp Val Ser Glu Asp
260 265 270

40 Asp Pro Asp Val His Val Ser Trp Phe Val Asn Asn Val Glu Val His
275 280 285

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Ile Arg
290 295 300

45 Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
305 310 315 320

50 Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

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

55 Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu
355 360 365

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	Thr	Cys	Met	Ile	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp
	370						375					380				
5	Thr	Asn	Asn	Gly	Gln	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val
	385					390					395					400
10	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu
					405					410					415	
15	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His
				420					425					430		
20	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro
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	Gly	Lys														
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<210> 178

<211> 1350

25 <212> DNA

<213> Mus musculus

<400> 178

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5	caaggaaaga ccctagagtg gataggagaa attaatccta acagtgggtg tgctggctac	180
	aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccac cacagcctac	240
	atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aaaattgggc	300
10	tacgatgata tctacgacga ctggtatttc gatgtctggg gcgcagggac cacggtcacc	360
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	acaactggct cctcgggtgac tctaggatgc ctgggtcaagg gttatttccc tgagccagtg	480
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	cagtctggcc tctacaccct cagcagctca gtgactgtaa ccacctggcc cagccagacc	600
20	atcacctgca atgtggccca cccggcaagc agcaccaaag tggacaagaa aattgagccc	660
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	ccatccgtct tcatcttccc tccaaagatc aaggatgtac tcatgatctc cctgagcccc	780
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	ttcgtgaaca acgtggaagt acacacagct cagacacaaa cccatagaga ggattacaac	900
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	gagttcaaat gcaaggtcaa caacaaagcc ctcccagcgc ccatcgagag aaccatctca	1020
	aaacccaaag ggccagtaag agctccacag gtatatgtct tgcctccacc agaagaagag	1080
35	atgactaaga aacaggtcac tctgacctgc atgatcacag acttcatgcc tgaagacatt	1140
	tacgtggagt ggaccaacaa cgggcaaaca gagctaaact acaagaacac tgaaccagtc	1200
	ctggactctg atggttctta cttcatgtac agcaagctga gagtggaaaa gaagaactgg	1260
40	gtggaaagaa atagctactc ctggtcagtg gtccacgagg gtctgcacaa tcaccacagc	1320
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	<211> 469	
	<212> PRT	
	<213> Mus musculus	
50	<400> 179	
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 5 Ser Val Thr Val Thr Thr Trp Pro Ser Gln Thr Ile Thr Cys Asn Val
 210 215 220
 10 Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg
 225 230 235 240
 15 Gly Ser Pro Thr His Lys Pro Cys Pro Pro Cys Pro Ala Pro Asn Leu
 245 250 255
 20 Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val
 260 265 270
 25 Leu Met Ile Ser Leu Ser Pro Met Val Thr Cys Val Val Val Asp Val
 275 280 285
 30 Ser Glu Asp Asp Pro Asp Val His Val Ser Trp Phe Val Asn Asn Val
 290 295 300
 35 Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser
 305 310 315 320
 40 Thr Ile Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met
 325 330 335
 45 Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
 340 345 350
 50 Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Pro Val Arg Ala Pro
 355 360 365
 55 Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln
 370 375 380
 Val Thr Leu Thr Cys Met Ile Thr Asp Phe Met Pro Glu Asp Ile Tyr
 385 390 395 400
 Val Glu Trp Thr Asn Asn Gly Gln Thr Glu Leu Asn Tyr Lys Asn Thr
 405 410 415
 Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu
 420 425 430
 Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser
 435 440 445

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Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser
450 455 460

5 Arg Thr Pro Gly Lys
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<210> 180

<211> 1407

10 <212> DNA

<213> Mus musculus

<400> 180

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 ggaaagaccc tagagtggat aggagaaatt aatcctaaca gtggtggtgc tggctacaac 240
 cagaagttca agggcaaggc cacattgact gtagacaagt cctccaccac agcctacatg 300
 10 gagctccgca gcctgacatc tgaggactct gcagtctatt actgtgcaaa attgggctac 360
 gatgatatct acgacgactg gtatttcgat gtctggggcg cagggaccac ggtcacctgc 420
 15 tcctcagcca aaacaacagc cccatcggtc tatccactgg cccctgtgtg tggagataca 480
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 40 gactctgatg gttcttactt catgtacagc aagctgagag tggaaaagaa gaactgggtg 1320
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<210> 181

<211> 214

<212> PRT

50 <213> Mus musculus

<400> 181

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Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
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 5 Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
 20
 10 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
 35 40 45
 15 Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 20 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr Asn Leu Glu Gln
 65 70 75 80
 25 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 30 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
 100 105 110
 35 Pro Thr Val Ser Ile Phe Pro Leu Ser Ser Glu Gln Leu Thr Ser Gly
 115 120 125
 40 Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
 130 135 140
 45 Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
 145 150 155 160
 50 Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
 165 170 175
 55 Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
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 60 Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
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 65 Phe Asn Arg Asn Glu Cys
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<210> 182

<211> 645

55 <212> DNA

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<400> 182

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 5 gatggaactt ttaaactcct tatctttctac acatcaagat tactctcagg agtcccatca 180
 aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttacia cctggagcaa 240
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 10 gggaccaaac tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacta 360
 tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420
 cccaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480
 15 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540
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<210> 183

<211> 234

<212> PRT

25 <213> Mus musculus

<400> 183

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 20 25 30

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

40 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe
 50 55 60

45 Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser
 65 70 75 80

50 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr
 85 90 95

55 Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp
 100 105 110

Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125

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	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Leu	Ser	Ser	Glu	Gln
	130						135					140				
5	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu	Asn	Asn	Phe	Tyr
	145					150					155					160
10	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	Glu	Arg	Gln
					165					170					175	
15	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	Asp	Ser	Thr
				180					185					190		
20	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	Glu	Tyr	Glu	Arg
			195					200					205			
25	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr	Ser	Thr	Ser	Pro
	210						215					220				
30	Ile	Val	Lys	Ser	Phe	Asn	Arg	Asn	Glu	Cys						
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<210> 184

<211> 705

<212> DNA

<213> Mus musculus

<400> 184

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	atcagttgca	gggcaagtca	agacattagc	aattatttaa	actggtatca	gcagaaacca	180
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	aggttcagtg	gcagtgggtc	tggaacagat	tattctctca	ccatttacia	cctggagcaa	300
	gaagattttg	ccacttactt	ttgccaacag	ggagatacgc	ttccgtacac	tttcggaggg	360
45	gggaccaaac	tggaataaaa	acgggctgat	gctgcaccaa	ctgtatccat	cttcccacta	420
	tccagtgagc	agttaacatc	tggaggtgcc	tcagtcgtgt	gcttcttgaa	caacttctac	480
50	cccaaagaca	tcaatgtcaa	gtggaagatt	gatggcagtg	aacgacaaaa	tggcgtcctg	540
	aacagttgga	ctgatcagga	cagcaaagac	agcacctaca	gcatgagcag	caccctcagc	600
	ttgaccaagg	acgagtatga	acgacataac	agctatacct	gtgaggccac	tcacaagaca	660
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<210> 185

<211> 447

<212> PRT
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1 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Ala
 5 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 10 Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Thr Leu Glu Trp Ile
 15 Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe
 20 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 25 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 30 Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
 35 Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro
 40 Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
 45 Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
 50 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
 55 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
 60 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 65 His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 70 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 75 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 80 245 250 255

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Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 260 265 270
 5
 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
 275 280 285
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 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
 290 295 300
 15
 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
 305 310 315 320
 20
 Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
 325 330 335
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 Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
 340 345 350
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 Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
 355 360 365
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 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
 370 375 380
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 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
 385 390 395 400
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 Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
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5	Val	Leu	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Met	Lys
				20					25					30		
10	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
			35					40					45			
15	Thr	Asp	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Asn	Gln	Gly	Lys	Thr	Leu
		50					55					60				
20	Glu	Trp	Ile	Gly	Glu	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Ala	Gly	Tyr	Asn
	65					70					75					80
25	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Thr
				85						90						95
30																
35																
40																
45																
50																
55																

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Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 5 Tyr Tyr Cys Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr
 115 120 125
 10 Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
 130 135 140
 Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
 145 150 155 160
 15 Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
 165 170 175
 20 Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
 180 185 190
 His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
 195 200 205
 25 Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
 210 215 220
 30 Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
 225 230 235 240
 35 Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
 245 250 255
 Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile
 260 265 270
 40 Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp
 275 280 285
 45 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
 290 295 300
 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 305 310 315 320
 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 55 Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
 340 345 350

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Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
 355 360 365
 5
 Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu
 370 375 380
 10
 Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp
 385 390 395 400
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 Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
 405 410 415
 20
 Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
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 Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
 435 440 445
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 Gly Lys
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50 <213> Mus musculus

<400> 189

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<400> 190

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25 <211> 235

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30 <400> 191

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Leu Ser Val Ser Pro Gly Asp Lys Val Thr Met Thr Cys Arg Ala Ser
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 5 Ser Ser Ile Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
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 10 Pro Arg Ser Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
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 25 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
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 30 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
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 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 165 170 175
 35 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 180 185 190
 40 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
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<212> DNA

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<400> 192

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 5 Ser Val Lys Val Ser Cys Thr Ala Ser Gly Phe Asp Ile Lys Asp Tyr
 10 Tyr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
 15 Gly Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala Pro Lys Phe
 20 Pro Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
 25 Gly Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
 30 Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser
 35 Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
 40 Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val
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Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 5 Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
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 195 200 205
 10 Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
 210 215 220
 Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
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 260 265 270
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 275 280 285
 25 Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
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 305 310 315 320
 35 Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 325 330 335
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 Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
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 45 Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
 370 375 380
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 385 390 395 400
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 55 Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn

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<211> 464
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 5 Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Asp Leu Val Gln
 10 Pro Gly Ala Ser Val Lys Val Ser Cys Thr Ala Ser Gly Phe Asp Ile
 15 Lys Asp Tyr Tyr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu
 20 Glu Trp Ile Gly Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala
 25 Pro Lys Phe Pro Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn
 30 Thr Ala Tyr Leu Gln Leu Arg Gly Leu Thr Ser Glu Asp Thr Ala Ile
 35 Tyr Tyr Cys Gly Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro
 40 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr
 45 Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn
 50 Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro
 55 Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr
 60 Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val
 65 Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val
 70 Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg
 75 Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser
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20	Ser	Glu	Leu	Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe
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25	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr
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	385					390					395					400
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					405					410					415	
50	Thr	Asp	Gly	Ser	Tyr	Phe	Ile	Tyr	Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser
				420					425					430		
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			435					440					445			
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 <211> 214
 50 <212> PRT
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 <400> 197

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

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5 Ala Arg Leu Gly Tyr Tyr Gly Asn Tyr Glu Asp Trp Tyr Phe Asp Val
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10 Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro
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Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
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15 Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
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20 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
165 170 175

25 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
180 185 190

30 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
195 200 205

35 His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
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Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
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40 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
245 250 255

45 Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
260 265 270

50 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
275 280 285

55 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
290 295 300

Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
305 310 315 320

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

Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro

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 <212> PRT
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55 <400> 203

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 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
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 Thr Asp Tyr Asn Met His Trp Met Lys Gln Asn Gln Gly Lys Ser Leu
 50 55 60
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 Glu Trp Ile Gly Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn
 65 70 75 80
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 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
 85 90 95
 30
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 35
 Tyr Tyr Cys Ala Arg Leu Gly Tyr Tyr Gly Asn Tyr Glu Asp Trp Tyr
 115 120 125
 40
 Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
 130 135 140
 45
 Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
 145 150 155 160
 50
 Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
 165 170 175
 55

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Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
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 5 His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
 195 200 205
 10 Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
 210 215 220
 15 Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
 225 230 235 240
 20 Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
 245 250 255
 25 Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile
 260 265 270
 30 Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp
 275 280 285
 35 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
 290 295 300
 40 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 305 310 315 320
 45 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 50 Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
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 55 Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
 355 360 365
 60 Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu
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 70 Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
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 75 Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
 420 425 430

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Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
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<212> DNA

15 <213> Mus musculus

<400> 204

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<211> 215

<212> PRT

50 <213> Mus musculus

<400> 205

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<211> 237

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25 <213> Mus musculus

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Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
40 35 40 45
Ser Ser Val Thr Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60
Ser Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
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Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
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Thr Ile Ser Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
55 100 105 110
Gln Tyr Asp Phe Phe Pro Ser Thr Phe Gly Gly Gly Thr Lys Leu Glu

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15	Asn	Phe	Tyr	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	
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20	Glu	Arg	Gln	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	
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25	Asp	Ser	Thr	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	Glu	
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<400> 209

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

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				275				280					285				
15	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu	Leu	
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20	Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe	Lys	Cys	Arg	
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25	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	
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30	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	
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35	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	Met	Ile	Thr	
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40	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	Asn	Gly	Gln	
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45	Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro	Ile	Met	Asp	Thr	Asp	Gly	
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50	Ser	Tyr	Phe	Ile	Tyr	Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser	Asn	Trp	Glu	
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55	Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu	His	Glu	Gly	Leu	His	Asn	
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	gccgttatta ctacgaatgc tatggactac tggggcaag gaacctcagt caccgtctcc	360
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 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
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 Thr Asp Tyr Tyr Met Asn Trp Val Lys Gln Ser His Gly Glu Ser Leu
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 Glu Trp Ile Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn
 65 70 75 80
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His Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn
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 5 Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
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 Tyr Tyr Cys Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp
 115 120 125
 10 Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr
 130 135 140
 15 Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn
 145 150 155 160
 20 Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr
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 30 Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val
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 35 Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg
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 245 250 255
 40 Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu
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 45 Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro
 275 280 285
 50 Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala
 290 295 300
 Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val
 305 310 315 320
 55 Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe
 325 330 335

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Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr
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 Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile
 355 360 365
 10
 Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys
 370 375 380
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 Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp
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 420 425 430
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 <223> Humanized Antibody Sequence

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<400> 213

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

10 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Thr Ser Ser
20 25 30

15 Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

20 Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

25 Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

30 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Phe Phe Pro
85 90 95

35 Ser Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

40 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

45 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

50 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

55 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

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

Ser Phe Asn Arg Gly Glu Cys
210 215

55 <210> 214
<211> 645
<212> DNA
<213> Artificial Sequence

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<220>

<223> Synthetic Polynucleotide

<220>

<221> misc_feature

<223> Humanized Antibody Sequence

<400> 214

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ccaggaaaag cacctaaact tcttatatac tctacatcta atctcgcac aggagttccc 180
15 tctcgatttt caggatctgg atcaggcaca gaatttacac ttactatatac atcactccaa 240
ccagaagact tcgccactta ttactgcca caatacgatt tttttccaag cacattcggga 300
20 ggaggtacaa aagtagaaat caagcgtacg gtggctgcac catctgtctt catcttcccg 360
ccatctgatg agcagttgaa atctggaact gcctctggtg tgtgcctgct gaataacttc 420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
25 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 215

<211> 237

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<220>

<221> MISC_FEATURE

<223> Humanized Antibody Sequence

<400> 215

EP 2 556 841 B9

<213> Artificial Sequence

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<223> Synthetic Polynucleotide

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<221> misc_feature

<223> Humanized Antibody Sequence

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<400> 216

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	gtaacaatca catgccgcgc ctcatcttca gttacatctt cttatcttaa ttggtatcaa	180
	caaaaaccag gaaaagcacc taaacttctt atatactcta catctaactc cgcacagga	240
20	gttcctctc gatcttcagg atctggatca ggcacagaat ttacacttac tataatcatca	300
	ctccaaccag aagacttcgc cacttattac tgccaacaat acgatttttt tccaagcaca	360
	ttcggaggag gtacaaaagt agaaatcaag cgtacgggtg ctgcaccatc tgtcttcac	420
25	ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctggtgtgtg cctgctgaat	480
	aacttctatc ccagagagggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt	540
30	aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc	600
	accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc	660
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<210> 217

<211> 447

<212> PRT

<213> Artificial Sequence

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<220>

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<220>

<221> MISC_FEATURE

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<223> Humanized Antibody Sequence

<400> 217

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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

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

5 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
 290 300

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

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

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

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

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

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

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

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

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

<210> 218

<211> 1341

<212> DNA

45 <213> Artificial Sequence

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<223> Synthetic Polynucleotide

50 <220>

<221> misc_feature

<223> Humanized Antibody Sequence

<400> 218

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	agttgcaaag catctggata cacatthacc gactactaca tgaattgggt acgacaagcc	120
5	cctggacaaa gacttgaatg gatgggagac attaaccctt ataacgacga cactacatac	180
	aatcataaat ttaaaggaag agttacaatt acaagagata catccgcatc aaccgcctat	240
10	atggaacttt cctcattgag atctgaagac actgctgttt attactgtgc aagagaaact	300
	gccgttatta ctactaacgc tatggattac tgggggtcaag gaaccactgt taccgtctct	360
	agtgcctcca ccaagggccc atcgggtcttc cccctggcgc cctgctccag gagcacctcc	420
15	gagagcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
	tcgtggaact caggcgtctc gaccagcggc gtgcacacct tcccagctgt cctacagtcc	540
20	tcaggactct actccctcag cagcgtggtg accgtgccct ccagcaactt cggcaccag	600
	acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gacagttgag	660
	cgcaaatggt gtgtcgagtg cccaccgtgc ccagcaccac ctgtggcagg accgtcagtc	720
25	ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcacg	780
	tgctgtggtg tggacgtgag ccacgaagac cccgaggtcc agttcaactg gtacgtggac	840
	ggcgtggagg tgcataatgc caagacaaag ccacgggagg agcagttcaa cagcacgttc	900
30	cgtgtggtca gcgtcctcac cgttgtgcac caggactggc tgaacggcaa ggagtacaag	960
	tgcaaggtct ccaacaaagg cctcccagcc cccatcgaga aaaccatctc caaaacaaa	1020
35	gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggagga gatgaccaag	1080
	aaccaggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag	1140
	tgggagagca atgggcagcc ggagaacaac tacaagacca cacctcccat gctggactcc	1200
40	gacggctcct tcttctctca cagcaagctc accgtggaca agagcaggtg gcagcagggg	1260
	aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1320
45	ctctccctgt ctccgggtaa a	1341
	<210> 219	
	<211> 466	
	<212> PRT	
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50	<220>	
	<223> Synthetic Polypeptide	
	<220>	
55	<221> MISC_FEATURE	
	<223> Humanized Antibody Sequence	
	<400> 219	

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

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	290		295		300												
5	Asn 305	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe 315	Asn	Ser	Thr	Phe	Arg 320	
10	Val	Val	Ser	Val	Leu 325	Thr	Val	Val	His	Gln 330	Asp	Trp	Leu	Asn	Gly 335	Lys	
15	Glu	Tyr	Lys	Cys 340	Lys	Val	Ser	Asn	Lys 345	Gly	Leu	Pro	Ala	Pro 350	Ile	Glu	
20	Lys	Thr	Ile 355	Ser	Lys	Thr	Lys	Gly 360	Gln	Pro	Arg	Glu	Pro 365	Gln	Val	Tyr	
25	Thr	Leu 370	Pro	Pro	Ser	Arg	Glu 375	Glu	Met	Thr	Lys	Asn 380	Gln	Val	Ser	Leu	
30	Thr 385	Cys	Leu	Val	Lys	Gly 390	Phe	Tyr	Pro	Ser	Asp 395	Ile	Ala	Val	Glu	Trp 400	
35	Glu	Ser	Asn	Gly 405	Gln	Pro	Glu	Asn	Asn	Tyr 410	Lys	Thr	Thr	Pro	Pro 415	Met	
40	Leu	Asp	Ser	Asp 420	Gly	Ser	Phe	Phe	Leu 425	Tyr	Ser	Lys	Leu	Thr 430	Val	Asp	
45	Lys	Ser	Arg 435	Trp	Gln	Gln	Gly	Asn 440	Val	Phe	Ser	Cys	Ser 445	Val	Met	His	
50	Glu	Ala 450	Leu	His	Asn	His	Tyr 455	Thr	Gln	Lys	Ser	Leu 460	Ser	Leu	Ser	Pro	
55	Gly 465	Lys															

45 <210> 220
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50 <220>
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<220>
 <221> misc_feature

55 <223> Humanized Antibody Sequence

<400> 220

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 5 tgcaaagcat ctggatacac atttaccgac tactacatga attgggtacg acaagcccct 180
 ggacaaagac ttgaatggat gggagacatt aacccttata acgacgacac tacatacaat 240
 10 cataaattta aaggaagagt tacaattaca agagatacat ccgcatcaac cgcctatatg 300
 gaactttcct cattgagatc tgaagacact gctgtttatt actgtgcaag agaaactgcc 360
 gttattacta ctaacgctat ggattactgg ggtcaaggaa ccaactgttac cgtctctagt 420
 15 gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 480
 agcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 540
 20 tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtctca 600
 ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg caccagacc 660
 tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc 720
 25 aaatgttgtg tcgagtgcc accgtgcca gcaccacctg tggcaggacc gtcagtcttc 780
 ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacgtgc 840
 gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggtc cgtggacggc 900
 30 gtggaggtgc ataatgcaa gacaaagcca cgggaggagc agttcaacag cacgttccgt 960
 gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc 1020
 aaggtctcca acaaaggcct cccagcccc atcgagaaaa ccatctcaa aaccaaggg 1080
 35 cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 1140
 caggtcagcc tgacctgcct ggtcaaaggc ttctaccca gcgacatcgc cgtggagtgg 1200
 40 gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac 1260
 ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320
 gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380
 45 tcctgtctc cgggtaaa 1398

<210> 221
 <211> 215
 50 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

55 <220>
 <221> MISC_FEATURE
 <223> Humanized Antibody Sequence

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<400> 221

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1 5 10

10 Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Thr Ile Ser Ser Asn
20 25 30

15 His Leu His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu
35 40 45

20 Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

25 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

30 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro
85 90 95

35 Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

40 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

45 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

50 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

55 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 222

<211> 645

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<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<220>
 <221> misc_feature
 <223> Humanized Antibody Sequence

<400> 222

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	cccggcaaag cacctaaatc acttatatac ggcacatcaa atctcgcac aggcgttcct	180
	tcaagatfff caggctctgg ctcaggcacc gactttactc ttacaatatc ctccctccaa	240
20	cccgaagact tcgcaaccta ttactgtcaa caatggctct catatccact cacatttggc	300
	ggcggcacia aagtagaaat taaacgtacg gtggctgcac catctgtctt catcttcccg	360
25	ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	420
	tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	480
	caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg	540
30	acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag	600
	ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt	645

<210> 223
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<220>
 <223> Synthetic Polypeptide

<220>
 <221> MISC_FEATURE
 <223> Humanized Antibody Sequence

<400> 223

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

<210> 224

<211> 711

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<212> DNA
 <213> Artificial Sequence

5 <220>
 <223> Synthetic Polynucleotide

10 <220>
 <221> misc_feature
 <223> Humanized Antibody Sequence

<400> 224

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 agatgtgaca tccagatgac ccagctcca tcctccctct cagcatccgt aggcgataga 120
 gttacaataa catgcagcgt atcatcaact atatcatcaa atcatcttca ttggttccaa 180
 20 cagaaacccg gcaaagcacc taaatcactt atatacggca catcaaatct cgcacagggc 240
 gttccttcaa gatthttcagg ctctggctca ggcaccgact ttactcttac aatatcctcc 300
 ctccaacccg aagacttgc aacctattac tgtcaacaat ggtcctcata tccactcaca 360
 25 tttggcggcg gcacaaaagt agaaattaa cgtacggcgg ctgcaccatc tgtcttcatc 420
 ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctggtgtgtg cctgctgaat 480
 aacttctatc ccagagagggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

30
 35 aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600
 accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660
 catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 711

40 <210> 225
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 <212> PRT
 <213> Artificial Sequence

45 <220>
 <223> Synthetic Polypeptide

50 <220>
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 <223> Humanized Antibody Sequence

<400> 225

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

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Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 180 185 190
 5 Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
 195 200 205
 10 Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
 210 215 220
 Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
 225 230 235 240
 15 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 20 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 25 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 290 295 300
 30 Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 35 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
 325 330 335
 40 Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 45 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 50 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 55 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

5 Pro Gly Lys
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<210> 226

<211> 1353

10 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

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<400> 226

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tccctgcaagg cttctgactt caacattaaa gacttctatc tacactgggt gcgacaggcc 120
5 cctggacaag ggcttgagtg gattggaagg attgatcctg agaatgggtga tactttatat 180
gacccgaagt tccaggacaa ggtcaccatg accacagaca cgtccaccag cacagcctac 240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagaggcg 300
10 gattatttcc acgatggtac ctccactagg tacttcgatg tctggggccg tggcaccctg 360
gtcaccgtct ctagtgcctc caccaagggc ccatcgggtct tccccctggc gccctgctcc 420
aggagcacct ccgagagcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
15 ccggtgacgg tgtcgtggaa ctccaggcct ctgaccagcg gcgtgcacac cttcccagct 540
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcaac 600
20 ttccggcacc agacctacac ctgcaacgta gatcacaagc ccagcaacac caaggtggac 660
aagacagttg agcgcaaatg ttgtgtcgag tgcccaccgt gccccagcacc acctgtggca 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
25 cctgaggtca cgtgcgtggt ggtggacgtg agccacgaag accccgaggt ccagttcaac 840
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30 aaggagtaca agtgcaaggc ctccaacaaa ggcctcccag ccccatcga gaaaccatc 1020
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35 gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta cccagcgcac 1140
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atgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260
40 tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320
acgcagaaga gcctctccct gtctccgggt aaa 1353

45 <210> 227
<211> 470
<212> PRT
<213> Artificial Sequence

50 <220>
<223> Synthetic Polypeptide

<220>
<221> MISC_FEATURE
55 <223> Humanized Antibody Sequence

<400> 227

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

50

55

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Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 210 215 220

5
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 225 230 235 240

10
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255

15
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270

20
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285

25
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 290 295 300

30
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 305 310 315 320

35
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
 325 330 335

40
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 340 345 350

45
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
 355 360 365

50
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 370 375 380

55
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 385 390 395 400

60
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 405 410 415

65
 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430

70
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445

75
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460

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Ser Leu Ser Pro Gly Lys
465 470

5 <210> 228
<211> 1410
<212> DNA
<213> Artificial Sequence

10 <220>
<223> Synthetic Polynucleotide

<220>
<221> misc_feature

15 <223> Humanized Antibody Sequence

<400> 228

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 gtgcagctgg tgcagtctgg ggctgagggtg aagaagcctg gggcctcagt gaaggtctcc 120
 5 tgcaaggctt ctgacttcaa cattaagac ttctatctac actgggtgcg acaggcccct 180
 ggacaagggc ttgagtggat tgggaaggatt gatcctgaga atggtgatac tttatatgac 240
 ccgaagttcc aggacaaggt caccatgacc acagacacgt ccaccagcac agcctacatg 300
 10 gagctgagga gcctgagatc tgacgacacg gccgtgtatt actgtgcgag agaggcggat 360
 tatttccacg atggtacctc ctactggtac ttogatgtct ggggccgtgg caccctggtc 420
 accgtctcta gtgcctccac caagggocca tgggtcttcc ccctggcgcc ctgctccagg 480
 15 agcacctccg agagcacagc ggccttgggc tgccctggtca aggactactt ccccgaaccg 540
 gtgacgggtg cgtggaactc aggcgctctg accagcggcg tgcacacctt cccagctgtc 600
 20 ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcaacttc 660
 ggcacccaga cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag 720
 acagttgagc gcaaatgttg tgtcgagtgc ccaccgtgcc cagcaccacc tgtggcagga 780
 25 ccgtcagtct tcctcttccc cccaaaacc aaggacacc tcatgatctc ccggaccct 840
 gaggtcacgt gcgtgggtgg ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg 900
 30 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cacgggagga gcagttcaac 960
 agcacgttcc gtgtggtcag cgtcctcacc gttgtgcacc aggactggct gaacggcaag 1020
 gagtacaagt gcaaggtctc caacaaaggc ctcccagccc ccatcgagaa aaccatctcc 1080
 35 aaaaccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1140
 atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1200
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctcccatg 1260
 40 ctggactccg acggctcctt ctctctctac agcaagctca ccgtggacaa gagcaggtgg 1320
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 45 cagaagagcc tctccctgtc tccgggtaaa 1410

<210> 229
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 50 <213> Artificial Sequence

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55 <220>
 <221> MISC_FEATURE
 <223> Humanized Antibody Sequence

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<400> 229

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1 5 10 15

10 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Ile Ser Tyr Ile
20 25 30

15 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45

20 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

25 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

30 Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asp Pro Leu Thr
85 90 95

35 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

40 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

45 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

50 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

55 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

55 <210> 230
<211> 639
<212> DNA
<213> Artificial Sequence

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<220>
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5 <220>
 <221> misc_feature
 <223> Humanized Antibody Sequence

<400> 230

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 aaagccccta agctcctgat ctatgccaca tccaacctgg cttctggggg cccatcaagg 180
 15 ttcagcggca gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa 240
 gattttgcaa cttattactg tcagcagtggt agtagtgacc cactcacggt cggcggaggg 300
 20 accaaggtgg agatcaaacg tacgggtggct gcaccatctg tcttcatctt cccgccatct 360
 gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420
 agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480
 25 agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg 600
 agctcgcccg tcacaaagag cttcaacagg ggagagtgt 639

30 <210> 231
 <211> 235
 <212> PRT
 <213> Artificial Sequence

35 <220>
 <223> Synthetic Polypeptide

40 <220>
 <221> MISC_FEATURE
 <223> Humanized Antibody Sequence

<400> 231

45 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

50 Leu Pro Gly Ala Arg Cys Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe

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<220>
<221> misc_feature
<223> Humanized Antibody Sequence

5 <400> 232

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10 agatgtgaca tccagttgac ccagctcca tccttcctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgcagggc cagctcaagt ataagttaca tacactggta tcagcaaaaa 180
ccagggaaag cccctaagct cctgatctat gccacatcca acctggcttc tgggggccca 240
15 tcaaggttca gcggcagtgg atctgggaca gaattcactc tcacaatcag cagcctgcag 300
cctgaagatt ttgcaactta ttactgtcag cagtggagta gtgacccact cacgttcggc 360
ggagggacca aggtggagat caaacgtacg gtggctgcac catctgtctt catcttcccg 420
20 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctcg 600
25 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

30 <210> 233
<211> 447
<212> PRT
<213> Artificial Sequence

35 <220>
<223> Synthetic Polypeptide

<220>
<221> MISC_FEATURE
40 <223> Humanized Antibody Sequence

<400> 233

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

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

10 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
 385 390 395 400

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

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

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

<210> 234
 <211> 1341
 25 <212> DNA
 <213> Artificial Sequence

<220>
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30 <220>
 <221> misc_feature
 <223> Humanized Antibody Sequence

35 <400> 234

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5	cctggacaag ggcttgagtg gatcgggaagg gttgatcctg acaatggtga gactgaattt	180
	gccccgaagt tcccgggcaa ggtcaccatg accacagaca cgtccatcag cacagcctac	240
10	atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaagac	300
	tacgatggta cctacacctg gtttccttat tggggccaag ggactctggt caccgtctct	360
	agtgcctcca ccaagggccc atcgggtcttc ccctggcgc cctgctccag gagcacctcc	420
15	gagagcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
	tcgtggaact caggcgctct gaccageggc gtgcacacct tcccagctgt cctacagtcc	540
	tcaggactct actccctcag cagcgtggtg accgtgccct ccagcaactt cggcaccag	600
20	acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gacagttgag	660
	cgcaaatggt gtgtcgagtg cccaccgtgc ccagcaccac ctgtggcagg accgtcagtc	720
25	ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcacg	780
	tgctgtgggg tggacgtgag ccacgaagac cccgaggtcc agttcaactg gtacgtggac	840
	ggcgtggagg tgcataatgc caagacaaag ccacgggagg agcagttcaa cagcacgttc	900
30	cgtgtggtca gcgtcctcac cgttgtgcac caggactggc tgaacggcaa ggagtacaag	960
	tgcaaggtct ccaacaaagg cctcccagcc cccatcgaga aaaccatctc caaaacaaa	1020
35	gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag	1080
	aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag	1140
	tgggagagca atgggcagcc ggagaacaac tacaagacca cacctcccat gctggactcc	1200
40	gacggctcct tcttctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1260
	aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1320
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50	<220>	
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55	<220>	
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	<400> 235	

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

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Tyr Tyr Cys Ala Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro
 115 120 125

5 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 130 135 140

10 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
 145 150 155 160

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

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

25 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205

30 Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
 210 215 220

35 Val Asp His Lys Pro Ser Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
 225 230 235 240

40 Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
 245 250 255

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

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

55 Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 290 295 300

60 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 305 310 315 320

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

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

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

80 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

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370

375

380

5 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

10 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
405 410 415

15 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

20 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

25 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

30 Gly Lys
465

35 <210> 236
<211> 1398
<212> DNA
<213> Artificial Sequence

40 <220>
<223> Synthetic Polynucleotide

45 <220>
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<223> Humanized Antibody Sequence

50 <400> 236

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5	tgcaaggctt ctggattcga cattaaggac tactatatac actgggtgcg acaggcccct	180
	ggacaagggc ttgagtggat cgggaagggtt gatcctgaca atggtgagac tgaatttgcc	240
	ccgaagttcc cgggcaaggt caccatgacc acagacacgt ccatcagcac agcctacatg	300
10	gagctgagca ggctgagatc tgacgacacg gccgtgtatt actgtgagag agaagactac	360
	gatggtacct acacctgggt tccttattgg ggccaagga ctctggtcac cgtctctagt	420
	gcctccacca agggcccac ggtcttcccc ctggcgccct gctccaggag cacctccgag	480
15	agcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgctg	540
	tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtctca	600
20	ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcaacttcgg caccagacc	660
	tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc	720
	aatggttggt tgcagtgccc accgtgcccc gcaccacctg tggcaggacc gtcagtcttc	780
25	ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacgtgc	840
	gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc	900
30	gtggaggtgc ataatgcaa gacaaagcca cgggaggagc agttcaacag cacgttccgt	960
	gtggtcagcg tcctcacctg tgtgcaccag gactggctga acggcaagga gtacaagtgc	1020
	aaggtctcca acaaaggcct cccagcccc atogagaaaa ccatctcaa aaccaaagg	1080
35	cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac	1140
	caggtcagcc tgacctgcct ggtcaaaggc ttctaccca gcgacatcgc cgtggagtgg	1200
40	gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac	1260
	ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac	1320
	gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1380
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<210> 237

<211> 7

<212> PRT

50 <213> Mus musculus

<400> 237

55 Gly Thr Ser Asn Leu Ala Ser

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<210> 238

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<211> 8
 <212> PRT
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5 <400> 238

Gln Gln Trp Thr Thr Thr Tyr Thr
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10 <210> 239
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 <212> PRT
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15 <400> 239

Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn
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20 <210> 240
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25 <400> 240

Ser Thr Ser Arg Leu Asn Ser
 1 5

30 <210> 241
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Gln Gln Asp Ile Lys His Pro Thr
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5 Trp Ala Ser Thr Arg His Thr
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15 Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
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25 Asp Tyr Asn Met His
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<400> 247

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<400> 248

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Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Gln Phe Lys
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Gly

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Asp Tyr Asn Met His
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<400> 255

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys
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Gly

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Asp Tyr Asn Met His
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 Asp Tyr Asn Met His
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Gly

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Asp Tyr Asn Met His
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Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe Lys
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Asp Tyr Tyr Ile His
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Arg Ile Asp Pro Asp Asn Gly Glu Ser Thr Tyr Val Pro Lys Phe Gln
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5 Gly

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Asp Tyr Ile Met His
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15 Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp Pro Lys Phe Gln
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Gly

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<400> 274

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<210> 275

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25 Gly Thr Ser Asn Leu Ala Ser
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Gln Gln Trp Ser Ser Asp Pro Leu Thr
1 5

15 <210> 284
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Arg Ala Ser Ser Ser Val Thr Ser Ser Tyr Leu Asn
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45 Gln Gln Tyr Asp Phe Phe Pro Ser Thr
1 5

50 <210> 287
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55 Asp Tyr Phe Ile His
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Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe Asp Val
 1 5 10 15

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Asp Tyr Tyr Ile His
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Gly

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Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr
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<400> 296

Asp Tyr Tyr Met Asn
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<210> 297
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<400> 297

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Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe Lys
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 Gly
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 Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp
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 20 <211> 130
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 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Met Leu Ile Ser Val Thr
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 30 Val Ile Leu Ser Ser Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Leu
 20 25 30
 35 Met Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Val Ser
 35 35 40 45
 Ser Ser Ile Ser Ser Ser Asn Leu His Trp Ser Gln Gln Lys Ser Gly
 50 55 60
 40 Thr Ser Pro Lys Leu Trp Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
 65 70 75 80
 45 Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 85 90 95
 50 Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 100 105 110
 55 Gln Trp Thr Thr Thr Tyr Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu
 115 120 125
 Lys Arg
 130

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 <211> 390
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 <213> Mus musculus

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 gtcaccatca cctgcagtgt cagctcgagt ataagttcca gcaacttaca ctgggtcccag 180
 15 cagaagtcag gaacctcccc caaactctgg atttatggca catccaacct tgcttctgga 240
 gtcctgttc gcttcagtgg cagtggatct gggacctctt attctctcac aatcagcagc 300
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 <211> 141
 <212> PRT
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 <400> 301

30 Met Gly Trp Asn Trp Ile Ile Phe Phe Leu Met Ala Val Val Thr Gly
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Val Asn Ser Glu Val Gln Leu Arg Gln Ser Gly Ala Asp Leu Val Lys
 20 25 30

35 Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
 35 40 45

40

45

50

55

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	Lys	Asp	Tyr	Tyr	Ile	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu
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5	Glu	Trp	Ile	Gly	Arg	Ile	Asp	Pro	Asp	Asn	Gly	Glu	Ser	Thr	Tyr	Val
	65					70				75						80
10	Pro	Lys	Phe	Gln	Gly	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn
				85						90					95	
15	Thr	Ala	Tyr	Leu	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Ile
				100					105					110		
20	Tyr	Tyr	Cys	Gly	Arg	Glu	Gly	Leu	Asp	Tyr	Gly	Asp	Tyr	Tyr	Ala	Val
			115					120					125			
25	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser			
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	gtgcagttgc	ggcagtctgg	ggcagacctt	gtgaagccag	gggcctcagt	caagttgtcc										120
35	tgcacagctt	ctggcttcaa	cattaaagac	tactatatac	actgggtgaa	gcagaggcct										180
	gaacagggcc	tggagtggat	tggaaggatt	gacctctgata	atggtgaaag	tacatatgtc										240
	ccgaagttcc	agggcaaggc	cactataaca	gcagacacat	catccaacac	agcctaccta										300
40	caactcagaa	gcctgacatc	tgaggacact	gccatctatt	attgtgggag	agaggggctc										360
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	agc															423
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	<223> Humanized Antibody Sequence															

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<400> 303

5 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
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10 Leu Pro Gly Ala Arg Cys Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe
 20 25 30

15 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Val Ser
 35 40 45

20 Ser Ser Ile Ser Ser Ser Asn Leu His Trp Tyr Gln Gln Lys Pro Gly
 50 55 60

25 Lys Ala Pro Lys Leu Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
 65 70 75 80

30 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
 85 90 95

35 Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
 100 105 110

40 Gln Trp Thr Thr Thr Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
 115 120 125

45 Lys Arg
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<210> 304

<211> 390

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Polynucleotide

<220>

<221> misc_feature

<223> Humanized Antibody Sequence

<400> 304

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5	gtgaccatta cctgcagcgt gagcagcagc attagcagca gcaacctgca ttggtatcag	180
	cagaaaccgg gcaaagcggc gaaactgctg atttatggca ccagcaacct gccgagcggc	240
10	gtgccgagcc gctttagcgg cagcggcagc ggcaccgaat ttaccctgac cattagcagc	300
	ctgcagccgg aagatcttgc gacctattat tgccagcagt ggaccaccac ctataccttt	360
	ggccagggca ccaaactgga aattaaacgt	390

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	<212> PRT
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	<221> MISC_FEATURE
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 5 ggccagggcc tggaatggat gggccgcatt gatccggata acggcgaaag cacctatgtg 240
 ccgaaatttc agggccgcgt gaccatgacc accgatacca gcaccagcac cgcgtatatg 300
 gaactgcgca gcctgcgcag cgatgatacc gcggtgtatt attgcgcgcg cgaaggcctg 360
 10 gattatggcg attattatgc ggtggattat tggggccagg gcaccctggt gaccgtctcg 420
 agc 423

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

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<210> 308
<211> 381
<212> DNA
<213> Mus musculus

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<400> 308

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atcagctgca gggcaagtca ggacattagc agttatttaa actggtatca gcagaaacca 180
15 gatggaactg ttaaactcct gatctactcc acatcaagat taaactcagg agtcccatca 240
aggttcagtg gcagtgggtc tgggacagat tattctctca ctattagcaa cctggcacia 300
gaagatattg ccacttactt ttgccaacag gatattaagc atccgacgtt cggaggaggc 360
20 accaagttgg agctgaaacg t 381

<210> 309
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<400> 309

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

5 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30

10 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe
 35 40 45

15 Thr Asp Tyr Ile Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn
 65 70 75 80

20 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
 85 90 95

25 Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Gly Ser Ala Val
 100 105 110

30 Tyr Tyr Cys Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135

35 <210> 310
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 <212> DNA
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 tgcaaggctt ctgggttcac attcactgac tacattatgc actgggtgaa gcagaagcct 180
 gggcagggcc ttgagtggat tggatatatt aatccttaca atgatgatac tgaatacaat 240
 50 gagaagttca aaggcaaggc cacactgact tcagacaaat cctccagcac agcctacatg 300
 gatctcagca gtctgacctc tgagggctct gcggtctatt actgtgcaag atcgatttat 360
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<213> Artificial Sequence

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<223> Synthetic Polypeptide

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<221> MISC_FEATURE

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

20

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

25

Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

30

Lys Leu Leu Ile Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

35

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Ile
100 105 110

40

Lys His Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

<210> 312

<211> 381

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<220>

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<223> Humanized Antibody Sequence

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<400> 312

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5 atcacttgcc gcgcaagtca ggatattagc agctatttaa attggtatca gcagaaacca 180
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cgcttcagtg gcagtggtc tgggacagat ttcactctca ccatcagcag tctgcaacct 300
10 gaagattttg caacttacta ctgtcaacag gatattaaac accctacgtt cggtaaggc 360
accaaggtgg agatcaaacg t 381

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<223> Synthetic Polypeptide
<220>
<221> MISC_FEATURE
25 <223> Humanized Antibody Sequence
<400> 313

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

55

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

5 Tyr Tyr Cys Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr
 115 120 125

10 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135

<210> 314
 <211> 107
 <212> PRT
 15 <213> Mus musculus

<400> 314

20 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

25 Asp Arg Val Asn Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr
 20 25 30

30 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

35 Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

40 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Ala Gln
 65 70 75 80

45 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Ile Lys His Pro Thr
 85 90 95

50 Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg
 100 105

55 <210> 315
 <211> 128
 <212> PRT
 <213> Mus musculus

<400> 315

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5 Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
 20 25 30

10 Thr Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 35 40 45

15 Val Phe Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
 50 55 60

20 Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
 65 70 75 80

25 Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

30 Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
 100 105 110

35 Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 115 120 125

<210> 316
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 <212> DNA
 <213> Mus musculus

<400> 316

40 atgaagtcac agaccaggt ctttgtatac atgttgctgt ggttgctctgg tgttgaagga 60
 gacattgtga tgaccagtc tcacaaattc atgtccacgt cagtaggaga cagggtcacc 120
 atcacctgca aggccagtc ggatgtcttt actgctgtag cctggtatca acagaaacca 180
 45 ggacaatctc ctaaactact gatttactgg gcatccacc gccacactgg agtccctgat 240
 cgcttcacag gcagtggatc tgggacagat ttcactctca ccattagcaa tgtgcagtct 300
 gaagacttgg cagattatct ctgtcaacaa tatagcagct atcctctcac gttcggtgct 360
 50 gggaccaagt tggagctgaa a 381

<210> 317
 <211> 138
 <212> PRT
 <213> Mus musculus

<400> 317

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

5 Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
 20 25 30

10 Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Asn Ile
 35 40 45

15 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp
 65 70 75 80

20 Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Thr Asp Thr Ser Ser Asn
 85 90 95

25 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Tyr Asp Ala Gly Asp Pro Ala Trp Phe Thr Tyr Trp
 115 120 125

30 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135

35 <210> 318
 <211> 411
 <212> DNA
 <213> Mus musculus

40 <400> 318

atgggatgga actggatcat cttcttcctg atggcagtggt ttacaggggt caattcagag 60
 45 gttcagctgc agcagctctgg ggctgagcct gtgaggccag ggccttagt caagttgtcc 120
 tgcaaagcct ctggcttcaa tattaagac tactatatgc actgggtgaa gcagaggcct 180
 gaacagggcc tggagtggat tggaaggatt gatcctgaga atggtgatata tatatatgac 240
 50 ccgaagttcc agggcaaggc cagtataaca acagacacat cctccaacac agcctacctg 300
 cagctcagca gcctgacgtc tgaggacact gccgtctatt actgtgctta cgatgctggt 360
 gaccccgctt ggtttactta ctggggccaa gggactctgg tcaccgtctc g 411

55 <210> 319
 <211> 130
 <212> PRT

EP 2 556 841 B9

<213> Mus musculus

<400> 319

5 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

10 Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

15 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
35 40 45

20 Gln Asp Val Phe Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

25 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
65 70 75 80

30 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

35 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100 105 110

40 Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125

45 Lys Arg
130

<210> 320

<211> 390

<212> DNA

<213> Mus musculus

<400> 320

45 atggatatgc gcgtgccggc gcagctgctg ggctgctgc tgctgtggct gcgcggcgcg 60
cgctgcgata tccagatgac ccagagcccg agcagcctga gcgcgagcgt gggcgatcgc 120
50 gtgaccatta cctgcaaagc gagccaggat gtgtttaccg cggtggcgtg gtatcagcag 180
aaaccgggca aagcgcggaa actgctgatt tattgggcga gcacccgcca taccggcgtg 240
ccgagtcgct ttagcggcag cggcagcggc accgatttta ccctgaccat tagcagcctg 300
55 cagccggaag attttgcgac ctattattgc cagcagtata gcagctatcc gctgaccttt 360
ggcggcggca ccaaagtgga aattaaacgt 390

EP 2 556 841 B9

<210> 321
 <211> 138
 <212> PRT
 <213> Artificial Sequence

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<220>
 <223> Synthetic Polypeptide

10

<220>
 <221> MISC_FEATURE
 <223> Humanized Antibody Sequence

<400> 321

15

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

20

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile
 35 40 45

25

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

30

Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp
 65 70 75 80

35

Pro Lys Phe Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
 85 90 95

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

40

Tyr Tyr Cys Ala Tyr Asp Ala Gly Asp Pro Ala Trp Phe Thr Tyr Trp
 115 120 125

45

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135

<210> 322
 <211> 414
 <212> DNA
 <213> Artificial Sequence

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<220>
 <223> Synthetic Polynucleotide

55

<220>
 <221> misc_feature
 <223> Humanized Antibody Sequence

EP 2 556 841 B9

<400> 322

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atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagcgaa      60
5  gtgcagctgg tgcagagcgg cgcggaagtg aaaaaaccgg gcgcgagcgt gaaagtgagc      120
tgcaaagcga gcggctttaa cattaagat tattatatgc attgggtgcg ccaggcgccg      180
10 ggccagggcc tggaatggat cggccgcatt gatccggaaa acggcgatat tatttatgat      240
ccgaaatttc agggccgcgt gaccatgacc accgatacca gcaccagcac cgcgtatatg      300
gaactgcgca gcctgcgcag cgatgatacc gcggtgtatt attgcgcgta tgatgcgggc      360
15 gatccggcgt ggtttaccta ttggggccag ggcaccctgg tgaccgtctc gagg      414

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<210> 323

<211> 106

<212> PRT

20 <213> Mus musculus

<400> 323

25 Thr Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln

1 5 10 15

30 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
20 25 30

35 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
35 40 45

40 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
50 55 60

45 Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
65 70 75 80

50 His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
85 90 95

55 Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
100 105

<210> 324

<211> 320

<212> PRT

55 <213> Mus musculus

<400> 324

EP 2 556 841 B9

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
 1 5 10 15

5
 Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
 20 25 30

10
 Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
 35 40 45

15
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 50 55 60

20
 Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
 65 70 75 80

25
 Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 85 90 95

30
 Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
 100 105 110

35
 Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
 115 120 125

40

45

50

55

EP 2 556 841 B9

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
 130 135 140

5

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
 145 150 155 160

10

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
 165 170 175

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
 180 185 190

15

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
 195 200 205

20

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
 210 215 220

25

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
 225 230 235 240

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
 245 250 255

30

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
 260 265 270

35

Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
 275 280 285

40

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
 290 295 300

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
 305 310 315 320

45

<210> 325
 <211> 106
 <212> PRT
 <213> Homo sapiens

50

<400> 325

55

EP 2 556 841 B9

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

30 <210> 326
 <211> 327
 <212> PRT
 <213> Homo sapiens

35 <400> 326

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45

50

55

EP 2 556 841 B9

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

5 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

10 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

15 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80

20 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

25 Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125

30 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

35 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160

40

45

50

55

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Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 5
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 10
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 15
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 20
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 25
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 30
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 35
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 40
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 45
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 50
 Leu Ser Leu Ser Leu Gly Lys
 325
 55

<210> 327

<211> 120

<212> PRT

<213> Mus musculus

<400> 327

EP 2 556 841 B9

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

<210> 328
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 328

EP 2 556 841 B9

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

<210> 329

<211> 120

<212> PRT

<213> Mus musculus

<400> 329

EP 2 556 841 B9

1 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 5 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
 10 Ile Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
 15 Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
 20 Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
 25 Met Asp Leu Ser Ser Leu Thr Ser Glu Gly Ser Ala Val Tyr Tyr Cys
 30 Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
 35 Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe
 40 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 45 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 50 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 55 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 60 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 65 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 70 Glu Cys
 75 225

<210> 331
 <211> 447

EP 2 556 841 B9

<212> PRT

<213> Mus musculus

<400> 331

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

10
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
 20 25 30

15
 Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

20
 Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
 50 55 60

25
 Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

30
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

35

40

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Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
100 105 110

5 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
10 130 135 140

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

15 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
20 180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

25 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
30 225 230 235 240

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

35 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
40 275 280 285

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

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

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
50 325 330 335

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

55 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu

<400> 333

5

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Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
1 5 10 15

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
5 20 25 30

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
10 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
50 55 60

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
15 65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
20 85 90 95

Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
100 105 110

Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
25 115 120 125

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
30 130 135 140

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
145 150 155 160

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
35 165 170 175

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
40 180 185 190

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
45 195 200 205

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
210 215 220

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
50 225 230 235 240

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
55 245 250 255

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln

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260

265

270

5 Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn
 275 280 285

10 Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
 290 295 300

15 Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
 305 310 315 320

15 Ser Pro Gly Lys

20 <210> 334

<211> 213

<212> PRT

<213> Mus musculus

<400> 334

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35

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45

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55

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

<210> 335

<211> 444

55 <212> PRT

<213> Mus musculus

<400> 335

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

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

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His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440

5 <210> 336
 <211> 108
 <212> PRT
 <213> Mus musculus

10 <400> 336

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Phe Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

40 <210> 337
 <211> 324
 <212> DNA
 <213> Mus musculus

<400> 337

45 gatatccaga tgaccagag cccgagcagc ctgagcgcga gcgtgggcca tcgctgacc 60
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 ggcaaagcgc cgaaactgct gatttattgg gcgagcacc gccataccgg cgtgccgagt 180
 50 cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240
 gaagattttg cgacctatta ttgccagcag tatagcagct atccgctgac ctttggcggc 300
 55 ggcaccaaag tggaaattaa acgt 324

<210> 338
 <211> 119

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<212> PRT
 <213> Mus musculus

<400> 338

5

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

10

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
 20 25 30

15

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

20

Gly Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp Pro Lys Phe
 50 55 60

25

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

30

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

Ala Tyr Asp Ala Gly Asp Pro Ala Trp Phe Thr Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
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<210> 339
 <211> 357
 <212> DNA
 <213> Mus musculus

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<400> 339

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<210> 340
 <211> 1395
 <212> DNA
 <213> Mus musculus

EP 2 556 841 B9

<400> 340

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 gagaagttca agggccgtgt cacgattacc gcgacaaat ccacgagcac agcctacatg 300
 15 gagctgagca gcctgcgctc tgaggacacg gccgtgtatt actgtgcgcg ttcgatttat 360
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 35 gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag 1020
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 agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc 1260
 45 tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1320
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50 <210> 341
 <211> 213
 <212> PRT
 <213> Mus musculus

55 <400> 341

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 5 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr
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 10 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 15 Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 20 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 25 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Ile Lys His Pro Thr
 85 90 95
 30 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 35 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 40 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 45 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 50 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 55 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 60 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 65 Asn Arg Gly Glu Cys
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<210> 342

<211> 639

55 <212> DNA

<213> Mus musculus

<400> 342

EP 2 556 841 B9

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 cgcttcagtg gcagtggtc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
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 20 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600
 agctcgcccg tcacaaagag cttcaacagg ggagagtgt 639

25 <210> 343
 <211> 235
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30 <400> 343

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EP 2 556 841 B9

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

<210> 344

EP 2 556 841 B9

<211> 705
 <212> DNA
 <213> Mus musculus

5 <400> 344

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 10 gtcaccatca cttgccgcg c aagtcaggat attagcagct atttaaattg gtatcagcag 180
 aaaccagga aagcccctaa gctcctgac tattctactt cccgtttgaa tagtggggtc 240
 15 ccatcacgct tcagtggcag tggctctggg acagatttca ctctcaccat cagcagctctg 300
 caacctgaag attttgcaac ttactactgt caacaggata ttaaaccacc tacgttcgggt 360
 caaggcacca aggtggagat caaacgtacg gtggctgcac catctgtctt catcttcccg 420
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 25 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660
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30 <210> 345
 <211> 446
 <212> PRT
 <213> Mus musculus

35 <400> 345

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
 20 25 30
 Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

55

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

5 Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

10 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

15 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

20 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

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

25 Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

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

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225 230 235 240

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

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

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

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

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

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

55 Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

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5	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
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10	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
		370					375					380				
15	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp
	385					390					395					400
20	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
					405					410					415	
25	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
				420					425					430		
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 <212> DNA
 <213> Mus musculus

<400> 346

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	aacgagaagt tcaagggccg tgtcacgatt accgcggaca aatccacgag cacagcctac	240
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	ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg caccagacc	600
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	aaatgttgtg togagtgcc accgtgcccga gcaccacctg tggcaggacc gtcagtcttc	720
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25	gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc	840
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30	gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc	960
35	aaggtctcca acaaaggcct cccagcccc atcgagaaaa ccatctcaa aaccaaaggg	1020
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	<212> PRT	
	<213> Mus musculus	
55	<400> 347	

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 Ala His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 5 20 25 30
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
 10 35 40 45
 Thr Asp Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 15 50 55 60
 Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
 20 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 25 100 105 110
 Tyr Tyr Cys Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr
 30 115 120 125
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 130 135 140
 Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
 35 145 150 155 160
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 40 165 170 175
 45
 50
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Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190
 5 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205
 10 Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
 210 215 220
 Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
 225 230 235 240
 15 Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
 245 250 255
 20 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 260 265 270
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 275 280 285
 25 Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 290 295 300
 30 Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
 305 310 315 320
 35 Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
 325 330 335
 Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
 340 345 350
 40 Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 355 360 365
 45 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 370 375 380
 50 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 385 390 395 400
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
 405 410 415
 55 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 420 425 430

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Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
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5 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
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15 <213> Mus musculus

<400> 348

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EP 2 556 841 B9

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<210> 349

<211> 417

<212> DNA

50 <213> Mus musculus

<400> 349

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EP 2 556 841 B9

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15 <210> 350
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 <212> PRT
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20 <400> 350

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Gly Thr Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Glu Ile Pro Ala
 50 55 60

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

Pro Val Glu Glu Glu Asp Ile Thr Thr Tyr Tyr Cys Gln Gln Ser Asn
 85 90 95

Glu Asp Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 115 120 125

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 130 135 140

55

EP 2 556 841 B9

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 145 150 155 160

5

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 165 170 175

10

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
 180 185 190

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His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
 195 200 205

20

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 351
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25

<400> 351

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<210> 352
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<400> 352

Ala Ala Ser Asn Leu Glu Ser
 1 5

40

<210> 353
 <211> 9
 <212> PRT
 <213> Mus musculus

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<400> 353

Gln Gln Ser Asn Glu Asp Pro Phe Thr
 1 5

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<210> 354
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 <212> DNA
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<400> 354

EP 2 556 841 B9

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 5 caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa tctagaatct 180
 gagatcccag ccaggtttag tggcaactggg tctgggacag acttcaccct caacatccat 240
 10 cctgtggagg aggaggatat cacaacctat tactgtcagc aaagtaatga ggatccgttc 300
 acgttcggag gggggaccaa gttggaaata aaacgggctg atgctgcacc aactgtatcc 360
 atcttcccac catccagtga gcagttaaca tctggagggtg cctcagtcgt gtgcttcttg 420
 15 aacaacttct acccceaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 480
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 20 agcacctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 600
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30 <400> 355

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EP 2 556 841 B9

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 1 5 10 15

5 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
 20 25 30

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

15 Val Asp Tyr Asp Gly Thr Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 50 55 60

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

20 Glu Ile Pro Ala Arg Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr
 85 90 95

25 Leu Asn Ile His Pro Val Glu Glu Glu Asp Ile Thr Thr Tyr Tyr Cys
 100 105 110

Gln Gln Ser Asn Glu Asp Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125

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

35 Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
 145 150 155 160

40 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
 165 170 175

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

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

50 Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
 210 215 220

55 Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 225 230 235

<210> 356

<211> 717

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<212> DNA
 <213> Mus musculus

<400> 356

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 gacattgtgt tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
 10 atcgcctgca aggccagcca aagtgttgat tatgatggta ctagttatat gaattggtac 180
 caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa tctagaatct 240
 gagatcccag ccaggtttag tggcactggg tctgggacag acttcaccct caacatccat 300
 15 cctgtggagg aggaggatat cacaacctat tactgtcagc aaagtaatga ggatccgttc 360
 acgttcggag gggggaccaa gttggaaata aaacgggctg atgctgcacc aactgtatcc 420
 20 atcttcccac catccagtga gcagttaaca tctggagggtg cctcagtcgt gtgcttcttg 480
 aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 540
 aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600
 25 agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 660
 actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgtag 717

<210> 357
 <211> 442
 <212> PRT
 <213> Mus musculus

<400> 357

35
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 1 5 10 15
 40 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Thr Tyr
 20 25 30

45

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

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Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met
 290 295 300
 5 His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser
 305 310 315 320
 10 Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly
 325 330 335
 15 Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln
 340 345 350
 20 Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe
 355 360 365
 25 Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu
 370 375 380
 30 Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe
 385 390 395 400
 35 Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn
 405 410 415
 40 Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr
 420 425 430
 45 Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440

<210> 358
 <211> 5
 <212> PRT
 <213> Mus musculus

<400> 358

45 Thr Tyr Trp Met Asn
 1 5

<210> 359
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 359

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	tcctgtaagg cttctggcta catcttcacc acctactgga tgaactgggt gaaacagagg	120
5	cctggacaag gccttgagtg gattggcatg attcatcctt ccgcaagtga aattaggttg	180
	gatcagaaat tcaaggacaa ggccacattg actcttgaca aatcctccag cacagcctat	240
10	atgcacctca gcggcccgac atctgtggat tctgcggtct attactgtgc aagatcaggg	300
	gaatgggggt ctatggacta ctgggggtcaa ggaacctcag tcaccgtctc ctccagccaaa	360
	acgacacccc catctgtcta tccactggcc cctggatctg ctgcccacaaac taactccatg	420
15	gtgaccctgg gatgcctggt caagggctat ttccctgagc cagtgcagct gacctggaac	480
	tctggatccc tgtccagcgg tgtgcacacc ttcccagctg tcctgcagtc tgacctctac	540
	actctgagca gctcagtgac tgtcccctcc agcacctggc ccagcgagac cgtcacctgc	600
20	aacgttgccc acccgccag cagcaccaag gtggacaaga aaattgtgcc cagggattgt	660
	ggttgtaagc cttgcatatg tacagtccca gaagtatcat ctgtcttcat cttccccca	720
25	aagccaaggg atgtgctcac cactactctg actcctaagg tcacgtgtgt tgtggtagac	780
	atcagcaagg atgatccga ggtccagttc agctggtttg tagatgatgt ggaggtgcac	840
	acagctcaga cgcaaccccg ggaggagcag ttcaacagca ctttccgctc agtcagtgaa	900
30	cttcccatca tgcaccagga ctggctcaat ggcaaggagt tcaaatgcag ggtcaacagt	960
	gcagctttcc ctgccccat cgagaaaacc atctccaaa ccaaaggcag accgaaggct	1020
	ccacaggtgt acaccattcc acctcccaag gagcagatgg ccaaggataa agtcagtctg	1080
35	acctgcatga taacagactt cttccctgaa gacattactg tggagtggca gtggaatggg	1140
	cagccagcgg agaactacaa gaacactcag cccatcatgg acacagatgg ctcttacttc	1200
40	atctacagca agctcaatgt gcagaagagc aactgggagg caggaaatac tttcacctgc	1260
	tctgtgttac atgagggcct gcacaaccac catactgaga agagcctctc ccactctcct	1320
	ggtaaatga	1329
45	<210> 362	
	<211> 461	
	<212> PRT	
	<213> Mus musculus	
50	<400> 362	
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Met Gly Trp Ser Ser Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Arg
 5 20 25 30
 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ile Phe
 10 35 40 45
 Thr Thr Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 15 50 55 60
 Glu Trp Ile Gly Met Ile His Pro Ser Ala Ser Glu Ile Arg Leu Asp
 65 70 75 80
 Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Leu Asp Lys Ser Ser Ser
 20 85 90 95
 Thr Ala Tyr Met His Leu Ser Gly Pro Thr Ser Val Asp Ser Ala Val
 25 100 105 110
 Tyr Tyr Cys Ala Arg Ser Gly Glu Trp Gly Ser Met Asp Tyr Trp Gly
 30 115 120 125
 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser
 130 135 140
 Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
 35 145 150 155 160
 Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val
 40 165 170 175
 Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
 45 180 185 190
 Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
 195 200 205
 Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
 50 210 215 220
 Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
 55 225 230 235 240

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Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
 245 250 255

5 Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
 260 265 270

10 Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
 275 280 285

15 Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
 290 295 300

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
 305 310 315 320

20 Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
 325 330 335

25 Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 340 345 350

30 Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
 355 360 365

Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
 370 375 380

35 Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
 385 390 395 400

40 Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
 405 410 415

Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
 420 425 430

45 Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
 435 440 445

50 His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 450 455 460

<210> 363

<211> 1386

55 <212> DNA

<213> Mus musculus

<400> 363

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 tgtaaggctt ctggctacat cttcaccacc tactggatga actgggtgaa acagaggcct 180
 ggacaaggcc ttgagtggat tggcatgatt catccttccg caagtgaaat taggttggat 240
 10 cagaaattca aggacaaggc cacattgact cttgacaaat cctccagcac agcctatatg 300
 cacctcagcg gcccgacatc tgtggattct gcggtctatt actgtgcaag atcaggggaa 360
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 15 acacccccat ctgtctatcc actggcccct ggatctgctg cccaaaactaa ctccatggtg 480
 accctgggat gcctgggtcaa gggctatttc cctgagccag tgacagtgac ctggaactct 540
 20 ggatccctgt ccagcgggtg gcacaccttc ccagctgtcc tgcagtctga cctctacact 600
 ctgagcagct cagtgactgt cccctccagc acctggccca gcgagaccgt cacctgcaac 660
 gttgccacc cggccagcag caccaagggtg gacaagaaaa ttgtgccag ggattgtggt 720
 25 tgtaagcctt gcatatgtac agtcccagaa gtatcatctg tcttcatctt cccccaaag 780
 cccaaggatg tgctcacat tactctgact cctaagggtca cgtgtgttgt ggtagacatc 840
 agcaaggatg atcccagggt ccagttcagc tggttttag atgatgtgga ggtgcacaca 900
 30 gctcagacgc aacccggga ggagcagttc aacagcactt tccgctcagt cagtgaactt 960
 cccatcatgc accaggactg gctcaatggc aaggagttca aatgcagggt caacagtgca 1020
 35 gctttccctg cccccatcga gaaaaccatc tccaaaacca aaggcagacc gaaggctcca 1080
 caggtgtaca ccattccacc tcccaggag cagatggcca aggataaagt cagtctgacc 1140
 tgcatgataa cagacttctt ccctgaagac attactgtgg agtggcagtg gaatgggag 1200
 40 ccagcggaga actacaagaa cactcagccc atcatggaca cagatggctc ttacttcatc 1260
 tacagcaagc tcaatgtgca gaagagcaac tgggaggcag gaaatacttt cacctgctct 1320
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 45 aaatga 1386

<210> 364
 <211> 106
 50 <212> PRT
 <213> Mus musculus
 <400> 364

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5	Gly	Glu	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Ala	Gly	Tyr	Asn	Gln	Lys	Phe
		50					55					60				
10	Lys	Gly	Arg	Val	Thr	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr
	65					70					75					80
15	Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85					90					95	
20	Ala	Arg	Leu	Gly	Tyr	Asp	Asp	Ile	Tyr	Asp	Asp	Trp	Tyr	Phe	Asp	Val
				100					105					110		
25	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser					
			115					120								

<210> 379
 <211> 369
 <212> DNA
 <213> Mus musculus

<400> 379

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	tcttgtaaag	caagcggata	tacatttaca	gattacaaca	tgattgggt	aagacaagcg	120
35	ccaggacaag	gattggaatg	gatgggcgaa	attaacccta	atagtggagg	agcaggctac	180
	aatcaaaaat	tcaaagggag	agttacaatg	acaacagaca	caagcacttc	aacagcatat	240
	atggaactgc	gatcacttag	aagcgacgat	acagctgtat	actattgcgc	acgacttggg	300
40	tatgatgata	tatatgatga	ctggtatttc	gatgtttggg	gccagggaac	aacagttacc	360
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<210> 380
 <211> 108
 <212> PRT
 <213> Mus musculus

<400> 380

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1 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 5 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 10 Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
 15 Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe
 20 Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
 25 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 30 Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp Tyr Trp Gly
 35 Gln Gly Thr Thr Val Thr Val Ser Ser
 40 <210> 383
 <211> 363
 <212> DNA
 <213> Mus musculus
 45 <400> 383

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 40 agttgcaaag catctggata cacatttacc gactactaca tgaattgggt acgacaagcc 120
 cctggacaaa gacttgaatg gatgggagac attaaccctt ataacgacga cactacatac 180
 aatcataaat ttaaaggaag agttacaatt acaagagata catccgcatc aaccgcctat 240
 45 atggaacttt cctcattgag atctgaagac actgctgttt attactgtgc aagagaaact 300
 gccgttatta ctactaacgc tatggattac tgggggtcaag gaaccactgt taccgtctct 360
 agt 363

50 <210> 384
 <211> 108
 <212> PRT
 <213> Mus musculus
 55 <400> 384

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<220>

<221> MISC_FEATURE

<223> Humanized Antibody Sequence

5 <400> 392

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

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	210					215						220				
5	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro
	225					230					235					240
10	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
					245						250				255	
15	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp
				260						265					270	
20	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn
			275					280					285			
25	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val
		290					295					300				
30	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
	305					310					315					320
35	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys
					325						330				335	
40	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
				340					345					350		
45	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
			355					360					365			
50	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
		370					375					380				
55	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu
	385					390					395					400
60	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys
					405						410				415	
65	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
				420						425				430		
70	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
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<210> 393
 <211> 446
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

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<220>

<221> MISC_FEATURE

<223> Humanized Antibody Sequence

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<400> 393

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

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Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
 225 230 235 240

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

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

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

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

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

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

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

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

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

40 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
 385 390 395 400

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

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

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

<210> 394

<211> 450

55 <212> PRT

<213> Artificial Sequence

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<223> Synthetic Polypeptide

<220>

<221> MISC_FEATURE

5 <223> Humanized Antibody Sequence

<400> 394

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

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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 5
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 10
 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 15
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 290 295 300
 20
 Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 25
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
 325 330 335
 30
 Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 35
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 40
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 45
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 50
 Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 55
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 60
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 65
 Pro Gly
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<210> 395

<211> 446

55 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<220>

<221> MISC_FEATURE

5 <223> Humanized Antibody Sequence

<400> 395

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1 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 5 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asp Ile Lys Asp Tyr
 10 Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 15 Gly Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala Pro Lys Phe
 20 Pro Gly Lys Val Thr Met Thr Thr Asp Thr Ser Ile Ser Thr Ala Tyr
 25 Ala Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
 30 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 35 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 40 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 45 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 50 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 55 Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
 Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
 Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
 225 230 235 240

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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 5 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 260 265 270
 10 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 15 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
 290 295 300
 20 Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 25 Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 30 Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 35 Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 40 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 45 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
 385 390 395 400
 50 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 405 410 415
 55 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
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 <213> Artificial Sequence
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 <223> Synthetic Polypeptide
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<223> Humanized Antibody Sequence

<400> 396

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

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- SEQ ID No:246 = Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys Gly;
- SEQ ID No:247 = Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val;
- SEQ ID No: 78 = Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn;
- SEQ ID No: 79 = Tyr Thr Ser Arg Leu Leu Ser; and
5 - SEQ ID No: 80 = Gln Gln Gly Asp Thr Leu Pro Tyr Thr; and
- SEQ ID NO: 284 = Arg Ala Ser Ser Ser Val Thr Ser Ser Tyr Leu Asn;
- SEQ ID NO: 285 = Ser Thr Ser Asn Leu Ala Ser;
- SEQ ID NO: 286 = Gln Gln Tyr Asp Phe Phe Pro Ser Thr;
- SEQ ID NO: 296 = Asp Tyr Tyr Met Asn;
10 - SEQ ID NO: 297 = Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe Lys Gly; and
- SEQ ID NO 298 = Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp.
2. The antibody or fragment for use of claim 1, wherein the amount of anti-sclerostin antibody administered is from 1 mg/kg to 3 mg/kg.
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3. The antibody or fragment for use of claim 1 or 2, wherein the amount of anti-sclerostin antibody administered is about 2 mg/kg.
4. The antibody or fragment for use of claim 1 or 2, wherein the amount of anti-sclerostin antibody administered is about 3 mg/kg.
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5. The antibody or fragment for use of claim 1, wherein the method comprises administering to a human the anti-sclerostin antibody at a dose of from 70 to 450 mg.
- 25 6. The antibody or fragment for use of claim 1, where the method comprises administering a dose of about 140 mg.
7. The antibody or fragment for use of claim 1, where the method comprises administering a dose of about 210 mg.
8. The antibody or fragment for use of any one of the preceding claims, wherein the amount of anti-sclerostin antibody is administered to the subject once every two weeks.
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9. The antibody or fragment for use of any one of claims 1 to 7, wherein the anti-sclerostin antibody is administered to the subject once a month.
- 35 10. The antibody or fragment for use of any one of the preceding claims, wherein the antibody is a human antibody, a humanized antibody, a monoclonal antibody, or a chimeric antibody.
- 40 11. The antibody or fragment for use of any one of the preceding claims, where the human is suffering from a bone-related disorder selected from the group consisting of achondroplasia, cleidocranial dysostosis, enchondromatosis, fibrous dysplasia, Gaucher's Disease, hypophosphatemic rickets, Marfan's syndrome, multiple hereditary exotoses, neurofibromatosis, osteogenesis imperfecta, osteopetrosis, osteopoikilosis, sclerotic lesions, pseudoarthrosis, pyogenic osteomyelitis, periodontal disease, anti-epileptic drug induced bone loss, primary and secondary hyperparathyroidism, familial hyperparathyroidism syndromes, weightlessness induced bone loss, osteoporosis in men, postmenopausal bone loss, osteoarthritis, renal osteodystrophy, infiltrative disorders of bone, oral bone loss, osteonecrosis of the jaw, juvenile Paget's disease, melorheostosis, metabolic bone diseases, mastocytosis, sickle cell anemia/disease, organ transplant related bone loss, kidney transplant related bone loss, systemic lupus erythematosus, ankylosing spondylitis, epilepsy, juvenile arthritides, thalassemia, mucopolysaccharidoses, Fabry Disease, Turner Syndrome, Down Syndrome, Klinefelter Syndrome, leprosy, Perthes' Disease, adolescent idiopathic scoliosis, infantile onset multi-system inflammatory disease, Winchester Syndrome, Menkes Disease, Wilson's Disease, ischemic bone disease, Legg-Calve-Perthes disease, regional migratory osteoporosis, anemic states, conditions caused by steroids, glucocorticoid-induced bone loss, heparin-induced bone loss, bone marrow disorders, scurvy, malnutrition, calcium deficiency, osteoporosis, osteopenia, alcoholism, chronic liver disease, postmenopausal state, chronic inflammatory conditions, rheumatoid arthritis, inflammatory bowel disease, ulcerative colitis, inflammatory colitis, Crohn's disease, oligomenorrhea, amenorrhea, pregnancy, diabetes mellitus, hyperthyroidism, thyroid disorders, parathyroid disorders, Cushing's disease, acromegaly, hypogonadism, immobilization or disuse, reflex sympathetic dystrophy syndrome, regional osteoporosis, osteomalacia, bone loss associated with joint replacement, HIV associated bone loss, bone loss associated with loss of growth hormone, bone loss associated with cystic fibrosis, chemotherapy associated bone loss, tumor induced bone loss, cancer-related bone loss, hormone ablative bone
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loss, multiple myeloma, drug-induced bone loss, anorexia nervosa, disease associated facial bone loss, disease associated cranial bone loss, disease associated bone loss of the jaw, disease associated bone loss of the skull, bone loss associated with aging, facial bone loss associated with aging, cranial bone loss associated with aging, jaw bone loss associated with aging, skull bone loss associated with aging, and bone loss associated with space travel.

12. The antibody or fragment for use of any one of the preceding claims, wherein the human is a post-menopausal woman.

13. The antibody or fragment for use of any one of the preceding claims, wherein the human is suffering from osteoporosis.

Patentansprüche

1. Anti-Sclerostin-Antikörper oder ein Fragment hiervon zur Verwendung in einer Methode zur Hemmung des Knochenabbaus in einem Menschen, die Methode umfassend die Verabreichung eines solchen Anti-Sclerostin-Antikörpers oder eines Fragments hiervon an einen Menschen in einer Menge zwischen 1 mg/kg und 5 mg/kg, wobei der Anti-Sclerostin-Antikörper oder ein Fragment hiervon eine Bindungsaffinität für Sclerostin der SEQ ID Nr. 1 von weniger als oder gleich 1×10^{-7} M zeigt und die Bindung zu Sclerostin eines Antikörpers, der CDR Sequenzen von SEQ ID Nr. 245, 246, 247, 78, 79 und 80 oder CDR Sequenzen von SEQ ID Nr. 284, 285, 286, 296, 297 und 298 umfasst, querverblockiert oder selbst von einer Bindung an das Sclerostin durch diesen Antikörper querverblockiert ist, wobei

- SEQ ID Nr. 245 = Asp Tyr Asn Met His;
- SEQ ID Nr.246 = Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys Gly;
- SEQ ID Nr.247 = Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val;
- SEQ ID Nr. 78 = Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn;
- SEQ ID Nr. 79 = Tyr Thr Ser Arg Leu Leu Ser; and
- SEQ ID Nr. 80 = Gln Gln Gly Asp Thr Leu Pro Tyr Thr; and
- SEQ ID Nr. 284 = Arg Ala Ser Ser Ser Val Thr Ser Ser Tyr Leu Asn;
- SEQ ID Nr. 285 = Ser Thr Ser Asn Leu Ala Ser;
- SEQ ID Nr. 286 = Gln Gln Tyr Asp Phe Phe Pro Ser Thr;
- SEQ ID Nr. 296 = Asp Tyr Tyr Met Asn;
- SEQ ID Nr. 297 = Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe Lys Gly; und
- SEQ ID Nr. 298 = Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp.

2. Antikörper oder Fragment zur Verwendung nach Anspruch 1, wobei die verabreichte Menge an Anti-Sclerostin-Antikörper zwischen 1 mg/kg und 3 mg/kg liegt.

3. Antikörper oder Fragment zur Verwendung nach Anspruch 1 oder 2, wobei die verabreichte Menge an Anti-Sclerostin-Antikörper bei etwa 2 mg/kg liegt.

4. Antikörper oder Fragment zur Verwendung nach Anspruch 1 oder 2, wobei die verabreichte Menge an Anti-Sclerostin-Antikörper bei etwa 3 mg/kg liegt.

5. Antikörper oder Fragment zur Verwendung nach Anspruch 1, wobei die Methode die Verabreichung eines Anti-Sclerostin-Antikörpers an einen Menschen mit einer Dosis von 70 bis 450 mg umfasst.

6. Antikörper oder Fragment zur Verwendung nach Anspruch 1, wobei die Methode die Verabreichung mit einer Dosis von 140 mg umfasst.

7. Antikörper oder Fragment zur Verwendung nach Anspruch 1, wobei die Methode die Verabreichung mit einer Dosis von 210 mg umfasst.

8. Antikörper oder Fragment zur Verwendung nach einem der vorhergehenden Ansprüche, wobei die Menge des Anti-Sclerostin-Antikörpers der Person einmal alle zwei Wochen verabreicht wird.

9. Antikörper oder Fragment zur Verwendung nach einem der Ansprüche 1 bis 7, wobei der Anti-Sclerostin-Antikörper der Person einmal monatlich verabreicht wird.

10. Antikörper oder Fragment zur Verwendung nach einem der vorhergehenden Ansprüche, wobei der Antikörper ein menschlicher Antikörper, ein humanisierter Antikörper, ein monoklonaler Antikörper oder ein chimärer Antikörper ist.

11. Antikörper oder Fragment zur Verwendung nach einem der vorhergehenden Ansprüche, wobei der Mensch an einer Knochen bezogenen Erkrankung leidet, die ausgewählt ist aus einer Gruppe, die Achondroplasie, kleidokraniale Dysostose, Enchondromatose, fibröse Dysplasie, die Gaucher-Krankheit, hypophosphatämische Knochenerweichung, das Marfan-Syndrom, multiple erbliche Exotosen, Neurofibromatose, Osteogenesis Imperfecta, Osteopetose, Osteopoikilose, sklerotische Läsionen, Pseudoarthrose, Pyogene Osteomyelitis, Parodontalerkrankung, anti-epileptischer Drogeninduzierter Knochenverlust, primären und sekundären Hyperparathyreoidismus, familiäre Hyperparathyreoidismus-Syndrome, durch Schwerelosigkeit induzierter Knochenverlust, Osteoporose bei Männern, postmenopausaler Knochenverlust, Arthrose, renale Osteodystrophie, infiltrative Erkrankungen der Knochen, oralen Knochenverlust, Osteonekrose des Kiefers, die juvenile Paget-Krankheit, Melorheostose, metabolische Knochenkrankheiten, Mastozytose, Sichelzellenanämie, Knochenverlust bedingt durch Organtransplantation, Knochenverlust bedingt durch Nierentransplantation, systemischer Lupus erythematodes, Morbus Bechterew, Epilepsie, juvenile Arthritiden, Thalassämie, Mukopolysaccharidosen, Morbus Fabry, das Turner-Syndrom, das Down-Syndrom, das Klinefelter-Syndrom, Lepra, die Perthes-Krankheit, idiopathische Skoliose bei Heranwachsenden, frühkindliche multisystemische Entzündungen, das Winchester-Syndrom, die Menkes-Krankheit, Morbus Wilson, ischämische Knochenenerkrankungen, die Legg-Calve-Perthes-Krankheit, regional wandernde Osteoporose, Blutarmut, durch Steroide hervorgerufene Zustände, Glukokortikoid-induzierten Knochenverlust, Heparin-induzierten Knochenverlust, Knochenmark-Erkrankungen, Skorbut, Mangelernährung, Calciummangel, Osteoporose, Osteopenie, Alkoholismus, chronische Lebererkrankung, postmenopausale Zustände, chronisch entzündliche Erkrankungen, rheumatoide Arthritis, entzündliche Darmerkrankungen, Colitis ulcerosa, entzündliche Kolitis, Morbus Crohn, Oligomenorrhoe, Amenorrhoe, Schwangerschaft, Diabetes Mellitus, Hyperthyreose, Erkrankungen der Schilddrüse, Erkrankungen der Nebenschilddrüse, Morbus Cushing, Akromegalie, Hypogonadismus, Immobilisation oder Nichtnutzung, das sympathetische Reflexdystrophie-Syndrom, regionale Osteoporose, Osteomalazie, Knochenverlust im Zusammenhang mit Gelenkersatz, HIV-bedingter Knochenverlust, Knochenverlust bei Verlust von Wachstumshormonen, Knochenverlust bei Mukoviszidose, Knochenverlust im Zusammenhang mit einer Chemotherapie, tumorinduzierter Knochenverlust, krebsbedingter Knochenverlust, hormonell bedingter ablativer Knochenverlust, Multiples Myelom, Arzneimittel-induzierter Knochenverlust, Magersucht, Krankheit bei Verlust von Gesichtsknochen, Krankheit bei Verlust von Schädelknochen, Krankheit bei Verlust von Kieferknochen, Krankheit bei Verlust von Knochen des Schädels mit dem Altern verbundener Knochenverlust, mit dem Altern verbundener Verlust von Gesichtsknochen, mit dem Altern verbundener Verlust von Schädelknochen, mit dem Altern verbundener Verlust von Kieferknochen, mit dem Altern verbundener Verlust von Knochen des Schädels, sowie Knochenabbau im Zusammenhang mit der Raumfahrt umfasst.

12. Antikörper oder Fragment zur Verwendung nach einem der vorhergehenden Ansprüche, wobei der Mensch eine Frau nach den Wechseljahren ist.

13. Antikörper oder Fragment zur Verwendung nach einem der vorhergehenden Ansprüche, wobei der Mensch an Osteoporose leidet.

Revendications

1. Anticorps anti-sclérostine, ou fragment d'un tel anticorps, pour utilisation dans un procédé d'inhibition de la résorption osseuse chez un humain, lequel procédé comporte le fait d'administrer audit humain ledit anticorps anti-sclérostine ou fragment d'un tel anticorps en une quantité de 1 mg/kg à 5 mg/kg, lequel anticorps anti-sclérostine ou fragment d'un tel anticorps montre, vis-à-vis de la sclérostine de Séquence N° 1, une affinité de liaison inférieure ou égale à 1.10^7 M et empêche, en réaction croisée, la liaison à la sclérostine d'un anticorps comprenant les régions CDR de Séquences N° 245, 246, 247, 78, 79 et 80 ou les régions CDR de Séquences N° 284, 285, 286, 296, 297 et 298, ou bien est empêché par un tel anticorps, en réaction croisée, de se lier à la sclérostine, étant entendu que :

- la Séquence N° 245 est : Asp Tyr Asn Met His ;
- la Séquence N° 246 est : Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys Gly ;
- la Séquence N° 247 est : Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val ;
- la Séquence N° 78 est : Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn ;
- la Séquence N° 79 est : Tyr Thr Ser Arg Leu Leu Ser ;
- la Séquence N° 80 est : Gln Gln Gly Asp Thr Leu Pro Tyr Thr ; et que

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- la Séquence N° 284 est : Arg Ala Ser Ser Ser Val Thr Ser Ser Tyr Leu Asn ;
- la Séquence N° 285 est : Ser Thr Ser Asn Leu Ala Ser ;
- la Séquence N° 286 est : Gln Gln Tyr Asp Phe Phe Pro Ser Thr ;
- la Séquence N° 296 est : Asp Tyr Tyr Met Asn ;
- la Séquence N° 297 est : Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe Lys Gly ;
- la Séquence N° 298 est : Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp.

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2. Anticorps ou fragment pour utilisation conforme à la revendication 1, dans laquelle la quantité d'anticorps anti-sclérostine administrée vaut de 1 mg/kg à 3 mg/kg.
3. Anticorps ou fragment pour utilisation conforme à la revendication 1 ou 2, dans laquelle la quantité d'anticorps anti-sclérostine administrée vaut à peu près 2 mg/kg.
4. Anticorps ou fragment pour utilisation conforme à la revendication 1 ou 2, dans laquelle la quantité d'anticorps anti-sclérostine administrée vaut à peu près 3 mg/kg.
5. Anticorps ou fragment pour utilisation conforme à la revendication 1, dans laquelle le procédé comporte le fait d'administrer à un humain l'anticorps anti-sclérostine en une dose de 70 à 450 mg.
6. Anticorps ou fragment pour utilisation conforme à la revendication 1, dans laquelle le procédé comporte le fait d'administrer une dose d'à peu près 140 mg.
7. Anticorps ou fragment pour utilisation conforme à la revendication 1, dans laquelle le procédé comporte le fait d'administrer une dose d'à peu près 210 mg.
8. Anticorps ou fragment pour utilisation conforme à l'une des revendications précédentes, dans laquelle la quantité d'anticorps anti-sclérostine est administrée au sujet une fois toutes les deux semaines.
9. Anticorps ou fragment pour utilisation conforme à l'une des revendications 1 à 7, dans laquelle la quantité d'anticorps anti-sclérostine est administrée au sujet une fois par mois.
10. Anticorps ou fragment pour utilisation conforme à l'une des revendications précédentes, lequel anticorps est un anticorps humain, un anticorps humanisé, un anticorps monoclonal, ou un anticorps chimérique.
11. Anticorps ou fragment pour utilisation conforme à l'une des revendications précédentes, dans laquelle le sujet humain souffre d'un trouble en rapport avec les os, choisi dans l'ensemble constitué par les suivants : achondroplasie, dysostose cléidocrânienne, enchondromatose, dysplasie fibreuse, maladie de Gaucher, rachitisme hypo-phosphatémique, syndrome de Marfan, exostoses multiples héréditaires, neurofibromatose, ostéogenèse imparfaite, ostéopétrose, ostéopoécilie, lésions sclérotiques, pseudarthrose, ostéomyélite à pyogène, parodontolyse, perte osseuse induite par antiépileptique, hyperparathyroïdisme primitif ou secondaire, syndromes d'hyperparathyroïdisme familial, perte osseuse induite par l'apesanteur, ostéoporose masculine, perte osseuse post-ménopausique, arthrose, ostéodystrophie rénale, maladies infiltrantes des os, perte osseuse orale, ostéonécrose de la mâchoire, maladie de Paget juvénile, mélorhéostose, maladies osseuses métaboliques, mastocytose, anémie falciforme, perte osseuse en relation avec une transplantation d'organe, perte osseuse en relation avec une transplantation de rein, lupus érythémateux aigu disséminé, spondylarthrite ankylosante, épilepsie, arthrite juvénile, thalassémie, mucopolysaccharidoses, maladie de Fabry, syndrome de Turner, syndrome de Down, syndrome de Klinefelter, lèpre, maladie de Perthes, scoliose idiopathique de l'adolescent, maladie inflammatoire multisystémique néonatale, syndrome de Winchester, maladie de Menkès, maladie de Wilson, maladie ischémique des os, maladie de Legg-Calvé-Perthes, ostéoporose migratoire régionale, états d'anémie, états induits par stéroïdes, perte osseuse induite par glucocorticoïdes, perte osseuse induite par héparine, troubles de la moelle osseuse, scorbut, malnutrition, manque de calcium, ostéoporose, ostéopénie, alcoolisme, maladie hépatique chronique, état post-ménopausique, états inflammatoires chroniques, polyarthrite rhumatoïde, affection intestinale inflammatoire, colite ulcéreuse, colite inflammatoire, maladie de Crohn, oligoménorrhée, aménorrhée, grossesse, diabète sucré, hyperthyroïdie, troubles thyroïdiens, troubles parathyroïdiens, maladie ou syndrome de Cushing, acromégalie, hypogonadisme, immobilisation ou inactivité, syndrome de dystrophie sympathique réflexe, ostéoporose régionale, ostéomalacie, perte osseuse associée à la mise en place d'une prothèse d'articulation, perte osseuse associée à une infection par VIH, perte osseuse associée à un déficit d'hormone de croissance, perte osseuse associée à la mucoviscidose, perte osseuse associée à une chimiothérapie, perte osseuse induite par une tumeur, perte osseuse en rapport avec un cancer, perte osseuse en

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rapport avec une hormonothérapie suppressive, myélome multiple, perte osseuse induite par un médicament, anorexie nerveuse, perte osseuse faciale associée à une maladie, perte osseuse crânienne associée à une maladie, perte osseuse à la mâchoire associée à une maladie, perte osseuse au crâne associée à une maladie, perte osseuse associée au vieillissement, perte osseuse faciale associée au vieillissement, perte osseuse crânienne associée au vieillissement, perte osseuse à la mâchoire associée au vieillissement, perte osseuse au crâne associée au vieillissement, et perte osseuse associée à un voyage spatial.

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12. Anticorps ou fragment pour utilisation conforme à l'une des revendications précédentes, dans laquelle le sujet humain est une femme ménopausée.

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13. Anticorps ou fragment pour utilisation conforme à l'une des revendications précédentes, dans laquelle le sujet humain souffre d'ostéoporose.

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Dose Related Increase Observed in PINP Following Single-dose SC Administration of Scl-Mab to Healthy Postmenopausal Women

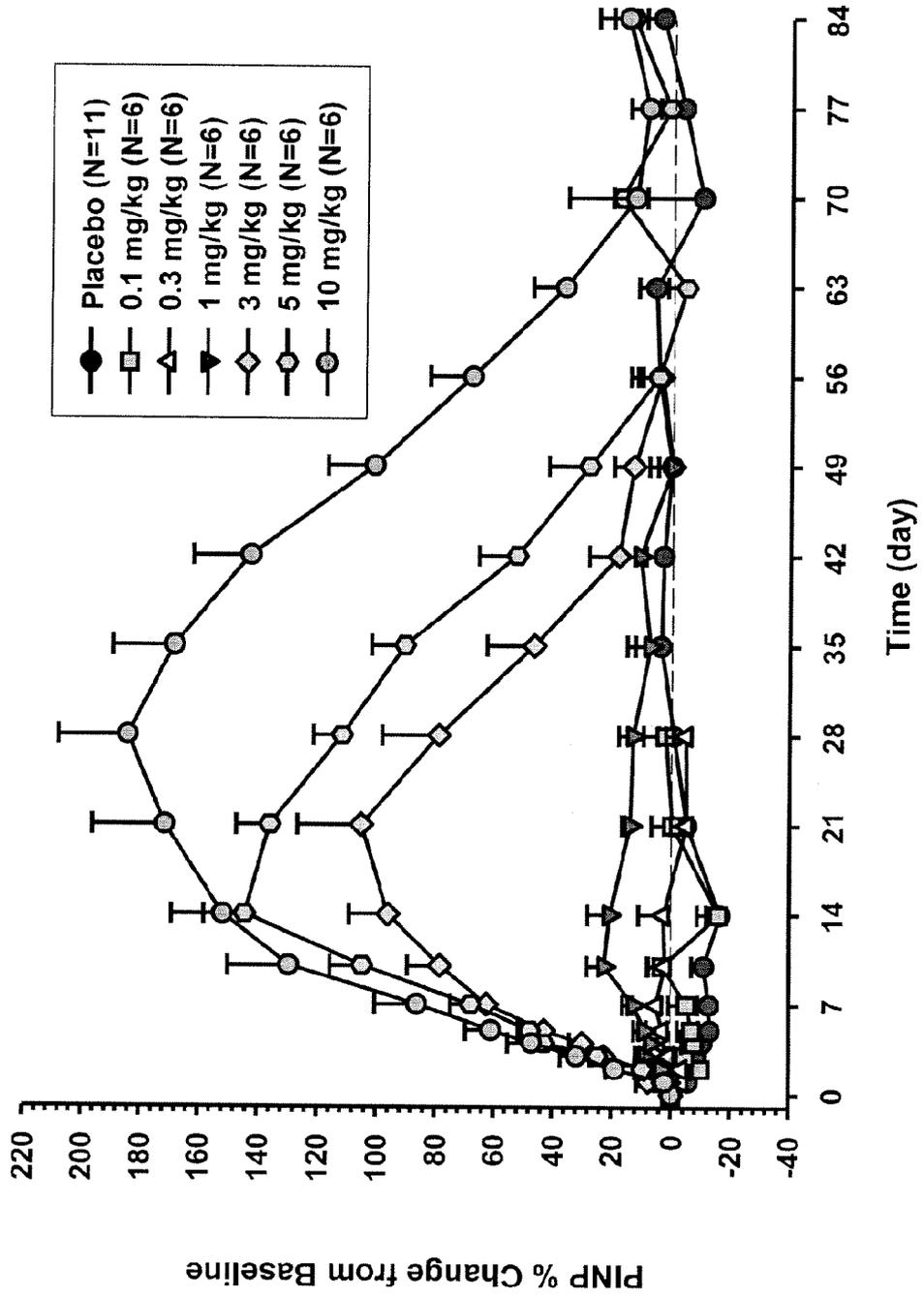
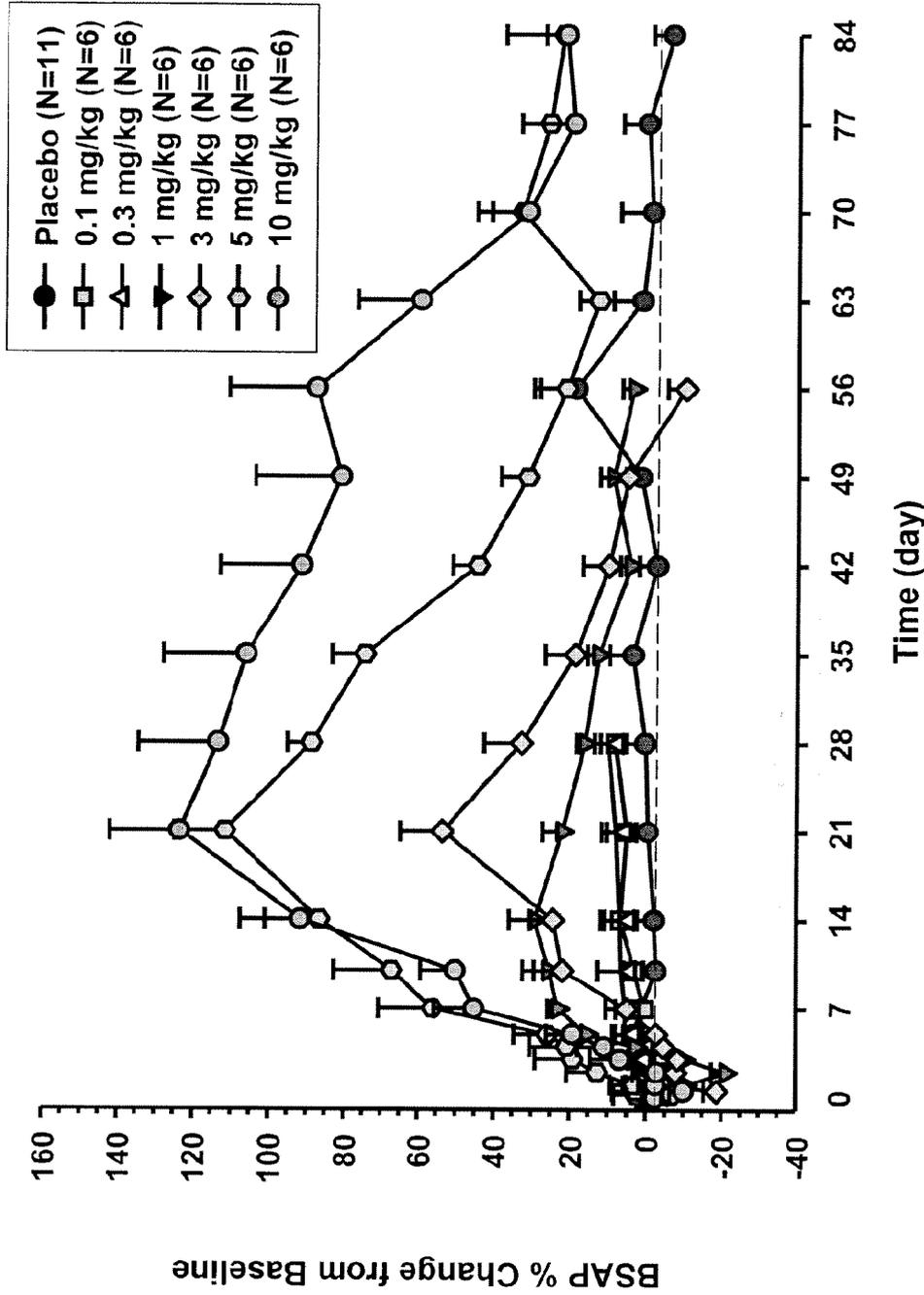


FIGURE 1

Dose Related Increase Observed in BSAP Following Single-dose SC Administration of Scl-Mab to Healthy Postmenopausal Women



Dose Related Increase Observed in Osteocalcin Following Single-dose SC Administration of Scl-Mab to Healthy Postmenopausal Women

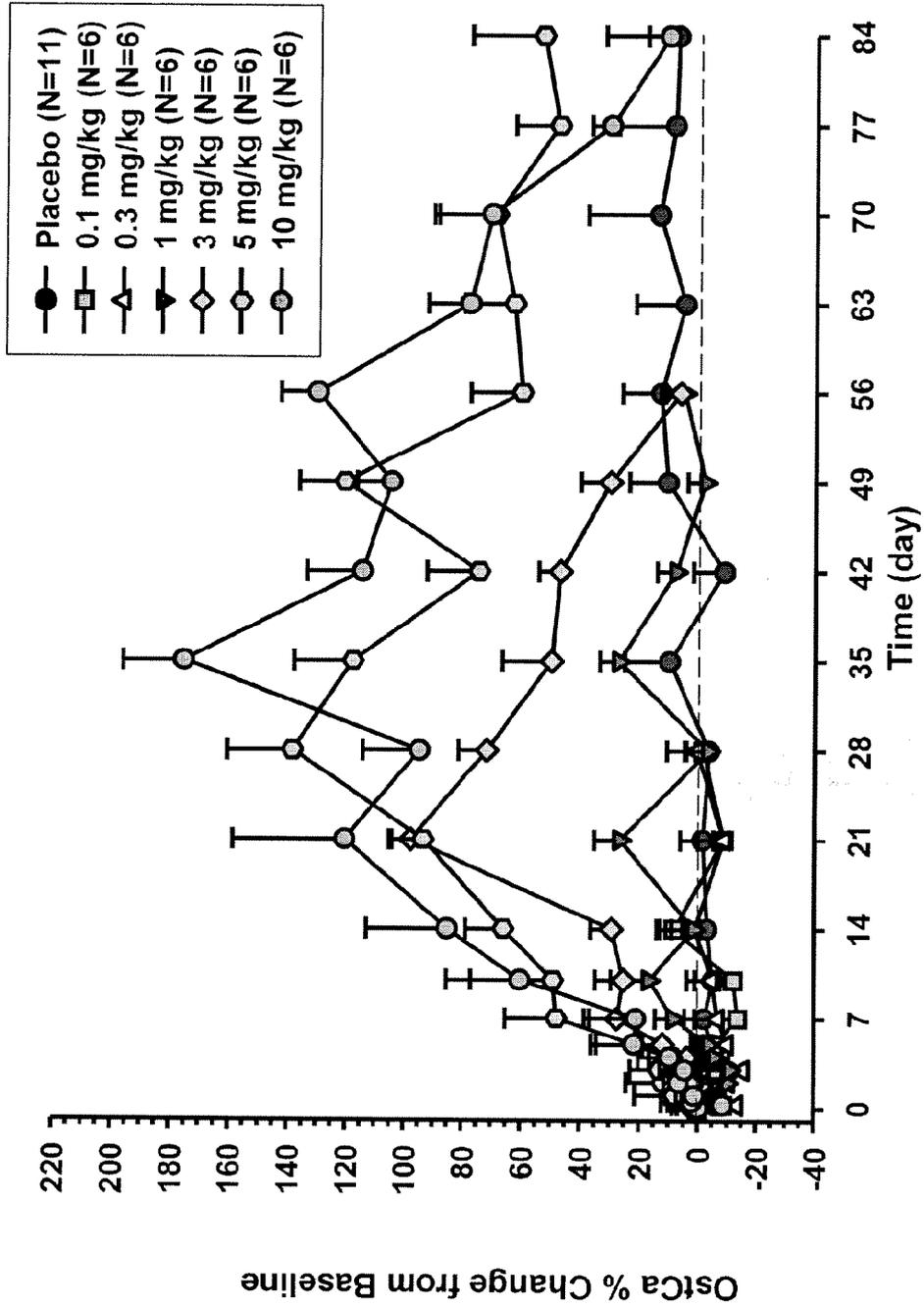


FIGURE 3

Dose Related Decrease in sCTX Following Single-dose SC Administration of Scl-Mab to Healthy Postmenopausal Women

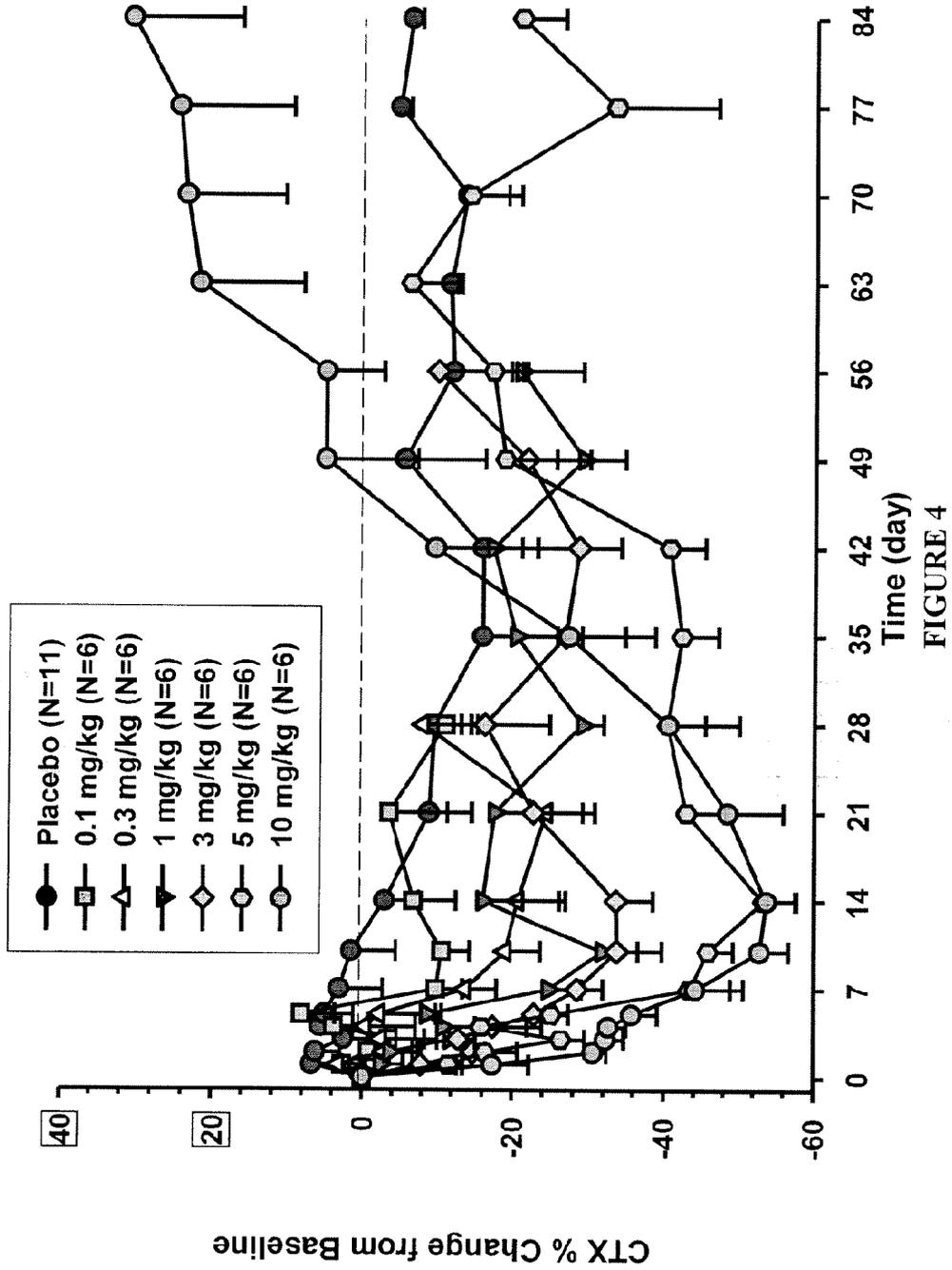


FIGURE 4

Large Anabolic Window Following Single SC Doses of 5 & 10 mg/kg Scl-Mab to Healthy Postmenopausal Women

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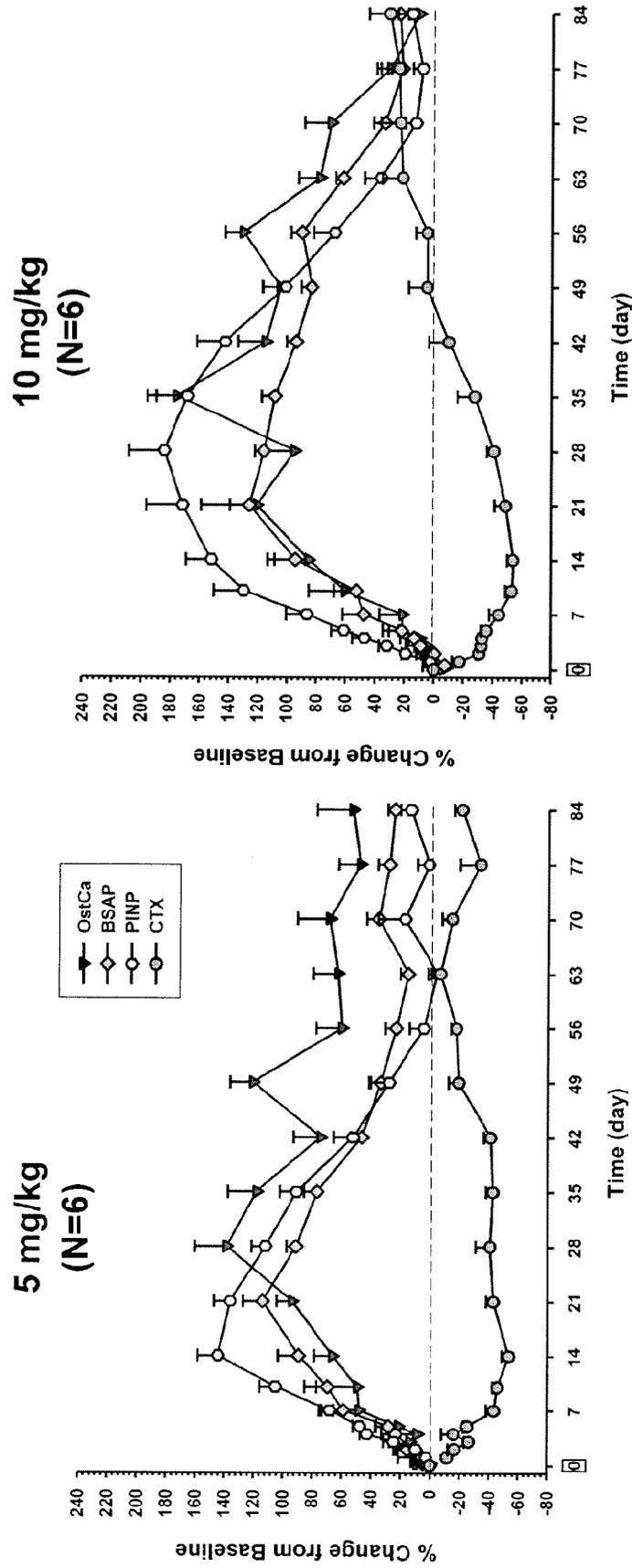


FIGURE 5

No Clinically Significant Changes in Serum Calcium Following Single-dose SC Administration of Scl-Mab to Healthy Postmenopausal Women

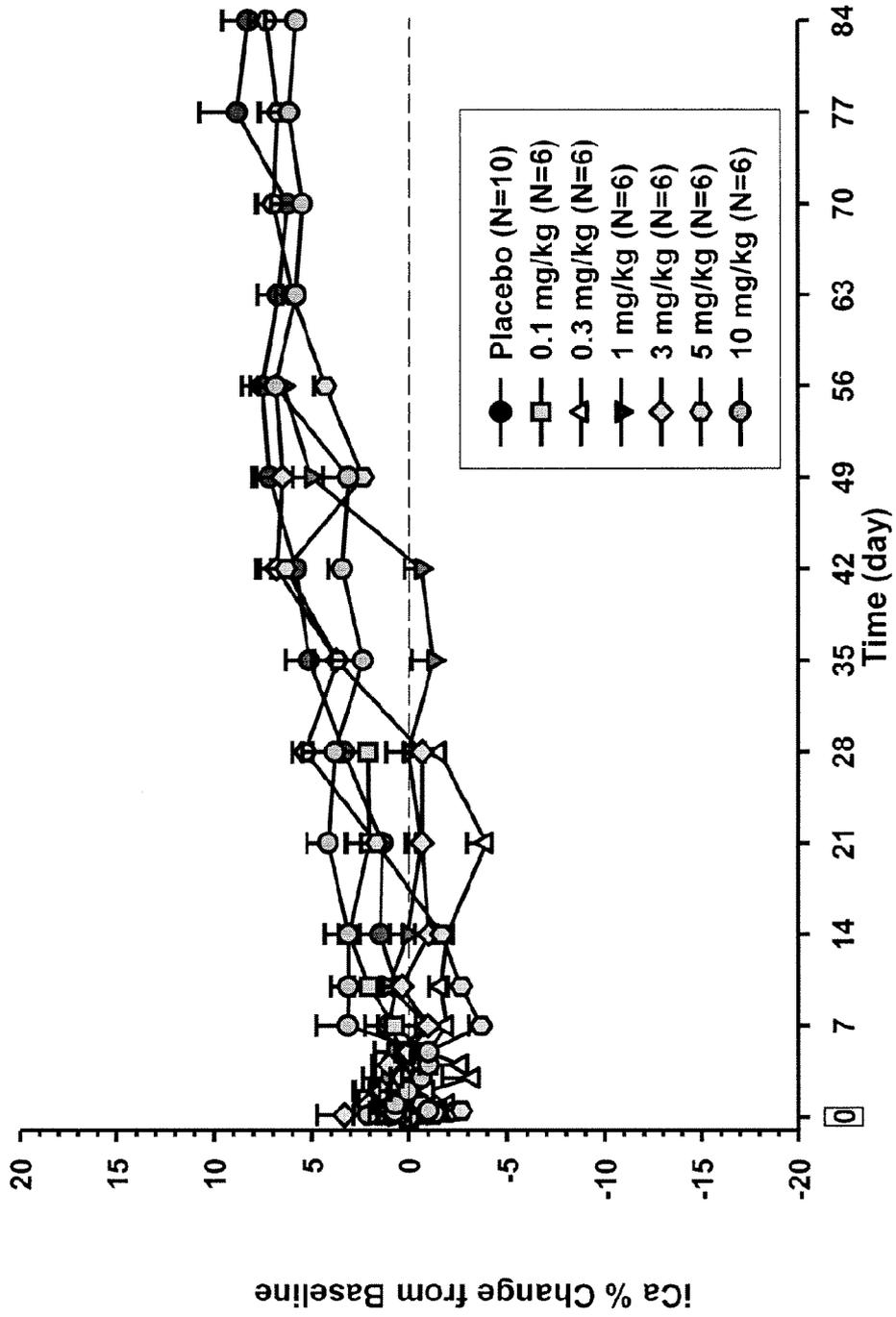


FIGURE 6

Single Doses of Scl-Mab Resulted in an Increase in BMD in Healthy Postmenopausal Women

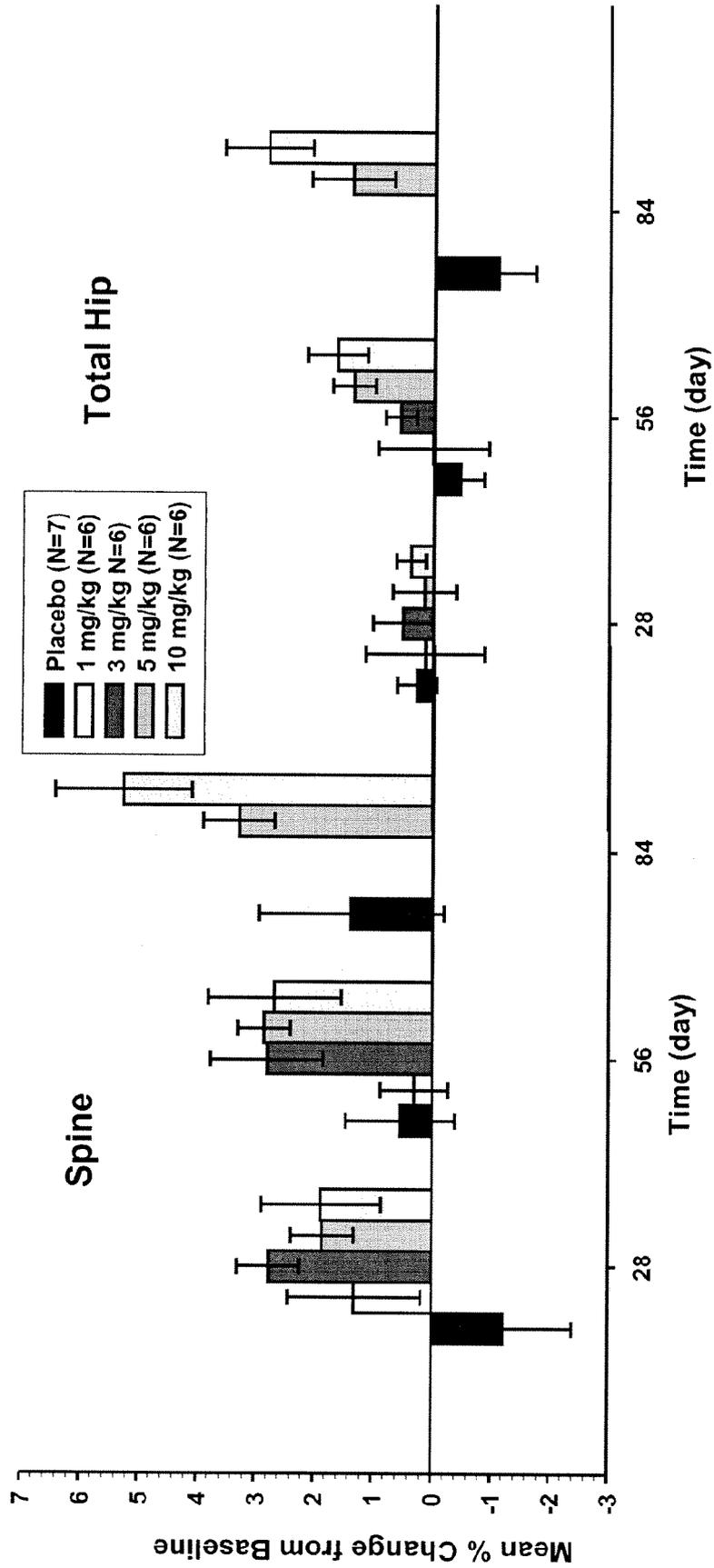


FIGURE 7

REFERENCES CITED IN THE DESCRIPTION

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