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Collagen-binding Agent Compositions And Methods Of Using The Same

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(54) **COLLAGEN-BINDING AGENT
COMPOSITIONS AND METHODS OF USING
THE SAME**

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(57) **ABSTRACT**

The invention generally relates to collagen-binding agent compositions and methods of using the same. More specifically, the invention relates in part to new collagen-binding agent compositions and methods that may be used to treat damaged collagen within tissues or used to specifically target therapeutics to tissues containing undamaged or damaged collagen.

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* cited by examiner

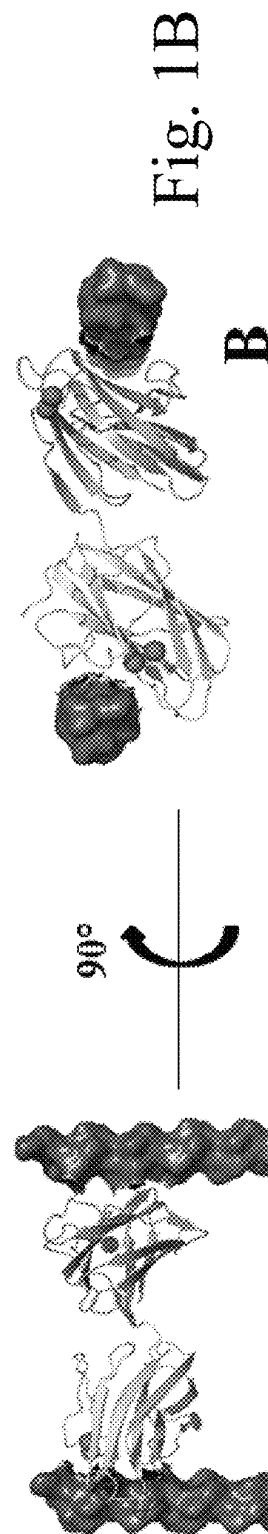
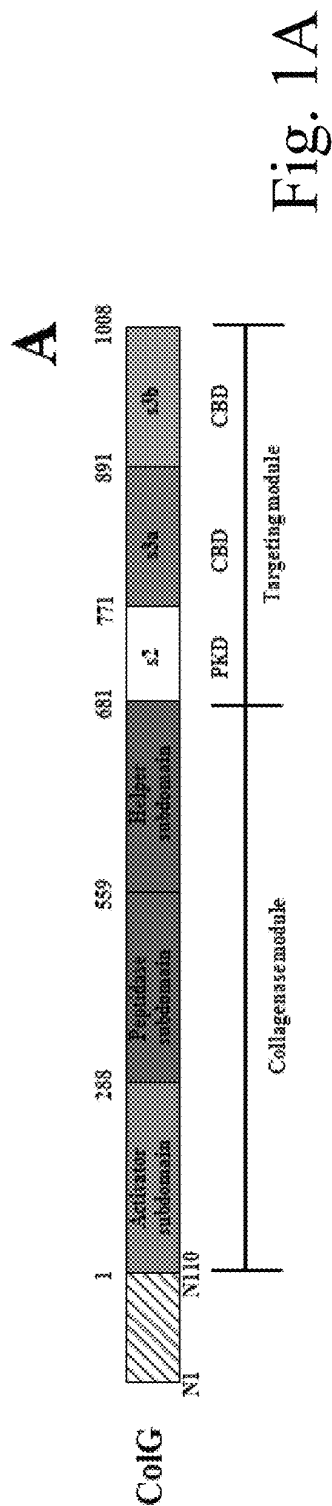


Fig. 1C



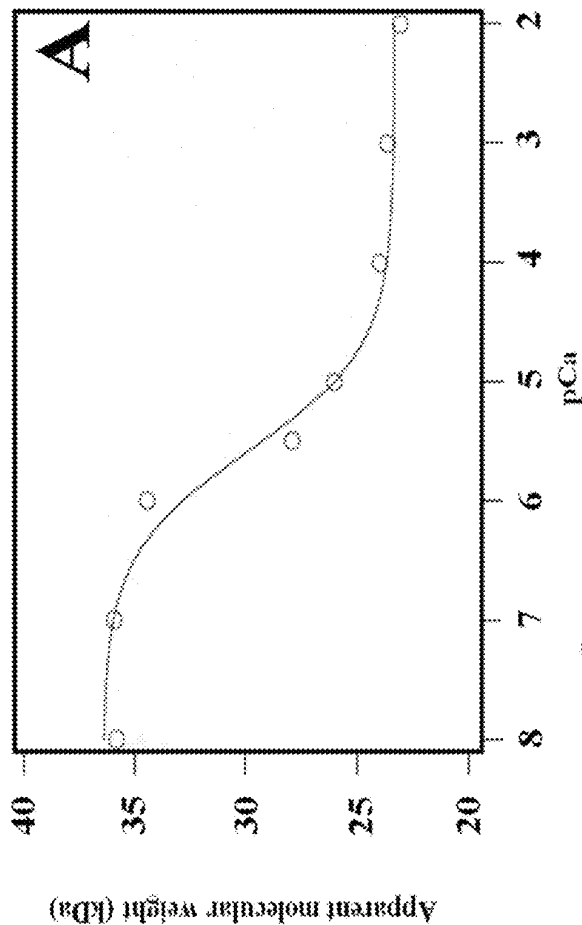


Fig. 2A

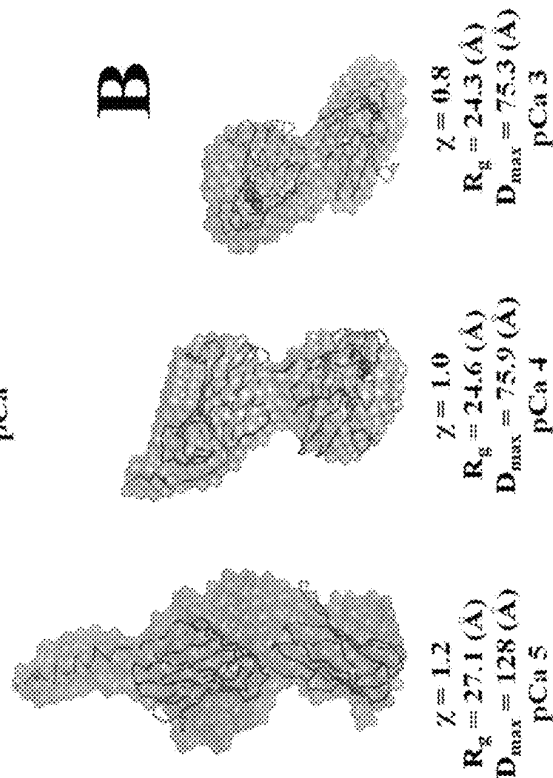


Fig. 2B

Fig. 3

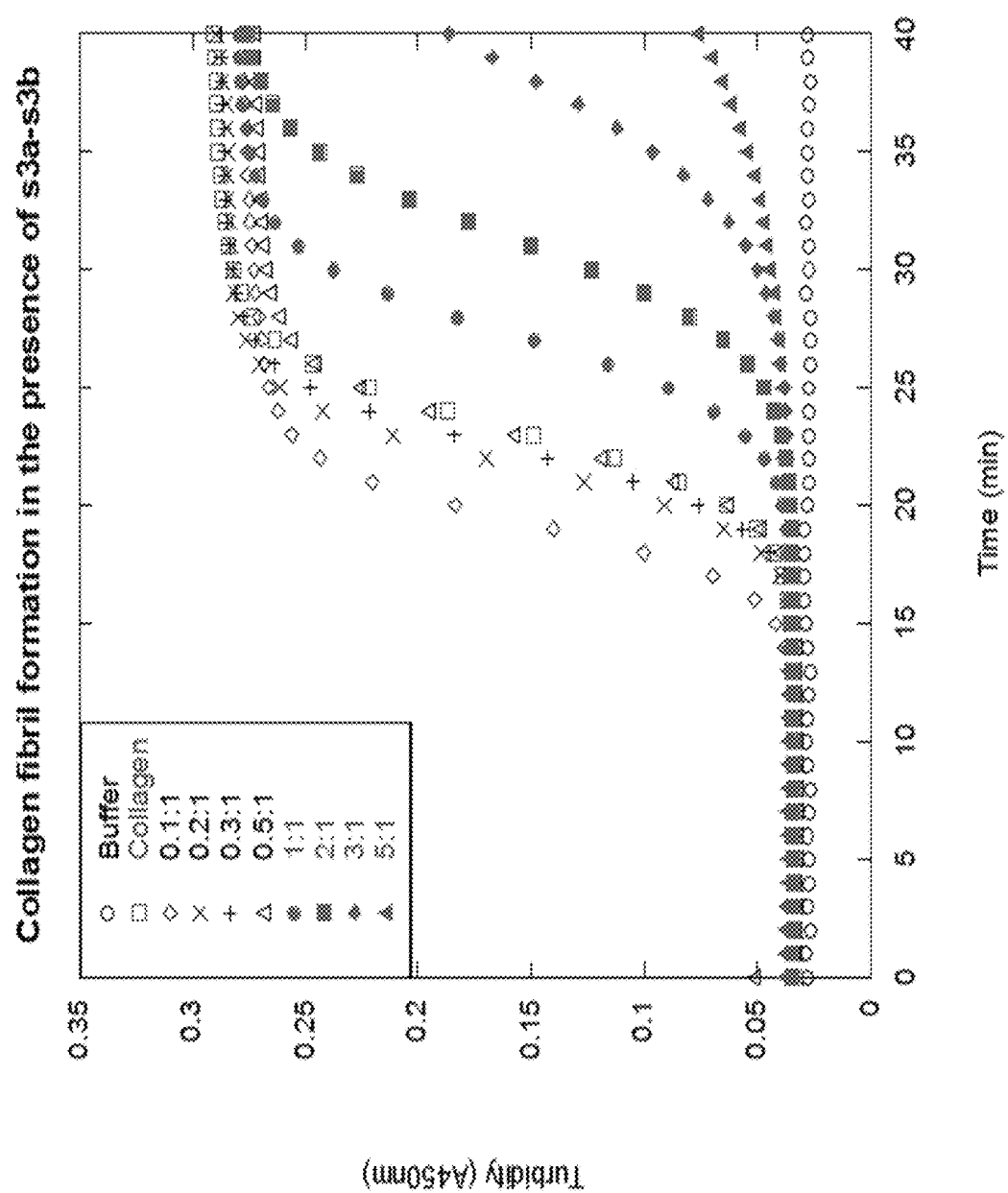


Fig. 4C

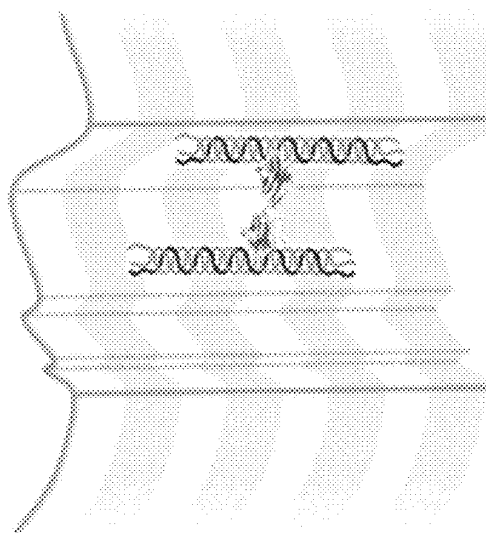


Fig. 4B

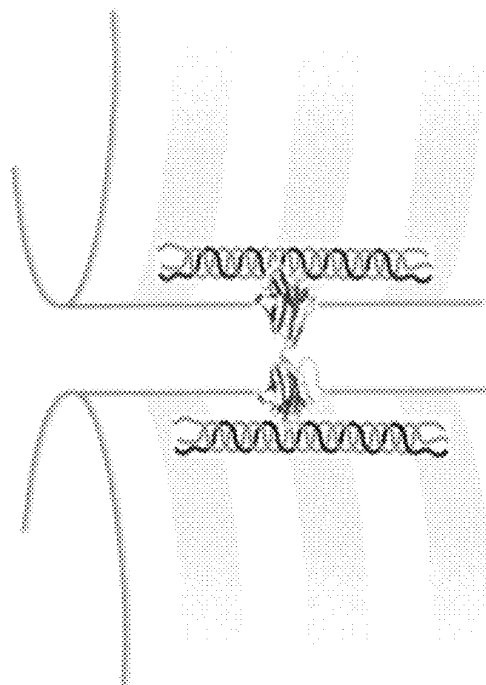


Fig. 4A

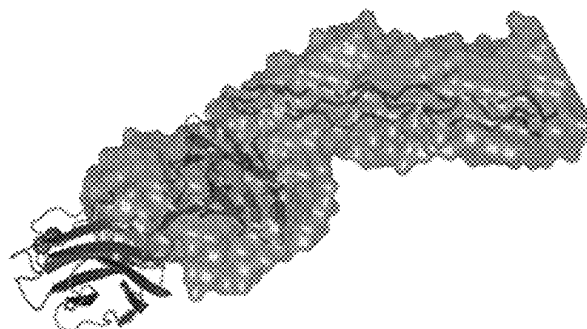


Fig. 5

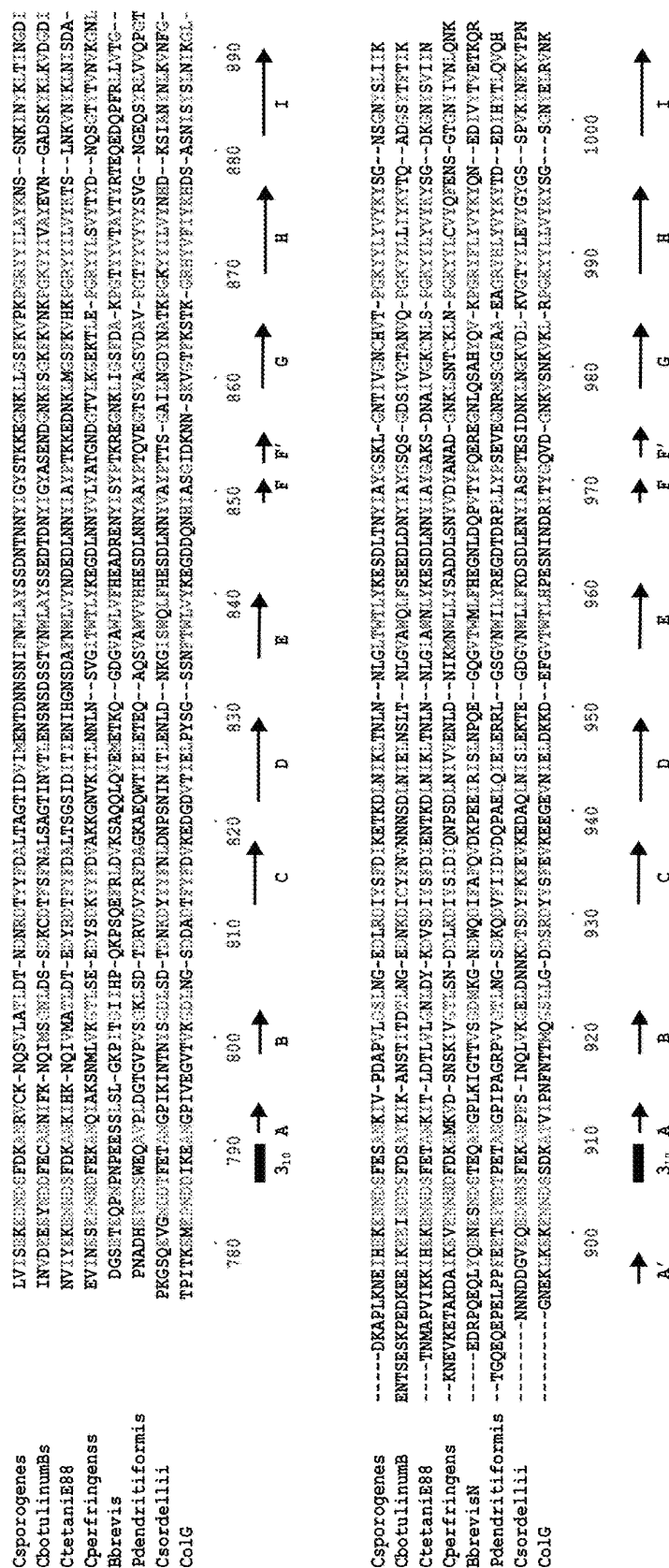


Fig. 6

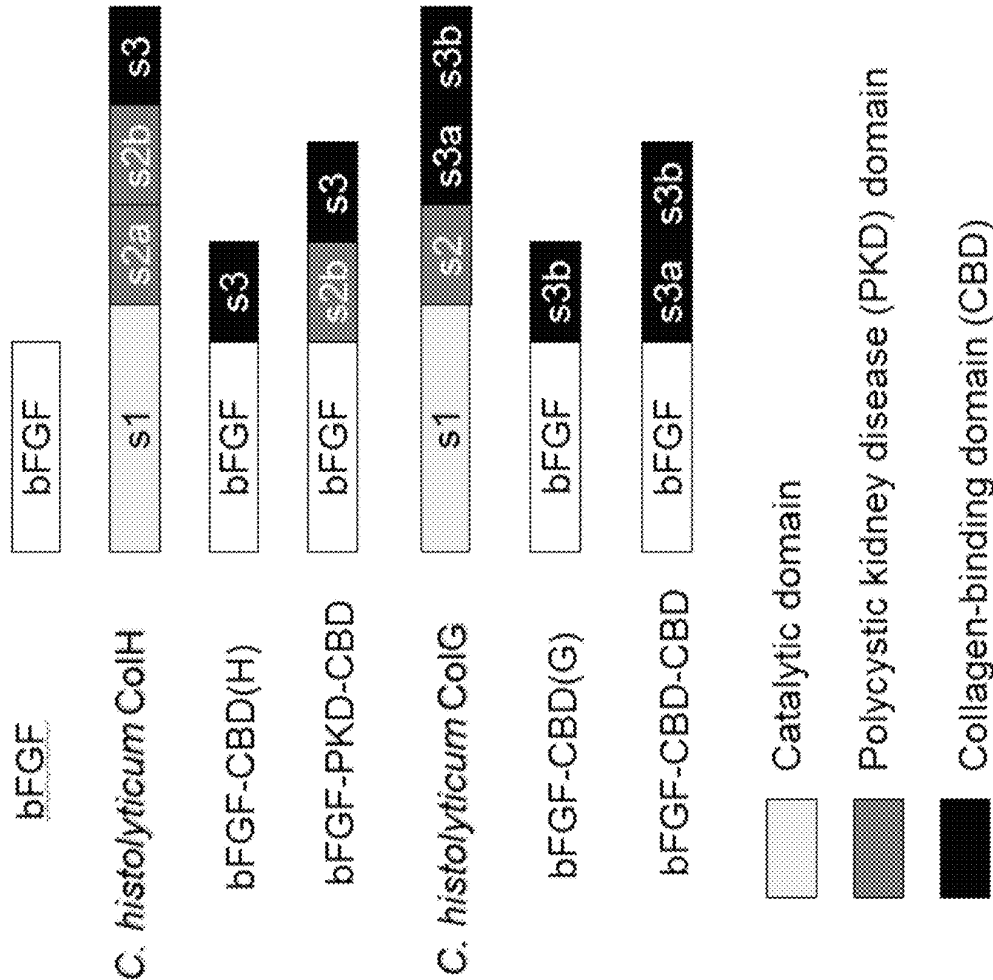


Fig. 7

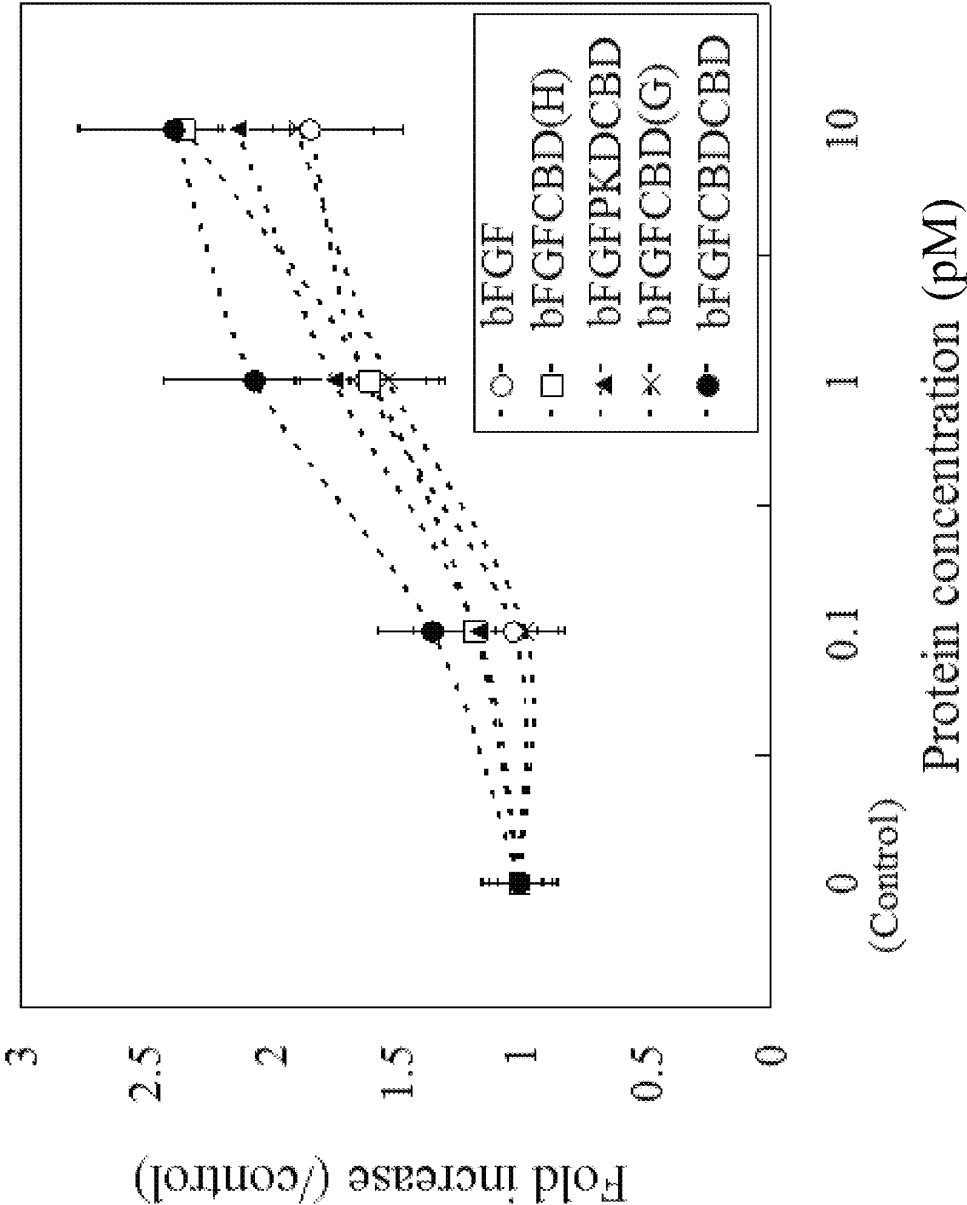


Fig. 8A Fig. 8B Fig. 8C

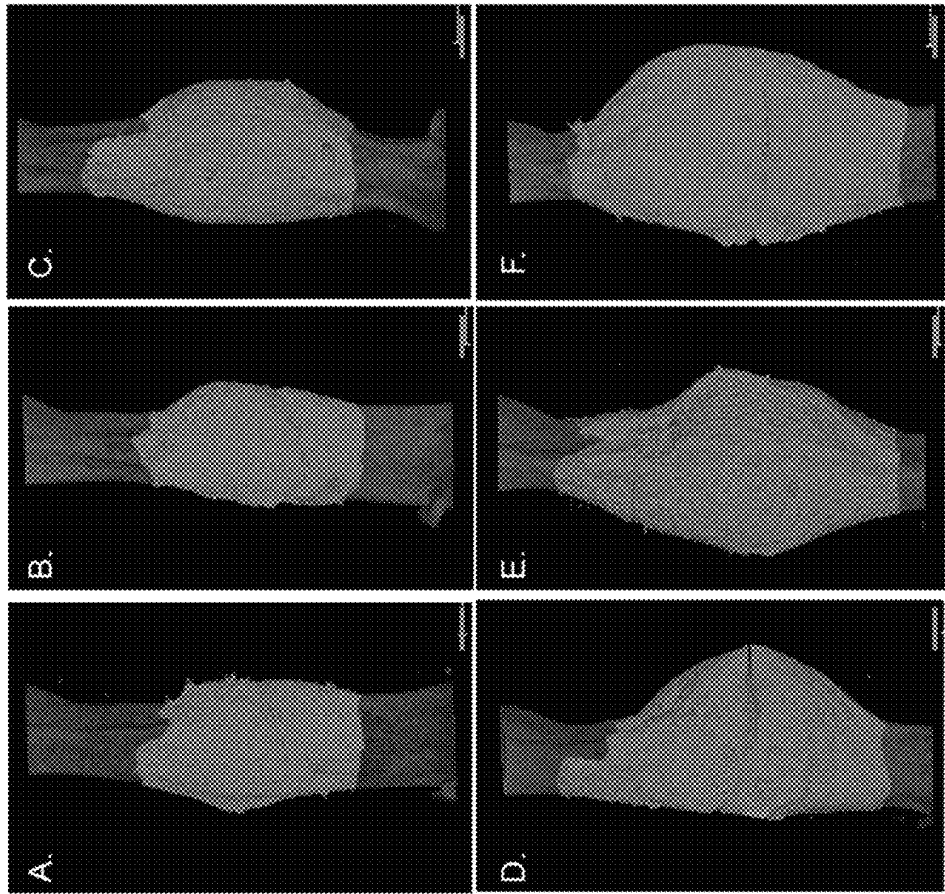


Fig. 8D Fig. 8E Fig. 8F

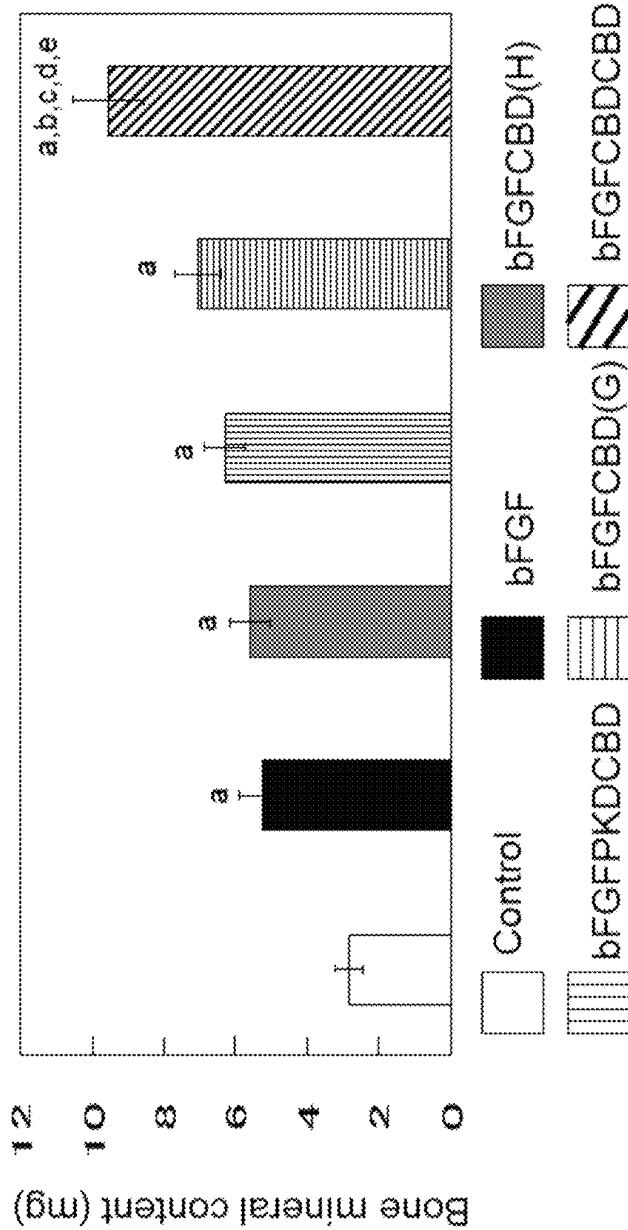
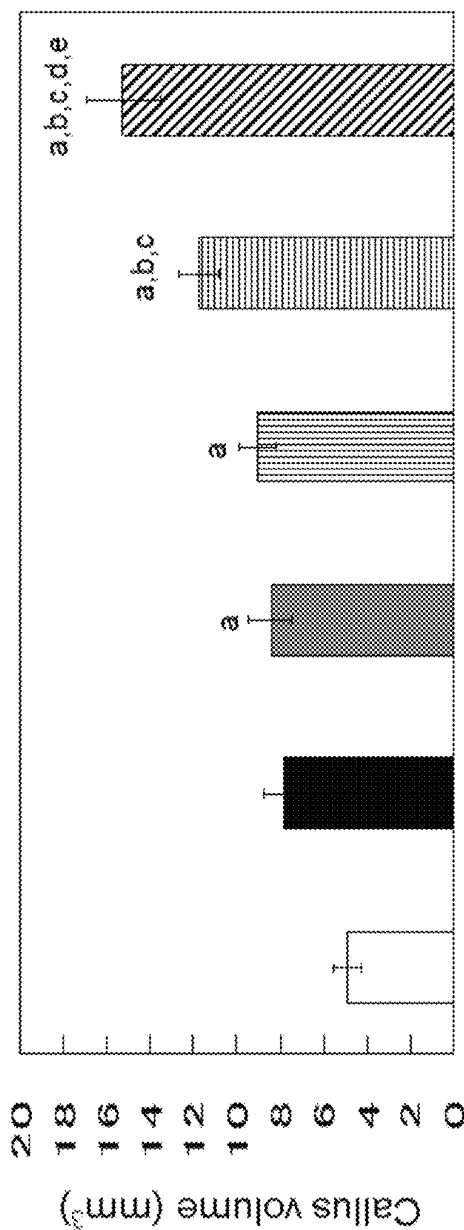


Fig. 10A

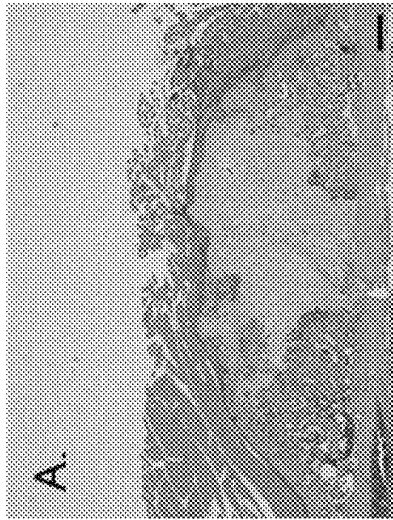


Fig. 10B



Fig. 10C

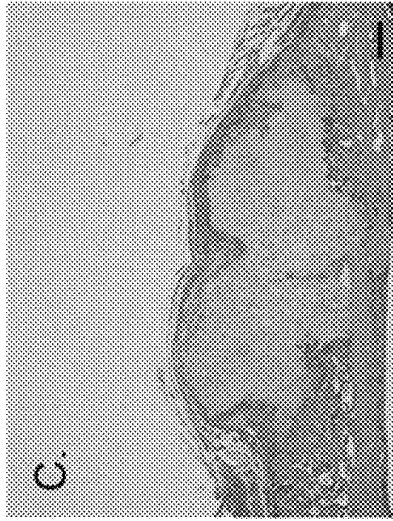


Fig. 10D

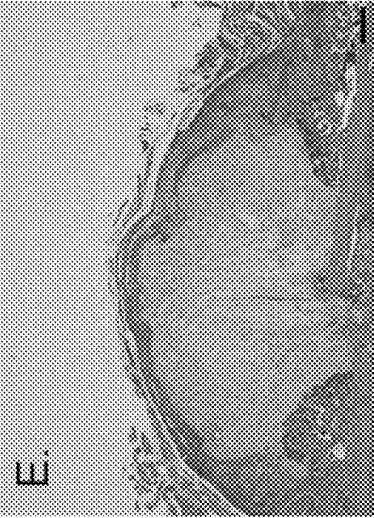


Fig. 10E



Fig. 10F

Fig. 11

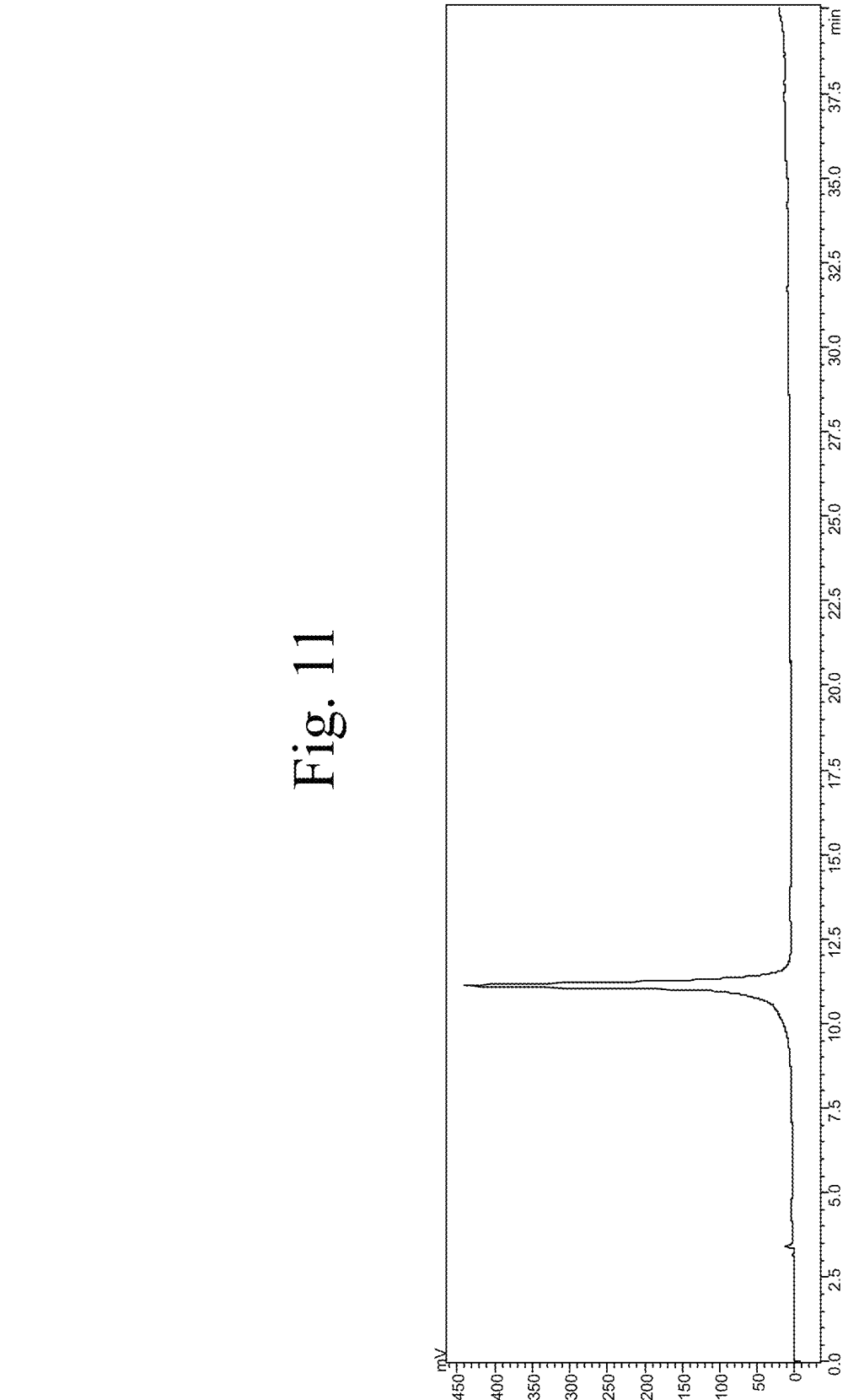


Fig. 12

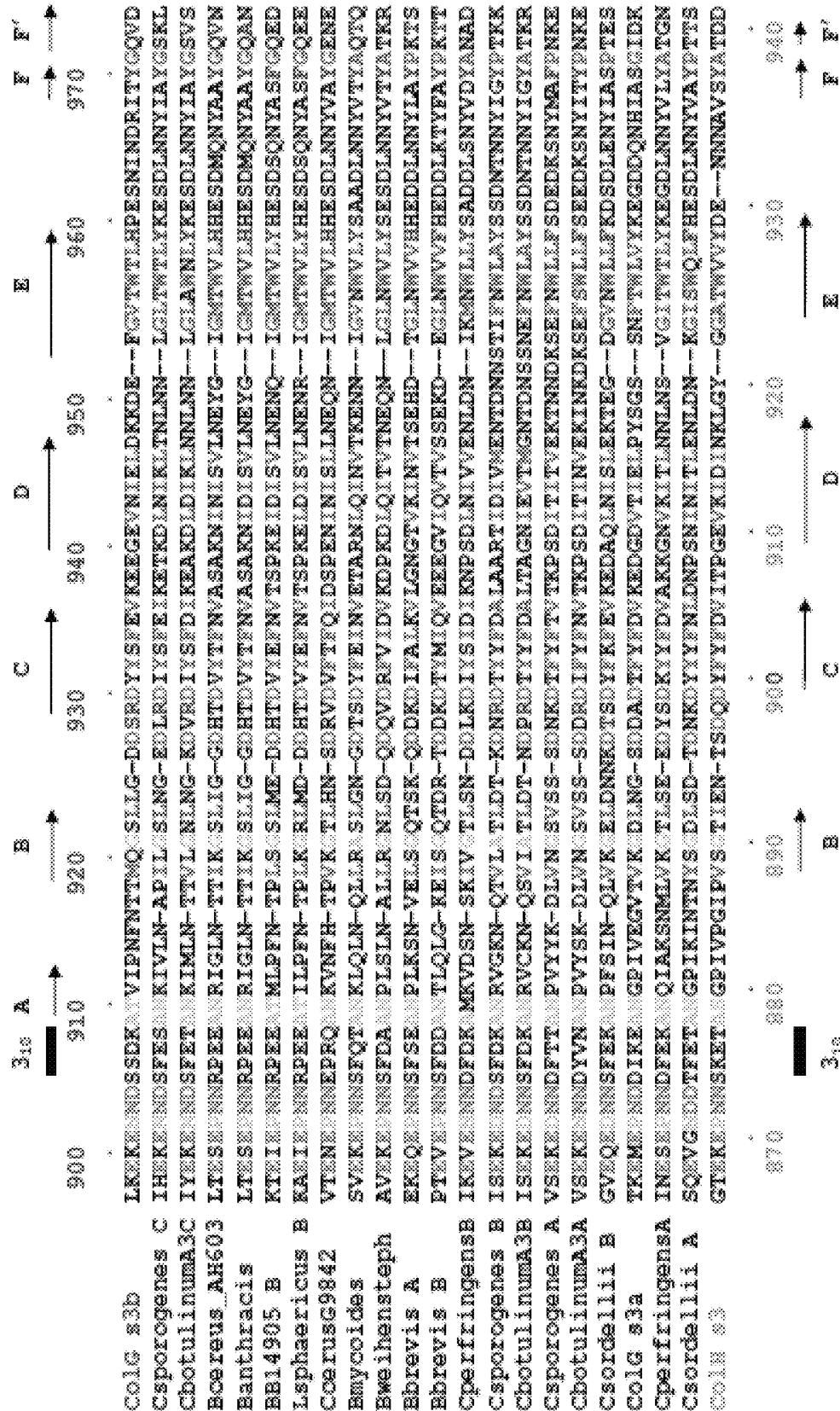


Fig. 12 (continued)

	G	H	I
	980	990	1000
ColG s3b	-GNKVS	NKVKL-RPGKY	LLVYKYSG--SGN ELRVN
Csporogenes C	-GSTIVG	NCHV-TRGKY	LYLVYKYSG-NNGN SILIK
CbotulinumA3C	-GNTIKG	KCNV-APGKY	LYLVYKYSG-DNGN SLAIK
Bcereus AH603	-GNHIEAN	FNA-KPGKY	LYLVYKYDN-GDGT ELSVK
Banthracis	-GNHIEAN	FNA-KPGKY	LYLVYKYDN-GDGT ELSVK
BB14905 B	-GNMINGK	UNA-KPGKY	LYLVYKFEN-ENGT TVHVQ
Lsphaericus B	-GNMINGK	IHA-EPGKY	LYLVYKFEN-ENGT TVQVQ
CcerusG9842	-GNVVKGT	YNA-KPGKY	LYLVYKYEN-KDGS VLNIK
Bmycoides	-GNKLVGS	YNA-HPGKY	LHVYQYGG-GTGN TVEVK
Bweihensteph	DGNKLLGN	YNA-KPGKY	LSVYKYG-GTGN TVEVK
Bbrevis A	-CKTLSGE	FEA-TGTYL	SVNFNG-ETIP KVTAE
Bbrevis B	-CKLTGE	FEA-KPGKY	LLVYNTNN-TKIP KAIYN
CperfringensB	-GNKLSNT	CKL-NPGKY	LCVYQFENS
Csporogenes B	EGNKIMG	SEKVPKPGRY	YLAYKNSS-NKIN KLTIN
CbotulinumA3B	EGNKITG	NFKVDKPGRY	YIVAYKTSS-NKIN KINIK
Csporogenes A	LGNQLS	NTVKINKPGKY	LVYKTLG-EKVD KFSIE
CbotulinumA3A	LENLFYST	VKIDKPGKY	LVYKVSG-EKSD EFNIE
Csordellii B	IDNKINGK	VDL-KVSTY	LEVYGYGS-SPVK NFKVT
ColG s3a	-NNSKVGT	FKSTK-GRIYV	FIYKHDSASNIS SILNIK
CperfringensA	EGTVLKG	EKTLE-PGRYLS	VYTYDN-QSGA TVNVK
Csordellii A	-GAILNGD	YNATKPGKY	LVVNHDK-SIAN NLKYN
ColH s3	-GQWLSCK	TKADKPGRY	IHLVNFNG-SYMP RINIE
	950	960	970
	G	H	I

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COLLAGEN-BINDING AGENT COMPOSITIONS AND METHODS OF USING THE SAME

CROSS-REFERENCE TO RELATED APPLICATIONS

The present application is a national stage filing under U.S.C. 371 of International Application No. PCT/US2018/017665 filed Feb. 9, 2018, which claims the benefit of priority of U.S. Provisional Patent Application No. 62/457,410, filed on Feb. 10, 2017, the contents of which are incorporated herein by reference in their entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with government support under grant number RR015569 and RR016460 awarded by the National Institute of Health. The United States government has certain rights in the invention.

SEQUENCE LISTING

This application is being filed electronically via EFS-Web and includes an electronically submitted Sequence Listing in .txt format. The .txt file contains a sequence listing entitled "2018-02-09_5965-00084_ST25.txt" created on Feb. 9, 2018 and is 72,312 bytes in size. The Sequence Listing contained in this .txt file is part of the specification and is hereby incorporated by reference herein in its entirety.

Introduction

Collagen is the primary structural protein found in the extracellular space of various animal tissues. Collagen, for example, can be found in fibrous tissues such as skin, ligaments, and tendons. It is also abundant in bones, cartilage, corneas, blood vessels, and muscle tissues.

Abnormal or damaged collagen underlies several medical conditions including wounding and collagenopathies. Collagenopathies represent a large number of diseases in which collagen structure or formation is not normal. This group of diseases results in a broad spectrum of symptoms including bone defects, vascular defects, and skin defects. Many of these diseases have no or only ineffective treatments available.

Collagen-targeting agents are also attractive agents for delivering therapeutics to different animal tissues or subsites within a particular tissue. 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. Targeted delivery systems allow the therapeutic agents to be most active at the sites where the agent is needed while minimizing the off-site effects of the therapeutic agent which may lead to unwanted toxicity and side effects. While use of targeted liposomes or polypeptides, such as antibodies, to target therapeutic agents to particular sites within the body has proved successful, additional delivery agents are needed. There thus is a need in the art for new collagen-targeting agents that may be used to treat tissues with damaged or normal collagen or to deliver appropriate therapeutics to such tissues.

SUMMARY

In one aspect, collagen-binding agents are provided. The collagen-binding agents may include two collagen-binding

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domains linked by a domain linker. The two collagen-binding domains may be selected from any one of the polypeptides of SEQ ID NOs: 1-47, a variant of the polypeptides of SEQ ID NOs: 1-47, or a fragment of the polypeptides of SEQ ID NOs: 1-47. SEQ ID NOs: 1-39 specify individual collagen-binding domains (i.e., ColG s3a, ColG s3b, ColH s3) from ColG and ColH proteins from various bacterial species. SEQ ID NOs: 40-47 specify tandem collagen-binding domains found in ColG proteins from various bacterial species. See, also, FIG. 5. The collagen-binding agents of the present invention may further include a therapeutic agent linked to the collagen-binding agent by a therapeutic agent linker. The therapeutic agent may be selected from FGF, parathyroid hormone (PTH), PTH/PTHrP receptor agonist, PTH/PTHrP receptor antagonist, bone morphogenic protein (BMP), G-CSF, BMP-2, BMP-3, anti-sclerostin antibody, growth hormone, IGF-1, VEGF, TGF- β , KGF, TGF- α , TGF- β 1, TGF- β receptor, CT, GH, GM-CSF, EGF, PDGF, celiprolol, activins and connective tissue growth factors.

In another aspect, pharmaceutical compositions are provided. The pharmaceutical compositions may include any of the collagen-binding agents described herein and a pharmaceutical carrier.

In a further aspect, methods of treating a condition are also provided. The methods may include administering any of collagen-binding agents or pharmaceutical compositions described herein to a subject in an amount effective to treat the condition.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1A shows a schematic diagram of the collagenases secreted by *C. histolyticum*. FIG. 1B shows pseudo-twofold symmetry in the structure of the tandem collagen-binding domain. FIG. 1C shows the two-fold axis is perpendicular to the plane of the page. The key residues for binding to collagen are highlighted: yellow for ColGS3a, blue for ColGS3b.

FIG. 2A shows the apparent molecular weights of the tandem CBD as a function of pCa determined by analytical size exclusion chromatography. FIG. 2B shows molecular envelopes of the tandem CBD at pCa 3, 4, and 5 based on SAXS scattering profiles.

FIG. 3 shows the influence of collagen binding on self-assembly of collagen type I.

FIG. 4A shows the molecular envelopes of the tandem CBD to mini-collagen based on SAXS scattering profiles. FIGS. 4B and 4C show models of the binding of tandem collagen-binding domain to collagen fibril.

FIG. 5 shows a sequence alignment of bacterial tandem collagen binding domains (See SEQ ID NOs: 40-47). Residues binding to collagen are highlighted in blue. Calcium-binding residues are in red, structurally important residues are shown in green.

FIG. 6 shows a scheme for the preparation of the four collagen binding-basic fibroblast growth factor constructs used in Example 2.

FIG. 7 shows the in-vitro proliferation activity of bFGF and CB-bFGFs. Dose-dependent induction of periosteal mesenchymal cell proliferation by bFGF and CB-bFGFs. Cell numbers were quantified three days after the treatment. Data are presented as the mean $\pm$ S.E. (n=8).

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FIGS. 8A-8F show 3D micro-CT analysis of femurs after injection of poly(Pro-Hyp-Gly)₁₀ loaded with bFGF and CB-bFGFs. 3D micro-CT images of fractured mouse femurs treated with (FIG. 8A) PBS, (FIG. 8B) bFGF, (FIG. 8C) bFGF-CBD(H), (FIG. 8D) bFGF-PKD-CBD, (FIG. 8E) bFGF-CBD-CBD (FIG. 8F) after 4 weeks of recovery. Red: newly formed bone; gray: existing bone. The scale bars indicate 3 mm.

FIGS. 9A-9B shows 3D micro-CT analysis of rat femurs four weeks after the injection of poly(Pro-Hyp-Gly)₁₀ loaded with bFGF and CB-bFGFs at femoral fracture sites. FIG. 9A is a graph showing callus volume (mm³) and FIG. 9B is a graph showing bone mineral content. Data are presented as the mean±S.E. (n=8). Lower case letters above the bars in the graph are defined as follows: a, P<0.05 compared with the control group. b, P<0.05 compared with the bFGF group. c, P<0.05 compared with the bFGF-CBD (H) group. d, P<0.05 compared with the bFGF-PKD-CBD group. e, P<0.05 compared with the bFGF-CBD(G) group.

FIGS. 10A-10F show representative hematoxylin and eosin-stained tissue sections on day 14 of fracture healing. Histological images of fractured mouse femurs treated with (FIG. 10A) PBS, (FIG. 10B) bFGF, (FIG. 10C) bFGF-CBD (ColH s3), (FIG. 10D) bFGF-PKD-CBD (ColH s2b-s3), (FIG. 10E) bFGF-CBD (ColG s3b), and (FIG. 10F) bFGF-CBD-CBD (s3a-s3b) after 14 days of recovery. Scale bar=500 μm.

FIG. 11 shows an HPLC profile of H-Gly-Pro-Arg-Gly-(Pro-Hyp-Gly)₁₂-NH₂ (SEQ ID NO: 60). HPLC gradient: 10-40% CH₃CN in 0.05% TFA over 30 min at 60° C.

FIG. 12 is a sequence alignment showing the alignment of several M9B bacterial collagenases from the *Bacillus* and *Clostridium* families (See SEQ ID NOS: 1-39). 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.

DETAILED DESCRIPTION

In the non-limiting Examples, the present inventors report the high-resolution structure of a bacterial tandem collagen-binding agent for the first time. The pseudo-symmetrical arrangement of the tandem collagen-binding agent, resulting from gene duplication and fusion, could allow it to recognize a unique niche in collagen fibril to facilitate degradation of collagen. The structure of the tandem collagen-binding agent also reveals that it could wedge between parallel collagen molecules. This structure combined with the previously identified collagen-binding domain preference for under-twisted regions of collagen suggests the tandem collagen-binding agent targets the bacterial collagenase, ColG, to damaged regions of the collagen fibril. Based on this new understanding of how tandem collagen-binding agent interacts with collagen, the present inventors disclose new collagen-binding agents that may be used to treat damaged collagen within tissues or used to specifically target therapeutics to tissues containing undamaged or damaged collagen. The tandem collagen binding agents provided herein may allow for tighter binding to collagen by bridging two collagen fibrils. This novel binding interaction of the collagen binding agents described herein will provide novel and unexpected therapeutic uses. The increased binding affinity and cross-linking of collagen molecules may make these tandem collagen binding agents more effective for certain

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applications than their single binding counterparts. Applications may include skin applications.

In one aspect, collagen-binding agents are provided. The collagen-binding agents may include two collagen-binding domains linked by a domain linker. As used herein, a “collagen-binding domain” refers to a polypeptide that binds collagen. In some embodiments, the collagen-binding domain may bind collagen with a K_d of less than 500 μM, 100 μM, 10 μM, 1 μM, 500 nM, 100 nM, 10 nM, 1 nM, or 0.1 nM. Determination of whether a collagen-binding domain binds collagen can be made, for example, as described in U.S. Patent Publication No. 2010/0129341, which is incorporated herein by reference in its entirety. Briefly, the collagen-binding domain may be incubated with collagen in binding buffer, and the mixture is then filtered through a filter that would otherwise allow the collagen-binding domain 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 collagen-binding domain. Suitably, at least 80%, 85%, 90%, 95%, 98% or more suitably at least 99% of the collagen-binding domain is retained by the filter in this assay, as compared to when the filtration is performed without collagen.

The collagen-binding domain may be a bacterial collagen-binding domain. Among other proteins, the collagen-binding domain may be derived from a bacterial ColG protein (Matsushita et al., (1999) J. Bacteriol. 181:923-933) or a bacterial ColH protein (Yoshihara et al., (1994) J. Bacteriol. 176: 6489-6496). As shown in FIG. 1, ColG is a class I collagenase found in various bacterial species including *Clostridium* species. ColH is a class II collagenase also found in various bacterial species including *Clostridium* species. The collagen-binding domain may also be any one of the polypeptides provided in SEQ ID NOS: 1-39, which specify collagen-binding domains from various bacterial species such as *Clostridium* and *Bacillus* species. Those of skill in the art will appreciate that other members of these collagen-binding protein families (i.e. ColG and ColH) may be useful in the compositions and methods described herein.

Suitably, the collagen-binding agents lack collagenase activity. “Collagenase activity” refers to the ability of a polypeptide to degrade or breakdown collagen. For example, as shown in FIG. 1A, ColG and ColH proteins have collagenase modules that include several subdomains that enable these proteins to degrade or breakdown collagen. In some embodiments, the collagen-binding agents lack these or similar collagenase modules.

The collagen-binding agents may include two collagen-binding domains that may be the same type of collagen-binding domain or may be different types of collagen-binding domains. For example, as exemplified in FIG. 1A, bacterial ColG proteins have two types of collagen-binding domains: a s3a collagen-binding domain and a s3b collagen-binding domain. Bacterial ColH proteins have a single collagen-binding domain known as an s3 domain. Thus, the two collagen-binding domains of the presently disclosed collagen-binding agents may be both ColG s3a domains, both ColG s3b domains, both ColH s3 domains, or any combinations thereof. Furthermore, the two collagen-binding domains of the presently disclosed collagen-binding agents may be from the same bacterial species or different species. For example, one of the collagen-binding domains may be a ColG s3a domain from *Clostridium histoliticum* while the other collagen-binding domain may be a ColG s3b domain from *Brevibacillus brevis*.

The two collagen-binding domains of the presently disclosed collagen-binding agents may be selected from any

one of the polypeptides of SEQ ID NOs: 1-47 or those polypeptides shown in FIGS. 5 and 12. SEQ ID NOs: 1-39 specify individual collagen-binding domains (i.e., ColG s3a, ColG s3b, ColH s3) from ColG and ColH proteins from various bacterial species. SEQ ID NOs: 40-47 specify tandem collagen-binding domains found in ColG proteins from various bacterial species. See, also, FIG. 5.

The collagen-binding domains of the present invention may be variants of the polypeptides of SEQ ID NOs: 1-47. As used herein the term “wild-type” is a term of the art understood by skilled persons and means the typical form of a polypeptide as it occurs in nature as distinguished from “variant” or “mutant” forms. As used herein, a “variant,” “mutant,” or “derivative” refers to a polypeptide molecule having an amino acid sequence that differs from a reference protein or polypeptide molecule. A variant may have one or more insertions, deletions, or substitutions of an amino acid residue relative to a reference molecule. A variant or mutant may include a fragment of a reference molecule. For example, a collagen-binding domain variant may have one or more insertions, deletions, or substitution of at least one amino acid residue relative to the “wild-type” collagen-binding domain polypeptide. The polypeptide sequences of “wild-type” collagen-binding domains from various bacterial species are presented as SEQ ID NOS: 1-47. These sequences may be used as reference sequences.

A “deletion” in a polypeptide refers to a change in the amino acid sequence resulting in the absence of one or more amino acid residues. A deletion may remove at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 50, 100, or more amino acids residues. A deletion may include an internal deletion and/or a terminal deletion (e.g., an N-terminal truncation, a C-terminal truncation or both of a reference polypeptide).

“Insertions” and “additions” in a polypeptide refer to changes in an amino acid sequence resulting in the addition of one or more amino acid residues. An insertion or addition may refer to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more amino acid residues. A variant of a collagen-binding domain may have N-terminal insertions, C-terminal insertions, internal insertions, or any combination of N-terminal insertions, C-terminal insertions, and internal insertions.

Regarding variant collagen-binding domains and agents, the phrases “% sequence identity,” “percent identity,” or “% identity” refer to the percentage of residue matches between at least two amino acid sequences aligned using a standardized algorithm. Methods of amino acid sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail below, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide. Percent identity for amino acid sequences may be determined as understood in the art. (See, e.g., U.S. Pat. No. 7,396,664, which is incorporated herein by reference in its entirety). A suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST), which is available from several sources, including the NCBI, Bethesda, Md., at its website. The BLAST software suite includes various sequence analysis programs including “blastp,” that is used to align a known amino acid sequence with other amino acids sequences from a variety of databases.

Polypeptide sequence identity may be measured over the length of an entire defined polypeptide sequence, for

example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

As described herein, variant collagen-binding domains and agents may have at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% 98%, or 99% sequence identity to any one of SEQ ID NOs: 1-47.

The polypeptide sequences of the variant collagen-binding domains and agents as contemplated herein may include conservative amino acid substitutions relative to a reference amino acid sequence. For example, variant collagen-binding domains and agents may include conservative amino acid substitutions relative to a reference molecule. “Conservative amino acid substitutions” are those substitutions that are a substitution of an amino acid for a different amino acid where the substitution is predicted to interfere least with the properties of the reference polypeptide. In other words, conservative amino acid substitutions substantially conserve the structure and the function of the reference polypeptide. Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

The disclosed variant collagen-binding domains and agents described herein may have one or more functional or biological activities exhibited by a reference polypeptide (e.g., one or more functional or biological activities exhibited by wild-type collagen-binding domains and agents (i.e., SEQ ID NOs: 1-47, See FIGS. 5 and 12). Suitably, the disclosed variant collagen-binding domains and agents retain at least 20%, 40%, 60%, 80%, or 100% of the collagen binding activity of the reference polypeptide (i.e., SEQ ID NOs: 1-47, See FIGS. 5 and 12).

FIG. 5 shows a sequence alignment of several bacterial tandem collagen-binding domains included as SEQ ID NOs: 40-47. As can be seen from the sequence alignment, these proteins have a relatively small amount of sequence identity, but they all are expected to bind to collagen in a similar fashion and are believed to have similar conformations. Thus any of the polypeptides shown in FIG. 5 (i.e., SEQ ID NOs: 40-47) or the collagen-binding domains, variants, or fragments thereof can be used in the compositions and methods described herein. In FIGS. 5 and 12, the amino acid residues important for collagen-binding activity are highlighted in blue. Calcium-binding residues are in red and structurally important residues are shown in green. Based on this alignment it becomes immediately apparent to a person of ordinary skill in the art that various amino acid residues may be altered (i.e. substituted, deleted, etc.) without substantially affecting the collagen-binding activity of the polypeptide. For example, a person of ordinary skill in the art would understand that amino acid residues shown in black likely could be modified without substantially affecting the collagen-binding activity of the polypeptide. A person of ordinary skill in the art would also appreciate that substitutions in a reference collagen-binding domain or agent could be based on alternative amino acid residues that occur at the same position in other collagen-binding domains or agents

from other bacterial species. At position 996, for example, the collagen-binding domains shown have either a tyrosine (Y) or phenylalanine (F) residue. Thus, one exemplary modification that is apparent from the sequence alignment in FIG. 5 is a Y996F substitution in a collagen-binding domain or agent. Similar modifications could be made at each position of the sequence alignment shown in FIG. 5.

SEQ ID NOs: 1-39 also include collagen-binding domains that are not shown in FIG. 5, several of these are included in FIG. 12. A person of ordinary skill in the art, however, could easily align these polypeptide sequences with the polypeptide sequences shown in FIGS. 5 and 12 to determine what additional variants could be made to these additional collagen-binding domains. Thus polypeptides having 85%, 88%, 90%, 92%, 94%, 95%, 96%, 97%, 98% or 99% amino acid identity to the collagen-binding polypeptides provided herein. The variant polypeptides are still able to bind collagen.

The collagen-binding domains of the present invention may be full-length versions of SEQ ID NOs: 1-47 or fragments of SEQ ID NOs: 1-47 having at least 8, 16, 32, 64, 100 or more consecutive amino acids of any one of SEQ ID NOs: 1-47. As used herein, a "fragment" is a portion of an amino acid sequence which is identical in sequence to, but shorter in length than, a reference sequence. A fragment may comprise up to the entire length of the reference sequence, minus at least one amino acid residue. In some embodiments, a fragment may comprise at least 8, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or more contiguous amino acid residues of a reference polypeptide (i.e., SEQ ID NOs: 1-47). Fragments may be preferentially selected from certain regions of a molecule. The term "at least a fragment" encompasses the full length polypeptide. A fragment of a collagen-binding domain or agent may comprise or consist essentially of a contiguous portion of an amino acid sequence of the full-length collagen-binding domain or agent (i.e., SEQ ID NOs: 1-47). A fragment may include an N-terminal truncation, a C-terminal truncation, or both truncations relative to the full-length collagen-binding domain or agent. The N-terminal and/or C-terminal truncations may include removal of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid residues from a reference polypeptide (i.e., SEQ ID NOs: 1-47).

The collagen-binding domains and agents contemplated herein may be further modified *in vitro* or *in vivo* to include non-amino acid moieties. These modifications may include but are not limited to acylation (e.g., O-acylation (esters), N-acylation (amides), S-acylation (thioesters)), acetylation (e.g., the addition of an acetyl group, either at the N-terminus of the protein or at lysine residues), formylation, lipoylation (e.g., attachment of a lipoate, a C8 functional group), myristoylation (e.g., attachment of myristate, a C14 saturated acid), palmitoylation (e.g., attachment of palmitate, a C16 saturated acid), alkylation (e.g., the addition of an alkyl group, such as an methyl at a lysine or arginine residue), isoprenylation or prenylation (e.g., the addition of an isoprenoid group such as farnesol or geranylgeraniol), amidation at C-terminus, glycosylation (e.g., the addition of a glycosyl group to either asparagine, hydroxylysine, serine, or threonine, resulting in a glycoprotein). Distinct from glycation, which is regarded as a nonenzymatic attachment of sugars, polysialylation (e.g., the addition of polysialic acid), glypiation (e.g., glycosylphosphatidylinositol (GPI) anchor formation, hydroxylation, iodination (e.g., of thyroid hormones), and phosphorylation (e.g., the addition of a phosphate group, usually to serine, tyrosine, threonine or histidine) represent other possible modifications.

The two collagen-binding domains may be a ColG or ColH collagen-binding domain from a bacterial species. In some embodiments, the two collagen-binding domains may be any one of the polypeptides of SEQ ID NOs: 1-39, a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% 98%, or 99% sequence identity to any one of SEQ ID NOs: 1-39, or a fragment of at least 8, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or more consecutive amino acids of any one of SEQ ID NOs: 1-39.

The two collagen-binding domains may be a bacterial ColG s3b domain and a bacterial ColG s3a domain, s3c domain, or ColH s3 domain. In some embodiments, the one of the collagen-binding domains may be any one of the polypeptides of SEQ ID NOs: 15-30, a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% 98%, or 99% sequence identity to any one of SEQ ID NOs: 15-30, or a fragment of at least 8, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or more consecutive amino acids of any one of SEQ ID NOs: 15-30 and wherein the other collagen-binding domain may be any one of the polypeptides of SEQ ID NOs: 1-14 and 31-39, a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% 98%, or 99% sequence identity to any one of SEQ ID NOs: 1-14 and 31-39, or a fragment of at least 8, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or more consecutive amino acids of any one of SEQ ID NOs: 1-14 and 31-39.

The two collagen-binding domains may both be a bacterial ColG s3b domain. In some embodiments, the two collagen-binding domains may be any one of the polypeptides of SEQ ID NOs: 15-30, a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% 98%, or 99% sequence identity to any one of SEQ ID NOs: 15-30, or a fragment of at least 8, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or more consecutive amino acids of any one of SEQ ID NOs: 15-30.

The two collagen-binding domains may be selected from a bacterial ColG s3a domain, a s3b domain, or a ColH s3 domain. In some embodiments, the two collagen-binding domains may be any one of the polypeptides of SEQ ID NOs: 1-14 and 31-39, a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% 98%, or 99% sequence identity to any one of SEQ ID NOs: 1-14 and 31-39, or a fragment of at least 8, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or more consecutive amino acids of any one of SEQ ID NOs: 1-14 and 31-39.

The two collagen-binding domains may be tandem collagen-binding domains from bacterial ColG proteins. In some embodiments, the collagen-binding agent may be any one of the polypeptides of SEQ ID NOs: 40-47, a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% 98%, or 99% sequence identity to any one of SEQ ID NOs: 40-47, or a fragment of at least 8, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 150 or more consecutive amino acids of any one of SEQ ID NOs: 40-47.

The collagen-binding agents may include two collagen-binding domains linked by a domain linker. As used herein, a "domain linker" may include a covalent bond and/or a linker or spacer moiety. For instance, the two collagen-binding domains may be linked directly through, e.g., a peptide bond or chemical cross-linking, or indirectly, through, e.g., a linker or spacer polypeptide. Useful domain linkers include polypeptides, amino acids, nucleic acids, as well as homofunctional linkers or heterofunctional linkers. Particularly useful conjugation reagents that can facilitate formation of a covalent bond between the two collagen-binding domains may include a N-hydroxysuccinimide (NHS) ester and/or a maleimide.

A domain linker may also include a spacer polypeptide. The spacer polypeptide may be any length and may include traditional or non-traditional amino acids. For example, the spacer polypeptide may be 1-100 amino acids long, suitably it is at least 2, 3, 5, 10, 15, 20, 25 or more amino acids long such that the two collagen-binding domains of the collagen-binding agent can mediate collagen binding. Spacer polypeptides may include, without limitation, any one of the polypeptides of SEQ ID NOs: 48-55, a GST tag, a His-tag, a Ser linker, or a Gly linker.

In some embodiments, the domain linker may include a tag system. A tag system includes any group of agents capable of binding one another with a high affinity. Several tag systems are well-known in the art and include, without limitation, biotin/avidin, biotin/streptavidin, or digoxigenin (DIG) systems. In some embodiments, said tag system comprises biotin/avidin or biotin/streptavidin.

The domain linker may include any one of the polypeptides of SEQ ID NOs: 48-55 or a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% sequence identity to any one of the polypeptides of SEQ ID NOs: 48-55.

The collagen-binding agents of the present invention may further include a therapeutic agent linked to the collagen-binding agent by a therapeutic agent linker. As used herein, a "therapeutic agent" may include any suitable pharmaceutical or other active agent, including, without limitation, osteogenic promoters, antimicrobials, anti-inflammatory agents, polypeptides such as recombinant proteins, cytokines or antibodies, small molecule chemicals, hormones, growth factors, polynucleotides, carbohydrates, lipids, or any combination thereof. Suitably the therapeutic agent(s) are capable of promoting bone growth, decreasing inflammation, promoting collagen stability. Suitably, the therapeutic agent is one whose therapeutic effect is in the region of collagen or damaged collagen. The therapeutic agent may include, without limitation, FGF, parathyroid hormone (PTH), PTH/PTHrP receptor agonist, PTH/PTHrP receptor antagonist, bone morphogenic protein (BMP), G-CSF, FGF, BMP-2, BMP-3, anti-sclerostin antibody, growth hormone, IGF-1, VEGF, TGF- β , KGF, TGF- α , TGF- β 1, TGF- β receptor, CT, GH, GM-CSF, EGF, PDGF, celiprolol, activins and connective tissue growth factors. Alternatively, the invention may also aid cell therapy. Cell therapy focuses on the administration of exogenous stem cells. One of the challenges is to deliver these cells at the lesion. Laminin could be attached to CBD. Cells decorated with anchoring collagen binder may seek a lesion and reside at injury site longer to aid in repair. PTH/PTHrP receptor agonists and PTH/PTHrP receptor antagonists have been described in WO 2013/090770, which is incorporated by reference in its entirety. Suitable FGF proteins include, without limitation, bFGF (FGF-2), FGF-4, or FGF-10 (See SEQ ID NO: 56).

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 WO2013/090770 and known to those skilled in the art 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 seg-

ment is a PTH or PTHrP polypeptide segment. One human isoform of PTH is SEQ ID NO: 62. One human isoform of PTHrP is SEQ ID NO:57. 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:62 (residues 1-33 of PTH (SEQ ID NO: 57)). The PTH/PTHrP receptor agonist polypeptide segment may be or may include residues 1-34 of PTH (SEQ ID NO: 62). In other embodiments, it is a fragment of residues 1-34 of PTH (SEQ ID NO: 62). In other embodiments, the PTH/PTHrP receptor agonist polypeptide segment may be or may include residues 1-84 of PTH (SEQ ID NO: 62). In other embodiments, the PTH/PTHrP receptor agonist polypeptide segment may be or may include residues 1-14 of PTH (SEQ ID NO: 62) or residues 1-7 of PTH (SEQ ID NO: 62). 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: 62). In another embodiment, it is or includes residues 7-33 of PTH (SEQ ID NO: 62). In other embodiments, it is a fragment of residues 7-34 of SEQ ID NO: 57. In another embodiment, the PTH/PTHrP receptor antagonist includes PTH(7-14), i.e., residues 7-14 of PTH (SEQ ID NO: 62). 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:58). In another embodiment, the PTH/PTHrP receptor antagonist includes PTHrP(7-34), i.e., residues 7-34 of SEQ ID NO:57, or a fragment of residues 7-34 of SEQ ID NO:57. 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:62. 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 in a 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 is linked directly or indirectly, e.g., through a therapeutic agent 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.

A "therapeutic agent linker" may include a covalent bond and/or a linker or spacer moiety. For instance, the collagen-binding agent and the therapeutic agent may be linked

directly through, e.g., a peptide bond or chemical cross-linking, or indirectly, through, e.g., a linker or spacer polypeptide. Useful therapeutic agent linkers include polypeptides, amino acids, nucleic acids, as well as homofunctional linkers or heterofunctional linkers. Particularly useful conjugation reagents that can facilitate formation of a covalent bond between the two collagen-binding domains may include a N-hydroxysuccinimide (NHS) ester and/or a maleimide.

A therapeutic agent linker may also include a spacer polypeptide. The spacer polypeptide may be any length and may include traditional or non-traditional amino acids. For example, the spacer polypeptide may be 1-100 amino acids long, suitably it is at least 2, 3, 5, 10, 15, 20, 25 or more amino acids long such that the two collagen-binding domains of the collagen-binding agent can mediate collagen binding. Spacer polypeptides may include, without limitation, a PKD (polycystic kidney disease) domain from a collagenase, a GST tag, a His-tag, a Ser linker, or a Gly linker. In some embodiments, the therapeutic agent linker may include a tag system. A tag system includes any group of agents capable of binding one another with a high affinity. Several tag systems are well-known in the art and include, without limitation, biotin/avidin, biotin/streptavidin, or digoxigenin (DIG) systems. In some embodiments, said tag system comprises biotin/avidin or biotin/streptavidin. The therapeutic agent(s) may be linked to the N-terminus or C-terminus of the collagen-binding agent by the therapeutic agent linker. In embodiments where the therapeutic agent includes a polypeptide, either the C-terminus or N-terminus of the therapeutic agent may be linked to the N-terminus or C-terminus of the collagen-binding agent by the therapeutic agent linker. Furthermore, either the same or different therapeutic agents may be linked to both the N-terminus and C-terminus of the collagen-binding agent by two or more therapeutic agent linkers.

Pharmaceutical compositions including any of the collagen-binding agents described herein are provided. The pharmaceutical compositions may include a pharmaceutical carrier, excipient, or diluent (i.e., agents), which are nontoxic to the cell or animal being exposed thereto at the dosages and concentrations employed. Often a pharmaceutical agent is in an aqueous pH buffered solution. Examples of pharmaceutical carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™ brand surfactant, polyethylene glycol (PEG), and PLURON-ICS™ surfactant.

Methods of treating a condition are also provided. The methods may include administering any of collagen-binding agents or pharmaceutical compositions described herein to a subject in an amount effective to treat the condition. The "condition" may include a wound (chronic and acute), hyperparathyroidism, a hair condition (either excessive hair growth or hair loss), a collagenopathy, and a bone condition. Bone conditions include fractures, osteoporosis, periodontal defects, or other bone defects. Collagenopathies include, without limitation, osteogenesis imperfecta (OI), Stickler's syndrome, Ehlers-Danlos syndrome, Alport's syndrome,

Caffey's disease, and localized collagen or cartilage damage. Many of these diseases are caused by genetic defects that result in the collagen in certain tissues being under twisted or partially untwisted.

Bone loss due to, for example, a collagenopathy such as osteogenesis imperfecta, Stickler's syndrome, osteoporosis or others which put an individual at higher risk for a bone fracture due to a collagen defect could be treated by administration of a collagen-binding agent linked to a bone anabolic peptide. The collagen-binding agent may target the bone anabolic agents to sites where the collagen is malformed and thus may prevent fracture.

Vascular fragility due to defects such as Ehlers-Danlos syndrome type IV, Alport's syndrome or other diseases where blood vessel rupture is more likely due to a defect in collagen formation may be administered collagen-binding agents including peptides that stimulate vascular growth or repair. The collagen binding agents will target the peptide to the areas having collagen damage and these areas are likely to have damaged vessels. The therapeutic agents will stimulate growth and repair at the site of damage and prevent vessel rupture.

Skin fragility due to disorders such as Ehlers-Danlos syndrome, Caffey's disease or other diseases where weakening of the skin due to a collagen defect leads to hyperelasticity, easy bruising or poor wound healing. Dermal and epidermal growth factors may serve as therapeutic agents which when linked to collagen-binding agents and delivered to areas of damaged collagen will stimulate growth and repair of the skin, prevent striae and improve healing.

Also provided herein are methods of treating hyperparathyroidism by administering, for example, collagen-binding agents linked to PTH 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. 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 IGI Pharmaceuticals were discontinued in phase 2 because of limited efficacy. Thus new compositions for treating alopecia are needed.

In another aspect, methods of treating a hair condition (excess hair loss or hair growth) The methods may include administering a collagen-binding agent 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 collagen-binding agent linked to a PTH/PTHrP receptor antagonist to a subject are provided. In one embodiment, the

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collagen-binding agent+PTH antagonist composition is applied locally, topically. The collagen-binding agent+PTH antagonist may be applied after a hair removal procedure to prevent or slow hair regrowth.

The subject of the present invention may be any mammal, suitably a human, domesticated animal such as a dog, cat, horse, cow, pig, or a mouse or rat. Treating the condition or treatment includes but is not limited to ameliorating at least one symptom of the condition, reducing or slowing further progression of the condition, reducing or slowing the spread of the condition to unaffected areas. Treating a subject refers to any type of treatment that imparts a benefit to a subject afflicted with a disease or at risk of developing the disease, including improvement in the condition of the subject (e.g., in one or more symptoms), delay in the progression of the disease, delay the onset of symptoms or slow the progression of symptoms, etc.

An effective amount or a therapeutically effective amount as used herein means the amount of a composition that, when administered to a subject for treating a state, disorder or condition is sufficient to effect a treatment (as defined above). The therapeutically effective amount will vary depending on the compound, formulation or composition, the disease and its severity and the age, weight, physical condition and responsiveness of the subject to be treated.

The compositions (i.e. collagen-binding agents and pharmaceutical 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, subcutaneous, intrathecal, transcutaneous, nasopharyngeal, intralesional, intra-tumoral, intradermal, or transmucosal absorption. Thus the compositions may be formulated as an ingestible, injectable, topical or suppository formulation. The compositions may also be delivered with in a liposomal or time-release vehicle. Administration of the compositions to a subject in accordance with the invention may 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 composition or 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 compositions 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, medications 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 described herein and of a known agent, such as by means of an appropriate conventional pharmacological 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 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 improve the condition being treated by at

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least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% or more as compared to no treatment.

The effective dosage amounts described herein refer to total amounts administered, that is, if more than one composition is administered, the effective dosage amounts correspond to the total amount administered. 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.

The collagen-binding agents or pharmaceutical compositions described herein may be administered one time or more than one time to the subject to effectively improve the condition being treated. Suitable dosage ranges are of the order of several hundred micrograms effective ingredient with a range from about 0.01 to 10 mg/kg/day, preferably in the range from about 0.1 to 1 mg/kg/day. Precise amounts of effective ingredient required to be administered depend on the judgment of the practitioner and may be peculiar to each subject. It will be apparent to those of skill in the art that the therapeutically effective amount of the collagen-binding agents and pharmaceutical compositions described herein will depend, inter alia, upon the administration schedule, whether the composition is administered in combination with other therapeutic agents, the status and health of the recipient, and the therapeutic activity of the particular composition.

The present disclosure is not limited to the specific details of construction, arrangement of components, or method steps set forth herein. The compositions and methods disclosed herein are capable of being made, practiced, used, carried out and/or formed in various ways that will be apparent to one of skill in the art in light of the disclosure that follows. The phraseology and terminology used herein is for the purpose of description only and should not be regarded as limiting to the scope of the claims. Ordinal indicators, such as first, second, and third, as used in the description and the claims to refer to various structures or method steps, are not meant to be construed to indicate any specific structures or steps, or any particular order or configuration to such structures or steps. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to facilitate the disclosure and does not imply any limitation on the scope of the disclosure unless otherwise claimed. No language in the specification, and no structures shown in the drawings, should be construed as indicating that any non-claimed element is essential to the practice of the disclosed subject matter. The use herein of the terms "including," "comprising," or "having," and variations thereof, is meant to encompass the elements listed thereafter and equivalents thereof, as well as additional elements. Embodiments recited as "including," "comprising," or "having" certain elements are also contemplated as "consisting essentially of" and "consisting of" those certain elements.

Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. For example, if a concentration range is stated as 1% to 50%, it is intended that values such as 2% to 40%, 10% to 30%, or 1% to 3%, etc., are expressly enumerated in this specification. These are only examples of what is specifi-

cally intended, and all possible combinations of numerical values between and including the lowest value and the highest value enumerated are to be considered to be expressly stated in this disclosure. Use of the word “about” to describe a particular recited amount or range of amounts is meant to indicate that values very near to the recited amount are included in that amount, such as values that could or naturally would be accounted for due to manufacturing tolerances, instrument and human error in forming measurements, and the like. All percentages referring to amounts are by weight unless indicated otherwise.

No admission is made that any reference, including any non-patent or patent document cited in this specification, constitutes prior art. In particular, it will be understood that, unless otherwise stated, reference to any document herein does not constitute an admission that any of these documents forms part of the common general knowledge in the art in the United States or in any other country. Any discussion of the references states what their authors assert, and the applicant reserves the right to challenge the accuracy and pertinence of any of the documents cited herein. All references cited herein are fully incorporated by reference in their entirety, unless explicitly indicated otherwise. The present disclosure shall control in the event there are any disparities between any definitions and/or description found in the cited references.

Unless otherwise specified or indicated by context, the terms “a”, “an”, and “the” mean “one or more.” For example, “a protein” or “an RNA” should be interpreted to mean “one or more proteins” or “one or more RNAs,” respectively.

As used herein, “about,” “approximately,” “substantially,” and “significantly” will be understood by persons of ordinary skill in the art and will vary to some extent on the context in which they are used. If there are uses of these terms which are not clear to persons of ordinary skill in the art given the context in which they are used, “about” and “approximately” will mean plus or minus $\leq 10\%$ of the particular term and “substantially” and “significantly” will mean plus or minus $>10\%$ of the particular term.

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.

EXAMPLES

Example 1—Activation and Binding Mechanism of Tandem Collagen-Binding Domains with Pseudo-Two Fold-Symmetry

Clostridium histolyticum secretes virulence factors, including highly active collagenases ColG (class I) and ColH (class II), to penetrate animal tissues. After the multi-domain ColG utilizes its tandem collagen-binding domain (CBD) to anchor itself onto insoluble collagen, subsequent degradation of the hierarchical substrate involves processive cleavage and rearrangement of fibrils. In this work, the structure of the calcium bound tandem CBD is presented at 1.9 Å resolution ($R_{work}=15.0\%$; $R_{free}=19.6\%$). The pseudo-two-fold arrangement of CBD would allow ColG to wedge between collagen molecules that are 55 Å apart in order to potentially aid in fibril rearrangement and processive cleavage. Indeed, between 0.1:1 and 0.5:1 molar ratios of tandem CBD and collagen, it accelerated collagen fiber formation. At 1:1 molar ratios and above, the tandem CBD retarded fibril formation. To toggle between collagen molecules, a tighter binding C-side CBD, may initiate binding as dem-

onstrated by small angle X-ray scattering (SAXS) of tandem CBD forming a 1:1 complex with [(Pro-Hyp-Gly)₁₀]₃. Subsequently, the weaker binding N-side CBD can latch onto a prone collagen molecule to provide the tightest known fibril binding. The conformational change of the tandem CBD is calcium dependent and cooperative as measured by size exclusion chromatography and by SAXS at pCa in the range of 3-6. At pCa >5 , the tandem CBD adopts an extended structure that is easier to be secreted from the bacterium. In the host pCa >3 , the compact structure seen in the crystal structure is adopted. The binding and activation mode described here will help guide site-directed drug delivery vehicle development.

Abbreviations used: CBD, collagen binding domain; MALDI-TOF-MS, matrix-assisted laser desorption/ionization-time of flight mass spectrometry; DLS, dynamic light scattering; SAXS, small angle X-ray scattering.

Clostridium histolyticum, which was recently proposed to be reclassified as *Hathewayia histolyticum* based on 16S rRNA gene comparison, produces collagenases that cause extensive tissue damage during myonecrosis (Lawson and Rainey 2015). The most significant of these enzymes, ColG (class I) and ColH (class II), are multi-domain enzymes that include a N-terminal collagenase module (Si), one or two polycystic kidney disease (PKD)-like domains, and one to three C-terminal collagen-binding domains (CBDs) (FIG. 1A), and division of roles in collagenolysis were suggested (Fields 2013).

The C-terminal domains of ColG (s3a, s3b), and ColH (s3), are homologs consisting of approximately 120 amino acids. The domains bind to soluble collagenous peptides and insoluble collagen fibril. Their role in binding to collagen fibril is essential in dismantling its hierarchical structure (Matsushita, Jung et al. 1998, Matsushita, Koide et al. 2001). Truncation of CBD from either full-length ColG or ColH incapacitates their abilities to degrade collagen fibril. Such enzymes can only degrade solubilized collagen or denatured collagen (gelatin). Mutagenesis and collagen-binding studies mapped the binding surface of s3b, while NMR and SAXS studies showed that s3b unidirectionally binds to under-twisted regions of mini-collagen collagen (Philominathan, Koide et al. 2009, Philominathan, Koide et al. 2012). High-speed atomic force microscopy has recently revealed ColG's ability to dismantle collagen in real time (Watanabe-Nakayama, Itami et al. 2016). During degradation, ColG moves processively along collagen fibril from C-terminus to N-terminus to dismantle the fibril. ColG also preferentially targeted less ordered region of collagen fibril. Structural insight for ColG's processivity and preference for disordered region are described.

Bacterial collagenases require calcium to attain both full catalytic activity and collagen-binding function. The activation of bacterial collagenase involves domain rearrangement triggered by the Ca²⁺ binding to the linker from α -helix to β -sheet (Wilson, Matsushita et al. 2003, Philominathan, Matsushita et al. 2009, Spiriti and van der Vaart 2010, Sides, Liyanage et al. 2012, Bauer, Wilson et al. 2013, Bauer, Janowska et al. 2015). The full-length apo-ColG is expected to be relatively flexible inside the bacteria where Ca²⁺ concentration is low ($0.2-0.3 \times 10^{-6}$ M) allowing the enzyme to be secreted more easily (Wilson, Matsushita et al. 2003). Upon secretion, the linker chelates to Ca²⁺ (~ 1.2 mM) in the ECM to adopt a rigid structure. Though it has not been shown for ColG, Ca²⁺ chelation indeed triggers a full-length ColH to adopt a less flexible and compact structure as demonstrated using SAXS and limited proteolysis (Ohbayashi, Matsumoto et al. 2013).

The clostridial collagenases have been successfully used for years as a wound debridement. Recently the mixture of ColG and ColH was approved for use in the treatment of excessive connective tissue build up found, for example, in Dupuytren's disease (Gaston, Larsen et al. 2015). Furthermore, the enzymes showed potential to treat different types of connective tissue build ups (Duarte, Correia et al. 2014) and to isolate pancreatic islets for transplantation (McCarthy, Breite et al. 2011). In addition to therapeutic use of full-length collagenase for removal of connective tissue, the non-catalytic segments are used for targeted drug-delivery to reduce dosage and to minimize side effects. Initially, Nishi et al. developed fusion proteins of the targeting segment (s2b-s3) and growth factors. When injected, the fusion proteins remained active at the site of injection for up to 10 days (Nishi, Matsushita et al. 1998). A fusion protein of s3 and parathyroid hormone (PTH-CBD) is being developed to treat osteoporosis (Ponnapakkam, Katikaneni et al. 2011, Ponnapakkam, Katikaneni et al. 2011, Ponnapakkam, Katikaneni et al. 2012), to prevent and to treat alopecia (Katikaneni, Ponnapakkam et al. 2012, Katikaneni, Ponnapakkam et al. 2014, Katikaneni, Ponnapakkam et al. 2014, Katikaneni, Seymour et al. 2015). The systemic application is based on the apparent targeting ability of s3 to blood accessible and regenerating collagen (Stratford, Vu et al. 2014). Although the lower affinity s3 is efficacious as a systemic drug delivery vehicle in vivo, the tighter collagen binder s2b-s3 is more efficacious in wound healing applications when it is applied at the site of injury with collagen-based bone graft material (An, Lin et al. 2015, Fujimaki, Inoue et al. 2015, Saito, Uchida et al. 2015, Uchida, Matsushita et al. 2015). Here we report crystal structures of tandem CBD in the presence of calcium. We also propose its mode of binding and interaction with the collagen substrate and the role of calcium based on gel filtration and SAXS results.

Methods and Materials

Production, Purification, Crystallization and Structure Determination

Individual s3a, s3b, as well as tandem CBD derived from the *C. histolyticum* ColG were expressed as glutathione S-transferase (GST)-fusion proteins using method as described previously (Matsushita, Jung et al. 1998). Initial conditions suitable to grow crystals of tandem CBD were identified by high-throughput screen (Hampton Research Crystal Screen HT). Subsequent crystallization trials using the initial conditions were carried out using the hanging-drop method. Crystals of tandem CBD, obtained in the presence of 3 mM calcium (21-26% PEG3350, HEPES pH 7.5 at 37° C.), were orthorhombic (space group, P2₁2₁2₁), with cell parameters a=51.5 Å, b=54.7 Å, c=92.0 Å. The crystals grew within 24 hours in 37° C. but not at 4, 16 and 24° C. The crystals were temperature sensitive and could not withstand cryogenic temperatures. Therefore diffraction data were collected by means of in-house X-ray facility at room temperature to 1.9 Å resolution using a Rigaku 007 generator with Cu Kα radiation. The data sets were processed with d*TREK (Pflugrath 1999) (Table 1). The structure was solved with the molecular replacement program MolRep from the CCP4 package, by using s3b (PDB code 2o8o) as the search model (Murshudov, Vagin et al. 1997). One tandem CBD was found in an asymmetric unit; and therefore, V_M was 2.5 Å³/Da and solvent content was 50% (Matthews 1968). Refinement of the tandem CBD was carried out using Refmac₆.1.13 (Murshudov, Vagin et al. 1997). TLS restraints were applied to main chain atoms with each CBD acting as a TLS group. Babinet scaling was used

for bulk solvent refinement. Five percent of the data were set aside to monitor R_{free}. The models were manually adjusted between each refinement cycle using MIFit (McRee 1999). Alternate confirmations were built for Lys818, Glu945, Tyr970, and Arg1005. The Ramachandran plot for the final structure obtained with the program Procheck (Laskowski, MacArthur et al. 1993) showed 91% of the residues in the core region and 9% in the additionally allowed region, with none in the generously allowed or disallowed regions. The final refinement statistics are shown in Table 1.

TABLE 1

Data collection statistics	
Data collection statistic	
Wavelength (Å)	1.5419
Temperature (K)	298
Resolution range (Å) ^a	19.7-1.90 (1.97-1.90)
Space group	P2 ₁ 2 ₁ 2 ₁
Unit cell dimension (Å)	
a (Å)	51.5
b (Å)	54.7
c (Å)	92.0
Unit cell angle (°)	α, β, γ = 90
Total reflections	89,473
Redundancy	4.47 (4.27)
Completeness (%) ^a	94.8 (94.2)
R _{meas} (%) ^{a, b}	7.1 (49.2)
I/σI ^b	11.2 (2.9)
Refinement statistic	
Unique reflections	18,987
Solvent molecules	211
R _{work} (%)	15.0 (25.5)
R _{free} (%) ^{b, c}	19.6 (26.8)
Average B value (Å ²)	37.68
Coordinates ESU based on R _{free} (Å)	0.13
Root mean square deviations	
Bond distance (Å)	0.011
Bond angles (°)	1.87
Chiral centers (Å ³)	0.17
Planar groups (Å)	0.01
B-factor restraints	
Main-chain bond (Å ²)	3.81
Main-chain angle (Å ²)	4.72
Side-chain bond (Å ²)	6.84
Long range B-factor (Å ²)	12.3
Ramachandran statistic	
Most favored region (%)	90.9
Allowed region (%)	9.1

$$^a R_{meas} = \frac{\sum_{hkl} \{N(hkl)/N(hkl) - 1\}^{1/2} \sum_i |I_i(hkl) - \langle I_i(hkl) \rangle|}{\sum_{hkl} \sum_i |I_i(hkl)|}$$

^bData for highest resolution shell are given in parentheses

^c5% of data excluded from refinement

Small Angle X-Ray Scattering

Suitable buffer conditions for small angle X-ray scattering (SAXS) measurements were identified using discontinuous Native-PAGE. For the pCa analysis the tandem CBD was equilibrated into 10 mM HEPES-Na (pH 7.5), 100 mM NaCl, and 2% glycerol. The pCa was maintained with 0.2 mM total EGTA with CaCl₂ added to bring pCa values to 3, 4, 5 and 6. The amount of Ca²⁺ needed to reach a given pCa was determined using MAXCHELATOR (Bers, Patton et al. 2010). For the tandem CBD:[(POG)₁₀]₃ complex analysis, the complex was equilibrated into 50 mM HEPES-Na (pH 7.5), 100 mM NaCl, and 2 mM CaCl₂. [(POG)₁₀]₃ was dissolved in 5 mM acetic acid to a concentration of 7.5 mg/mL and stored at 4° C. for 24 h. The peptide was then mixed with tandem CBD in a 1:2 molar ratio of tandem CBD to mini-collagen. Measurements were completed for three

concentration series per sample. For the pCa series, the concentration of tandem CBD used at pCa 4 and 5 and 6 was 1, 3, and 5 mg/mL. At pCa 3, the concentration series used was 2, 4, and 6 mg/mL. For the complexes with $[(\text{POG})_{10}]_3$, the concentration series used was 1, 3, and 5 mg/mL. All SAXS data were collected at 10° C. at the Advanced Light Source at Berkley National Lab (SIBYLS beamline, 12.3.1). All data processing was accomplished using primusqt from the ATAS 2.6.1 software package. For CBD at each pCa, exposure data from the concentration gradient that were not affected by either aggregation or detector saturation were extrapolated to infinite dilution. Determination of the radius of gyration (R_g), maximum diameter (D) as well as ab initio shape reconstruction of the extrapolated data was carried out using the dammif function in primusqt. The χ values calculated at the end of each run indicated the agreement between the calculated scattering curve and the experimental scattering curve. For the pCa series, the χ values for each shape ranges between 0.8 And 1.2. For the complex with $[(\text{POG})_{10}]_3$, the χ value is 0.8.

Collagen Fibril Formation

The impact of addition of tandem CBD on self-assembly of collagen molecules was monitored by measuring turbidity as an increase in optical density at 450 nm, at 37° C. On ice, a solution of 2 mg/ml of rat collagen was diluted with 40 mM HEPES buffer pH 7.5, with addition of 300 mM NaCl, 2 mM CaCl_2 , to final concentration of 0.5 mg/ml (2.4 μM). In the next step collagen binding was added in ratios: 0.1 to 1; 0.2 to 1; 0.3:1; 0.5 to 1; 1 to 1; 2 to 1; 3 to 1; 5 to 1 of molar concentration. The turbidity measurement was taken in 96 well plates with 1-minute intervals with spectrophotometer Filter Max F5 (Molecular Devices). From the turbidity curve the following parameters were estimated t_{lag} -time at the end of lag phase, maximum turbidity, and V the maximum fibril growth rate.

Analytical Size Exclusion Chromatography

Size exclusion chromatography was performed at room temperature on a HPLC system equipped with a Superdex 75 column (1x30 cm, Pharmacia) at a flow rate of 0.5 ml/min as described (Wilson, Matsushita et al. 2003). The following proteins were used as molecular mass standards: bovine serum albumin, 67.0 kDa; chicken ovalbumin, 43.0 kDa; and ribonuclease A, 13.7 kDa (Pharmacia). The measurement was carried out in triplicate.

Quantitative Analysis of the Binding to a Collagenous Peptide

Binding of various CBD proteins to a collagenous peptide was measured by surface plasmon resonance using a BIA-CORE apparatus (Biacore, Uppsala, Sweden) with a sensor chip (CMS, Biacore) on which a peptide, Gly-(Pro-Hyp-Gly)₁₂, was covalently immobilized as described (Wilson, Matsushita et al. 2003).

Collagen Fibril Binding Assay

Binding affinities for three CBDs, s3a, s3b, and s3as3b, to collagen fiber were analyzed. Initially, 10 mg of porcine skin fiber (Nippi, Inc; Japan) was placed on a 0.2 nm spin column and washed with 50 mM Tris-HCl (pH 7.5), supplemented with 200 mM NaCl and 5 mM CaCl_2 . Then, 20 μL of a protein mixtures containing 0.5 mg/mL BSA (internal control), and a varied concentration (between 2.5 and 20 mg/mL) of tandem CBD, equilibrated in the buffer above, was added and thoroughly mixed with the fiber. After a 30 min incubation at room temperature, the supernatant containing unbound tandem CBD was collected and quantified using SDS-PAGE. For this step, an equal volume of unused protein mixture was used as a control. After electrophoresis, proteins were stained with Coomassie Brilliant Blue R-250,

and their relative amounts were estimated by ImageJ software (version 1.4.2; National Institutes of Health). Based on these estimations a calibration curve was constructed for each CBD and was used to quantify CBD amounts in each supernatant. The results obtained by triplicate assay were analyzed on a Scatchard plot to obtain the dissociation constant (K_d) and the number of binding sites (B_{max}) for each CBD.

Results and Discussion

Structure Description of Tandem CBD

Crystal structure of tandem CBD consisting of s3a and s3b was solved at 1.9 Å resolution. Although the s3b segment has been described before, the s3a segment is described for the first time in this paper. Both s3a and s3b adopt a very similar β -sandwich "jelly-roll" composed of ten β -strands. The CBDs are related by a pseudo two-fold rotational symmetry that is stabilized by salt-bridges and hydrogen-bonding interactions. The pseudo symmetry axis, which is perpendicular to the plane of the page in FIG. 1B, positions the collagen-binding pockets in the tandem CBD to be 55 Å apart. Each domain chelates to two Ca^{2+} i.e., one Ca^{2+} is bound with pentagonal bipyramidal geometry and the other is bound with square antiprismatic geometry as described (Bauer, Wilson et al. 2013). The electron density allowed us to observe a prolyl-cis-peptide bond between Glu792 and Pro793 and non-prolyl-cis-peptide bond between Glu899 and Asn992. Overlay based on 110 equivalent C_α atoms shows that the s3a and s3b share r.m.s.d. of 0.9 Å and only significantly deviate at loops (r.m.s.d. of 1.1-2.5 Å). Loops in both CBDs exhibited the highest B-factor values, while β -sheet residues exhibited low B-factor values. As expected, B-factor values for residues that interact with Ca^{2+} were amongst the lowest. The average temperature factor for s3a is lower than s3b due to crystal packing. In the previously reported structure of holo-s3b (PDB code 4HIPK), the protease sensitive and highly dynamic loop 960-968 was not observed (Philominathan, Koide et al. 2009, Sides, Liyanage et al. 2012, Bauer, Wilson et al. 2013). In the structure presented here, the dynamics of this loop are suppressed by crystal packing contacts. Otherwise the s3b alone and s3b in the tandem CBD are virtually identical to each other (C_α r.m.s.d. 0.6 Å).

Ca^{2+} -Induced Transformation of the Tandem CBD

The difference in Ca^{2+} concentration inside bacterium and ECM in host could be taken advantage of to efficiently secrete bacterial collagenases into the host. The intracellular Ca^{2+} concentration of *Clostridium* is likely to be similar to that of *Escherichia coli* (0.2-0.3 $\times 10^{-6}\text{M}$) (Holland, Jones et al. 1999), which is well below the tandem CBD's apparent K_d for Ca^{2+} (FIG. 2A). However, extracellular tissue fluids contain Ca^{2+} concentrations at ~1.2 mM (Maurer and Hohenester, 1997). Monitored by size exclusion chromatography, the domain reorientation of s3a-s3b is a cooperative event induced by Ca^{2+} , and SAXS data corroborated the magnitude of the structural change (FIG. 2B). The SAXS derived envelope for tandem CBD at pCa less than or equal to 5 (10 μM) adopts a rod like shape (FIG. 2B). A bump in the envelope resembles how α -helical linker appeared in SAXS (Sides, Liyanage et al. 2012). At pCa=6, the β -strand A' of s3b also unfolds to greatly increase the linker's dynamic (Sides, Liyanage et al. 2012). Upon increasing Ca^{2+} concentrations, the tandem CBD steadily adopts more compact shapes (FIG. 2B). At pCa=4 (100 μM) the shape resembles the crystal structure with the exception of a bulge that suggests the linker of s3a remained dynamic. At pCa=3 (1 mM) it agrees well with the crystal structure of tandem CBD. The domain rearrangement modeled in the SAXS

derived envelope is consistent with the observations made for s3b with its 12-residue-long linker. The linker between s3a and s3b has been shown to undergo secondary structure transformation from α -helix to β -sheet that is induced by Ca^{2+} binding and results in tighter contact between the domains (Wilson, Matsushita et al. 2003, Sides, Liyanage et al. 2012). The β -strand A' of s3b also unfolds to greatly increase the linker's dynamic (Sides, Liyanage et al. 2012). Free energy simulations have determined that the calcium ions not only stabilize the cis-peptide bond thermodynamically but also catalyze its formation (Spiriti and van der Vaart 2010). Calcium dependent structural change was monitored for full length ColH by size exclusion chromatography and by SAXS (Ohbayashi, Matsumoto et al. 2013). Expanding upon the findings for tandem CBD, the full length ColG and ColH is also likely to undergo Ca^{2+} -induced domain rearrangement. Dynamic ColG and ColH inside bacterium should allow for rapid secretion inducing maximum damage to host.

Mini Collagen-Tandem CBD Interaction

Our results suggest a unique interaction between tandem CBD and either collagen fibril or mini-collagen. Collagen fibril is built by a staggered array of triple-helical tropocollagen, and is insoluble in water. Meanwhile, synthetic collagenous peptide, or mini-collagen, which mimics the structure of native tropocollagen and is soluble in water, has been used to investigate the individual collagen-protein interactions. Use of mini-collagen also allows quantitative analysis of CBD-collagen interaction. The K_d values have been evaluated for various forms of CBDs to insoluble collagen fibril and to mini-collagen, and they come to a good agreement (Matsushita, Koide et al. 2001). Tandem CBD binds to the collagen fibril the tightest ($K_d \sim$) among CBDs tested and much tighter than the sum of s3a or s3b alone ($K_d \sim 100 \mu\text{M}$). However, tandem CBD binds to mini-collagen only as tightly as s3b does. Tandem CBD did show cooperative binding when the immobilized mini-collagen density was high. SAXS results of tandem CBD:mini-collagen also revealed a 1:1 complex. Given the binding affinities of s3a and s3b to mini-collagen, s3b segment of tandem CBD bound unidirectionally to the C-terminus of [(POG)₁₀]₃ (Philominathan, Koide et al. 2009, Philominathan, Koide et al. 2012, Bauer, Wilson et al. 2013), thus it was modeled in the envelope as such (FIG. 2B).

The s3a binds less tightly than s3b to collagen possibly because it is missing one of the conserved tyrosine residues. When CBD sequences were aligned, three Tyr residues (970, 994 and 996 in s3b) are well conserved, and mutagenesis of any of these residues diminished binding to mini-collagen (Wilson, Matsushita et al. 2003). When the sequences of tandem CBDs were aligned instead difference in N-side CBD and C-side CBD emerged. The equivalent to Tyr 996 in the N-side CBD was not well conserved, but all three Tyr residues were well conserved in the C-side CBD (FIG. 2B; FIG. 5). The s3a also lacks conserved Tyr970 equivalent and Ser851 occupies the position instead. Neighboring His848 of s3a does occupy approximately the same space near this residue and could, to a lesser extent, fulfill its role. The gene duplication of CBD apparently required a loss of functionally importance at position 877 in order to prevent the domain from becoming stuck at the surface of the fibril. The CBD domains are positioned by an extra 0-strand (β -strand A') and interdomain interactions. While β -strand A' is present in both s3a and s3b, it is absent in s3, and hence, could be unique to collagenases with multiple CBDs. The extra

0-strand is stabilized by unconserved side-chain interactions, which suggests that gene duplication was a relatively recent event.

The observed 1:1 complex of CBD to mini-collagen indicates that the tighter binding s3b initiates binding. This proposed mechanism is supported by the observation that the tandem CBD binds to mini-collagen just as tightly as s3b alone. Nevertheless, the tandem CBD binds tighter to collagen fibril than s3b alone (Toyoshima, Matsushita et al. 2001). While s3b initiates binding and serves the central role, s3a plays an auxiliary, yet pivotal role in intercalating into a space created between collagen molecules that are 55 Å apart. Although it was suggested that CBDs could lie side by side to bind to one tropocollagen molecule (Eckhard and Brandstetter 2011), our structure suggests this mode is less likely.

ColH, unlike ColG, possesses two PKD-like domains (s2a and s2b) but only a single CBD, s3. Though not a collagen-binder by itself, s2b does enhance s3's affinity to collagen (Matsushita, Jung et al. 1998). While s3a is a collagen-binder, it may work similarly to s2b by serving as the source of weak interactions that allows the segment to scan a single tropocollagen for opportunistic binding sites as well as contribute to an overall tighter collagen-binder. Development of the tandem PKD and tandem CBD segments allowed ColG and ColH to potentially seek different niches in collagen fiber.

Collagen Fibril-Tandem CBD Interaction

The pseudo-two fold symmetry orients the collagen-binding surface at the opposite ends of the molecule and allows the tandem CBD to bind to parallelly oriented two collagen molecules (FIG. 1B). Collagen self assembles to form collagen fibril in a process that can be monitored by change in absorbance at 450 nm. Collagen-binding molecules, such as s3b, bind to collagen and retard fibril formation (Okano-Kosugi, Matsushita et al. 2009). However, since the tandem CBD appears to be able to wedge itself between two collagen molecules, we tested its ability to promote fibril self-assembly. To investigate the influence tandem CBD has on collagen fibril formation, the turbidity of mixtures of tandem CBD and collagen was monitored (FIG. 3). Remarkably, the ratio of tandem CBD to collagen has contrasting influences on the lag time prior to fiber formation. In the absence of tandem CBD (control), the lag time for fibril formation is 19 min and is consistent with previous observations (Okano-Kosugi, Matsushita et al. 2009). At a 0.1:1 ratio of tandem CBD to collagen, the lag time is reduced to 15 min. When the concentration of tandem CBD is relatively high compared to the ratio of collagen the lag time increases. At a tandem CBD to collagen ratio of 5:1, the lag time is 31 min. The fibril growth for lower ratios of CBD resulted in a much higher absorption of 0.0217 compared to samples with higher ratios of tandem CBD, where the absorption was 0.005. Influence on lag time inversely correlated to collagen fibril thickness. The 0.1:1 and 0.2:1 mixtures of tandem CBD to collagen resulted in fibril that is about 14% thicker than the collagen fibril control. At a 5:1 ratio, the thickness is 2% less than the control. At low concentrations, tandem CBD aids in collagen alignment, and thus accelerates the formation of nuclei for collagen self-assembly. The seemingly opposite effects of this two ratio ranges of CBD to collagen on self-assembly may provide an important clue to understanding how ColG disassemble and breakdown collagen fibril as recently being revealed (Watanabe-Nakayama, Itami et al. 2016).

Collagenolysis by ColG

Hydrolysis of collagen fibril by ColG monitored in real time by high-speed atomic force microscopy revealed as following: (1) the interactions of inter-fibril collagen molecules prevented collagenase molecules from engaging; (2) collagen molecules were rearranged onto other fibrils when subjected to ColG; (3) disordered D-periodicity made the collagen fibril susceptible to degradation by ColG; (4) ColG moves from C-terminus to N-terminus processively; (5) At every pass, ColG evenly trimmed the thickness of the collagen fibril. The structure of tandem CBD sheds some light into the ColG's action.

Given the binding clefts' positions on opposite faces of the domain, we propose the following collagen-binding modes: (i) tandem CBD wedges into interfibrillar space (FIG. 4B), (ii) tandem CBD wedges into crevices found in damaged or remodeling collagen fiber (FIG. 4C). The effort necessary to toggle into interfibrillar space may appear as though ColG was stalled. The tandem CBD's ability to facilitate fibril formation could explain how ColG rearranged collagen fibrils. Mechanically disrupting D-periodicity in collagen fibril may introduce pockets for ColG binding. If the fibril is damaged by removing the outermost tropocollagen, the CBD could wedge itself between the exposed tropocollagen. Such action raises the interesting possibility that the tandem CBD could be used to target drugs to damaged collagen. Alternatively, the tandem CBD could toggle between two fibrils. The median of the surface-to-surface distance of one fibril to another is ~3.2 nm in skin (Kuwaba, Kobayashi et al. 2001). Nearly 15% of the interfibrillar space in skin should be in the order of ~6 nm. The results suggest that the tandem CBD could be useful to anchor drugs to damaged tissues. Once toggled between collagen molecules, ColG's processive C→N-terminal movement is likely driven by the collagenase module, and thus, evenly trimmed collagen fibril is produced (Eckhard and Brandstetter 2011, Eckhard, Schonauer et al. 2011).

The high-resolution structure of bacterial tandem collagen binding domain is reported for the first time. The pseudo-symmetrical arrangement of CBD, resulting from gene duplication and fusion, could allow it to recognize unique niche in collagen fibril to facilitate degradation of collagen. The structure of tandem CBD reveals that it could wedge between parallelly oriented collagen molecules. The structure combined with previously identified CBD preference for under-twisted regions of collagen suggest the tandem CBD targets ColG to damaged regions of the collagen fibril. Such targeting also opens new drug targeting avenues in which the tandem CBD tightly anchors drugs to the injury site.

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Example 2—Acceleration of Bone Formation During Fracture Healing by Basic Fibroblast Growth Factor Fused with Tandem Collagen-Binding Domains from *Clostridium histolyticum* Class I Collagenase

The increased retention of recombinant basic fibroblast growth factor (bFGF) at fracture sites accelerates bone formation during fracture healing. We previously constructed a fusion protein consisting of bFGF and a polycystic kidney disease domain (PKD; s2b) and a collagen-binding domain (CBD; s3) derived from the *Clostridium histolyticum* class II collagenase (ColH); and reported the combination of the fusion protein and a collagen-like peptide, poly(Pro-Hyp-Gly)₁₀ (SEQ ID NO: 59), induced mesenchymal cell proliferation and callus formation at fracture sites. It is known that *C. histolyticum* also produces class I collagenase (ColG), which possesses tandem CBDs (s3a and s3b) at the C-terminus. First, we examined binding affinity of the four collagen anchors derived from two clostridial collagenases to a collagenous peptide, H-Gly-Pro-Arg-Gly-(Pro-Hyp-Gly)₁₂-NH₂ (SEQ ID NO: 60), by surface plasmon resonance, which revealed that the tandem CBDs (s3a-s3b) shows the highest affinity to a collagenous peptide. Then, we constructed fusion proteins consisting of bFGF

and single CBD (bFGF-s3b) or tandem CBDs (bFGF-s3a-s3b) to compare their biological abilities to those of the previous fusion construct (bFGF-s2b-s3). A fracture-model study showed that bFGF-s3a-s3b exhibit the highest abilities to induce mesenchymal cell proliferation and bone formation. Taken together, collagen anchors with higher collagen-binding affinity exert bFGF to show higher biological activities. The poly(Pro-Hyp-Gly)₁₀/bFGF-(CBD)₂ composite therefore appears to have the potential to promote bone fracture healing in the clinical setting.

Basic fibroblast growth factor (bFGF) is a mitogenic protein with angiogenic properties and is involved in bone remodeling during early bone repair [1;2]. Recombinant human bFGF has demonstrated efficacy in animal models of osteoporosis for regenerating bone fractures and defects [3;4]. In two recent clinical trials, bFGF treatment accelerated bone union at osteotomy and tibial fracture sites [5;6]. Although the findings from these studies strongly indicate that bFGF promotes bone remodeling and regeneration, exogenously added bFGF is rapidly diffused from bone defect sites.

Clostridium histolyticum, a pathogenic bacterium of gas gangrene, secretes two classes of collagenase, (class I, ColG and class II, ColH). These enzymes commonly contain a catalytic domain (s1), polycystic kidney disease domain (PKD, s2; SEQ ID NO: 61), and collagen-binding domain (CBD, s3). However copy numbers of PKD and CBD in the C-terminal collagen-anchors are different in ColG and ColH, being s2-s3a-s3b and s2a-s2b-s3 respectively [7;8]. We previously demonstrated that fusion proteins consisting of bFGF and either CBD (bFGF-s3) or PKD-CBD (bFGF-s2b-s3) derived from ColH accelerated bone formation in rat femurs when loaded onto collagen sheets compared to native bFGF [9]. When combined with high-density collagen sheets, bFGF-s2b-s3 promoted greater bone formation than bFGF-s3[10]. The combination of bFGF-s2b-s3 with the collagen-like peptide poly(Pro-Hyp-Gly)₁₀ (SEQ ID NO: 59) also induced greater bone formation compared to bFGF alone in mice bone fracture models[11]. In a more recent study, a fusion protein consisting of galectin-9 and tandem CBDs (s3a and s3b) derived from ColG displayed higher collagen-binding activity than the corresponding protein fused with PKD and CBD (s2b and s3) derived from ColH [12]. Based on these findings, we speculated that a bFGF fusion protein containing tandem CBDs from ColG would increase the retention of bFGF at the fracture site through the enhancement of collagen-binding activity, leading to improved bone formation and fracture repair.

Here, we evaluated dissociation constants between various collagen-anchors and mini-collagen in vitro. Following the results, we constructed fusion proteins consisting of bFGF and either single (bFGF-s3b) or tandem CBD(s) (bFGF-s3a-s3b) derived from ColG, and examined the bone formation ability of these fusion proteins with previously constructed two fusion proteins consisting of bFGF and collagen-anchors derived from ColH.

Materials and Methods

A Mini-Collagen Peptide and a Collagen-Like Polypeptide

A mini-collagen peptide, H-Gly-Pro-Arg-Gly-(Pro-Hyp-Gly)₁₂-NH₂ (SEQ ID NO: 60), was synthesized by a N-(9-fluorenyl) methoxycarbonyl (Fmoc)-based strategy on Rink-amide resins (Novabiochem, San Diego, Calif.). In each cycle, Fmoc-amino acids (5 equivalents; Novabiochem) were reacted in the presence of N,N'-diisopropylcarbodiimide (5 equivalents; Wako Pure Chemical, Osaka, Japan) and 1-hydroxybenzotriazole (5 equivalents; Wako Pure Chemical) in N,N-dimethylformamide for 90 min. Fmoc depro-

tection was performed by 20% (v/v) piperidine in DMF for 20 min. Peptide cleavage and deprotection steps were performed by treatment with a standard trifluoroacetic acid (TFA) scavenger cocktail (TFA: m-cresol:thioanisole:water:ethanedithiol: 82.5:5:5:5:2.5, v/v) for 4 hours at room temperature. The peptides were purified by HPLC on a Cosmosil 5C18-AR-II column (20×250 mm, Nacalai Tesque, Kyoto, Japan) with CH₃CN in water, both containing 0.05% (v/v) TFA. Purity of the product was confirmed by RP-HPLC on a Cosmosil 5C18-AR-II (4.6×250 mm, Nacalai Tesque) with a linear gradient of CH₃CN in water, both containing 0.05% (v/v) TFA. Mass spectrometric analysis was performed with a Bruker Autoflex III MALDI-TOF MS (Bruker Daltonics, Leipzig, Germany). H-Gly-Pro-Arg-Gly-(Pro-Hyp-Gly)₁₂-NH₂ (SEQ ID NO: 60): MS (MALDI-TOF) m/z calcd. for C₁₅₉H₂₃₂N₄₄O₅₂ ([M+H]⁺): 3590.7 found 3590.6. A HPLC profile of H-Gly-Pro-Arg-Gly-(Pro-Hyp-Gly)₁₂-NH₂ (SEQ ID NO: 60) is shown in FIG. 11. A collagen-like polypeptide, poly(Pro-Hyp-Gly)₁₀ (SEQ ID NO: 59) was obtained from PHG Co., Ltd. (Hyogo, Japan) [13].

Collagen-Anchors Derived from Clostridial Collagenases, ColG and ColH

CBD (s3) and PKD-CBD (s2b-s3) derived from the *C. histolyticum* class II collagenase ColH were purified as described previously[14]. CBD (s3b) and CBD-CBD (s3a-s3b) derived from the *C. histolyticum* class I collagenase ColG were purified as described previously[17].

Quantitative Analysis of Collagen Anchor Binding to a Collagenous Peptide

Binding of collagen-anchors to the mini-collagen peptide was measured by surface plasmon resonance using a BIA-CORE apparatus (Biacore, Uppsala, Sweden) in the same manner as reported previously [15]. Briefly, the peptide was dissolved in 10 mM sodium acetate (pH 6.0) at a concentration of 0.1 mg/ml, and was covalently immobilized on a CMS sensor chip (Biacore) using the standard amine coupling procedure recommended by the manufacturer. Resonance was measured in 10 mM sodium HEPES (pH 7.4), 150 mM NaCl, 1 mM CaCl₂, and 0.005% Tween-20 at a flow rate of 20 µl/min at 25° C. After each binding step, the chip was regenerated with a 180-s pulse of 0.1 M HCl. Values for the apparent dissociation constant, K_D(app), were calculated from equilibrium binding data for eight protein concentrations (100 nM-300 µM) by direct fitting to the following equation by the least squares method,

$$cRU = cRU_{max} \times [\text{protein}] / (K_D + [\text{protein}]) \quad (\text{Eq. 1})$$

where cRU is the response at equilibrium corrected for bulk refractive index errors using a sham-coupled flow cell blocked with ethanolamine, [protein] is the analyte concentration, and K_D is the dissociation constant.

Collagen-Binding bFGF

Four collagen-binding bFGF fusion proteins (CB-bFGFs) were used in this study (FIG. 6). Two fusion proteins, bFGF-s3 and bFGF-s2b-s3, consisting of human bFGF, and CBD or PKD-CBD derived from ColH were prepared as previously described [10]. In order to prepare bFGF-s3b (ColG), an expression plasmid, pCHG115 DNA encoding a fusion protein between GST and a C-terminal collagen-binding domain (s3b, ColG) was digested with BamHI and EcoRI at the linker region, and ligated with a hbFGF-encoding DNA fragment pretreated with BglII and EcoRI. *Escherichia coli* DH5a was transformed with the ligation mixture, to confirm the nucleotide sequence of resultant plasmid (pCHG115-hbFGF) by Sanger sequencing. *E. coli* BL21 CodonPlus RIL (Agilent Technologies, Santa Clara,

Calif.) was transformed with the plasmid to express the GST-bFGF-s3b fusion protein. The fusion protein was purified, and the GST moiety was cleaved off as described previously [10]. Another fusion protein consisting of bFGF and tandem CBDs derived from ColG (bFGF-s3a-s3b) was produced in the same manner using another expression plasmid, pCHG112.

Proliferation Assay

Periosteum was collected from the distal femurs of 10-week-old Wistar rats as previously described [9], and was then digested with 0.2% type I collagenase (Wako Pure Chemical Industries, Ltd., Tokyo, Japan) for 2 h at 37° C. The digested sample was passed through a 40- μ m filter to obtain single-cell suspensions of nucleated cells, which were then seeded at 1×10^4 cells/cm² in 6-well culture plates containing α -minimum essential medium (α -MEM) supplemented with 10% fetal bovine serum, 100 U/ml penicillin, and 100 μ g/ml streptomycin. The plates were incubated at 37° C. for 7 days in a 5% CO₂ atmosphere and the passage 0 (P0) cells were then detached from the plate surface by treatment with 0.25% trypsin and 1 mM EDTA for 5 min. The cells were collected and seeded at 1.25×10^3 cells/well in 96-well plates. α -MEM containing either bFGF, bFGF-s3 (ColH), bFGF-s2b-s3 (ColH), bFGF-s3b (ColG), or bFGF-s3a-s3b (ColG) was then added to the culture supernatant at concentrations of 0 (control), 0.1, 1, and 10 pM. Cell proliferation was evaluated after 2 days of treatment using a water-soluble tetrazolium (WST) assay kit (Cell Count Reagent SF; Nacalai Tesque, Kyoto, Japan) following the manufacturer's protocol and a previously described procedure [9].

Fracture Model

A femur fracture model was generated using 9-week-old C57BL/6J mice. The mice were fed standard rodent chow (CRF-1; Oriental Yeast, Tokyo, Japan), and were housed under controlled environmental conditions (temperature, 23 $\pm$ 2° C.; humidity, 55 $\pm$ 10%; lighting, 12-h light/dark cycle) in a semi-barrier system at Nippon Charles River Laboratories (Kanagawa, Japan). Femur fractures were generated by first making a 4-mm medial parapatellar incision in the left knee under sterile conditions. After drilling a 0.5-mm hole in the intracondylar notch, a 0.2-mm tungsten guide wire was inserted retrograde into the intramedullary canal, and a section of the femur was removed using a wire saw (0.22 mm in diameter) with a lateral approach. To stabilize the fracture, a stainless steel screw (0.5 mm in diameter) was inserted into the intramedullary canal after removing the guide wire. After generating the fracture, PBS (control), poly(Pro-Hyp-Gly)₁₀ (SEQ ID NO: 59) gel containing 0.058 nmoles of bFGF, bFGF-s3, bFGF-s2b-S3, bFGF-s3b, or bFGF-s3a-s3b was immediately injected into the fracture site (n=8, each treatment). The dose of bFGF was determined based on the results of a previous study [11]. All animal procedures followed the guidelines of the Animal Ethics Committee of Kitasato University.

Quantification of New Bone Volume and Bone Mineral Content

To quantify the new bone volume and bone mineral content in the control and treated region, femurs were removed from sacrificed mice four weeks after the fracture treatment, and stored in 4% paraformaldehyde for 48 h at 4° C. The femurs were transferred to PBS and imaged using an inspeXio SMX-90CT microfocal X-ray CT system (Shimadzu, Tokyo, Japan) with the following settings: acceleration voltage, 90 kV; current, 110 mA; voxel size, 20 μ m/pixel; and matrix size, 1024 $\times$ 1024. New bone volume and bone mineral content were quantified in the micro-CT

images of whole femurs using Tri-3D-Bon three-dimensional (3D) image analysis software (Ratoc System Engineering, Tokyo, Japan) at 10-mm regions of interest (500 slices) of the midfemur, as previously described [14;16]. Bone mineral content was estimated by comparing the measured densities of each femur sample in the micro-CT images to those in a hydroxyapatite (HA) calibration curve, which was constructed by plotting the data generated from phantom images prepared with 200, 300, 400, 500, 600, 700, and 800 mg HA/cm³. New bone was defined as having a threshold density value of ≥ 300 mg/cm³.

Histological Evaluation

To examine the effects of poly(Pro-Hyp-Gly)₁₀/bFGF-s3a-s3b (ColG) treatment on bone formation, femurs were excised from control and treated animals 14 days after the creation of fractures. The femur samples were demineralized in a 20% EDTA solution for 28 days, and the remaining tissue was then embedded in paraffin. The femurs were sectioned (3 μ m) through the long axis in the coronal plane, and the obtained sections were stained with hematoxylin and eosin (HE) for morphological analysis.

Statistical Analysis

Differences among the PBS (control), bFGF, bFGF-s3, bFGF-s2b-s3, bFGF-s3b and bFGF-s3a-s3b groups were examined using one-way ANOVA with Fisher's least significant difference (LSD) test. The level of significance was set at p<0.05. All statistical analyses were conducted using SPSS software (Version 19.0; SPSS Inc., Chicago, Ill.).

Results

Binding Affinity of Collagen-Anchors

Dissociation constants of four collagen-anchors to the mini-collagen peptide, H-Gly-Pro-Arg-Gly-(Pro-Hyp-Gly)₁₂-NH₂ (SEQ ID NO: 60), were measured by surface plasmon resonance (Table 2). Although s2b-s3 (PKD-CBD, ColH) showed a lower K_D value compared to the s3 alone (CBD, ColH), the values of s3b (CBD, ColG) and s3a-s3b (CBD-CBD, ColG) were approx. 10-fold lower than those of the ColH anchors. It can be expected that the ColG-derived anchors bind more tightly to collagenous peptides than the ColH-derived anchors.

TABLE 2

Binding affinity of various collagen anchors		
Collagen anchor	K _D ($\times 10^{-5}$ M)	Ratio
ColGS3aS3b	4.46 $\pm$ 0.45	0.100
ColGS3b	4.54 $\pm$ 0.15	0.102
ColHS2bS3	44.5 $\pm$ 0.55	1.00
ColHS3	75.2 $\pm$ 0.41	1.69

Regarding Table 2, anchor proteins were dissolved in HBS-Ca buffer at concentrations ranging from 1×10^{-7} M to 3×10^{-4} M. Binding to the collagenous peptide, H-Gly-Pro-Arg-Gly-(Pro-Hyp-Gly)₁₂-NH₂ (SEQ ID NO: 60), was measured by surface plasmon resonance. Data were directly fit to an equation described in Materials and Methods section by least squares method to calculate values for the apparent dissociation constant (K_D) and uncertainty.

In-Vitro Biological Activities of Fusion Proteins

The biological activities of the four CB-bFGF's were evaluated by measuring the proliferation of rat periosteal mesenchymal cells in vitro (FIG. 7). Two days after treatment with 0.1 pM bFGF-s3a-s3b (ColG), the number of cultured periosteal mesenchymal cells had significantly increased compared to the control (α -MEM) treatment group. In contrast, no significant increase was detected in the

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bFGF, bFGF-s3 (ColH), bFGF-s2b-s3 (ColH), or bFGF-s3b (ColG)-treated cells. However, when the concentration of the bFGF or CB-bFGF's was increased to 1 or 10 pM, the cell number had increased significantly in all forms of the growth factors compared to α -MEM-treated cells.

In-Vivo Callus Formation Induced by CB-bFGF/Poly(Pro-Hyp-Gly)₁₀ Composite Material

Poly(Pro-Hyp-Gly)₁₀ gel was mixed with either PBS, bFGF (controls) or one of the four prepared CB-bFGF's, and applied at fractured site in mice femurs. After 4 weeks of recovery, callus formation at the fracture sites was evaluated by micro-CT image analysis (FIGS. 8A-8F). Compared with PBS-injected fracture sites, callus volume and bone mineral content was significantly higher at sites treated with poly (Pro-Hyp-Gly)₁₀ in combination with bFGF or the CB-bFGF fusion proteins (FIG. 9, $P < 0.05$). Notably, however, bFGF-s2b-s3 (ColH), bFGF-s3b (ColG) and bFGF-s3a-s3b (ColG) resulted in higher callus volume and bone mineral content compared to bFGF (FIG. 9, $P < 0.05$). Among the three fusion proteins, bFGF-s3a-s3b (ColG) exhibited the highest efficacy for bone repair, as the callus volume and bone mineral content were significantly higher than those of all the other groups (FIG. 9, $P < 0.05$).

Histomorphometric Findings

To investigate the mechanism by which poly(Pro-Hyp-Gly)₁₀/bFGF-s3a-s3b (ColG) accelerated new bone formation, histological evaluation of the treated fracture sites was performed after 2 weeks when soft callus formation was first detected in the mouse femur fracture model. Compared to the control group, large calluses were observed at the fracture sites treated with either bFGF-s2b-s3 (ColH), bFGF-s3b (ColG) or bFGF-s3a-s3b (FIGS. 10A-10F). Notably, the calluses formed by the bFGF-s3a-s3b-treatment were clearly larger than those observed in the other treatment groups (FIGS. 10A-10F). This finding indicated that poly(Pro-Hyp-Gly)₁₀/bFGF-s3a-s3b (ColG) accelerated periosteal cell proliferation in the early stages of fracture healing.

Discussion

Clostridial collagenases possess collagen-anchors at their C-termini. The anchors bind to collagen fibrils and collagenous peptides with triple-helical conformation, but not to denatured collagen (gelatin) [17]. The anchors are made of two types of domains, PKD and CBD, where former enhances the binding of the latter. The enzymes possess collagen anchors made of various copy numbers of PKD(s) and CBD(s). Previously we have shown the callus-inducing potential of composite materials made of collagen-carrier (high density collagen sheet/powder or demineralized bone matrix) and bFGF fused with an anchor made of a single copy each of PKD and CBD (bFGF-PKD-CBD) derived from *Clostridium histolyticum* class II collagenase, ColH [14;16]. Recently we tried to use collagenous-peptide gel instead of collagen-carrier since the former is more easily applicable by injection. In aged mice fracture models, a novel composite material made of poly(Pro-Hyp-Gly)₁₀ and bFGF-PKD-CBD induced greater bone formation than one made of poly(Pro-Hyp-Gly)₁₀ and bFGF [11]. Hence, we could speculate that efficacies of this composite material can be optimized by switching anchors with various binding affinity to the collagenous peptide carrier.

In order to estimate the binding affinity of various anchors to the peptide carrier, poly(Pro-Hyp-Gly)₁₀, we synthesized a longer collagenous peptide, H-Gly-Pro-Arg-Gly-(Pro-Hyp-Gly)₁₂-NH₂ as a ligand for surface plasmon resonance assay, where the first triplet, Pro-Arg-Gly, was introduced to keep its water-solubility and triple-helical conformation.

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Since the peptide was immobilized to the sensor chip at the N-terminus, it could be safely expected that the alteration near the N-terminus does not affect the binding significantly. A single CBD (ColG s3b) showed a K_D value ($4.54 \pm 0.15 \times 10^{-5}$ M) to this peptide similar to that ($5.72 \pm 0.473 \times 10^{-5}$ M) reported previously to a shorter collagenous peptide, (G(POG)₈) [15], indicating that the quantitative analysis performed here is reproducible. Collagen anchors (s3a-s3b and s3b) derived from class I enzyme (ColG) showed significantly higher affinity to this peptide than ones (s2b-s3 and s3) derived from class II enzyme (ColH), suggesting that the formers are more appropriate anchors toward the peptide carrier than the latters. Presence of an additional CBD (s3a) did not significantly enhance binding of ColG s3b to the synthetic peptide, suggesting that the peptide used for this assay is still too short to allow simultaneous binding of the two CBDs. An alternative possibility is that the binding between S3a and the collagen peptide is sufficiently weak to be reflected in the apparent K_D value. Binding assay and/or small-angle X-ray diffraction study using a longer collagenous peptide would be necessary to solve this question.

Provided that the efficacy correlates with the binding affinity, we could expect more callus formation using bFGF fused with the ColG anchors when combined with the collagenous peptide. Hence, we prepared four CB-bFGF's with one of the anchors described above. In order to confirm that bFGF moiety in each CB-bFGF construct is intact, cell proliferation assay was performed in vitro. Four CB-bFGF and bFGF promoted cell proliferation in dose dependent manner, which indicates that bFGF moiety is active regardless to the various anchor moiety. Specific activity of the bFGF-CBD-CBD (s3a-s3b) seems to be slightly higher than the other CB-bFGF's at the lower concentrations (0.1-1.0 pM), which might be due to the binding of this CB-bFGF to collagen produced by the mesenchymal cells.

Then, osteogenic potential of the composite materials made of poly(Pro-Hyp-Gly)₁₀ and either of the four CB-bFGF's was compared using a mouse femur fracture model. When combined with the gel-like carrier made of poly(Pro-Hyp-Gly)₁₀, bFGF-CBD (ColG) and bFGF-CBD-CBD (ColG) induced large soft callus formation at 2 weeks and significantly more callus during fracture healing compared to bFGF, bFGF-PKD-CBD (ColH), or bFGF-CBD (ColH). Among the examined, bFGF-CBD-CBD (ColG) resulted in the highest callus volume and bone mineral content.

The binding affinity of collagen anchors may affect the osteogenic activity of the corresponding fusion proteins, as the rapid diffusion of target molecules from defect sites would limit their osteogenic potential [10]. We previously demonstrated that bFGF-PKD-CBD (ColH) has higher binding affinity to collagen-carrier and induces greater bone formation compared to bFGF-CBD (ColH) [10]. Among the collagen anchors used in the present study, ColG CBD(s) showed approximately 10-times higher affinity than ColH anchors to a collagenous peptide. This finding is consistent with the in-vivo results, where the treatment with bFGF fused with ColG anchors accelerated osteogenesis more efficiently compared to bFGF fused with ColH anchors when combined with a collagenous peptide carrier.

Taken together, osteogenic potentials seem to correlate with the binding affinity of collagen-anchors at least in the range we examined. It also seems likely that the tandem CBDs (ColG) increase the retention time of bFGF most at fracture sites when introduced together with collagen-like polypeptide poly(Pro-Hyp-Gly)₁₀ and thereby accelerate bone formation. These results suggest that bFGF-CBD-CBD

(ColG) combined with poly(Pro-Hyp-Gly)₁₀ is a promising therapeutic material for stimulating bone repair in the clinical setting.

Previous studies have demonstrated that fusion proteins between growth factors and CBDs have superior biological activity compared to native growth factor [18;19]. For example, Han et al. [18] reported that bone morphogenetic protein containing a CBD derived from von Willebrand factor increased the in-vitro alkaline phosphatase activity of the mouse osteoblastic cell line MC3T3-E1. As bFGF stimulates periosteal mesenchymal cells [9;10;16], here, we examined the proliferation ability of bFGF and several CB-bFGF fusion proteins using rat periosteal mesenchymal cells and demonstrated that bFGF-CBD-CBD stimulated the highest cell proliferation activity of the examined proteins at a concentration as low as 1 pM. Taken together, the findings from this study indicate that bFGF-CBD-CBD possess both high collagen-binding affinity and biological activity, including the ability to stimulate callus formation during fracture healing. A recombinant collagen-binding bFGF fusion protein containing tandem CBDs from *C. histolyticum* class I collagenase ColG strongly induced bone formation when injected in combination with the collagen-like peptide poly(Pro-Hyp-Gly)₁₀ into mouse femur fracture sites. The high osteogenic properties of bFGF-CBD-CBD/ poly(Pro-Hyp-Gly)₁₀ suggest that this composite material has the potential to promote fracture healing in the clinical setting.

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SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 62

<210> SEQ ID NO 1
 <211> LENGTH: 113
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 <213> ORGANISM: Clostridium histolyticum
 <220> FEATURE:
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 <222> LOCATION: (1)..(113)
 <223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 1

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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 2
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: B. brevis
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 2

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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 3
 <211> LENGTH: 115
 <212> TYPE: PRT
 <213> ORGANISM: C. sporogenes
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(115)
 <223> OTHER INFORMATION: ColG s3a domain

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<400> SEQUENCE: 3

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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 4

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: C. botulinum

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(115)

<223> OTHER INFORMATION: C. botulinumA3 ColG s3a domain

<400> SEQUENCE: 4

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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 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
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 5

<211> LENGTH: 113

<212> TYPE: PRT

<213> ORGANISM: C. perfringens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(113)

<223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 5

```

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

```

-continued

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 6
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: C. sordellii
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(113)
 <223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 6

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 7
 <211> LENGTH: 116
 <212> TYPE: PRT
 <213> ORGANISM: C. histolyticum
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(116)
 <223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 7

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

-continued

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65          70          75          80
Lys Asn Asn Ser Lys Val Gly Thr Phe Lys Ser Thr Lys Gly Arg His
      85          90          95
Tyr Val Phe Ile Tyr Lys His Asp Ser Ala Ser Asn Ile Ser Tyr Ser
      100        105        110
Leu Asn Ile Lys
      115

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<210> SEQ ID NO 8
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: C. sporogenes
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(117)
<223> OTHER INFORMATION: ColG s3a domain

```

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<400> SEQUENCE: 8
Leu Val Ile Ser Glu Lys Glu Asp Asn Asp Ser Phe Asp Lys Ala Asn
1      5      10      15
Arg Val Cys Lys Asn Gln Ser Val Leu Ala Thr Leu Asp Thr Asn Asp
      20      25      30
Asn Arg Asp Thr Tyr Tyr Phe Asp Ala Leu Thr Ala Gly Thr Ile Asp
      35      40      45
Val Ile Met Glu Asn Thr Asp Asn Asn Ser Asn Ile Phe Asn Trp Leu
      50      55      60
Ala Tyr Ser Ser Asp Asn Thr Asn Asn Tyr Ile Gly Tyr Ser Thr Lys
65      70      75      80
Lys Glu Gly Asn Lys Leu Leu Gly Ser Phe Lys Val Pro Lys Pro Gly
      85      90      95
Arg Tyr Tyr Ile Leu Ala Tyr Lys Asn Ser Ser Asn Lys Ile Asn Tyr
      100     105     110
Lys Leu Thr Ile Asn
      115

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<210> SEQ ID NO 9
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: C. botulinum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(117)
<223> OTHER INFORMATION: C. botulinumB ColG s3a domain

```

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<400> SEQUENCE: 9
Ile Asn Val Asp Glu Glu Glu Tyr Asn Asp Asp Phe Glu Cys Ala Asn
1      5      10      15
Asn Ile Phe Lys Asn Gln Ile Met Ser Gly Asn Leu Asp Ser Ser Asp
      20      25      30
Lys Cys Asp Thr Phe Ser Phe Asn Ala Leu Ser Ala Gly Thr Ile Asn
      35      40      45
Val Thr Leu Glu Asn Ser Asn Ser Asp Ser Ser Thr Val Asn Trp Leu
      50      55      60
Ala Tyr Ser Ser Glu Asp Thr Asp Asn Tyr Ile Gly Tyr Ala Ser Glu
65      70      75      80
Asn Asp Gly Asn Lys Phe Ser Gly Lys Phe Lys Val Asn Lys Pro Gly
      85      90      95
Lys Tyr Tyr Ile Val Ala Tyr Glu Val Asn Gly Ala Asp Ser Lys Tyr
      100     105     110

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-continued

Lys Leu Lys Val Asp
115

<210> SEQ ID NO 10
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: C. tetani E88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(117)
<223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 10

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

<210> SEQ ID NO 11
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: C. perfringens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(115)
<223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 11

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

<210> SEQ ID NO 12
<211> LENGTH: 115

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<212> TYPE: PRT
<213> ORGANISM: B. brevis
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<223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 12
Asp Gly Ser Glu Thr Glu Gln Pro Asn Pro Asn Pro Glu Glu Ser Ser
1      5      10      15
Leu Ser Leu Gly Lys Pro Ile Thr Gly Ile Ile His Pro Gln Lys Pro
20     25     30
Ser Gln Glu Phe Arg Leu Asp Val Lys Ser Ala Gln Gln Leu Gln Val
35     40     45
Glu Met Glu Thr Lys Gln Gly Asp Gly Val Ala Trp Leu Val Phe His
50     55     60
Glu Ala Asp Arg Glu Asn Tyr Ile Ser Tyr Pro Thr Lys Arg Glu Gly
65     70     75     80
Asn Lys Leu Ile Gly Ser Phe Asp Ala Lys Pro Gly Thr Tyr Tyr Val
85     90     95
Thr Ala Tyr Thr Tyr Arg Thr Glu Gln Glu Asp Gln Pro Phe Arg Leu
100    105    110
Leu Val Thr
115

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<210> SEQ ID NO 13
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: P. dendritiformis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(114)
<223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 13
Pro Asn Ala Asp His Glu Pro Asn Asp Ser Trp Glu Gln Ala Val Pro
1      5      10      15
Leu Asp Gly Thr Gly Val Pro Val Ser Gly Lys Leu Ser Asp Thr Asp
20     25     30
Arg Val Asp Val Tyr Arg Phe Asp Ala Gly Lys Ala Glu Gln Trp Thr
35     40     45
Ile Glu Leu Glu Thr Glu Gln Ala Gln Ser Val Ala Trp Val Val His
50     55     60
His Glu Ser Asp Leu Asn Asn Tyr Ala Ala Tyr Pro Thr Gln Val Glu
65     70     75     80
Gly Thr Ser Val Ala Gly Ser Val Asp Ala Val Pro Gly Thr Tyr Tyr
85     90     95
Val Tyr Val Tyr Ser Val Gly Asn Gly Glu Gln Ser Tyr Arg Leu Val
100    105    110
Val Gln

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<210> SEQ ID NO 14
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: C. sordellii
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(116)
<223> OTHER INFORMATION: ColG s3a domain

<400> SEQUENCE: 14

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

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```

<210> SEQ ID NO 15
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Clostridium histolyticum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(111)
<223> OTHER INFORMATION: ColG s3b domain

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<400> SEQUENCE: 15

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```

Leu Lys Glu Lys Glu Asn Asn Asp Ser Ser Asp Lys Ala Thr Val Ile
1      5      10      15
Pro Asn Phe Asn Thr Thr Met Gln Gly Ser Leu Leu Gly Asp Asp Ser
20      25      30
Arg Asp Tyr Tyr Ser Phe Glu Val Lys Glu Glu Gly Glu Val Asn Ile
35      40      45
Glu Leu Asp Lys Lys Asp Glu Phe Gly Val Thr Trp Thr Leu His Pro
50      55      60
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 16
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Bacillus sp.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(111)
<223> OTHER INFORMATION: ColG s3b domain

```

```

<400> SEQUENCE: 16

```

```

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

```

-continued

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 17
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: *L. sphaericus*
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: ColG s3b domain

<400> SEQUENCE: 17

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 18
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: *B. brevis*
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: ColG s3b domain

<400> SEQUENCE: 18

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				
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			

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<210> SEQ ID NO 19
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: C. perfringens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(112)
<223> OTHER INFORMATION: ColG s3b domain

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<400> SEQUENCE: 19

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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

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<210> SEQ ID NO 20
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: C. sporogenes
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(115)
<223> OTHER INFORMATION: ColG s3b domain

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<400> SEQUENCE: 20

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```

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

```

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<210> SEQ ID NO 21
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: C. botulinum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(115)
<223> OTHER INFORMATION: C. botulinumA3 ColG s3b domain

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<400> SEQUENCE: 21

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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 22
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: C. sordellii
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(113)
<223> OTHER INFORMATION: ColG s3b domain

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<400> SEQUENCE: 22

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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

```

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<210> SEQ ID NO 23
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: C. histolyticum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(112)
<223> OTHER INFORMATION: ColG s3b domain

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<400> SEQUENCE: 23

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

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35	40	45
Glu Leu Asp Lys Lys Asp	Glu Phe Gly Val Thr Trp	Thr Leu His Pro
50	55	60
Glu Ser Asn Ile Asn Asp	Arg Ile Thr Tyr Gly Gln	Val Asp Gly Asn
65	70	75
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 Lys
100	105	110

<210> SEQ ID NO 24
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: C. sporogenes
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: ColG s3b domain

<400> SEQUENCE: 24

Ile His Glu Lys	Glu Asn Asn Asp	Ser Phe Glu Ser	Ala Asn Lys Ile
1	5	10	15
Val Pro Asp Ala	Pro Val Leu Gly	Ser Leu Asn Gly	Glu Asp Leu Arg
20	25	30	
Asp Ile Tyr Ser	Phe Asp 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 Thr	Asn Tyr Ile Ala	Tyr Gly Ser Lys	Leu Gly Asn 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 Ser Gly	Asn Tyr Ser Leu	Ile Ile Lys
100	105	110	

<210> SEQ ID NO 25
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: C. botulinum
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: C. botulinumB ColG s3b domain

<400> SEQUENCE: 25

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

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<210> SEQ ID NO 26
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: C. tetani E88
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(111)
<223> OTHER INFORMATION: ColG s3b domain

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<400> SEQUENCE: 26

Ile His Glu Lys Glu Asn Asn Asp Ser Phe Glu Thr Ala Asn Lys Ile
1          5          10          15

Thr Leu Asp Thr Leu Val Leu Gly Asn Leu Asp Tyr Lys Asp Val Ser
          20          25          30

Asp Ile Tyr Ser Phe Asp Ile Glu Asn Thr Lys Asp Leu Asn Ile Lys
          35          40          45

Leu Thr Asn Leu Asn Asn Leu Gly Ile Ala Trp Asn Leu Tyr Lys Glu
          50          55          60

Ser Asp Leu Asn Asn Tyr Ile Ala Tyr Gly Ala Lys Ser Asp Asn Ala
          65          70          75          80

Ile Val Gly Lys Cys Asn Leu Ser Pro Gly Lys Tyr Tyr Leu Tyr Val
          85          90          95

Tyr Lys Tyr Ser Gly Asp Lys Gly Asn Tyr Ser Val Ile Ile Asn
          100          105          110

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<210> SEQ ID NO 27
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: C. perfringens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(114)
<223> OTHER INFORMATION: ColG s3b domain

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<400> SEQUENCE: 27

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 Gln 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 Ile Val Asn Leu Gln
          100          105          110

Asn Lys

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<210> SEQ ID NO 28
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: B. brevis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(115)
<223> OTHER INFORMATION: ColG s3b domain

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<400> SEQUENCE: 28

```

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

```

<210> SEQ ID NO 29

<211> LENGTH: 114

<212> TYPE: PRT

<213> ORGANISM: *P. dendritiformis*

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(114)

<223> OTHER INFORMATION: ColG s3b domain

<400> SEQUENCE: 29

```

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

```

<210> SEQ ID NO 30

<211> LENGTH: 115

<212> TYPE: PRT

<213> ORGANISM: *C. sordellii*

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(115)

<223> OTHER INFORMATION: ColG s3b domain

<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

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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 Pro Asn
 115

<210> SEQ ID NO 31
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: C. sporogenes
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: ColG s3c domain

<400> SEQUENCE: 31

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 32
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: C. botulinum
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: C. botulinumA3 ColG s3c domain

<400> SEQUENCE: 32

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

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	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 33
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: B. cereus
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: AH603 domain

<400> SEQUENCE: 33

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	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 34
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: B. anthracis
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: ColG domain

<400> SEQUENCE: 34

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 35
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: C. cerus
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)

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<223> OTHER INFORMATION: G9842 domain

<400> SEQUENCE: 35

```

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 36

<211> LENGTH: 111

<212> TYPE: PRT

<213> ORGANISM: B. mycoides

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(111)

<223> OTHER INFORMATION: ColG domain

<400> SEQUENCE: 36

```

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
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 37

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: B. weihensteph

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(112)

<223> OTHER INFORMATION: ColG domain

<400> SEQUENCE: 37

```

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

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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 38
 <211> LENGTH: 125
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium histolyticum
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(125)
 <223> OTHER INFORMATION: ColH s3 domain

<400> SEQUENCE: 38

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

<210> SEQ ID NO 39
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium histolyticum
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(111)
 <223> OTHER INFORMATION: ColH s3 domain

<400> SEQUENCE: 39

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	
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	

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100	105	110
<210> SEQ ID NO 40		
<211> LENGTH: 234		
<212> TYPE: PRT		
<213> ORGANISM: C. histolyticum		
<220> FEATURE:		
<221> NAME/KEY: misc_feature		
<222> LOCATION: (1)..(234)		
<223> OTHER INFORMATION: ColG s3a + s3b domains		
<400> SEQUENCE: 40		
Thr Pro Ile Thr Lys Glu Met Glu Pro Asn Asp Asp Ile Lys Glu Ala		
1 5 10 15		
Asn Gly Pro Ile Val Glu Gly Val Thr Val Lys Gly Asp Leu Asn Gly		
20 25 30		
Ser Asp Asp Ala Asp Thr Phe Tyr Phe Asp Val Lys Glu Asp Gly Asp		
35 40 45		
Val Thr Ile Glu Leu Pro Tyr Ser Gly Ser Ser Asn Phe Thr Trp Leu		
50 55 60		
Val Tyr Lys Glu Gly Asp Asp Gln Asn His Ile Ala Ser Gly Ile Asp		
65 70 75 80		
Lys Asn Asn Ser Lys Val Gly Thr Phe Lys Ser Thr Lys Gly Arg His		
85 90 95		
Tyr Val Phe Ile Tyr Lys His Asp Ser Ala Ser Asn Ile Ser Tyr Ser		
100 105 110		
Leu Asn Ile Lys Gly Leu Gly Asn Glu Lys Leu Lys Glu Lys Glu Asn		
115 120 125		
Asn Asp Ser Ser Asp Lys Ala Thr Val Ile Pro Asn Phe Asn Thr Thr		
130 135 140		
Met Gln Gly Ser Leu Leu Gly Asp Asp Ser Arg Asp Tyr Tyr Ser Phe		
145 150 155 160		
Glu Val Lys Glu Glu Gly Glu Val Asn Ile Glu Leu Asp Lys Lys Asp		
165 170 175		
Glu Phe Gly Val Thr Trp Thr Leu His Pro Glu Ser Asn Ile Asn Asp		
180 185 190		
Arg Ile Thr Tyr Gly Gln Val Asp Gly Asn Lys Val Ser Asn Lys Val		
195 200 205		
Lys Leu Arg Pro Gly Lys Tyr Tyr Leu Leu Val Tyr Lys Tyr Ser Gly		
210 215 220		
Ser Gly Asn Tyr Glu Leu Arg Val Asn Lys		
225 230		
<210> SEQ ID NO 41		
<211> LENGTH: 239		
<212> TYPE: PRT		
<213> ORGANISM: C. sporogenes		
<220> FEATURE:		
<221> NAME/KEY: misc_feature		
<222> LOCATION: (1)..(239)		
<223> OTHER INFORMATION: ColG s3a + s3b domains		
<400> SEQUENCE: 41		
Leu Val Ile Ser Glu Lys Glu Asp Asn Asp Ser Phe Asp Lys Ala Asn		
1 5 10 15		
Arg Val Cys Lys Asn Gln Ser Val Leu Ala Thr Leu Asp Thr Asn Asp		
20 25 30		
Asn Arg Asp Thr Tyr Tyr Phe Asp Ala Leu Thr Ala Gly Thr Ile Asp		
35 40 45		

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Val Ile Met Glu Asn Thr Asp Asn Asn Ser Asn Ile Phe Asn Trp Leu
  50                      55                      60

Ala Tyr Ser Ser Asp Asn Thr Asn Asn Tyr Ile Gly Tyr Ser Thr Lys
  65                      70                      75                      80

Lys Glu Gly Asn Lys Leu Leu Gly Ser Phe Lys Val Pro Lys Pro Gly
                      85                      90                      95

Arg Tyr Tyr Ile Leu Ala Tyr Lys Asn Ser Ser Asn Lys Ile Asn Tyr
      100                      105                      110

Lys Leu Thr Ile Asn Gly Asp Ile Asp Lys Ala Pro Leu Lys Asn Glu
      115                      120                      125

Ile His Glu Lys Glu Asn Asn Asp Ser Phe Glu Ser Ala Asn Lys Ile
      130                      135                      140

Val Pro Asp Ala Pro Val Leu Gly Ser Leu Asn Gly Glu Asp Leu Arg
  145                      150                      155                      160

Asp Ile Tyr Ser Phe Asp Ile Lys Glu Thr Lys Asp Leu Asn Ile Lys
      165                      170                      175

Leu Thr Asn Leu Asn Asn Leu Gly Leu Thr Trp Thr Leu Tyr Lys Glu
      180                      185                      190

Ser Asp Leu Thr Asn Tyr Ile Ala Tyr Gly Ser Lys Leu Gly Asn Thr
      195                      200                      205

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

Tyr Lys Tyr Ser Gly Asn Ser Gly Asn Tyr Ser Leu Ile Ile Lys
  225                      230                      235

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<210> SEQ ID NO 42
<211> LENGTH: 244
<212> TYPE: PRT
<213> ORGANISM: C. botulinum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(244)
<223> OTHER INFORMATION: C. botulinumB ColG s3a + s3b domains

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<400> SEQUENCE: 42

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Ile Asn Val Asp Glu Glu Glu Tyr Asn Asp Asp Phe Glu Cys Ala Asn
  1                      5                      10                      15

Asn Ile Phe Lys Asn Gln Ile Met Ser Gly Asn Leu Asp Ser Ser Asp
      20                      25                      30

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

Val Thr Leu Glu Asn Ser Asn Ser Asp Ser Ser Thr Val Asn Trp Leu
      50                      55                      60

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

Asn Asp Gly Asn Lys Phe Ser Gly Lys Phe Lys Val Asn Lys Pro Gly
      85                      90                      95

Lys Tyr Tyr Ile Val Ala Tyr Glu Val Asn Gly Ala Asp Ser Lys Tyr
      100                      105                      110

Lys Leu Lys Val Asp Gly Asp Ile Glu Asn Thr Ser Glu Ser Lys Pro
      115                      120                      125

Glu Asp Lys Glu Glu Ile Lys Glu Glu Ile Asn Asp Asp Ser Phe Asp
      130                      135                      140

Ser Ala Thr Lys Ile Lys Ala Asn Ser Thr Ile Thr Asp Thr Leu Asn
  145                      150                      155                      160

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Gly Glu Asp Asn Lys Asp Ile Cys Tyr Phe Asn Val Asn Asn Asn Ser
 165 170 175

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

Gln Leu Phe Ser Glu Glu Asp Leu Asp Asn Tyr Ile Ala Tyr Gly Ser
 195 200 205

Gln Ser Gly Asp Ser Ile Val Gly Thr Ala Asn Val Gln Pro Gly Lys
 210 215 220

Tyr Tyr Leu Leu Ile Tyr Lys Tyr Thr Gln Ala Asp Gly Ser Tyr Thr
 225 230 235 240

Phe Thr Ile Lys

<210> SEQ ID NO 43
 <211> LENGTH: 239
 <212> TYPE: PRT
 <213> ORGANISM: C. tetani E88
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(239)
 <223> OTHER INFORMATION: ColG s3a + s3b domains

<400> SEQUENCE: 43

Asn Val Ile Tyr Glu Lys Glu Asn Asn Asp Ser Phe Asp Lys Ala Asn
 1 5 10 15

Lys Ile His Lys Asn Gln Ile Val Met Ala Thr Leu Asp Thr Glu Asp
 20 25 30

Tyr Arg Asp Thr Phe Tyr Phe Asp Ala Leu Thr Ser Gly Ser Ile Asp
 35 40 45

Ile Thr Ile Glu Asn Ile His Gly Asn Ser Asp Ala Phe Asn Trp Leu
 50 55 60

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

Lys Glu Asp Asn Lys Leu Met Gly Ser Phe Lys Val His Lys Pro Gly
 85 90 95

Arg Tyr Tyr Ile Leu Val Tyr Lys Thr Ser Leu Asn Lys Val Asn Tyr
 100 105 110

Lys Leu Asn Ile Ser Asp Ala Thr Asn Met Ala Pro Val Ile Lys Lys
 115 120 125

Ile His Glu Lys Glu Asn Asn Asp Ser Phe Glu Thr Ala Asn Lys Ile
 130 135 140

Thr Leu Asp Thr Leu Val Leu Gly Asn Leu Asp Tyr Lys Asp Val Ser
 145 150 155 160

Asp Ile Tyr Ser Phe Asp Ile Glu Asn Thr Lys Asp Leu Asn Ile Lys
 165 170 175

Leu Thr Asn Leu Asn Asn Leu Gly Ile Ala Trp Asn Leu Tyr Lys Glu
 180 185 190

Ser Asp Leu Asn Asn Tyr Ile Ala Tyr Gly Ala Lys Ser Asp Asn Ala
 195 200 205

Ile Val Gly Lys Cys Asn Leu Ser Pro Gly Lys Tyr Tyr Leu Tyr Val
 210 215 220

Tyr Lys Tyr Ser Gly Asp Lys Gly Asn Tyr Ser Val Ile Ile Asn
 225 230 235

<210> SEQ ID NO 44
 <211> LENGTH: 243
 <212> TYPE: PRT
 <213> ORGANISM: C. perfringens

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1) .. (243)
<223> OTHER INFORMATION: ColG s3a + s3b domains

<400> SEQUENCE: 44

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

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

Asp Tyr Ser Asp Lys Tyr Tyr Phe Asp Val Ala Lys Lys Gly Asn Val
35          40          45

Lys Ile Thr Leu Asn Asn Leu Asn Ser Val Gly Ile Thr Trp Thr Leu
50          55          60

Tyr Lys Glu Gly Asp Leu Asn Asn Tyr Val Leu Tyr Ala Thr Gly Asn
65          70          75          80

Asp Gly Thr Val Leu Lys Gly Glu Lys Thr Leu Glu Pro Gly Arg Tyr
85          90          95

Tyr Leu Ser Val Tyr Thr Tyr Asp Asn Gln Ser Gly Thr Tyr Thr Val
100         105         110

Asn Val Lys Gly Asn Leu Lys Asn Glu Val Lys Glu Thr Ala Lys Asp
115         120         125

Ala Ile Lys Glu Val Glu Asn Asn Asn Asp Phe Asp Lys Ala Met Lys
130         135         140

Val Asp Ser Asn Ser Lys Ile Val Gly Thr Leu Ser Asn Asp Asp Leu
145         150         155         160

Lys Asp Ile Tyr Ser Ile Asp Ile Gln Asn Pro Ser Asp Leu Asn Ile
165         170         175

Val Val Glu Asn Leu Asp Asn Ile Lys Met Asn Trp Leu Leu Tyr Ser
180         185         190

Ala Asp Asp Leu Ser Asn Tyr Val Asp Tyr Ala Asn Ala Asp Gly Asn
195         200         205

Lys Leu Ser Asn Thr Cys Lys Leu Asn Pro Gly Lys Tyr Tyr Leu Cys
210         215         220

Val Tyr Gln Phe Glu Asn Ser Gly Thr Gly Asn Tyr Ile Val Asn Leu
225         230         235         240

Gln Asn Lys

<210> SEQ ID NO 45
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: B. brevis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1) .. (239)
<223> OTHER INFORMATION: ColG s3a + s3b domains

<400> SEQUENCE: 45

Asp Gly Ser Glu Thr Glu Gln Pro Asn Pro Asn Pro Glu Glu Ser Ser
1          5          10          15

Leu Ser Leu Gly Lys Pro Ile Thr Gly Ile Ile His Pro Gln Lys Pro
20          25          30

Ser Gln Glu Phe Arg Leu Asp Val Lys Ser Ala Gln Gln Leu Gln Val
35          40          45

Glu Met Glu Thr Lys Gln Gly Asp Gly Val Ala Trp Leu Val Phe His
50          55          60

Glu Ala Asp Arg Glu Asn Tyr Ile Ser Tyr Pro Thr Lys Arg Glu Gly

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65	70	75	80
Asn Lys Leu Ile Gly Ser Phe Asp Ala Lys Pro Gly Thr Tyr Tyr Val	85	90	95
Thr Ala Tyr Thr Tyr Arg Thr Glu Gln Glu Asp Gln Pro Phe Arg Leu	100	105	110
Leu Val Thr Gly Glu Asp Arg Pro Gln Glu Gln Leu Tyr Gln Glu Asn	115	120	125
Glu Ser Asn Asp Ser Thr Glu Gln Ala Asn Gly Pro Leu Lys Ile Gly	130	135	140
Thr Thr Val Ser Gly Asp Met Lys Gly Asn Asp Trp Gln Asp Ile Phe	145	150	155
Ala Phe Gln Val Asp Lys Pro Glu Glu Ile Arg Ile Ser Leu Asn Pro	165	170	175
Gln Glu Gly Gln Gly Val Thr Trp Met Leu Phe His Glu Gly Asn Leu	180	185	190
Asp Gln Pro Val Thr Tyr Pro Gln Glu Arg Glu Gly Asn Leu Gln Ser	195	200	205
Ala His Tyr Gln Val Lys Pro Gly Arg Tyr Phe Leu Tyr Val Tyr Lys	210	215	220
Tyr Gln Asn Glu Asp Ile Val Tyr Thr Val Glu Thr Lys Gln Arg	225	230	235

<210> SEQ ID NO 46
 <211> LENGTH: 242
 <212> TYPE: PRT
 <213> ORGANISM: P. dendritiformis
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(242)
 <223> OTHER INFORMATION: ColG s3a + s3b domains

<400> SEQUENCE: 46

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

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Glu Gly Asp Thr Asp Arg Pro Leu Leu Tyr Pro Ser Glu Val Glu Gly
 195 200 205

Asn Arg Met Ser Gly Gly Phe Ala Ala Glu Ala Gly Arg Tyr His Leu
 210 215 220

Tyr Val Tyr Lys Tyr Thr Asp Glu Asp Ile His Tyr Thr Leu Gln Val
 225 230 235 240

Gln His

<210> SEQ ID NO 47
 <211> LENGTH: 238
 <212> TYPE: PRT
 <213> ORGANISM: *C. sordellii*
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(238)
 <223> OTHER INFORMATION: ColG s3a + s3b domains

<400> SEQUENCE: 47

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

Asn Gly Pro Ile Lys Ile Asn Thr Asn Tyr Ser Gly Asp Leu Ser Asp
 20 25 30

Thr Asp Asn Lys Asp Tyr Tyr Tyr Phe Asn Leu Asp Asn Pro Ser Asn
 35 40 45

Ile Asn Ile Thr Leu Glu Asn Leu Asp Asn Lys Gly Ile Ser Trp Gln
 50 55 60

Leu Phe His Glu Ser Asp Leu Asn Asn Tyr Val Ala Tyr Pro Thr Thr
 65 70 75 80

Ser Gly Ala Ile Leu Asn Gly Asp Tyr Asn Ala Thr Lys Pro Gly Lys
 85 90 95

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

Leu Lys Val Asn Phe Gly Asn Asn Asn Asp Asp Gly Val Glu Gln Glu
 115 120 125

Asp Asn Asn Ser Phe Glu Lys Ala Asn Pro Phe Ser Ile Asn Gln Leu
 130 135 140

Val Lys Gly Glu Leu Asp Asn Asn Lys Asp Thr Ser Asp Tyr Phe Lys
 145 150 155 160

Phe Glu Val Lys Glu Asp Ala Gln Leu Asn Ile Ser Leu Glu Lys Thr
 165 170 175

Glu Gly Asp Gly Val Asn Trp Leu Leu Phe Lys Asp Ser Asp Leu Glu
 180 185 190

Asn Tyr Ile Ala Ser Pro Thr Glu Ser Ile Asp Asn Lys Leu Asn Gly
 195 200 205

Lys Val Asp Leu Lys Val Gly Thr Tyr Tyr Leu Glu Val Tyr Gly Tyr
 210 215 220

Gly Ser Ser Pro Val Lys Tyr Asn Phe Lys Val Thr Pro Asn
 225 230 235

<210> SEQ ID NO 48
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: *Clostridium histolyticum*
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(6)
 <223> OTHER INFORMATION: ColG domain linker

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<400> SEQUENCE: 48

Gly	Leu	Gly	Asn	Glu	Lys
1				5	

<210> SEQ ID NO 49

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: C. sporogenes

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(11)

<223> OTHER INFORMATION: ColG domain linker

<400> SEQUENCE: 49

Gly	Asp	Ile	Asp	Lys	Ala	Pro	Leu	Lys	Asn	Glu
1				5					10	

<210> SEQ ID NO 50

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: C. botulinumB

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(16)

<223> OTHER INFORMATION: C. botulinumB ColG domain linker

<400> SEQUENCE: 50

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

<210> SEQ ID NO 51

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: C. tetani E88

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(11)

<223> OTHER INFORMATION: ColG domain linker

<400> SEQUENCE: 51

Asp	Ala	Thr	Asn	Met	Ala	Pro	Val	Ile	Lys	Lys
1				5					10	

<210> SEQ ID NO 52

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: C. perfringens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(14)

<223> OTHER INFORMATION: ColG domain linker

<400> SEQUENCE: 52

Gly	Asn	Leu	Lys	Asn	Glu	Val	Lys	Glu	Thr	Ala	Lys	Asp	Ala
1				5					10				

<210> SEQ ID NO 53

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: B. brevis

<220> FEATURE:

<221> NAME/KEY: misc_feature

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

<223> OTHER INFORMATION: ColG domain linker

<400> SEQUENCE: 53

Gly	Glu	Asp	Arg	Pro	Gln	Glu	Gln	Leu
1					5			

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<210> SEQ ID NO 54
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: P. dendritiformis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(14)
<223> OTHER INFORMATION: ColG domain linker

<400> SEQUENCE: 54

Pro Gly Thr Thr Gly Gln Glu Gln Glu Pro Glu Leu Pro Pro
1          5          10

<210> SEQ ID NO 55
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: C. sordellii
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(7)
<223> OTHER INFORMATION: ColG domain linker

<400> SEQUENCE: 55

Phe Gly Asn Asn Asn Asp Asp
1          5

<210> SEQ ID NO 56
<211> LENGTH: 288
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(288)
<223> OTHER INFORMATION: Human bFGF protein sequence

<400> SEQUENCE: 56

Met Val Gly Val Gly Gly Gly Asp Val Glu Asp Val Thr Pro Arg Pro
1          5          10          15

Gly Gly Cys Gln Ile Ser Gly Arg Gly Ala Arg Gly Cys Asn Gly Ile
20          25          30

Pro Gly Ala Ala Ala Trp Glu Ala Ala Leu Pro Arg Arg Arg Pro Arg
35          40          45

Arg His Pro Ser Val Asn Pro Arg Ser Arg Ala Ala Gly Ser Pro Arg
50          55          60

Thr Arg Gly Arg Arg Thr Glu Glu Arg Pro Ser Gly Ser Arg Leu Gly
65          70          75          80

Asp Arg Gly Arg Gly Arg Ala Leu Pro Gly Gly Arg Leu Gly Gly Arg
85          90          95

Gly Arg Gly Arg Ala Pro Glu Arg Val Gly Gly Arg Gly Arg Gly Arg
100         105         110

Gly Thr Ala Ala Pro Arg Ala Ala Pro Ala Ala Arg Gly Ser Arg Pro
115         120         125

Gly Pro Ala Gly Thr Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala
130         135         140

Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys
145         150         155         160

Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile
165         170         175

His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His
180         185         190

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Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys
    195                      200                205

Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu
    210                      215                220

Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu
    225                      230                235                240

Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp
    245                      250                255

Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr
    260                      265                270

Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
    275                      280                285

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<210> SEQ ID NO 57
<211> LENGTH: 141
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(141)
<223> OTHER INFORMATION: human PTHrP

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<400> SEQUENCE: 57

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

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<210> SEQ ID NO 58
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: PTH(1-33) with Gly-Ser amino
        terminal extension

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<400> SEQUENCE: 58

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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
    35

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<210> SEQ ID NO 59

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<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (23)..(23)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline

<400> SEQUENCE: 59

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 60
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (24)..(24)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: Xaa is 4-hydroxyproline
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: Xaa is 4-hydroxyproline

<400> SEQUENCE: 60

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

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

Xaa Gly Pro Xaa Gly Pro Xaa Gly
35          40

<210> SEQ ID NO 61
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 61

Pro Glu Ile Lys Asp Leu Ser Glu Asn Lys Leu Pro Val Ile Tyr Met
1           5           10          15

His Val Pro Lys Ser Gly Ala Leu Asn Gln Lys Val Val Phe Tyr Gly
20          25          30

Lys Gly Thr Tyr Asp Pro Asp Gly Ser Ile Ala Gly Tyr Gln Trp Asp
35          40          45

Phe Gly Asp Gly Ser Asp Phe Ser Ser Glu Gln Asn Pro Ser His Val
50          55          60

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

Ser Gly Gln Met Ser Glu Lys Thr Met Lys Ile Lys Ile Thr Asp
85          90          95

<210> SEQ ID NO 62
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<212> TYPE: PRT
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<222> LOCATION: (1)..(84)
<223> OTHER INFORMATION: human parathyroid hormone
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<400> SEQUENCE: 62

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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

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We claim:

1. A collagen-binding agent comprising a first collagen-binding domain and a second collagen-binding domain linked by a domain linker and a therapeutic agent linked to at least one of the collagen-binding domains by a therapeutic agent linker,

wherein the collagen-binding agent lacks collagenase activity;

wherein the therapeutic agent is fibroblast growth factor (FGF);

wherein the two collagen-binding domains bind to collagen with a K_D of between 100 μ M and 0.1 nM;

wherein the first collagen-binding domain is selected from the group consisting of the polypeptides of SEQ ID NOs: 1-14, and the second collagen-binding domain is selected from the group consisting of the polypeptides of SEQ ID NOs: 15-30; and

wherein the C-terminus of the first collagen-binding domain is linked to the N-terminus of the second collagen-binding domain by the domain linker.

2. The collagen-binding agent of claim 1, wherein the domain linker comprises a polypeptide.

3. The collagen-binding agent of claim 1, wherein the domain linker comprises a polypeptide selected from the group consisting of the polypeptides of SEQ ID NOs: 48-55 or a polypeptide having at least 80% sequence identity to any one of the polypeptides of SEQ ID NOs: 48-55.

4. The collagen-binding agent of claim 1, wherein the therapeutic agent linker comprises a polypeptide.

5. The collagen-binding agent of claim 4, wherein the C-terminus of the therapeutic agent is linked to the N-terminus of the collagen-binding domains by the therapeutic agent linker.

6. A pharmaceutical composition comprising the collagen-binding agent of claim 1 and a pharmaceutical carrier.

7. A method of stimulating bone formation in a subject having a bone condition comprising administering to the subject a therapeutically effective amount of the collagen-binding agent of claim 1.

8. The method of claim 7, wherein the subject is a mammal.

9. The method of claim 8, wherein the mammal is a human.

* * * * *