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Delivery of therapeutic agents by a collagen binding protein

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(54) **DELIVERY OF THERAPEUTIC AGENTS BY A COLLAGEN BINDING PROTEIN**

(58) **Field of Classification Search**
None
See application file for complete search history.

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(57) **ABSTRACT**

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Methods of delivering therapeutic agents by administering compositions including a bacterial collagen-binding polypeptide segment linked to the therapeutic agent to subjects in need of treatment with the therapeutic agent are provided. Methods of treating hyperparathyroidism, and hair loss using compositions comprising a collagen binding polypeptide and a PTH/PTHrP receptor agonist are provided. In addition, methods of reducing hair regrowth by administering a composition including a collagen binding polypeptide and a PTH/PTHrP receptor antagonist are provided.

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Fig. 1

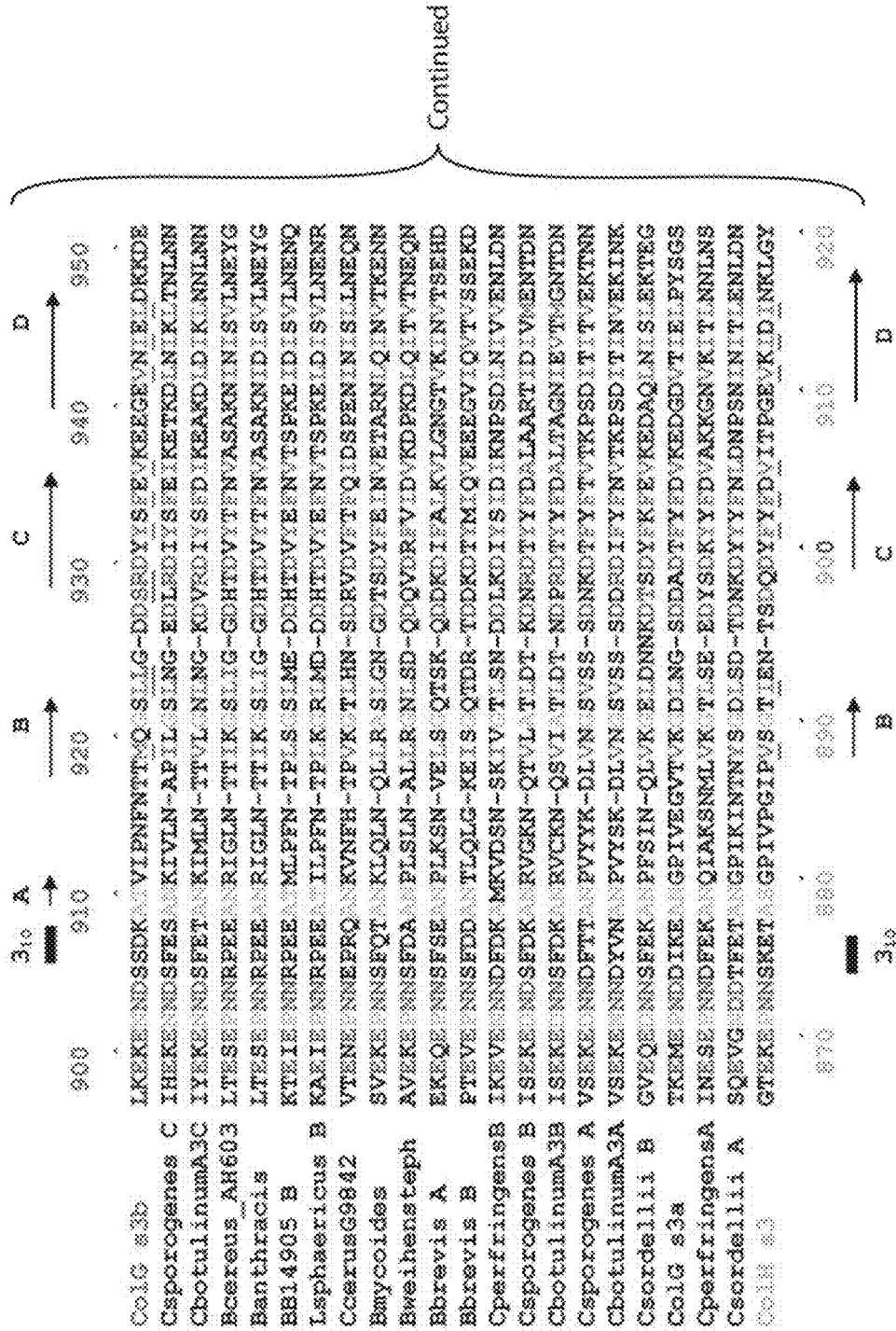


Fig. 1 (Continued)

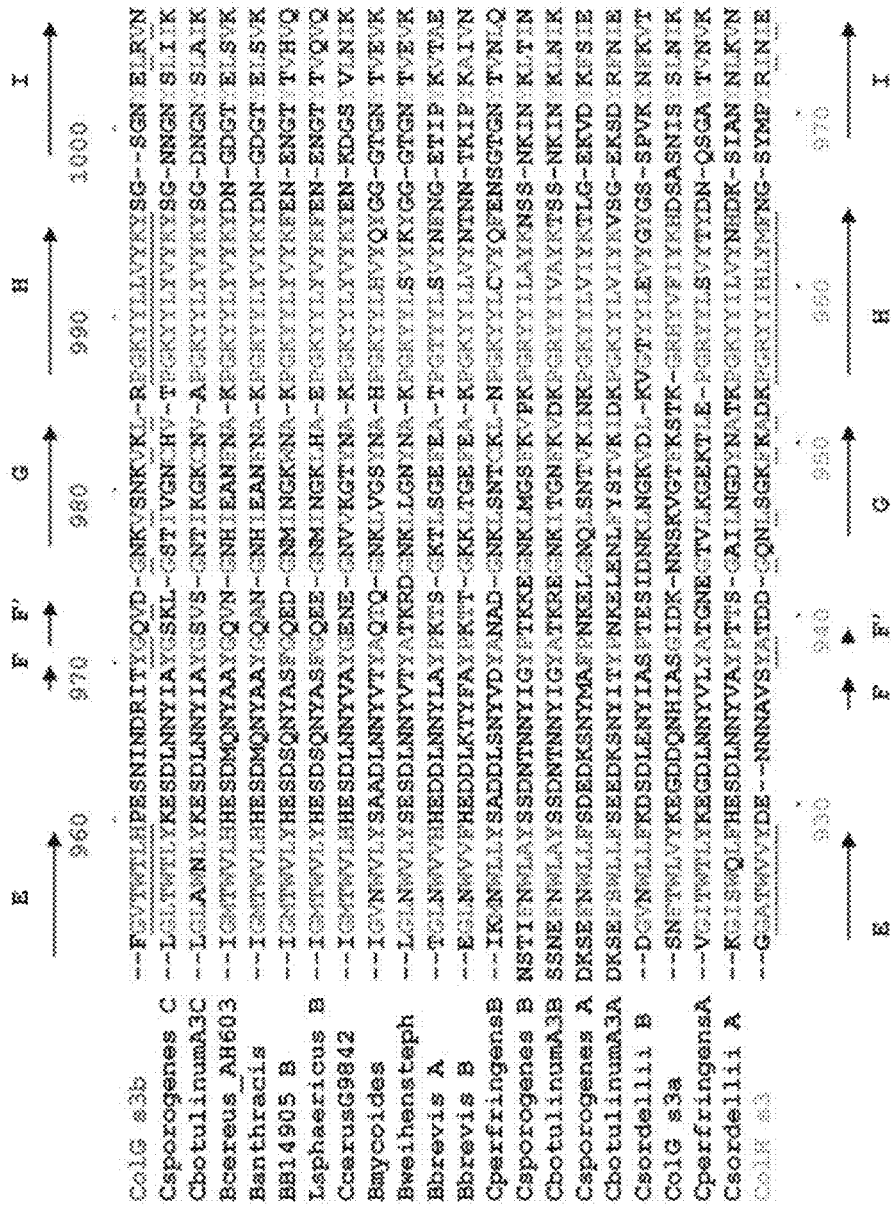


Fig. 2

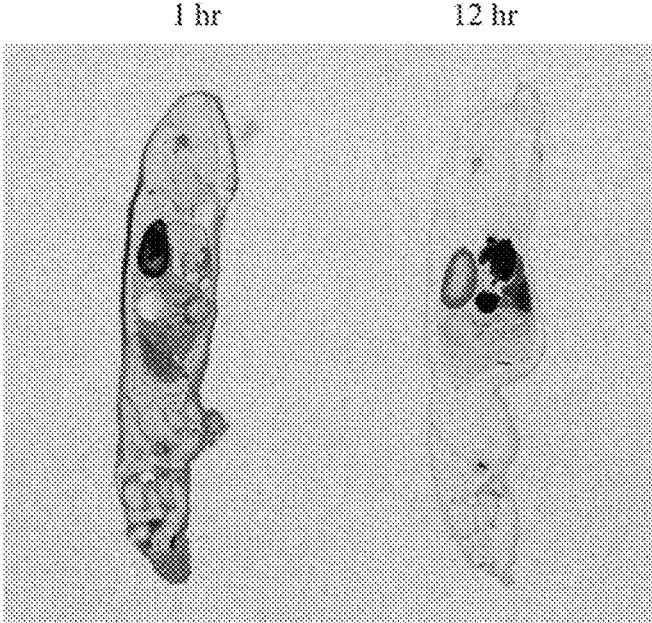


Fig. 3

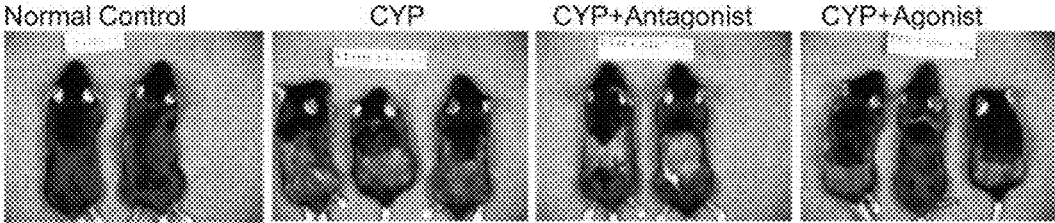


Fig. 4

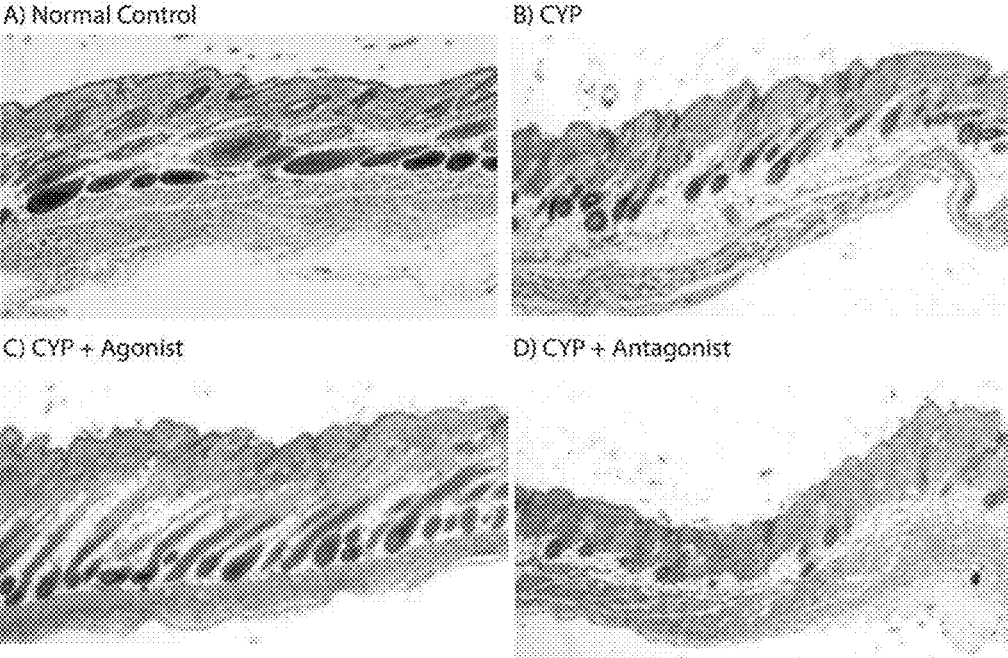


Fig. 5

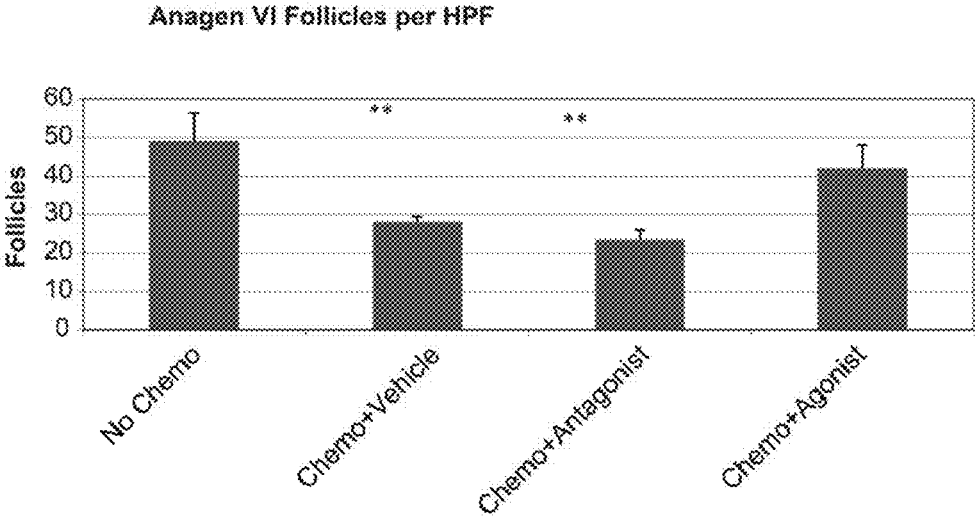
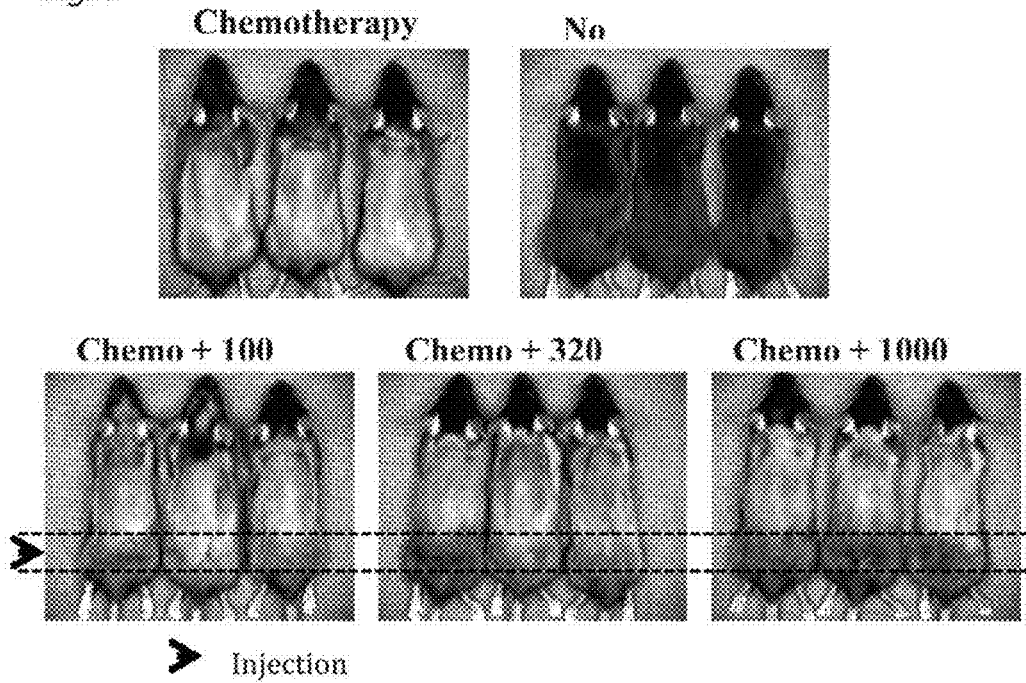


Fig. 6



Grey Scale Analysis at Injection Site

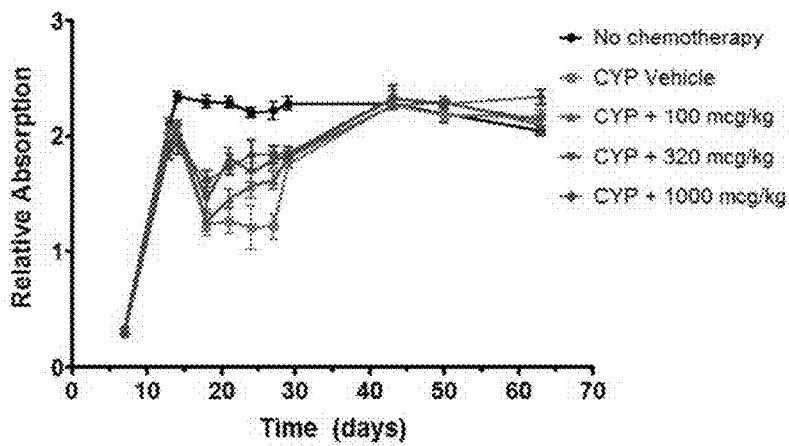


Fig. 7

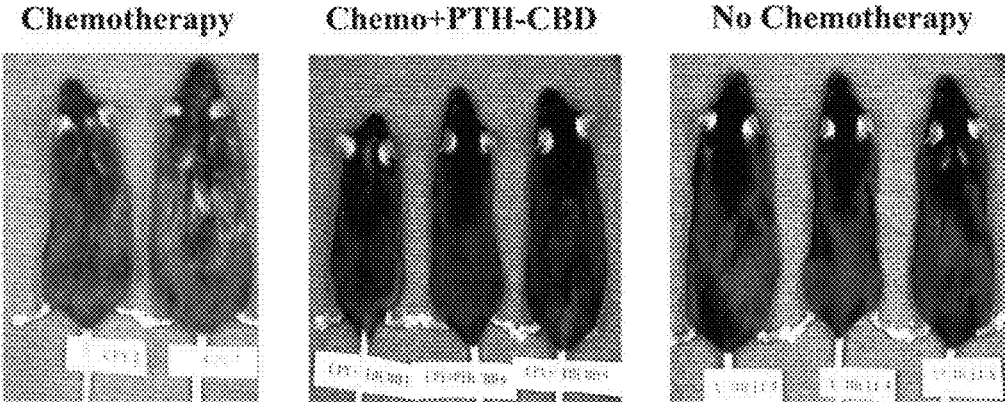


Fig. 8

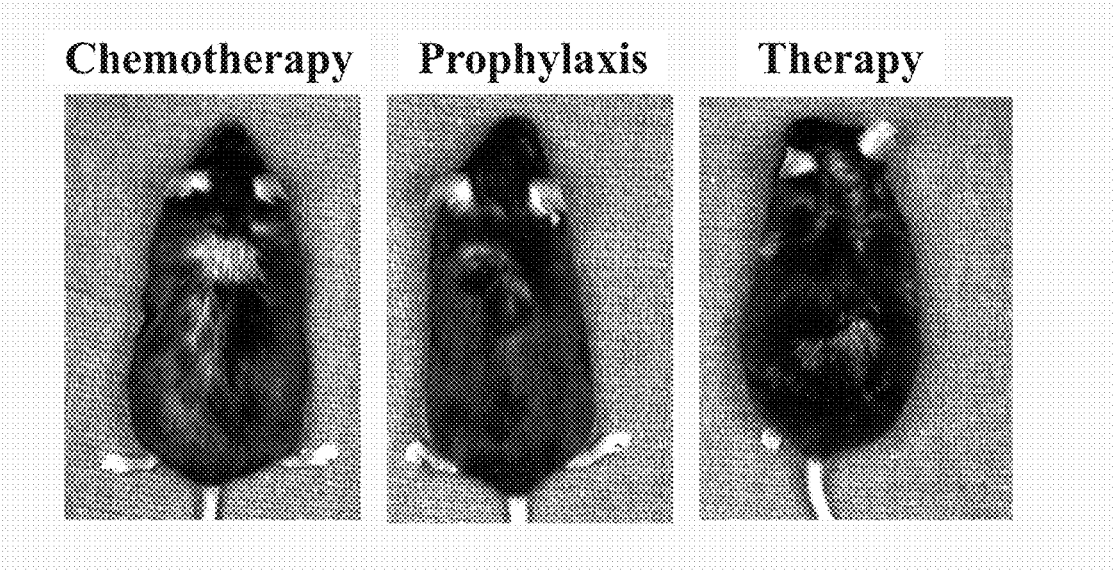
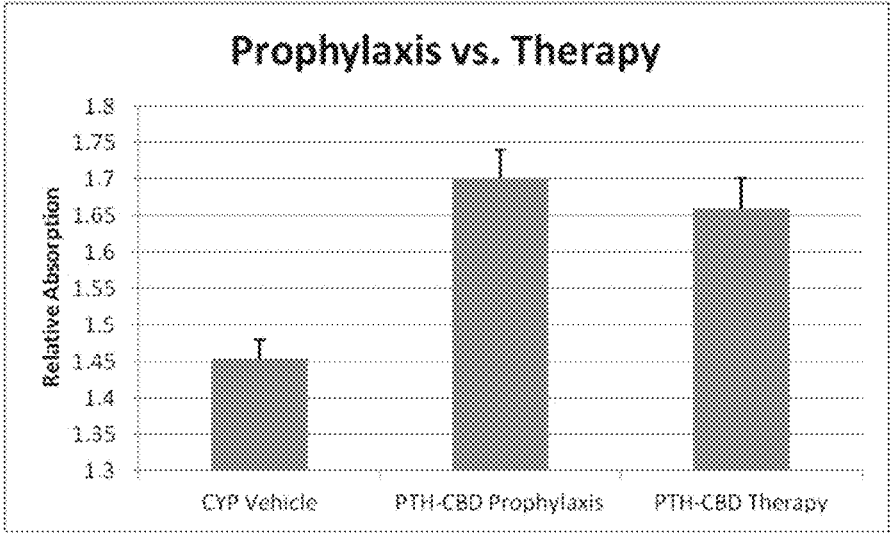


Fig. 9

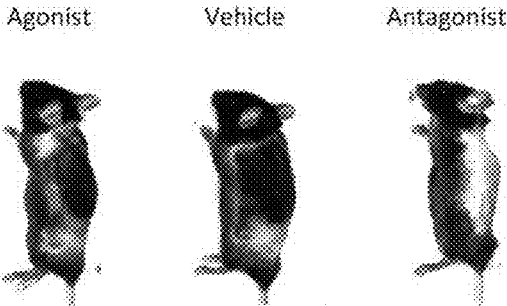


Fig. 10

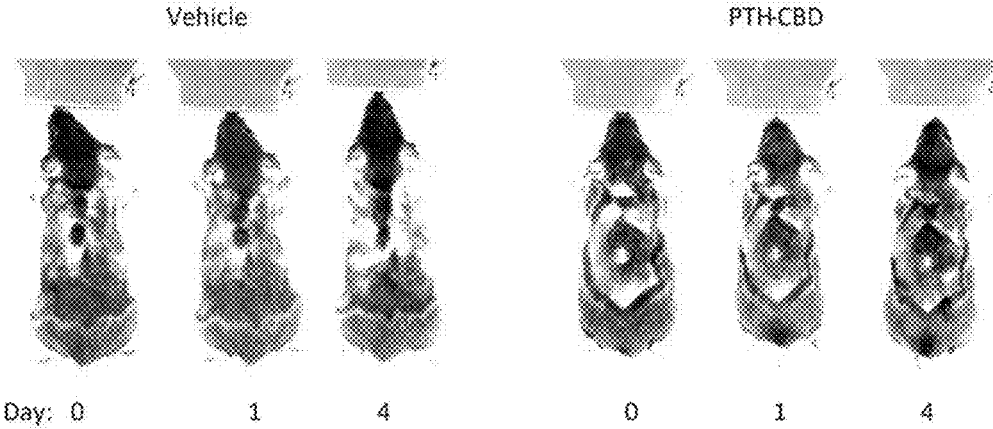
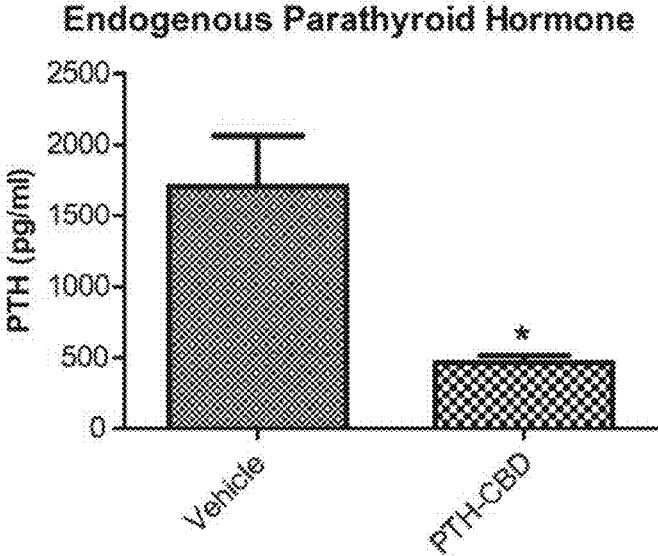


Fig. 11



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DELIVERY OF THERAPEUTIC AGENTS BY A COLLAGEN BINDING PROTEIN

CROSS-REFERENCE TO RELATED APPLICATIONS

This patent application is a national stage filing under 35 U.S.C. of International Application No. PCT/US2013/025541, filed Feb. 11, 2013, which claims the benefit of priority of U.S. Provisional Patent Application No. 61/596,869, filed Feb. 9, 2012, and of International Application No. PCT/US2012/069831, filed Dec. 14, 2012, all of which are incorporated herein by reference in their entireties.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with United States government support awarded by the National Institutes of Health grant number NCRR COBRE 8P30GM103450 and INBRE GM103429. The United States may have certain rights in this invention.

SEQUENCE LISTING

A Sequence Listing accompanies this application and is incorporated herein by reference in its entirety. The Sequence Listing was filed with the application as a text file on Feb. 11, 2013.

INTRODUCTION

Delivery of therapeutic agents to sites within the body of a subject where a particular therapeutic agent is needed in order to be effective is a developing area. Such delivery systems will allow more efficient use of therapeutic agents while reducing toxicity caused by some therapeutic agents. Use of targeted liposomes or polypeptides, such as antibodies, to target therapeutic agents to particular sites within the body has proved successful, but additional delivery agents are needed.

Alopecia (hair loss) is a psychologically and emotionally distressing event with multiple causes. Alopecia occurs most commonly in male-pattern baldness, affecting approximately two thirds of males by age 35; a similar pattern of hair loss can be observed in females with polycystic ovarian syndrome. In both of these disorders, the hair loss is androgen mediated. Alopecia can also occur as an autoimmune disease, termed alopecia areata; a disorder which affects 1.7% of the population. It can occur as a side-effect of medical treatments, particularly in chemotherapy, with 65-85% of chemotherapy patients experiencing some degree of alopecia. Psychological consequences of hair loss have been well studied in the chemotherapy setting. Chemotherapy-induced alopecia (CIA) can result in anxiety, depression, a negative body image, lowered self-esteem and a reduced sense of well-being. In fact, 47-58% of female cancer patients consider hair loss to be the most traumatic aspect of chemotherapy, and 8% would decline treatment for fear of hair loss. In addition to these studies in chemotherapy patients, evidence exists in other forms of alopecia to support therapy to reduce psychological consequences of hair loss. Thus a new treatment to stop hair loss or speed hair regrowth would be beneficial.

While drugs with mild anti-androgenic effects (i.e. spironolactone) had been used with limited success as therapy for alopecia, the first effective medication for alo-

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pecia was minoxidil (Rogaine). This antihypertensive has an observed side-effect of causing hair growth, and is now used as topical therapy for many forms of alopecia. However, responses are incomplete, with some subjects showing only slowing of hair loss rather than actual regrowth. Finasteride (Propecia) is a newer agent that blocks conversion of testosterone to dihydrotestosterone, resulting in improvements in androgenic alopecia at the expense of partial systemic androgen blockade. However, response rates with long-term (10 years) therapy are only around 50%. Overall, despite considerable research in this area, there is still no adequate therapy for hair loss.

In addition, unwanted hair growth is a cosmetic issue many people deal with on a regular basis. Unwanted hair growth on the face, legs, arms, chest or back is a growing cosmetic problem. Many people use laser therapy, waxing or other therapies to remove unwanted hair. There are currently no topical pharmaceuticals to limit hair growth.

SUMMARY

Provided herein are methods of delivering therapeutic agents by administering compositions including a bacterial collagen-binding polypeptide segment linked to the therapeutic agent to subjects in need of treatment with the therapeutic agent.

In one aspect, methods of treating hyperparathyroidism by administering a composition comprising a bacterial collagen-binding polypeptide segment linked to a PTH/PTHrP receptor agonist to a subject are provided.

In a further aspect, methods of slowing hair growth or regrowth after removal by administering a composition comprising a bacterial collagen-binding polypeptide segment linked to a PTH/PTHrP receptor antagonist to a subject are provided.

In a still further aspect, methods of increasing hair growth or the speed of hair re-growth after removal or loss by administering a composition comprising a bacterial collagen-binding polypeptide segment linked to a PTH/PTHrP receptor agonist to a subject are provided.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a sequence alignment showing the alignment of several M9B bacterial collagenases from the *Bacillus* and *Clostridium* families. The sequences are also provided in the Sequence Listing, filed herewith as follows: ColG s3b (SEQ ID NO: 13); Csporogenes C (SEQ ID NO: 14); CbotulinumA3C (SEQ ID NO: 15); Bcereus_AH603 (SEQ ID NO: 16); Banthraxis (SEQ ID NO: 17); BB14905 B (SEQ ID NO: 18); Lsphaericus B (SEQ ID NO: 19); CcereusG9842 (SEQ ID NO: 20); Bmycoides (SEQ ID NO: 21); Bweihensteph (SEQ ID NO: 22); Bbrevis A (SEQ ID NO: 23); Bbrevis B (SEQ ID NO: 24); CperfringensB (SEQ ID NO: 25); Csporogenes B (SEQ ID NO: 26); CbotulinumA3B (SEQ ID NO: 27); Csporogenes A (SEQ ID NO: 28); CbotulinumA3A (SEQ ID NO: 29); Csordellii B (SEQ ID NO: 30); ColG s3a (SEQ ID NO: 31) CperfringensA (SEQ ID NO: 32) Csordellii A (SEQ ID NO: 33) and ColH s3 (SEQ ID NO: 34). The residues shown in blue are important for collagen binding activity, those shown in green are important for maintaining the architecture or protein folding. Both of these are also underlined for the top and bottom sequences. Residues shown in red are critical for Ca²⁺ binding and those in orange are critical for positioning the Ca²⁺ binding residues.

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FIG. 2 shows the tissue distribution of S³⁵-PTH-CBD 1 hour and 12 hours after subcutaneous injection. Note the skin outline.

FIG. 3 is a set of photographs documenting the hair growth on the back of mice at day 36 after depilation, treatment groups as indicated (Antagonist PTH(7-33)-CBD, Agonist PTH-CBD).

FIG. 4 is a set of photographs showing the histology at Day 36 after the indicated treatment. Skin samples were taken from the dorsal region and processed for Hematoxylin and Eosin (H&E) staining. Representative sections are shown from each treatment group as indicated. (Antagonist=PTH(7-33)-CBD, Agonist=PTH-CBD).

FIG. 5 is a graph showing the hair follicle counts per high powered field. Anagen VI hair follicles were counted by two independent observers in a blinded fashion. Results are expressed as mean±standard deviation. **=p<0.01 vs. no chemo ANOVA followed by Dunnett's test. (Antagonist=PTH(7-33)-CBD, Agonist PTH-CBD).

FIG. 6 is a set of photographs showing the hair growth on the back of the mice after each of the indicated treatments and a graph showing the results of a grey scale analysis of the hair at the injection site over time after the injection.

FIG. 7 is a set of photographs showing the hair on the back of mice after the indicated treatment without prior depilation.

FIG. 8 is a set of photographs and a graph showing the grey scale analysis of hair growth on the backs of mice comparing the indicated treatments with the PTH-CBD being administered prior to the chemotherapy as opposed to after chemotherapy began.

FIG. 9 is a photograph of three mice 13 days after waxing to remove hair and treatment with PTH-CBD, PTH antagonist-CBD or vehicle alone.

FIG. 10 is a set of photographs of mice showing hair regrowth in a model of alopecia areata after treatment with a control or with PTH-CBD.

FIG. 11 is a graph showing the endogenous parathyroid hormone levels in ovariectomized aged rats injected with a single dose of human PTH-CBD 6 months prior to sacrifice.

DETAILED DESCRIPTION

The effects of PTH agonists and antagonists on hair growth have been studied for over almost 15 years. PTH has a common receptor with PTH-related peptide (PTHrP), which is normally produced by dermal fibroblasts. PTHrP affects keratinocyte proliferation/differentiation and modulates the hair cycle. Most of the testing on hair growth effects has been performed with PTH antagonists, as indications from initial testing were that these were the most effective agents. Both injected and topical formulations have been tested in animal models of chemotherapy-induced alopecia and in the SKH-1 hairless mouse. Part of the effect of PTH antagonists on hair growth is to transition the hair follicles into a dystrophic catagen stage, which protects them from chemotherapeutic damage. However, clinical trials of topical PTH antagonists for chemotherapy-induced alopecia by MI Pharmaceuticals were discontinued in phase 2 because of limited efficacy. Thus new compositions for treating alopecia are needed.

The problems of delivery and retention of PTH to the skin can be overcome by using collagen-targeted PTH analogs. To accomplish this, we synthesized several fusion proteins of different PTH agonists and antagonists linked to a collagen binding domain derived from the Col1H1 collagenase of *Clostridium histolyticum*, in the studies described in the

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Examples, we found that the agonist compound PTH-CBD promotes transition of hair follicles to the anagen phase and has potent effects on hair growth. The antagonist compound PTH(7-33)-CBD had little effect on hair growth in chemotherapy models and had a deleterious effect on hair regrowth after depilation. Compounds such as PTH-CBD, which promote anagen phase transition of hair follicles, have been sought after due to their potential to treat a large variety of disorders of hair loss. PTH-CBD appears to have a similar mechanism of action to cyclosporine, which also promotes transition of hair follicles to anagen phase, although the mechanism is less likely to be the result of direct effects on WNT signaling. While clinical use of cyclosporine for this purpose is limited by systemic toxicity, PTH-CBD has not shown toxic effects, even with systemic administration.

Thus in another aspect, methods of increasing hair growth are provided herein. The methods include administering a CBD linked to a PTH/PTHrP receptor agonist to a subject in need of treatment to induce hair growth or stop hair loss. The method is applicable to individuals with alopecia, including chemotherapy induced alopecia, but also alopecia areata, alopecia caused by male pattern baldness, polycystic ovarian syndrome or other hair loss. The compositions may be administered locally or topically to treat hair loss.

In another aspect, methods of slowing hair growth or regrowth after a hair removal procedure by administering a CUD linked to a PTH/PTHrP receptor antagonist to a subject are provided. In one embodiment, the PTH antagonist composition is applied locally, topically. The PTH antagonist may be applied after a hair removal procedure to prevent or slow hair regrowth. As described in the Examples, we have demonstrated that hair regrowth is slowed after waxing in animals treated with CBD-PTH antagonist as compared to control animals treated with PTH CBD or vehicle alone. The compositions may be administered locally or topically to block hair growth.

Also provided herein are methods of treating hyperparathyroidism by administering PTH-CBD to a subject in need of treatment for hyperparathyroidism. In one embodiment the PTH administered to the subject may be a PTH from a different species. As shown in the Examples a single administration of CBD-PTH to ovariectomized aged rats was able to reduce the amount of endogenous PTH produced by the animal. Thus, administration of PTH-CBD to individuals suffering from hyperparathyroidism may experience a decrease in symptoms associated with hyperparathyroidism and have decreased levels of PTH after administration of PTH-CBD.

The collagen-binding polypeptide segment and the therapeutic agent may be chemically cross-linked to each other or may be polypeptide portions of a fusion protein. The terms "fusion protein" and "fusion polypeptide" may be used to refer to a single polypeptide comprising two functional segments, e.g., a collagen-binding polypeptide segment and a polypeptide based therapeutic agent, such as PTH/PTHrP receptor agonist polypeptide segment. The fusion proteins may be any size, and the single polypeptide of the fusion protein may exist in a multimeric form in its functional state, e.g. by cysteine disulfide connection of two monomers of the single polypeptide. A polypeptide segment may be a synthetic polypeptide or a naturally occurring polypeptide. Such polypeptides may be a portion of a polypeptide or may comprise one or more mutations. The two polypeptide segments of the fusion proteins can be linked directly or indirectly. For instance, the two segments may be linked directly through, e.g., a peptide bond or chemical cross-linking, or indirectly, through, e.g., a linker segment or

linker polypeptide. The peptide linker may be any length and may include traditional or non-traditional amino acids. For example, the peptide linker may be 1-100 amino acids long, suitably it is 5, 10, 15, 20, 25 or more amino acids long such that the collagen binding portion of the fusion polypeptide can mediate collagen binding and the therapeutic agent can have its therapeutic effect. Peptide linkers may include but are not limited to a PKD (polycystic kidney disease) domain from a collagenase or other protein such as in SEQ ID NO: 2, a GST or His-tag, or a Ser or Gly linker.

The collagen-binding polypeptide segment is a polypeptide that binds collagen and may be part of a larger fusion protein, bioactive agent, or pharmaceutical agent. Determination of whether a composition, polypeptide segment, fusion protein, or pharmaceutical or bioactive agent binds collagen can be made as described in U.S. Patent Publication No. 2010/0129341, which is incorporated herein by reference in its entirety. Briefly, the composition is incubated with collagen in binding buffer, and the mixture is then filtered through a filter that would otherwise allow it to pass through but that blocks the collagen and therefore holds back materials that bind to the collagen. The filtrate is then assayed for the presence of the composition, polypeptide segment, fusion protein, or pharmaceutical or bioactive agent. Suitably, at least 80%, 85%, 90%, 95%, 98% or more suitably at least 99% of the collagen-binding composition, polypeptide segment, fusion protein, or pharmaceutical or bioactive agent is retained by the filter in this assay, as compared to when the filtration is performed without collagen.

The collagen-binding polypeptide segment may be a bacterial collagen-binding polypeptide segment. It may be a *Clostridium* collagen-binding polypeptide segment. The collagen-binding polypeptide segment may be a segment of a collagenase, or a bacterial collagenase, or a *Clostridium* collagenase. Suitably the polypeptide segment is only a portion of the collagenase and the collagen-binding polypeptide segment does not have collagenase activity. The collagen-binding polypeptide may be a bacterial M9B (including those derived from *Bacillus* spp. and *Clostridium* spp.) or M9A (including those derived from *Vibrio* spp.) collagen-binding protein or a collagen-binding peptide derived from such a protein. By "derived from" we mean that the peptide is a fragment of the full-length protein, a peptide that has amino acid changes relative to the wild-type protein or a combination thereof. The key is that the peptide retains the ability to bind collagen. For example, a peptide may be derived from a protein by selecting a region of the protein capable of binding to collagen. Compositions including a bacterial collagenase as a collagen binding peptide are described in US Patent Publication No. 2010/0129341, which is hereby incorporated herein by reference in its entirety.

FIG. 1 shows a sequence alignment of the collagen-binding region of several M9B bacterial collagen-binding proteins included as SEQ ID NOs: 13-34. As can be seen from the sequence alignment, these proteins have a relatively small amount of sequence identity (about 30%), but they all bind to collagen in a similar fashion and are believed to have similar conformation as discussed in the Examples. Notably, the proteins share several amino acids critical for binding to collagen. Thus any of the peptides shown in FIG. 1 or collagen-binding fragments thereof can be used in the compositions and methods described herein (i.e., SEQ ID NOs: 13-34 can be used interchangeably).

In FIG. 1, the amino acid residues critical for the conformation of the peptide and for the collagen-binding activity

are underlined and shown in green and blue respectively. The key amino acid residues for collagen-binding are as follows:

a phenylalanine, histidine or tyrosine at position 959 of ColG in FIG. 1 (position 63 of SEQ ID NO: 13), position 968 of the ColH sequence of SEQ ID NO: 6, position 928 of the ColH sequence of FIG. 1 (position 63 of SEQ ID NO: 34) or a similar position of one of the other sequences shown in FIG. 1;

a tyrosine, serine or phenylalanine at position 970 of ColG in FIG. 1 (position 74 of SEQ ID NO: 13), position 977 of the ColH sequence of SEQ ID NO: 6, position 937 of the ColH sequence of FIG. 1 (position 72 of SEQ ID NO: 34) or a similar position of one of the other sequences shown in FIG. 1;

a tyrosine at position 994 of ColG in FIG. 1 (position 98 of SEQ ID NO: 13), position 1002 of the ColH sequence of SEQ ID NO: 6, position 962 of the Corn sequence in FIG. 1 (position 97 of SEQ ID NO: 34) or a similar position of one of the other sequences shown in FIG. 1;

a tyrosine, phenylalanine or histidine at position 996 of ColG in FIG. 1 (position 100 of SEQ ID NO: 13), position 1004 of the ColH sequence of SEQ ID NO: 6, position 964 of the ColH sequence in FIG. 1 (position 99 of SEQ ID NO: 34) or a similar position of one of the other sequences shown in FIG. 1. The critical segment for collagen binding is amino acids 90-100 of SEQ ID NO: 13 which corresponds to amino acids 89-97 of SEQ ID NO: 34 or the equivalent thereof from another bacterial collagen binding protein such as the sequences provided in the alignment of FIG. 1 (SEQ ID NOs: 14-33). Thus a peptide with relatively low sequence identity, sharing the structure and function of the ColG protein may also be used as a collagen binding domain (CBD) herein.

In one embodiment, the collagenase is ColH, SEQ ID NO: 6. The collagen-binding polypeptide segment may be or may include residues 901-1021 of SEQ ID NO:6 (residues 34-158 of SEQ ID NO:1), or a fragment of residues 34-158 of SEQ ID NO:1 at least 8, 10, 12, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 110 or 120 amino acid residues in length. The collagen-binding polypeptide segment is at least 50%, 60%, 70%, 80%, or at least 85%, at least 90%, at least 95%, at least 96%, at least 98%, or at least 99% identical to residues 34-158 of SEQ ID NO: 1 or to any one of SEQ ID NO: 13-34. The collagen-binding polypeptide segment may be or may comprise a fragment of residues 901-1021 of SEQ NO:6, e.g., a fragment of at least 8, at least 10, at least 20, at least 30 at least 40, or at least 50 consecutive amino acid residues of residues 901-1021 of SEQ ID NO:6. Suitably the collagen-binding polypeptide consists of residues 894-1008, 894-1021, 901-1021, or 901-1008 of SEQ ID NO: 6 or a homolog thereof as shown by the sequence alignment in FIG. 1. As described more fully in the examples, the entire collagen binding polypeptides shown in FIG. 1 are not required for collagen binding. The collagen binding segment may be as short as eight amino acids and may include, e.g., amino acids 89-97 of SEQ ID NO: 34, 90-98 of SEQ ID NO: 13 or 994-1002 of SEQ ID NO: 6. A ten amino acid collagen binding peptide may include e.g., amino acids 89-99 SEQ ID NO: 34, 90-100 SEQ ID NO 13 or 994-1004 SEQ ID NO 6. A 30 amino acid collagen binding segment may include e.g., amino acids 70-100 of SEQ ID NOs: 13 or 34 or 975-1005 of SEQ ID NO: 6. A forty amino acid collagen binding peptide may include e.g., amino acids 60-100 of SEQ ID NOs: 13, 34 or 964-1004 of SEQ ID NO: 6, or 59-99 of SEQ ID NO: 34. A fifty amino acid collagen binding segment may include e.g., amino acids 50-100 or 55-105 of SEQ ID NOs:

13-34 or 9060-1010 of SEQ ID NO: 6. Similar shorter peptides derived for corresponding sequences of SEQ ID NOs: 14-33 may also be used.

The collagen-binding polypeptide segment may be or may include residues 807-1021 of SEQ ID NO: 6 (residues 37-251 of SEQ ID NO: 2), or a fragment of residues 807-1021 of SEQ ID NO:6 at least 8, 10, 12, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 110 or 120 amino acid residues in length. Residues 807-901 comprise the polycystic kidney disease (PKD) domain of the collagen-binding protein. Those of skill in the art will appreciate that other linkers could be used to link the collagen-binding peptide to a therapeutic agent as outlined above.

Among other proteins the collagen-binding segment can be derived from are ColG (Matsushita et al., (1999) J. Bacteria 181:923-933), a class I collagenase from *Clostridium histolyticum*. ColH is a class II collagenase (Yoshihara et al., (1994) J. Bacteriol. 176: 6489-6496). The collagen-binding polypeptide segment may also be a polypeptide segment from any one of the protein sequences provided in FIG. 1 which aligns collagen-binding peptides from members of *Clostridium* and *Bacillus*. Those of skill in the art will appreciate that other members of this collagen-binding protein family may be useful in the methods described herein.

The PTH/PTHrP receptor agonist polypeptide segment may be a synthetic polypeptide or a naturally occurring polypeptide. Such polypeptides may be a portion of a polypeptide or may comprise one or more mutations. The mutations may make the PTH/PTHrP receptor agonist a better or worse agonist as compared to the wild-type PTH/PTHrP. Agonist activity with the PTH/PTHrP receptor can be assayed as described in Example 3 below by a cAMP stimulation assay. An agonist will stimulate cAMP synthesis in the assay described. Suitably, an agonist can activate receptor activity at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% or even 110% or 120% as much as wild-type PTH(1-34).

The PTH/PTHrP receptor agonist polypeptide segment is a PTH or PTHrP polypeptide segment. One human isoform of PTH is SEQ ID NO: 7. One human isoform of PTHrP is SEQ ID NO:8. While the human isoforms are provided, those of skill in the art will appreciate that other non-human-derived isoforms may be used as well. Such non-human-derived isoforms may be able to interact with human PTH/PTHrP receptor and vice versa. The PTH/PTHrP receptor agonist polypeptide segment may be or may include residues 1-33 of SEQ ID NO:1 (residues 1-33 of PTH (SEQ ID NO: 7)). The PTH/PTHrP receptor agonist polypeptide segment may be or may include residues 1-34 of PTH (SEQ ID NO: 7). In other embodiments, it is a fragment of residues 1-34 of PTH (SEQ ID NO: 7). In other embodiments, the PTH/PTHrP receptor agonist polypeptide segment may be or may include residues 1-84 of PTH (SEQ ID NO:7). In other embodiments, the PTH/PTHrP receptor agonist polypeptide segment may be or may include residues 1-14 of PTH (SEQ ID NO 7) or residues 1-7 of PTH (SEQ ID NO: 7). The key amino acids for binding to the PTH receptor as an agonist are amino acids 1, 2 and 5 of PTH. In still other embodiments, the PTH/PTHrP receptor agonist is a PTH or PTHrP polypeptide segment for any other species.

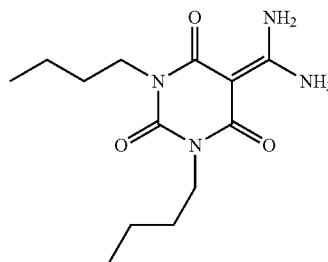
The PTH/PTHrP receptor antagonist can include in one embodiment PTH(7-34), i.e., residues 7-34 of PTH (SEQ ID NO: 7). In another embodiment, it is or includes residues 7-33 of PIE (SEQ ID NO: 7). In other embodiments, it is a fragment of residues 7-34 of SEQ ID NO: 8. In another embodiment, the PTH/PTHrP receptor antagonist includes

PIE (7-14), residues 7-14 of PTH (SEQ ID NO: 7). In another embodiment, the PTH/PTHrP receptor antagonists include ((-1)-33) of PTH/PTHrP. In another embodiment, the PTH/PTHrP receptor antagonists include residues 1-14 of PTH with an N-terminal extension. Adding an N-terminal extension to PTH or active N-terminal fragments of PTH converts the PTH peptides to antagonists. The N-terminal extension can be 1, 2, 3, 4, 5, or more amino acids in length. The identity of the amino acids in the N-terminal extension is typically not important. In one embodiment, the PTH/PTHrP receptor antagonist includes residues 1-33 of PTH with a Gly-Ser extension at the N-terminus (SEQ ID NO:11). In another embodiment, the PTH/PTHrP receptor antagonist includes PTHrP(7-34), i.e., residues 7-34 of SEQ ID NO:8, or a fragment of residues 7-34 of SEQ NO:8. In another embodiment, the PTH/PTHrP receptor antagonist includes mouse TIP(7-39) (See Hoare S R, Usdin T B. 2002. Specificity and stability of a new PTH1 receptor antagonist, mouse TIP(7-39). Peptides 23:989-98.). Other PTH/PTHrP receptor antagonists that may be used in the fusion proteins are also disclosed in Hoare et al. The PTH/PTHrP receptor antagonist may be a fragment of at least 8, 10, 12 or more amino acids from residues 1-34 of SEQ ID NO:7. In other embodiments the PTH/PTHrP receptor antagonist may be PTH/PTHrP receptor antagonist polypeptide from another species.

In one embodiment, the therapeutic agent or PTH/PTHrP receptor agonist or antagonist polypeptide segment is N terminal to the collagen-binding polypeptide segment in the fusion protein. That is, the two polypeptide segments each have an N-terminal and a C-terminal, and the N-terminal of the collagen-binding polypeptide segment is linked directly or indirectly, e.g., through a linker polypeptide segment (such as PKD, a Glycine or Serine linker) to the C-terminal of the therapeutic agent or PTH/PTHrP agonist or antagonist polypeptide segment.

The fusion proteins described above comprising (a) a collagen-binding polypeptide segment linked to (b) a therapeutic agent or a PTH/PTHrP receptor agonist or antagonist polypeptide segment can be replaced by pharmaceutical agents comprising (a) a collagen-binding polypeptide segment linked to (b) a therapeutic agent or PTH/PTHrP receptor agonist or a non-peptidyl PTH/PTHrP receptor agonist. An example of a non-peptidyl PTH/PTHrP receptor agonist is compound AH3960 (Rickard et al., (2007) Bone 39:1361-1372).

AH3960



AH3960 contains two amino groups. Amino groups in small chemical molecules such as AH3960 can be used to cross-link the therapeutic agent to amino groups on the collagen-binding polypeptide segment through a cross-linker such as DSG (disuccinimidyl glutarate) or through the combination of SANK (succinimidyl-4-hydrazinonicotinate acetone hydrazone) and SFB (succinimidyl-4-formyl ben-

zoate). Therapeutic agents can be cross-linked through their amino group to a carboxyl group of the collagen-binding polypeptide segment by EDC (1-ethyl-3-[3-dimethylaminopropyl]carbodiimide hydrochloride) or vice versa. These cross-linking products are available from Pierce (pierce.com, Thermo Fisher Scientific Inc., Rockford, Ill.). Protocols and reaction conditions are also available in the product literature from Pierce (pierce.com).

In another embodiment of the pharmaceutical agents comprising (a) a collagen-binding polypeptide segment; linked to (b) a polypeptide therapeutic agent or a PTH/PTHrP receptor agonist or antagonist polypeptide segment, segment (a) and segment (b) are separate polypeptides, and the two polypeptides are linked by chemical cross-linking. The two polypeptides can be cross-linked through amino groups by reagents including DSG (disuccinimidyl glutarate) or glutaraldehyde. They can also be cross-linked through amino groups by derivatizing one polypeptide with SANH (succinimidyl-4-hydrazinonicotinate acetone hydrazone) and the other with SFB (succinimidyl-4-formyl benzoate), and then mixing the two derivatized polypeptides to cross-link. The two polypeptides can be cross-linked between an amino group of one polypeptide and a carboxyl of the other by reaction with EDC (1-ethyl-3-[3-dimethylaminopropyl]carbodiimide hydrochloride). The polypeptides can also be cross-linked (e.g., covalently coupled) by any other suitable method known to a person of ordinary skill in the art. These cross-linking reagents are available from Pierce (pierce.com, Thermo Fisher Scientific Inc., Rockford, Ill.). Protocols and reaction conditions are also available in the product literature from Pierce (pierce.com). These and other applicable cross-linking methods are described in U.S. published patent applications 2006/0258569 and 2007/0224119.

The compositions described herein may be administered by any means known to those skilled in the art, including, but not limited to, oral, topical, intranasal, intraperitoneal, parenteral, intravenous, intramuscular, intradermal or subcutaneous. Thus the compositions may be formulated as an ingestible, injectable, topical or suppository formulation. The composition may be formulated for administration by injection to result in systemic administration or local administration. The compositions may also be delivered with in a liposomal or time-release vehicle. The compositions may also be delivered in a site-directed delivery vehicle, such as but not limited to, a targeted liposome or an absorbable collagen sponge carrier or other implant.

The inventors have found that when administering compositions including a CBD subcutaneously it binds locally at the site of injection if the composition is dissolved in neutral pH buffer. But if the composition is dissolved in a low pH buffer, for example a buffer having pH 5.0 or pH 4.5 or below, the collagen-binding domain does not bind collagen, and the composition has time to disperse systemically before it binds collagen elsewhere in the body at neutral pH. Thus systemic administration of the compositions involves administering the composition dissolved in buffer or aqueous solution at a pH lower than about 5.0 or at pH 4.5 or below. In another embodiment, systemic administration of the compositions involves administering the fusion proteins dissolved in aqueous solution at lower than about 6.0. Alternatively, if the skin condition is localized, the compositions described herein may be administered in a buffer with a pH of 6.0, 6.5, 7.0, 7.5 or above in order to allow for localized delivery of the compositions to the affected area of the skin.

Pharmaceutical compositions for topical administration may also be formulated using methods and compositions such as those available to those skilled in the art. For example, gels, creams or liposome preparations may be suitable for topical delivery. These delivery vehicles may be formulated to mediate delivery to the lower layers of the skin or to allow for extended release of the pharmaceutical at the site of application.

The compositions can be administered as a single dose or as divided doses. For example, the composition may be administered two or more times separated by 4 hours, 6 hours, 8 hours, 12 hours, a day, two days, three days, four days, one week, two weeks, or by three or more weeks. Optionally, such treatment may be repeated, for example, every 1, 2, 3, 4, 5, 6, or 7 days, or every 1, 2, 3, 4, and 5 weeks or every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 months. The composition is expected to be more effective than a comparable or control composition comprising the therapeutic agent or a PTH/PTHrP receptor agonist that is not linked to a collagen-binding protein. In one embodiment, a smaller amount of the composition may be used or the composition may be administered less frequently than a comparable composition comprising the therapeutic agent or a PTH/PTHrP receptor agonist which is not linked to a collagen-binding protein.

The dosage amounts and frequencies of administration provided herein are encompassed by the terms therapeutically effective and prophylactically effective. The individual doses of pharmaceutical agents comprising a collagen-binding polypeptide segment linked to a therapeutic agent may be approximately the same on a molar basis as doses used for the therapeutic agent alone. It is expected that the pharmaceutical agents comprising a collagen-binding polypeptide segment linked to a therapeutic agent may be administered less frequently, because linking the agent to the collagen-binding polypeptide segment gives it much more prolonged activity *in vivo*.

Administration of the compositions to a subject in accordance with the invention appears to exhibit beneficial effects in a dose-dependent manner. Thus, within broad limits, administration of larger quantities of the compositions is expected to achieve increased beneficial biological effects than administration of a smaller amount. Moreover, efficacy is also contemplated at dosages below the level at which toxicity is seen.

It will be appreciated that the specific dosage administered in any given case will be adjusted in accordance with the compositions being administered, the disease to be treated or inhibited, the condition of the subject, and other relevant medical factors that may modify the activity of the agent or the response of the subject, as is well known by those skilled in the art. For example, the specific dose for a particular subject depends on age, body weight, general state of health, diet, the timing and mode of administration, the rate of excretion, medicaments used in combination and the severity of the particular disorder to which the therapy is applied. Dosages for a given patient can be determined using conventional considerations, e.g., by customary comparison of the differential activities of the compositions of the invention and of the therapeutic agent administered alone, such as by means of an appropriate conventional pharmacological or prophylactic protocol.

The maximal dosage for a subject is the highest dosage that does not cause undesirable or intolerable side effects. The number of variables in regard to an individual prophylactic or treatment regimen is large, and a considerable range of doses is expected. The route of administration will also

impact the dosage requirements. It is anticipated that dosages of the compositions will reduce symptoms of the condition being treated by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% compared to pre-treatment symptoms or symptoms is left untreated. It is specifically contemplated that pharmaceutical preparations and compositions may palliate or alleviate symptoms of the disease without providing a cure, or, in some embodiments, may be used to cure the disease or disorder.

Suitable effective dosage amounts for administering the compositions may be determined by those of skill in the art, but typically range from about 1 microgram to about 10,000 micrograms per kilogram of body weight weekly, although they are typically about 1,000 micrograms or less per kilogram of body weight weekly. In some embodiments, the effective dosage amount ranges from about 10 to about 10,000 micrograms per kilogram of body weight weekly. In another embodiment, the effective dosage amount ranges from about 50 to about 5,000 micrograms per kilogram of body weight weekly. In another embodiment, the effective dosage amount ranges from about 75 to about 1,000 micrograms per kilogram of body weight weekly. The effective dosage amounts described herein refer to total amounts administered, that is, if more than one compound is administered, the effective dosage amounts correspond to the total amount administered.

The effectiveness of the compositions described herein may be enhanced by at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 100% relative to a control treated with the therapeutic agent alone. It will be appreciated that the effectiveness of the treatment in any given case will be enhanced variably in accordance with the specific compositions used, the type of disease being treated, the condition of the subject, the specific formulations of the compounds and other relevant medical factors that may modify the activity of the compositions or the responses of the subject as is appreciated by those of skill in the art.

The following examples are meant only to be illustrative and are not meant as limitations on the scope of the invention or of the appended claims. All references cited herein are hereby incorporated by reference in their entireties.

EXAMPLES

Example 1

Structural Comparison of ColH and ColG Collagen-Binding Domains

The C-terminal collagen-binding domain (CBD) of collagenase is required for insoluble collagen fibril binding and for subsequent collagenolysis. The high resolution crystal structures of ColG-CBD (s3b) and ColH-CBD (s3) the molecules resemble one another closely (r.m.s.d. C_{α} =1.5 Å), despite sharing only 30% sequence identity. Five out of six residues chelating Ca^{2+} are conserved. The dual Ca^{2+} binding sites in s3 are completed by a functionally equivalent aspartate. The three most critical residues for collagen interaction in s3b are conserved in s3. The general shape of the binding pocket is retained by altered loop structures and side-chain positions. Small angle X-ray scattering data revealed that s3 also binds asymmetrically to mini-collagen. Besides the calcium-binding sites and the collagen-binding

pocket, architecturally important hydrophobic residues and hydrogen-bonding network around the cis-peptide bond are well-conserved in metallopeptidase subfamily M9B.

Common structural features described above and in Bauer et (2012) J Bacteriol November 9 (which is incorporated herein by reference in its entirety), enabled us to update the sequence alignment of the CBD in the M9B subfamily (FIG. 1). Conserved residues are important for one of four reasons: calcium chelation (red), cis-trans isomerization of the linker (yellow), collagen-binding (blue) or protein folding (green). FIG. 1 also indicates the strands of the structure along the top of the figure.

The dual calcium-binding site is formed by four chelating residues (Glu899, Glu901, Asn903, and Asp904) within the N-terminal linker, two chelating residues (Asp927 and Asp930) from the β -strand C and invariant Tyr1002 hydrogen-bonds and orients Asp930. Residue numbers used in this paragraph are of s3b. Likewise other supporting cast such as Gly921 is conserved in the middle of β -strand strategically placed to make room for Glu899. The dual calcium chelation site is fashioned sometimes by functionally equivalent residues. As mentioned, Asp897 of s3 acts equivalently to Asp927 of s3b. Asp897 equivalents are tentatively identified in *B. brevis* s3a and s3b, *C. botulinum* A3 s3a and *C. histolyticum* ColG s3a. Tridentate and divalent Asp and Glu residues are conserved with only *C. sordellii* s3a as the exception. The monodentate Asp904 residue is sometimes substituted by Asn. For those substituted, the net charge of the dual calcium site is neutral rather than -1.

The peptide between residues 901-902 has cis conformation in the holo state for both s3b and s3. The position 902 in other CBD molecules is Pro, Asp or Asn. Pro frequently succeeds the peptide bond to ease trans-cis isomerization. The s3 molecule has Pro. In s3b, OD of Asn902 hydrogen-bonds with the main-chain N of Asp904. The hydrogen-bond is critical for the peptide isomerization. Spiriti and van der Vaart. (2010) Biochemistry 49:5314-5320, which is incorporated herein by reference in its entirety. For the remainder of CBD molecules with Asp at the position, OD of Asp could play the same role as that of Asn902. Other hydrogen-bonds identified by simulation studies important in stabilizing the transition states are well conserved. These donor-acceptor pairs in s3 and s3b are tabulated (Table 1). Calcium ions could catalyze the isomerization in all the CBD molecules and their transition states and catalytic mechanism may look very similar.

TABLE 1

Hydrogen-bonds important in trans-cis peptide isomerization in s3b and their counterparts in s3.

Important H-bonds in s3b for transition state formation	Corresponding H-bonds in s3
T910_OG1 . . . N903_NH2	S879_OG1 . . . N872_ND2
T910_OG1 . . . N900_N	S879_OG1 . . . K86_N
E899_OE1 . . . N903_ND2	E868_OE1 . . . N872_ND2
E899_OE2 . . . S922_N	E868_OE2 . . . T891_N
N902_OD1 . . . D904_N	NA (N902 replaced with P871)
D930_OD2 . . . Y1002_OH	D939_OD2 . . . Y97_OH
Y1002_OH . . . Y932_OH	NA (Y932 replaced with F901)

Non-functional residues that are important in either folding or architectural stability are conserved. Hydrophobic residues packed between the β -sheets are better conserved if they are located in the vicinity of functionally critical residues. For example, invariant Trp956 of strand E is packed between the β -sheets. The residues flanking (Thr955

& Thr957) interact with mini-collagen. Tyr932 is packed between the sheets and helps positioning Tyr1002. Residues at tight turns are conserved as well. Gly975 is well conserved to allow a type II' turn in s3b, Gly942 (Gly975 equivalent) in s3 allows Asp941 side-chain to stabilize the reverse turn. A highly conserved six-residue stretch, between residues 986 and 991, adopts a tight turn and precedes the functionally important strand H. The region is well ordered in the crystal structures with low B-factors, and is the least dynamic based on NMR and limited proteolysis MALDI-TOF MS. Philominathan, et al. (2009) J Biol Chem 284: 10868-10876 and Sides et al. J Am Soc Mass Spectrom. (2012) 23(3):505-19 both of which are incorporated herein by reference in their entireties. The main-chain carbonyl and amino groups of Arg985 hydrogen-bond with OH of Tyr989 to stabilize the turn. Only Gly987 can make room for the bulky Tyr989 side chain. Try990 packs against the invariant Ala909 and conserved 3_{10} helix. Ala909 is at the base of the linker that undergoes α -helix \rightarrow β -strand transformation. The tight turn may ensure that collagen interacting Leu992, Tyr994, and Tyr996 would be correctly positioned. Tyr994 is the most critical residue in interacting with collagenous peptides. Wilson, et al. (2003) EMBO J. 22:1743-1752. The strands adjacent to strand H, i.e. strands C and E, are very well conserved. The three antiparallel strands mold the collagen-binding pocket. Strand F staples the β -sheets by interacting with both sheets. The β -strand first interacts in an antiparallel orientation with strand E then breaks its direction at Gly971 to interact with strand G. In place of Gly971, Ala or Pro is found at the location where the strand switches its allegiance. The dual interaction of the strand helps positioning Tyr970 to interact with mini-collagen.

Three residues shown to interact strongly with mini-collagen are conserved. The invariant Tyr994 and well conserved Tyr970 and Tyr996 constitute the "hot spot". Y994A mutation lost binding capability. Since Y994F resulted in 12-fold reduction in binding to mini-collagen, the hydroxyl group of Tyr994 may interact with collagen through a hydrogen-bond. Tyr996, which is a critical residue in binding mini-collagen, is not so well conserved. Y996A caused 40-fold reduction in binding to the mini-collagen. Y996 is s3b is replaced with Phe in s3, though both side chains have identical orientation. In other CBD molecules, an aromatic residue, such as Phe or His, is sometimes found at the site. Y970A results in 12-fold reduction in binding to mini-collagen. Thr957 was found to interact with mini-collagen by ^{15}N -HSQC-NMR titration. The β -branched amino acid residues or Leu are found at the positions equivalent to Thr957 in most of the CBDs. Six other residues were identified by ^{15}N -HSQC-NMR titration to interact with mini-collagen are not very well conserved. Since divergent CBDs (s3 and s3b) adopted a similar saddle-shaped binding pocket, other CBDs may also adopt similar collagen-binding strategy.

Divergent CBD could target different collagen sequences and could possibly target different collagen types; however, this structural study suggest otherwise. Rather, all the CBD domains may bind similarly to an under-twisted region such as the C-terminus of a collagen fibril. The C-terminus of type I collagen is exposed in the fibril surface based on X-ray fiber diffraction experiments, and it is the most accessible site for the bacterial collagenase to initiate assaults. However CBD binding only at the C-terminal region of tropocollagen is unfounded. Gold particle-labeled tandem ColG-CBD (s3a-s3b) labeled with gold particle bound to type I collagen fibrils exhibited no periodicity. In the collagen fibrils, the molecules are staggered from each other by about

67 nm. Therefore CBD could target partially under-twisted regions in the middle of a tropocollagen that are also vulnerable for assaults.

Much like s3b, s3 is both compact, and extremely stable in the presence of physiological Ca^{2+} . Thus, the enzyme could degrade extracellular matrix for prolonged time. The linker that induced structural transformation is a common feature found in M9B collagenase. It could act as Ca^{2+} to trigger domain rearrangement as means of enzyme activation. Ca^{2+} concentration in extracellular matrix is higher than that inside a bacterium. Both s3 and s3b bind similarly to a mini-collagen, thus M9B collagenase molecules could initiate collagenolysis from analogous structural features in various collagen fibril. Fusion protein of any CBD derived from M9B collagenase and a growth factor should result in comparable clinical outcome.

Example 2

CBD-PTH Agonist Spurs Hair Growth and CBD-PTH Antagonist Inhibits Hair Growth

In-Vitro Characterization of CBD-Linked PTH Compounds:

Collagen binding of each peptide was verified in flow-through collagen binding assays as previously described in U.S. Patent Publication No. 2010/0129341, which is incorporated herein by reference in its entirety. PTH-CBD, consisting of the first 33 amino acids of PTH linked directly to the collagen binding domain (SEQ ID NO 1), was the most potent agonist, having a similar effect to that of PTH(1-34) (SEQ ID NO: 7) on cAMP accumulation. Ponnappakkam et al. (2011) Calcif 88:511-520. Epub 2011 April 2022. Among the antagonists, PTH(7-33)-CBD (SEQ ID NO: 10) had the best combination of low intrinsic activity and high receptor blockade (not shown), similar to those seen in other PTH antagonists, including those used in hair growth studies. Peters, et al. (2001) J Invest Dermatol 117:173-178.

In Vivo Distribution of PTH-CBD:

Tissue distribution was assessed by administering ^{35}S -labelled PTH-CBD via subcutaneous injection, followed by whole mount frozen and whole-body autoradiography. PTH-CBD with a phosphorylation site between PTH(1-33) and the CBD was purified, activated and labeled with [γ - ^{35}S] ATP as described previously. Tamai et al. (2003) Infect Immun. 71:5371-5375. Approximately 10.8 meg of ^{35}S -PTH-CBD (122 kcm/mcg) was injected subcutaneously in 7 week-old mice (32-35 g). Mice were sacrificed at 1 hour or 12 hours post-injection, and then frozen in dry ice-acetone. Frozen sections (50 μm) were prepared with an autocryotome, dried at -20°C ., and exposed to an image plate for 4 weeks. There appeared to be an initial distribution of ^{35}S -PTH-CBD to a broad area of skin around the site of injection, followed by a rapid redistribution to the skin of the entire animal, as well as to several other tissues (i.e. bone, intestine, bladder) (FIG. 2). PTH-CBD thus showed the desired properties of distribution and retention to skin with subcutaneous administration.

PTH-CBD Reverses Hair Loss in Chemotherapy-Induced Alopecia in Mice:

We compared efficacy of CBD linked PTH agonists and antagonists in chemotherapy-induced alopecia, utilizing an experimental design published by Peters, et al., for non-CBD linked PTH compounds. Peters, et al. (2001) J Invest Dermatol 117:173-178. C57BL/6J mice (Jackson Laboratories, Bar Harbor, Me.) were depilated to synchronize the hair follicles, and cyclophosphamide (CYP, 150 mg/kg) was

administered on day 9 to maximize the chemotherapy-induced damage. The agonist (PTH-CBD) and the antagonist (PTH(7-33)-CBD) were administered 2 days prior to chemotherapy, and given the long-term retention of the compounds in the skin, we administered only a single dose to cover the timing of the multiple injections of PTH agonist and antagonist in the study by Peters, et. al. The administered dose of CBD-linked compounds (320 meg/kg) is well tolerated in mice. Ponnappakkam et al. (2011) *Calcif* 88511-520. Epub 2011 April 2022.

The results of the photodocumentation record indicate that the agonist, PTH-CBD, was far more effective at stimulating hair growth than was the antagonist (FIG. 3). Histological examination revealed morphological changes in the hair follicles after CYP therapy, which were more superficially located and exhibited clumped melanocytes around the bulb, characteristics of the dystrophic anagen and catagen phase (FIG. 4). While the antagonist PTH(7-33)-CBD had no beneficial effect, treatment with the agonist PTH-CBD led to deeper rooting and reduced melanocyte clumping, thus reversing the dystrophic changes. Counts of anagen VI hair follicles per high-powered field (HPF) were compared between groups; animals treated with PTH-CBD had a higher number of hair follicles, approaching those of animals which did not receive chemotherapy (FIG. 5), while the antagonist PTH(7-33)-CBD had no beneficial effect.

Importantly, we saw no evidence of adverse effects from PTH-CBD administration. While PTH injections are known to elevate blood calcium and can cause kidney stones, PTH-CBD had no effect on serum calcium. In addition, there was no evidence of excess hair length on the body or of excess hair growth on the ears and tail, where a full coat is normally not present. The effects of PTH-CBD on hair growth have been confirmed in models of chemotherapy-induced alopecia without depilation, which more closely mimic clinical protocols.

Quantification of Effects of PTH-CBD in Chemotherapy-Induced Alopecia:

We followed these studies by comparing the effects of different doses of PTH-CBD in chemotherapy-induced alopecia. In these studies, we applied the injections more distally on the back and applied a gray-scale analysis to quantify the amount of hair growth. Injecting more distally in the back allows us to compare regrowth of hair after PTH-CBD treatment with less interference from the normal hair regrowth, which normally proceeds from head to tail in mice. The results are shown in FIG. 6, indicating a dose-dependent effect on hair regrowth both qualitatively and quantitatively.

Chemotherapy-Induced Alopecia without Depilation:

While the depilated model of chemotherapy-induced alopecia provides a uniform model for comparison of drug effects, the depilation process is known to cause hair follicle injury, and may alter the response of the animals to the PTH-CBD administration. We therefore tested the effects of PTH-CBD in another model of chemotherapy-induced alopecia, where the animals were given 3 courses of cyclophosphamide therapy (50 mg/kg/wk), similar to the usual manner in which cancer patients might be treated. In this model, it takes much longer (4-6 months) for alopecia to develop. Animals that received a single dose of PTH-CBD (320 meg/kg subcutaneous) prior to the first cycle did not develop hair loss as shown in FIG. 7.

In a second study, we compared the effects of PTH-CBD when given prophylactically, at the time of the first cycle of chemotherapy, vs. therapeutically, after the hair loss had developed. While PTH-CBD was effective in both instances,

the effects were more prominent when given prophylactically. This is evident both visually and quantitatively in FIG. 8, using the same grey scale analysis used in our dose-response study.

Depilation Alopecia:

The agonist PTH-CBD appears to increase hair growth by increasing the number of anagen phase hair follicles. As such, there is no reason to believe that hair growth effects should be limited to the chemotherapy model. We therefore tested both PTH-CBD and antagonist compound, PTH(7-33)-CBD, after removing hair from C57/BL6J mice by waxing (FIG. 9). The results were quite interesting; agonist (PTH-CBD) treated animals had earlier anagen eruption (day 7 vs. day 9 for vehicle controls), and exhibited more complete regrowth of hair by the end of the study (day 18). Antagonist (PTH(7-33)-CBD) treated animals also had an early anagen eruption, but the hair growth which followed was markedly curtailed, and the hair cycle was arrested after this point, resulting no further observed regrowth of hair. Thus, it appears that agonist therapy is acting to promote more rapid regrowth of hair by promoting more rapid transition to the anagen phase, while the antagonist inhibited hair regrowth by blocking this transition.

PTH-CBD is a fusion protein of the first 33 amino acids of parathyroid hormone (PTH) and a bacterial collagen binding domain. The collagen binding activity causes PTH-CBD to be retained at its site of action in the dermal collagen, maximizing efficacy and reducing systemic side-effects. PTH-CBD stimulates hair growth by causing hair follicles to enter an anagen VI or growth phase, presumably by activating WNT signaling and increasing production of beta-catenin. We therefore plan to conduct the following additional studies to confirm this mechanism of action and to determine the effect of PTH-CBD in two distinct genetic mouse models with WNT signaling inhibition. These data will be used in formulating clinical trials for PTH-CBD as a therapy for alopecia.

Alopecia Areata Alopecia:

Areata is a disease of patchy hair loss due to autoimmune destruction of the hair follicles. We tested the efficacy of PTH-CBD in promoting regrowth of hair in an animal model of alopecia areata, the engrafted C3H/HeJ mouse. In this model, hair loss develops variably over the first 2 months of life. Shown in FIG. 10 is the results of a single dose of PTH-CBD (320 meg/kg subcutaneous) administered into the engrafted site, the center of the back, where there was maximal hair loss. Compared to vehicle control animals, which continued to lose hair at this site, animals receiving PTH-CBD began to show regrowth of hair within the next 1-4 days. Importantly, the response was found to be sustained during the 2 month course of the experiment.

Example 3

CBD-PTH can Prevent or Treat Hyperparathyroidism

In this experiment, rats had their ovaries surgically removed at age 3 months. At age 9 months, rats were injected with either a single dose of PTH-CBD (320 mcg/kg) or vehicle control. Animals were sacrificed 6 months after therapy (age 15 months). Human intact PTH levels were measured to assess serum levels of PTH-CBD, and were found to be undetectable in both groups. Serum calcium was measured and there were no differences between groups (Vehicle: 13.5+/-1.1 vs. PTH-CBD: 14.3+/-1.1 mg/dl, NS). Rat intact PTH levels were measured to assess endogenous PTH production, and PTH-CBD suppressed the normal

increase in endogenous PTH levels seen in aged, ovariectomized rats (FIG. 11). These findings indicate that a single injection of PTH-CBD can provide long-term suppression of

endogenous PTH production, preventing the normal rise seen with age in the ovariectomized rat model, and thus may serve as a therapy for hyperparathyroidism.

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agcgtgcccg gaaagctggc tggagtgcga tcttctgag gccgatactg tcgtcgtccc 5280
ctcaaacctg cagatgcacg gttacgatgc gccatctac accaacgtaa cctatcccat 5340
tacggtcaat ccgcccgttg ttcccacgga gaatccgacg gggtgttact cgctcacatt 5400
taatgttgat gaaagctggc tacaggaagg ccagacgcga attatctttg atggcggttg 5460
aatt 5464

```

<210> SEQ ID NO 4

<211> LENGTH: 383

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic GST-PTH-CBD fusion protein

<400> SEQUENCE: 4

```

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

```

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu

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-continued

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

<210> SEQ ID NO 5

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide: Factor Xa recognition sequence

<400> SEQUENCE: 5

-continued

Ile Glu Gly Arg
1

<210> SEQ ID NO 6
<211> LENGTH: 1021
<212> TYPE: PRT
<213> ORGANISM: Clostridium histolyticum

<400> SEQUENCE: 6

Met Lys Arg Lys Cys Leu Ser Lys Arg Leu Met Leu Ala Ile Thr Met
1 5 10 15
Ala Thr Ile Phe Thr Val Asn Ser Thr Leu Pro Ile Tyr Ala Ala Val
20 25 30
Asp Lys Asn Asn Ala Thr Ala Ala Val Gln Asn Glu Ser Lys Arg Tyr
35 40 45
Thr Val Ser Tyr Leu Lys Thr Leu Asn Tyr Tyr Asp Leu Val Asp Leu
50 55 60
Leu Val Lys Thr Glu Ile Glu Asn Leu Pro Asp Leu Phe Gln Tyr Ser
65 70 75 80
Ser Asp Ala Lys Glu Phe Tyr Gly Asn Lys Thr Arg Met Ser Phe Ile
85 90 95
Met Asp Glu Ile Gly Arg Arg Ala Pro Gln Tyr Thr Glu Ile Asp His
100 105 110
Lys Gly Ile Pro Thr Leu Val Glu Val Val Arg Ala Gly Phe Tyr Leu
115 120 125
Gly Phe His Asn Lys Glu Leu Asn Glu Ile Asn Lys Arg Ser Phe Lys
130 135 140
Glu Arg Val Ile Pro Ser Ile Leu Ala Ile Gln Lys Asn Pro Asn Phe
145 150 155 160
Lys Leu Gly Thr Glu Val Gln Asp Lys Ile Val Ser Ala Thr Gly Leu
165 170 175
Leu Ala Gly Asn Glu Thr Ala Pro Pro Glu Val Val Asn Asn Phe Thr
180 185 190
Pro Ile Leu Gln Asp Cys Ile Lys Asn Ile Asp Arg Tyr Ala Leu Asp
195 200 205
Asp Leu Lys Ser Lys Ala Leu Phe Asn Val Leu Ala Ala Pro Thr Tyr
210 215 220
Asp Ile Thr Glu Tyr Leu Arg Ala Thr Lys Glu Lys Pro Glu Asn Thr
225 230 235 240
Pro Trp Tyr Gly Lys Ile Asp Gly Phe Ile Asn Glu Leu Lys Lys Leu
245 250 255
Ala Leu Tyr Gly Lys Ile Asn Asp Asn Asn Ser Trp Ile Ile Asp Asn
260 265 270
Gly Ile Tyr His Ile Ala Pro Leu Gly Lys Leu His Ser Asn Asn Lys
275 280 285
Ile Gly Ile Glu Thr Leu Thr Glu Val Met Lys Val Tyr Pro Tyr Leu
290 295 300
Ser Met Gln His Leu Gln Ser Ala Asp Gln Ile Lys Arg His Tyr Asp
305 310 315 320
Ser Lys Asp Ala Glu Gly Asn Lys Ile Pro Leu Asp Lys Phe Lys Lys
325 330 335
Glu Gly Lys Glu Lys Tyr Cys Pro Lys Thr Tyr Thr Phe Asp Asp Gly
340 345 350
Lys Val Ile Ile Lys Ala Gly Ala Arg Val Glu Glu Glu Lys Val Lys
355 360 365

-continued

Arg Leu Tyr Trp Ala Ser Lys Glu Val Asn Ser Gln Phe Phe Arg Val
 370 375 380
 Tyr Gly Ile Asp Lys Pro Leu Glu Glu Gly Asn Pro Asp Asp Ile Leu
 385 390 395 400
 Thr Met Val Ile Tyr Asn Ser Pro Glu Glu Tyr Lys Leu Asn Ser Val
 405 410 415
 Leu Tyr Gly Tyr Asp Thr Asn Asn Gly Gly Met Tyr Ile Glu Pro Glu
 420 425 430
 Gly Thr Phe Phe Thr Tyr Glu Arg Glu Ala Gln Glu Ser Thr Tyr Thr
 435 440 445
 Leu Glu Glu Leu Phe Arg His Glu Tyr Thr His Tyr Leu Gln Gly Arg
 450 455 460
 Tyr Ala Val Pro Gly Gln Trp Gly Arg Thr Lys Leu Tyr Asp Asn Asp
 465 470 475 480
 Arg Leu Thr Trp Tyr Glu Glu Gly Gly Ala Glu Leu Phe Ala Gly Ser
 485 490 495
 Thr Arg Thr Ser Gly Ile Leu Pro Arg Lys Ser Ile Val Ser Asn Ile
 500 505 510
 His Asn Thr Thr Arg Asn Asn Arg Tyr Lys Leu Ser Asp Thr Val His
 515 520 525
 Ser Lys Tyr Gly Ala Ser Phe Glu Phe Tyr Asn Tyr Ala Cys Met Phe
 530 535 540
 Met Asp Tyr Met Tyr Asn Lys Asp Met Gly Ile Leu Asn Lys Leu Asn
 545 550 555 560
 Asp Leu Ala Lys Asn Asn Asp Val Asp Gly Tyr Asp Asn Tyr Ile Arg
 565 570 575
 Asp Leu Ser Ser Asn Tyr Ala Leu Asn Asp Lys Tyr Gln Asp His Met
 580 585 590
 Gln Glu Arg Ile Asp Asn Tyr Glu Asn Leu Thr Val Pro Phe Val Ala
 595 600 605
 Asp Asp Tyr Leu Val Arg His Ala Tyr Lys Asn Pro Asn Glu Ile Tyr
 610 615 620
 Ser Glu Ile Ser Glu Val Ala Lys Leu Lys Asp Ala Lys Ser Glu Val
 625 630 635 640
 Lys Lys Ser Gln Tyr Phe Ser Thr Phe Thr Leu Arg Gly Ser Tyr Thr
 645 650 655
 Gly Gly Ala Ser Lys Gly Lys Leu Glu Asp Gln Lys Ala Met Asn Lys
 660 665 670
 Phe Ile Asp Asp Ser Leu Lys Lys Leu Asp Thr Tyr Ser Trp Ser Gly
 675 680 685
 Tyr Lys Thr Leu Thr Ala Tyr Phe Thr Asn Tyr Lys Val Asp Ser Ser
 690 695 700
 Asn Arg Val Thr Tyr Asp Val Val Phe His Gly Tyr Leu Pro Asn Glu
 705 710 715 720
 Gly Asp Ser Lys Asn Ser Leu Pro Tyr Gly Lys Ile Asn Gly Thr Tyr
 725 730 735
 Lys Gly Thr Glu Lys Glu Lys Ile Lys Phe Ser Ser Glu Gly Ser Phe
 740 745 750
 Asp Pro Asp Gly Lys Ile Val Ser Tyr Glu Trp Asp Phe Gly Asp Gly
 755 760 765
 Asn Lys Ser Asn Glu Glu Asn Pro Glu His Ser Tyr Asp Lys Val Gly
 770 775 780

-continued

Thr Tyr Thr Val Lys Leu Lys Val Thr Asp Asp Lys Gly Glu Ser Ser
 785 790 795 800
 Val Ser Thr Thr Thr Ala Glu Ile Lys Asp Leu Ser Glu Asn Lys Leu
 805 810 815
 Pro Val Ile Tyr Met His Val Pro Lys Ser Gly Ala Leu Asn Gln Lys
 820 825 830
 Val Val Phe Tyr Gly Lys Gly Thr Tyr Asp Pro Asp Gly Ser Ile Ala
 835 840 845
 Gly Tyr Gln Trp Asp Phe Gly Asp Gly Ser Asp Phe Ser Ser Glu Gln
 850 855 860
 Asn Pro Ser His Val Tyr Thr Lys Lys Gly Glu Tyr Thr Val Thr Leu
 865 870 875 880
 Arg Val Met Asp Ser Ser Gly Gln Met Ser Glu Lys Thr Met Lys Ile
 885 890 895
 Lys Ile Thr Asp Pro Val Tyr Pro Ile Gly Thr Glu Lys Glu Pro Asn
 900 905 910
 Asn Ser Lys Glu Thr Ala Ser Gly Pro Ile Val Pro Gly Ile Pro Val
 915 920 925
 Ser Gly Thr Ile Glu Asn Thr Ser Asp Gln Asp Tyr Phe Tyr Phe Asp
 930 935 940
 Val Ile Thr Pro Gly Glu Val Lys Ile Asp Ile Asn Lys Leu Gly Tyr
 945 950 955 960
 Gly Gly Ala Thr Trp Val Val Tyr Asp Glu Asn Asn Asn Ala Val Ser
 965 970 975
 Tyr Ala Thr Asp Asp Gly Gln Asn Leu Ser Gly Lys Phe Lys Ala Asp
 980 985 990
 Lys Pro Gly Arg Tyr Tyr Ile His Leu Tyr Met Phe Asn Gly Ser Tyr
 995 1000 1005
 Met Pro Tyr Arg Ile Asn Ile Glu Gly Ser Val Gly Arg
 1010 1015 1020

<210> SEQ ID NO 7
 <211> LENGTH: 84
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

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

<210> SEQ ID NO 8
 <211> LENGTH: 141
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly Lys Ser Ile Gln

-continued

```

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

```

```

<210> SEQ ID NO 9
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Gly-Ser-PTH(1-33)-CBD fusion protein

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<400> SEQUENCE: 9

```

```

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

```

```

<210> SEQ ID NO 10
<211> LENGTH: 152
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic PTH(7-33)-CBD fusion protein

```

```

<400> SEQUENCE: 10

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```

Leu Met His Asn Leu Gly Lys His Leu Asn Ser Met Glu Arg Val Glu
1           5           10           15

```


-continued

Glu Ser Asn Ile Asn Asp Arg Ile Thr Tyr Gly Gln Val Asp Gly Asn
 65 70 75 80
 Lys Val Ser Asn Lys Val Lys Leu Arg Pro Gly Lys Tyr Tyr Leu Leu
 85 90 95
 Val Tyr Lys Tyr Ser Gly Ser Gly Asn Tyr Glu Leu Arg Val Asn
 100 105 110

<210> SEQ ID NO 14
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: C. sporogenes

<400> SEQUENCE: 14

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

<210> SEQ ID NO 15
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: C. botulinum

<400> SEQUENCE: 15

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

<210> SEQ ID NO 16
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: B. cereus

<400> SEQUENCE: 16

Leu Thr Glu Ser Glu Pro Asn Asn Arg Pro Glu Glu Ala Asn Arg Ile
 1 5 10 15

-continued

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

<210> SEQ ID NO 17
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: B. anthracis

<400> SEQUENCE: 17

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

<210> SEQ ID NO 18
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: Bacillus sp.

<400> SEQUENCE: 18

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

<210> SEQ ID NO 19
 <211> LENGTH: 111

-continued

<212> TYPE: PRT

<213> ORGANISM: *L. sphaericus*

<400> SEQUENCE: 19

```

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

```

<210> SEQ ID NO 20

<211> LENGTH: 111

<212> TYPE: PRT

<213> ORGANISM: *C. cerus*

<400> SEQUENCE: 20

```

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

```

<210> SEQ ID NO 21

<211> LENGTH: 111

<212> TYPE: PRT

<213> ORGANISM: *B. mycooides*

<400> SEQUENCE: 21

```

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

```

-continued

85 90 95
 Tyr Gln Tyr Gly Gly Gly Thr Gly Asn Tyr Thr Val Glu Val Lys
 100 105 110

<210> SEQ ID NO 22
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: B. weihensteph

<400> SEQUENCE: 22

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

<210> SEQ ID NO 23
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: B. brevis

<400> SEQUENCE: 23

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

<210> SEQ ID NO 24
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: B. brevis

<400> SEQUENCE: 24

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

-continued

Val Ser Ser Glu Lys Asp Glu Gly Leu Asn Trp Val Val Phe His Glu
 50 55 60
 Asp Asp Leu Lys Thr Tyr Phe Ala Tyr Pro Lys Thr Thr Gly Lys Lys
 65 70 75 80
 Leu Thr Gly Glu Phe Glu Ala Lys Pro Gly Lys Tyr Tyr Leu Leu Val
 85 90 95
 Tyr Asn Thr Asn Asn Thr Lys Ile Pro Tyr Lys Ala Ile Val Asn
 100 105 110

<210> SEQ ID NO 25
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: C. perfringens

<400> SEQUENCE: 25

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

<210> SEQ ID NO 26
 <211> LENGTH: 115
 <212> TYPE: PRT
 <213> ORGANISM: C. sporogenes

<400> SEQUENCE: 26

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

<210> SEQ ID NO 27
 <211> LENGTH: 115
 <212> TYPE: PRT
 <213> ORGANISM: C. botulinum

-continued

<400> SEQUENCE: 27

```

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

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<210> SEQ ID NO 28

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: C. sporogenes

<400> SEQUENCE: 28

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

```

<210> SEQ ID NO 29

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: C. botulinum

<400> SEQUENCE: 29

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

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-continued

Ser Glu Glu Asp Lys Ser Asn Tyr Ile Thr Tyr Pro Asn Lys Glu Leu
65 70 75 80

Glu Asn Leu Phe Tyr Ser Thr Val Lys Ile Asp Lys Pro Gly Lys Tyr
85 90 95

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

Asn Ile Glu
115

<210> SEQ ID NO 30
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: *C. sordellii*

<400> SEQUENCE: 30

Gly Val Glu Gln Glu Asp Asn Asn Ser Phe Glu Lys Ala Asn Pro Phe
1 5 10 15

Ser Ile Asn Gln Leu Val Lys Gly Glu Leu Asp Asn Asn Lys Asp Thr
20 25 30

Ser Asp Tyr Phe Lys Phe Glu Val Lys Glu Asp Ala Gln Leu Asn Ile
35 40 45

Ser Leu Glu Lys Thr Glu Gly Asp Gly Val Asn Trp Leu Leu Phe Lys
50 55 60

Asp Ser Asp Leu Glu Asn Tyr Ile Ala Ser Pro Thr Glu Ser Ile Asp
65 70 75 80

Asn Lys Leu Asn Gly Lys Val Asp Leu Lys Val Gly Thr Tyr Tyr Leu
85 90 95

Glu Val Tyr Gly Tyr Gly Ser Ser Pro Val Lys Tyr Asn Phe Lys Val
100 105 110

Thr

<210> SEQ ID NO 31
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: *Clostridium histolyticum*

<400> SEQUENCE: 31

Thr Lys Glu Met Glu Pro Asn Asp Asp Ile Lys Glu Ala Asn Gly Pro
1 5 10 15

Ile Val Glu Gly Val Thr Val Lys Gly Asp Leu Asn Gly Ser Asp Asp
20 25 30

Ala Asp Thr Phe Tyr Phe Asp Val Lys Glu Asp Gly Asp Val Thr Ile
35 40 45

Glu Leu Pro Tyr Ser Gly Ser Ser Asn Phe Thr Trp Leu Val Tyr Lys
50 55 60

Glu Gly Asp Asp Gln Asn His Ile Ala Ser Gly Ile Asp Lys Asn Asn
65 70 75 80

Ser Lys Val Gly Thr Phe Lys Ser Thr Lys Gly Arg His Tyr Val Phe
85 90 95

Ile Tyr Lys His Asp Ser Ala Ser Asn Ile Ser Tyr Ser Leu Asn Ile
100 105 110

Lys

<210> SEQ ID NO 32
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: *C. perfringens*

-continued

<400> SEQUENCE: 32

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

Lys

<210> SEQ ID NO 33

<211> LENGTH: 113

<212> TYPE: PRT

<213> ORGANISM: *C. sordellii*

<400> SEQUENCE: 33

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

Asn

<210> SEQ ID NO 34

<211> LENGTH: 111

<212> TYPE: PRT

<213> ORGANISM: *Clostridium histolyticum*

<400> SEQUENCE: 34

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

-continued

Ser Gly Lys Phe Lys Ala Asp Lys Pro Gly Arg Tyr Tyr Ile His Leu
 85 90 95

Tyr Met Phe Asn Gly Ser Tyr Met Pro Tyr Arg Ile Asn Ile Glu
 100 105 110

<210> SEQ ID NO 35
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic peptide
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(30)
 <223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 35

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro
 1 5 10 15

Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 20 25 30

<210> SEQ ID NO 36
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic peptide
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(30)
 <223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 36

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro
 1 5 10 15

Xaa Gly Pro Xaa Ala Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 20 25 30

<210> SEQ ID NO 37
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic peptide
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(30)
 <223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 37

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro
 1 5 10 15

Xaa Ala Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 20 25 30

<210> SEQ ID NO 38
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic peptide
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(30)
 <223> OTHER INFORMATION: Any Xaa is hydroxyproline

-continued

<400> SEQUENCE: 38

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Ala Pro
 1 5 10 15

Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 20 25 30

<210> SEQ ID NO 39

<211> LENGTH: 30

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(30)

<223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 39

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Ala Pro Xaa Gly Pro
 1 5 10 15

Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 20 25 30

<210> SEQ ID NO 40

<211> LENGTH: 24

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(24)

<223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 40

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Cys Gly Pro Xaa Gly Pro
 1 5 10 15

Xaa Gly Pro Xaa Gly Pro Xaa Gly
 20

<210> SEQ ID NO 41

<211> LENGTH: 31

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(31)

<223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 41

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Ala Pro
 1 5 10 15

Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Cys
 20 25 30

<210> SEQ ID NO 42

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(22)

<223> OTHER INFORMATION: Any Xaa is hydroxyproline

-continued

<400> SEQUENCE: 42

Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 1 5 10 15

Pro Xaa Gly Pro Xaa Gly
 20

<210> SEQ ID NO 43

<211> LENGTH: 31

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(31)

<223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 43

Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 1 5 10 15

Pro Xaa Gly Pro Xaa Gly Pro Arg Gly Pro Arg Gly Pro Arg Gly
 20 25 30

<210> SEQ ID NO 44

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(9)

<223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 44

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 1 5

<210> SEQ ID NO 45

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(9)

<223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 45

Pro Xaa Gly Pro Xaa Gly Pro Xaa Ala
 1 5

<210> SEQ ID NO 46

<211> LENGTH: 26

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(26)

<223> OTHER INFORMATION: Any Xaa is hydroxyproline

<400> SEQUENCE: 46

Gly Pro Arg Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly
 1 5 10 15

-continued

Pro Xaa Gly Pro Xaa Gly Pro Xaa Gly Cys
 20 25

<210> SEQ ID NO 47
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic peptide: GST Tag

<400> SEQUENCE: 47

Gly Ser Pro Gly Ile Pro Gly
 1 5

We claim:

1. A method of slowing hair growth comprising administering a composition comprising a bacterial collagen-binding polypeptide segment linked to a PTH/PTHrP receptor antagonist to a subject to slow hair growth relative to the hair growth the subject would experience without treatment, wherein the bacterial collagen-binding polypeptide segment comprises a collagen-binding polypeptide derived from an M9 peptidase selected from the group consisting of, one of SEQ ID NOs: 13-34 or a fragment of at least 8 consecutive amino acids of SEQ ID NOs: 13-34, residues 34-158 of SEQ ID NO: 1, a fragment of at least 8 consecutive amino acids from residues 34-158 of SEQ ID NO: 1, and a peptide that is at least 90% identical to residues 34-158 of SEQ ID NO: 1 or SEQ ID NOs: 13-34, and wherein the PTH/PTHrP receptor antagonist comprises a sequence selected from the group consisting of residues 7-33 of SEQ ID NO: 7, residues 7-14 of SEQ ID NO: 7, a fragment of at least 8 consecutive amino acids from residues 7-34 of SEQ ID NO: 7, and residues ((-1)-33) of PTH.

2. The method of claim 1, wherein the composition is administered locally.

3. The method of claim 2, wherein the composition is administered topically.

4. The method of claim 1, wherein and the N-terminus of the collagen-binding polypeptide segment is linked directly

or through a linker polypeptide segment to the C-terminus of the PTH/PTHrP receptor antagonist polypeptide.

5. The method of claim 1, wherein the collagen-binding polypeptide segment and the PTH/PTHrP receptor antagonist polypeptide are chemically cross-linked to each other or are polypeptide portions of a fusion protein.

6. The method of claim 1, wherein the subject is human.

7. The method of claim 1, wherein the bacterial collagen-binding polypeptide segment comprises residues 34-158 of SEQ ID NO: 1 or a peptide that is at 90% identical to residues 34-158 of SEQ ID NO: 1.

8. The method of claim 1, wherein the PTH/PTHrP receptor antagonist comprises residues 7-33 of SEQ ID NO: 7.

9. The method of claim 1, wherein the bacterial collagen-binding polypeptide segment linked to the PTH/PTHrP receptor antagonist is a fusion protein comprising SEQ ID NO: 10.

10. The method of claim 4, wherein the linker polypeptide segment comprises a PKD domain.

11. The method of claim 10, wherein the PKD domain comprises residues 807-901 of SEQ ID NO: 6.

12. The method of claim 1, wherein the composition is administered after the subject undergoes a hair removal procedure.

* * * * *