

AMENDED 1

WE CLAIM :

1. A vector comprising each of the following elements arranged sequentially to form a module open reading frame, said vector comprising

5 a) a first restriction site that codes for a first group of amino acids, wherein the first group of amino acids comprises at least two amino acids;

b) a first open reading frame coding for a polypeptide of interest, wherein the coding sequence of the polypeptide of interest is in frame with the coding sequence of at least two amino acids of the first restriction site;

10 c) a second restriction site that codes for a second group of amino acids, wherein the second group of amino acids comprises at least two amino acids, wherein the coding sequence of the second group of amino acids of the second restriction site is in frame with the coding sequence of the polypeptide of interest of the first open reading frame, and wherein the polynucleotide sequence of the second restriction site is not the
15 same as the polynucleotide sequence of the first restriction site;

d) a spacer polynucleotide sequence, wherein the spacer polynucleotide sequence codes for at least three spacer amino acids, and wherein the coding sequence for the spacer sequence is in frame with the polynucleotide sequence of the second restriction site; and

20 e) a third restriction site that codes for a third group of amino acids, wherein the third group of amino acids comprises at least two amino acids, wherein the coding sequence of the third group of amino acids of the third restriction site are in frame with the coding sequence of the at least three spacer amino acids and wherein the polynucleotide sequence of the third restriction site is not the same as the polynucleotide sequence of the
25 first restriction site and the third restriction site is not the same as the polynucleotide sequence of the second restriction site,

wherein elements (a) through (e) are in-frame linked to one another to form the module open reading frame,

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wherein the first restriction site is susceptible to a restriction enzyme that would produce a first single-stranded overhang comprising at least 2 nucleotides, wherein the second restriction site is susceptible to a restriction enzyme that would produce a second single-stranded overhang comprising at least 2 nucleotides, and

- 5 wherein said first and second overhangs are complementary to one another, whereupon the annealing of the first and second overhangs, the first restriction site and the second restriction site are destroyed.

2. The vector as claimed in claim 1, wherein the polypeptide of interest is a full length protein or polypeptide, a protein functional domain, a protein structural domain, a
10 protein enzymatic domain, a protein inhibition domain, a protein binding domain, a protein localization domain, or an epitope.

3. The vector as claimed in any one of claim 1 or claim 2, wherein said first restriction site comprises a polynucleotide sequence recognized by the NgoM IV restriction enzyme.

- 15 4. The vector as claimed in any one of claims 1-3, wherein the second restriction site comprises a polynucleotide sequence recognized by the Xma I restriction enzyme.

5. The vector as claimed in any one of claims 1-4, wherein the third restriction site comprises a polynucleotide sequence recognized by the Cla I restriction enzyme.

6. The vector as claimed in any one of claims 1-5, wherein the spacer polynuc-
20 leotide sequence codes for three glycine amino acids.

7. The vector as claimed in any one of claims 1-6, wherein at least one additional open reading frame is inserted between the first open reading frame and the second restriction site, wherein each of the at least one additional open reading frames is in frame with both the first open reading frame and the second restriction group, and wherein each

AMENDED 1

of the additional open reading frames codes for at least one additional polypeptide of interest.

8. The vector as claimed in claim 7, wherein there are no restriction sites in any of the open reading frames between the first and second restriction groups that occur in
5 either the first or second restriction sites.

9. A method of making a fusion polypeptide comprising

a) digesting the vector as claimed in any one of claims 3 to 8 with restriction enzymes that recognize the second and third restriction sites to create a linear vector with a first and second singlestranded overhang, wherein the first and second overhangs are in-
10 compatible with one another;

b) providing a first insert, wherein the first insert comprises at least one additional open reading frame, wherein the at least one additional open reading frame comprises 5' and 3' overhangs that are compatible with the first and second overhangs, wherein each of the at least one additional open reading frames codes for at least one ad-
15 ditional polypeptide of interest;

c) ligating the first insert into the linear vector to form a ligated expression vector, wherein the ligation of the 5' overhang of the at least one open reading frame anneals with the first singlestranded overhang of the linear vector, wherein the ligation of the 3' overhang of the at least one open reading frame anneals with the second single-
20 stranded overhang of the linear vector, and wherein the ligation of the 3' overhang recreates the third restriction site,

wherein the first open reading frame and the at least one additional open reading frames are ligated in frame with one another.

10. A method of making fusion protein DNA constructs comprising,

25 a) providing first and second polynucleotide reagents, wherein each reagent contains an open reading frame of interest, and wherein each open reading frame of interest is flanked by at least 3 predetermined restriction endonuclease sites, wherein the

AMENDED 1

first restriction site is susceptible to a restriction enzyme that would produce a first single-stranded overhang comprising at least 2 nucleotides, wherein the second restriction site is susceptible to a restriction enzyme that would produce a second single-stranded overhang comprising at least 2 nucleotides, and wherein said first and second overhangs
5 are complementary to one another, whereupon the annealing of the first and second overhangs, the first restriction site and the second restriction site are destroyed.

b) digesting the first polynucleotide reagent with 2 different restriction endonucleases that cleave at 2 of the predetermined restriction endonuclease sites, generating a polynucleotide with 2 different overhangs,

10 c) digesting the second polynucleotide reagent with 2 different restriction endonucleases that cleave at 2 of the predetermined restriction endonuclease sites, wherein a polynucleotide containing an open reading frame of interest is released, wherein the released polynucleotide has 2 different overhangs, and wherein one of the overhangs is compatible with an overhang of the polynucleotide digested in step b),

15 d) mixing together, annealing, and ligating the polynucleotide generated in step b) and the released polynucleotide containing an open reading frame of interest of step c), wherein a third polynucleotide containing a fusion of open reading frames is generated, wherein a junction between the open reading frames of interest is no longer susceptible to digestion with any of the endonucleases that cut at the 3 predetermined restriction sites, and wherein sequences flanking the fusion of open reading frames of interest
20 contain the 3 predetermined restriction sites.

11. A method of making fusion protein DNA constructs comprising,

a) providing first and second polynucleotide reagents, wherein each reagent contains an open reading frame of interest, and wherein each open reading frame of interest
25 is flanked by at least 3 predetermined restriction endonuclease sites, wherein the first restriction site is susceptible to a restriction enzyme that would produce a first single-stranded overhang comprising at least 2 nucleotides, wherein the second restriction site is susceptible to a restriction enzyme that would produce a second single-stranded overhang

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comprising at least 2 nucleotides, and wherein said first and second overhangs are complementary to one another, whereupon the annealing of the first and second overhangs, the first restriction site and the second restriction site are destroyed,

b) digesting the first polynucleotide reagent with 2 different restriction endonucleases that cleave at 2 of the predetermined restriction endonuclease sites, generating a polynucleotide with 2 incompatible overhangs,

c) digesting the second polynucleotide reagent with 2 different restriction endonucleases that cleave at 2 of the predetermined restriction endonuclease sites, wherein 1 of the restriction endonucleases is identical to a restriction endonuclease of step b), and wherein a polynucleotide containing an open reading frame of interest is released, and wherein the released polynucleotide has 2 incompatible overhangs,

d) mixing together, annealing, and ligating the polynucleotide generated in step b) and the released polynucleotide containing an open reading frame of interest of step c), wherein a third polynucleotide containing a fusion of open reading frames is generated, wherein the fusion of open reading frames of interest is flanked by said predetermined restriction sites, and wherein a junction between the open reading frames of interest lacks said 3 predetermined restriction endonuclease sites.

12. The method as claimed in claims 10 or 11, wherein the predetermined restriction sites are sequences cleavable by NgoM IV, Xma I, and Cla I.

20 Dated 5th May, 2008.



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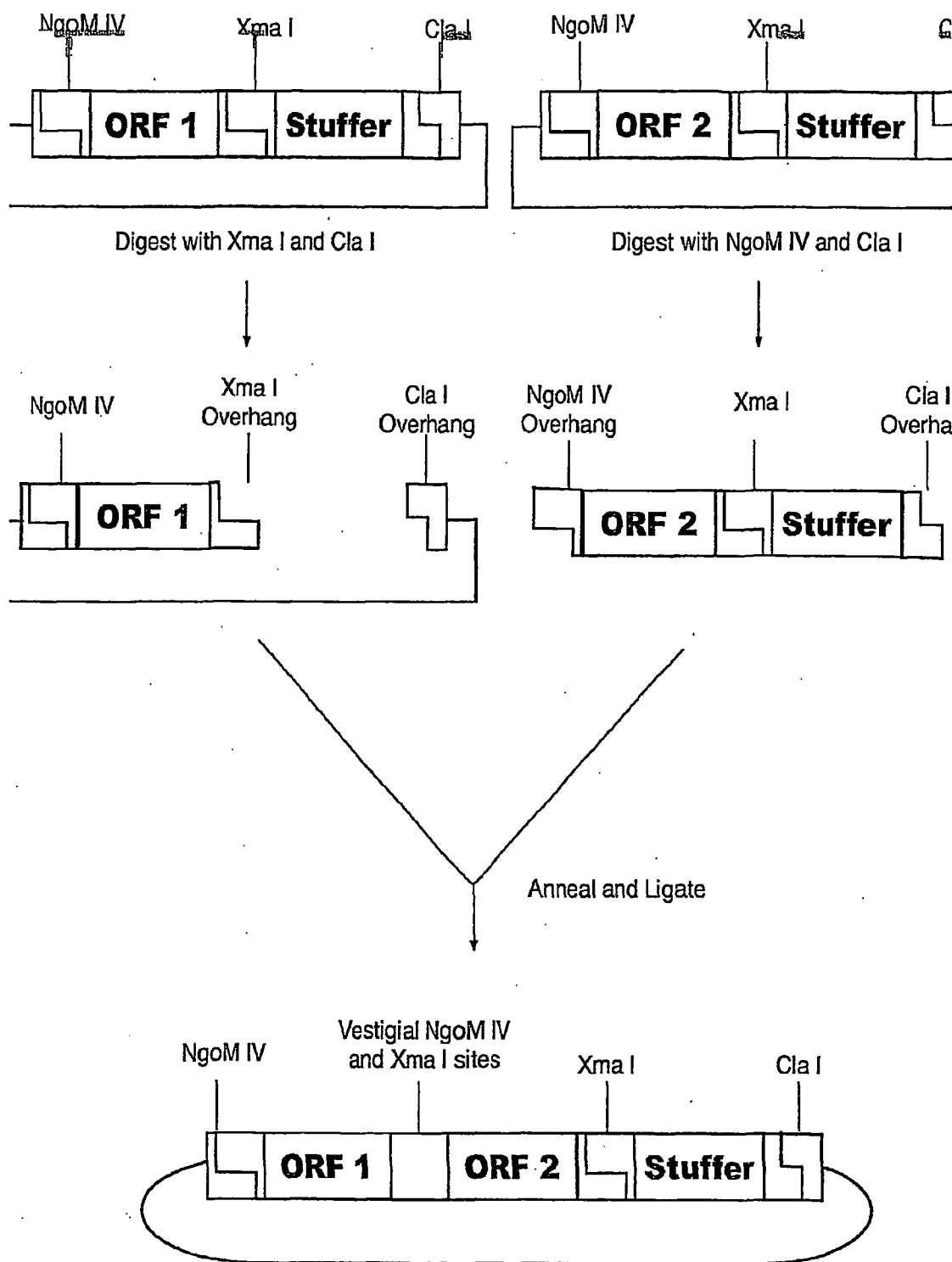


FIGURE 1

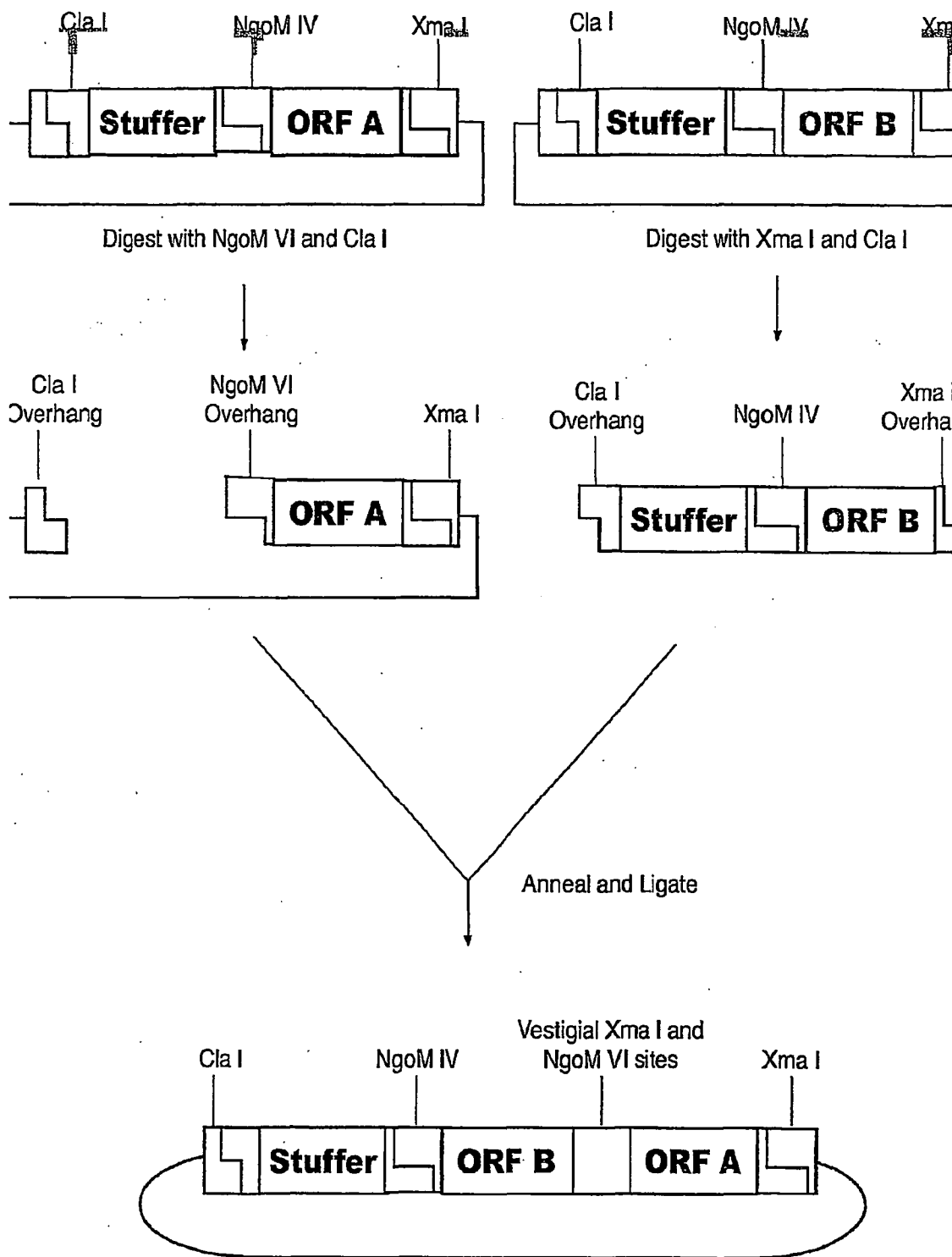


FIGURE 2

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S. D. Ahuja
S. D. AHUJA
of D. P. AHUJA & CO.
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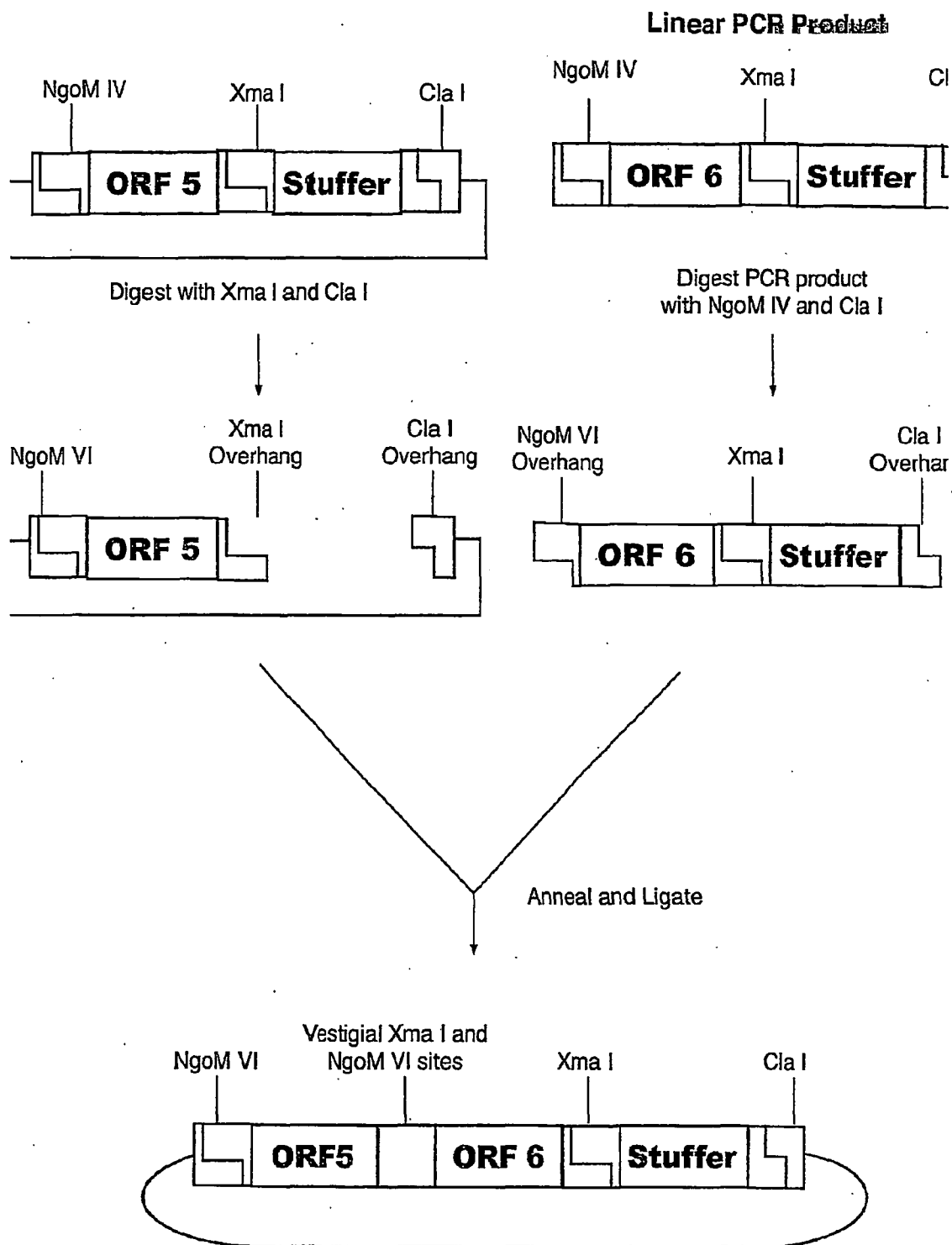


FIGURE 3

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of D. P. AHUJA & CO.
APPLICANT'S AGENT

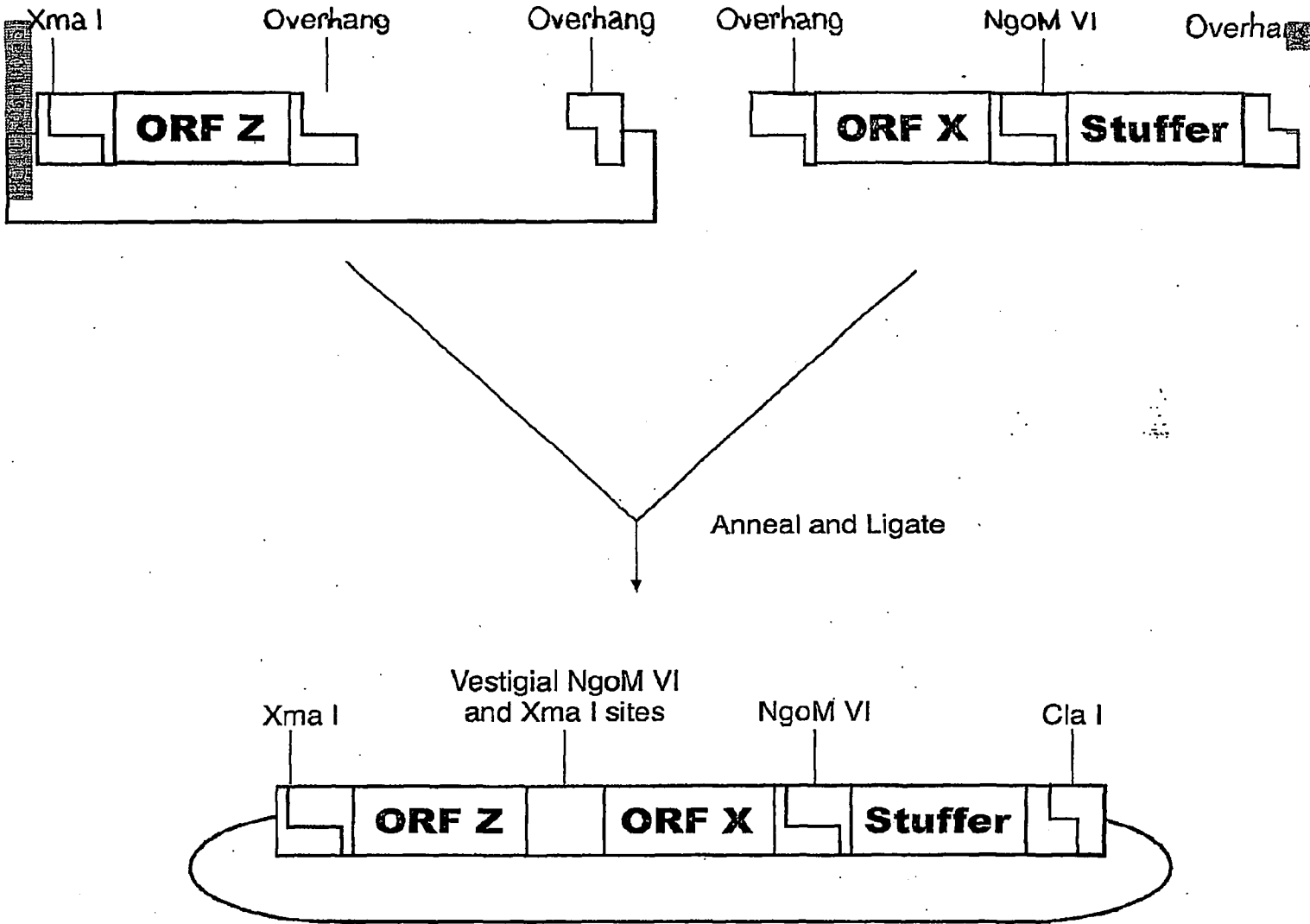


FIGURE 4

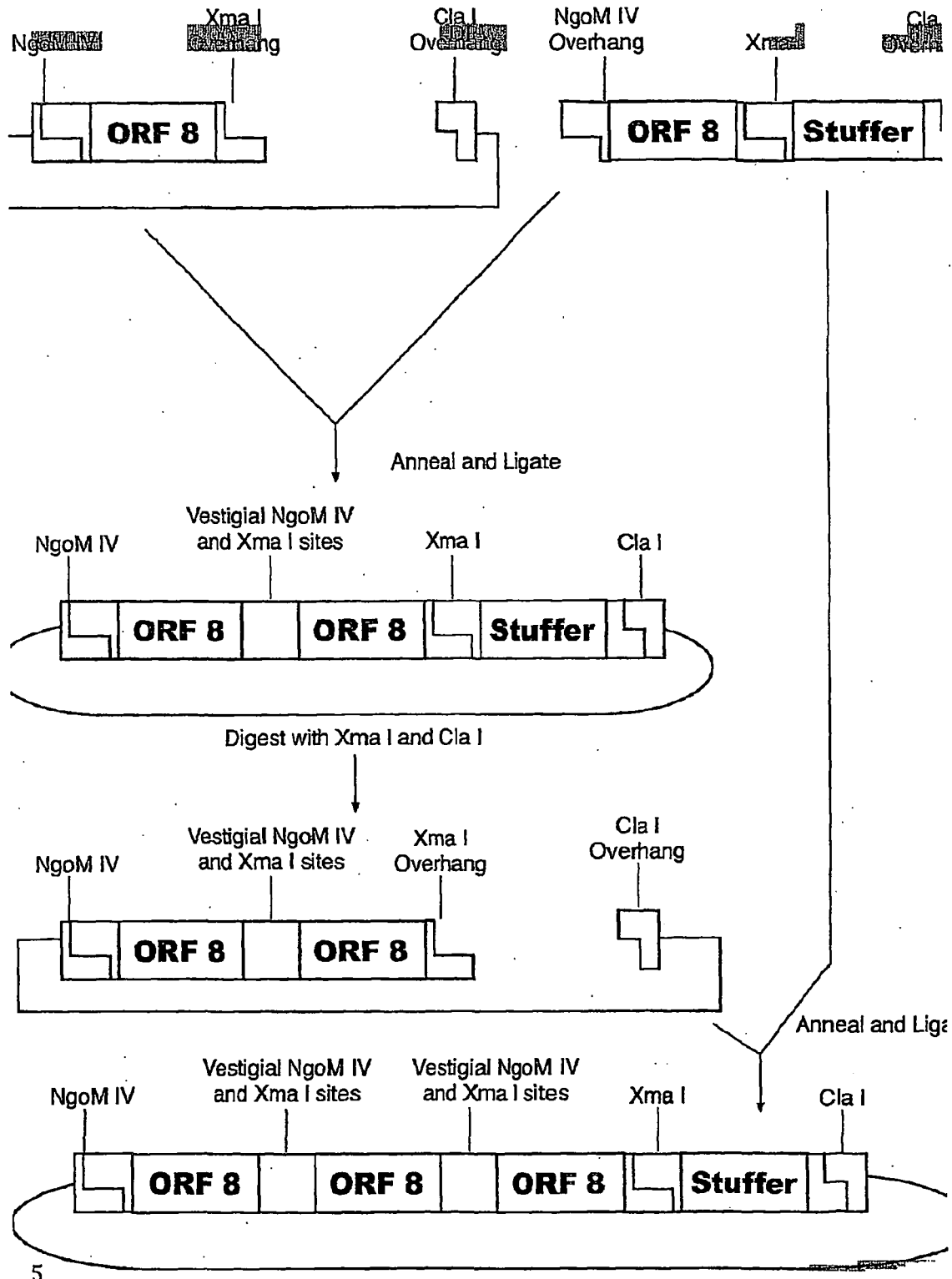


FIGURE 5

Site I	EXON R segment	Vestigial Sites	EXON T segment	Site II	stuffer	Site III
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FIGURE 6A

Site I	EXON D segment	Vestigial Sites	EXON A segment	Vestigial Sites	EXON H segment	Site II	stuffer	Site III
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FIGURE 6B

Site I	EXON A segment	Vestigial Sites	EXON P segment	Vestigial Sites	EXON L segment	Vestigial Sites	EXON C segment	Site II	stuffer	Site III
-----------	---------------------------	--------------------	---------------------------	--------------------	---------------------------	--------------------	---------------------------	------------	---------	-------------

FIGURE 6C

Site I	ORF Y	Vestigial Sites	ORF Z	Vestigial Sites	LOCALIZATION SIGNAL	Site II	stuffer	Site III
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FIGURE 7A

Site I	LOCALIZATION SIGNAL	Vestigial Sites	PEPTIDE 3	Vestigial Sites	PEPTIDE 4	Vestigial Sites	PEPTIDE 5	Site II	stuffer	Site III
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FIGURE 7B

Site I	LIGAND X	Vestigial Sites	LIGAND X	Vestigial Sites	LIGAND X	Vestigial Sites	LOCALIZATION SIGNAL	Site II	stuffer	Site III
-----------	---------------------	--------------------	---------------------	--------------------	---------------------	--------------------	--------------------------------	------------	---------	-------------

FIGURE 7C

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S. D. AHUJA

of D. P. AHUJA & CO.
APPLICANT'S AGENT

Site I	EPITOPE	Vestigial Sites	LIGAND	Site II	stuffer	Site III
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FIGURE 8A

Site I	EXON S segment	Vestigial Sites	EXON V segment	Vestigial Sites	EPITOPE	Site II	stuffer	Site III
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FIGURE 8B

Site I	ORF 3	Vestigial Sites	ORF 9	Vestigial Sites	EPITOPE	Vestigial Sites	ORF 7	Site II	stuffer	Site III
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FIGURE 8C

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S. D. AHUA
of D. P. AHUA & CO.
APPLICANTS AGENT

Site I	CYTOPLASMIC DOMAIN	Vestigial Sites	TRANSMEMBRANE DOMAIN	Vestigial Sites	EXTRACELLULAR DOMAIN	Site II	stuffer	Site III
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FIGURE 9A

Site I	DNA BINDING DOMAIN	Vestigial Sites	HORMONE BINDING DOMAIN	Vestigial Sites	DIMERIZATION DOMAIN	Vestigial Sites	ACTIVATION DOMAIN	Site II	stuffer	Site III
--------	---------------------------	-----------------	-------------------------------	-----------------	----------------------------	-----------------	--------------------------	---------	---------	----------

FIGURE 9B

Site I	SUBSTRATE RECOGNITION DOMAIN	Vestigial Sites	CATALYTIC DOMAIN	Vestigial Sites	INHIBITION DOMAIN	Vestigial Sites	BINDING DOMAIN	Site II	stuffer	Site III
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FIGURE 9C

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[Signature]
S-D-AHUA
of D. P. AHUA & CO.
APPLICANT'S AGENT

PROMOTER	CHIMERIC PROTEIN CODING SEQUENCE	STOP	POLY-A
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FIGURE 10

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S. D. AHUA
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of D. P. AHUA & CO.
APPLICANT'S AGENT

<----- Module Open Reading Frame ----->				
NgoM IV	ORF of interest	Xma I	Stuffer	Cla I
GCCGGC	AAGAAGAAAAAGAAGAAG	CCCGGG	GGCGGAGGC	ATCGAT
AlaGly	LysLysLysLysLysLys	ProGly	GlyGlyGly	IleAsp

FIGURE 11

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Site I	Phosphorylation Domain	Site II	Stuffer	Site III	Site I	Catalytic Domain	Site II	Stuffer	Site III
Site I	Zinc Finger Region	Site II	Stuffer	Site III	Site I	DNA Binding Domain	Site II	Stuffer	Site III
Site I	Peptide Inhibitor	Site II	Stuffer	Site III	Site I	Leucine Zipper Region	Site II	Stuffer	Site III
Site I	Hormone Binding Domain	Site II	Stuffer	Site III	Site I	Transmembrane Domain	Site II	Stuffer	Site III
Site I	Epitope	Site II	Stuffer	Site III	Site I	Activation Domain	Site II	Stuffer	Site III
Site I	Dimerization Domain	Site II	Stuffer	Site III	Site I	Inhibition Domain	Site II	Stuffer	Site III
Site I	Lipid Binding Domain	Site II	Stuffer	Site III	Site I	G Protein Binding Region	Site II	Stuffer	Site III
Site I	Glycosylation Domain	Site II	Stuffer	Site III	Site I	Highly Acidic Region	Site II	Stuffer	Site III
Site I	Peptide Hormone	Site II	Stuffer	Site III	Site I	Ligand	Site II	Stuffer	Site III
Site I	Ion Pore Region	Site II	Stuffer	Site III	Site I	Protein Subunit	Site II	Stuffer	Site III
Site I	Reporter Peptide	Site II	Stuffer	Site III	Site I	Localization Signal	Site II	Stuffer	Site III

FIGURE 12

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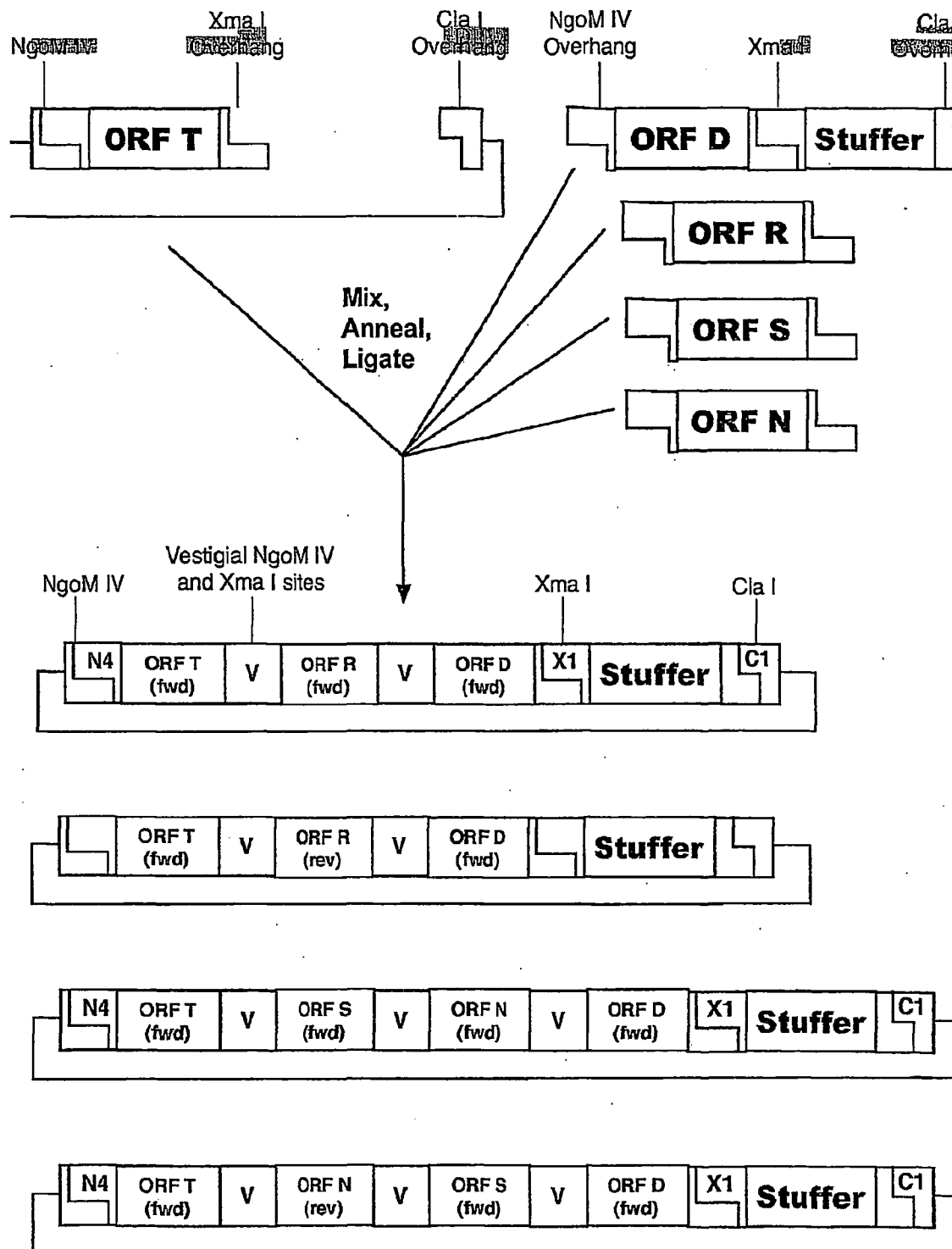


FIGURE 13

[Signature]

S. D. AHUJA
of D. P. AHUJA & CO.
APPLICANT'S AGENT

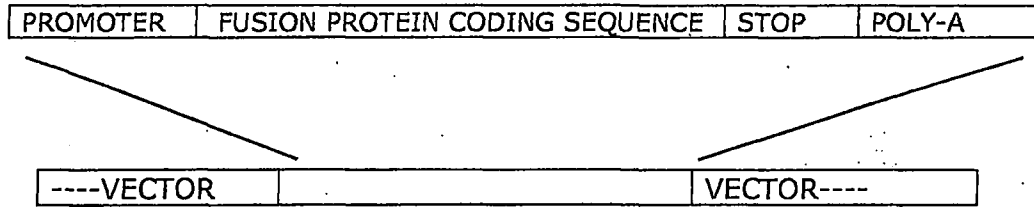


FIGURE 14A

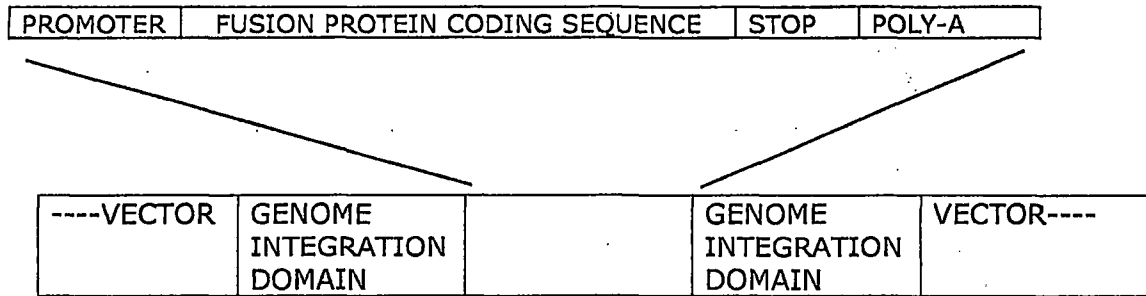


FIGURE 14B

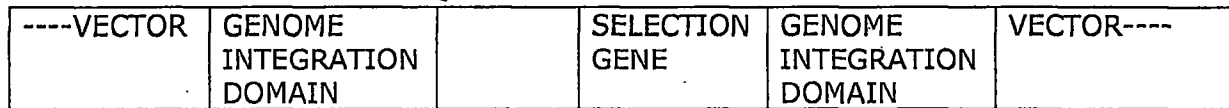


FIGURE 14C



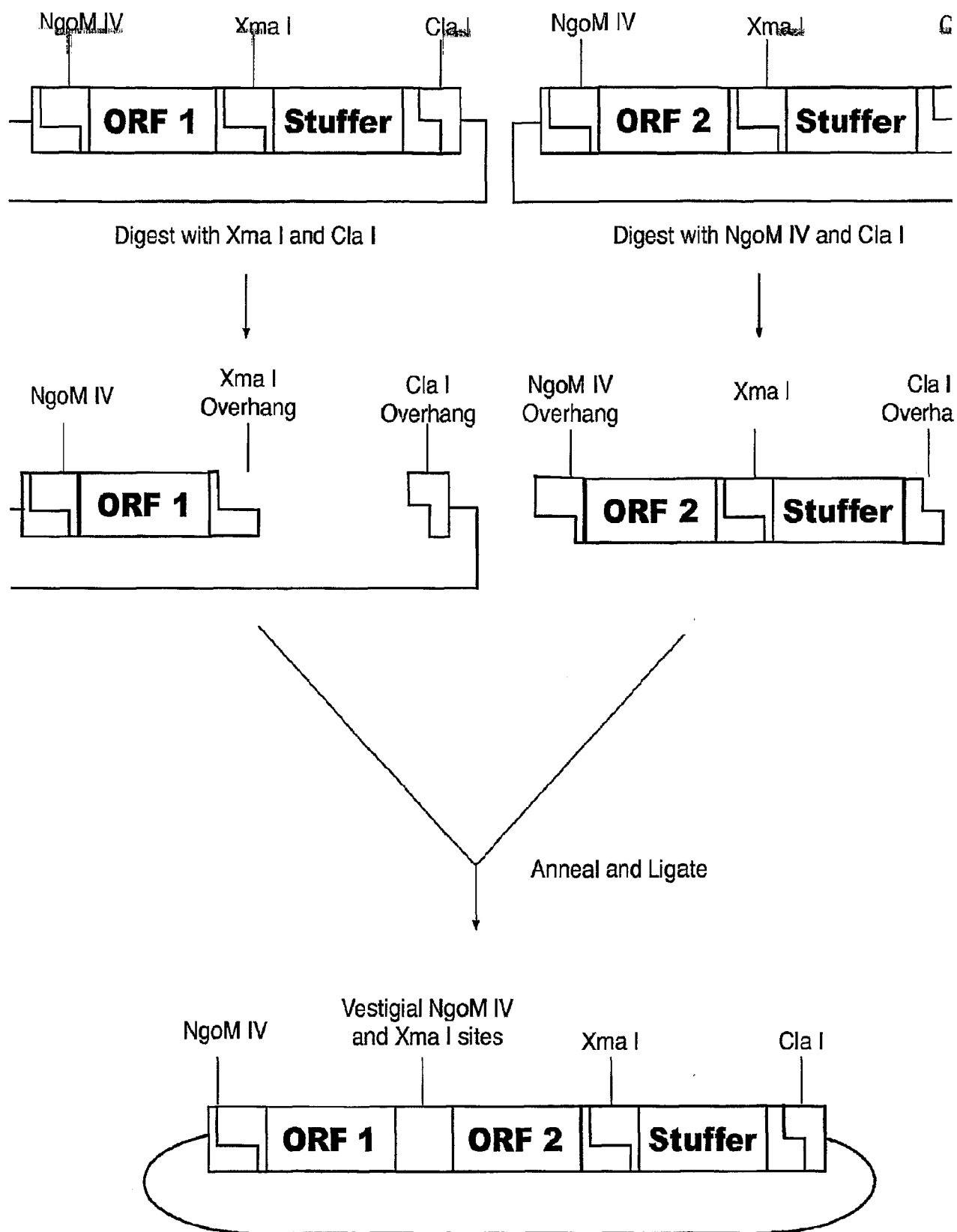
FIGURE 14D

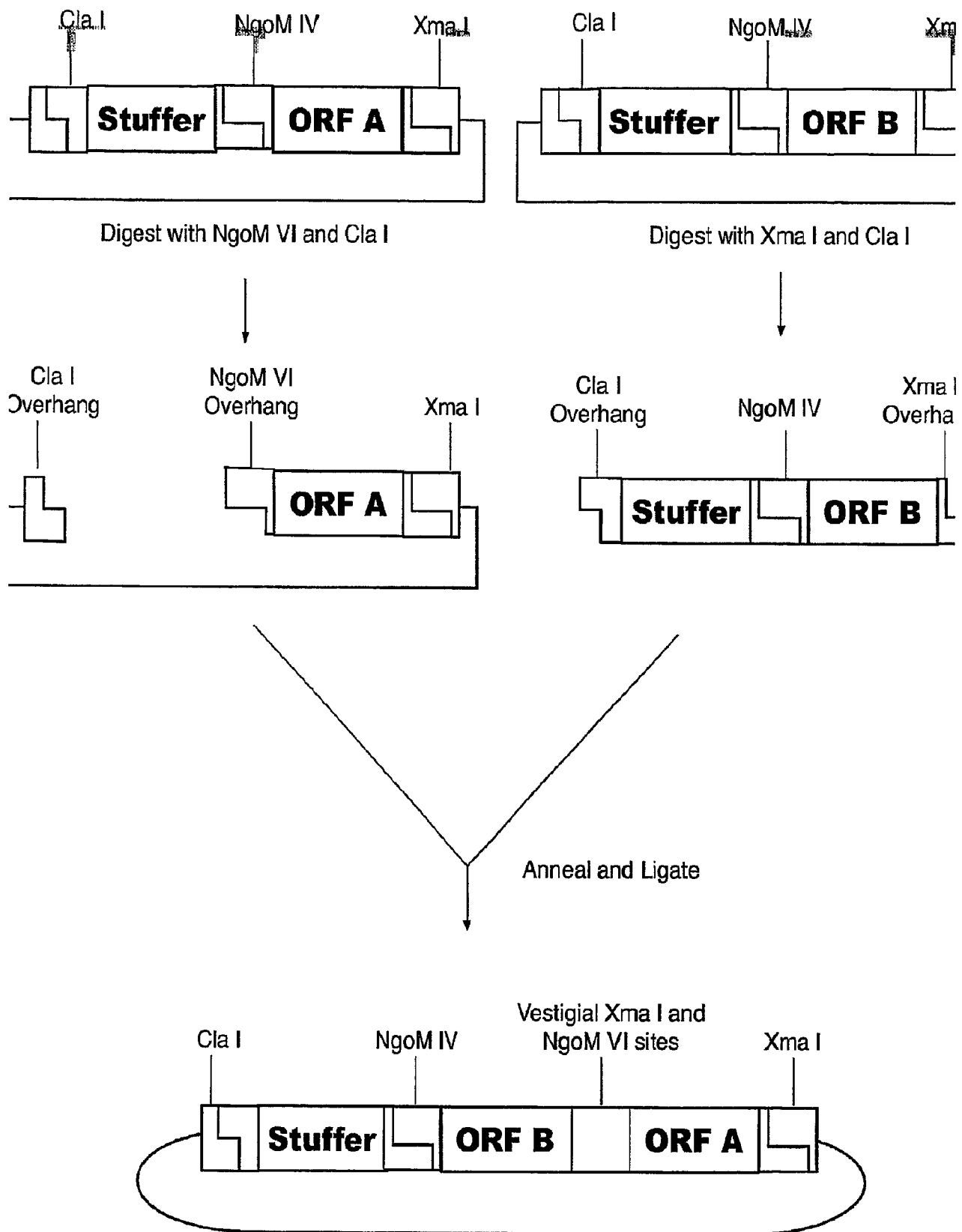
ABSTRACT

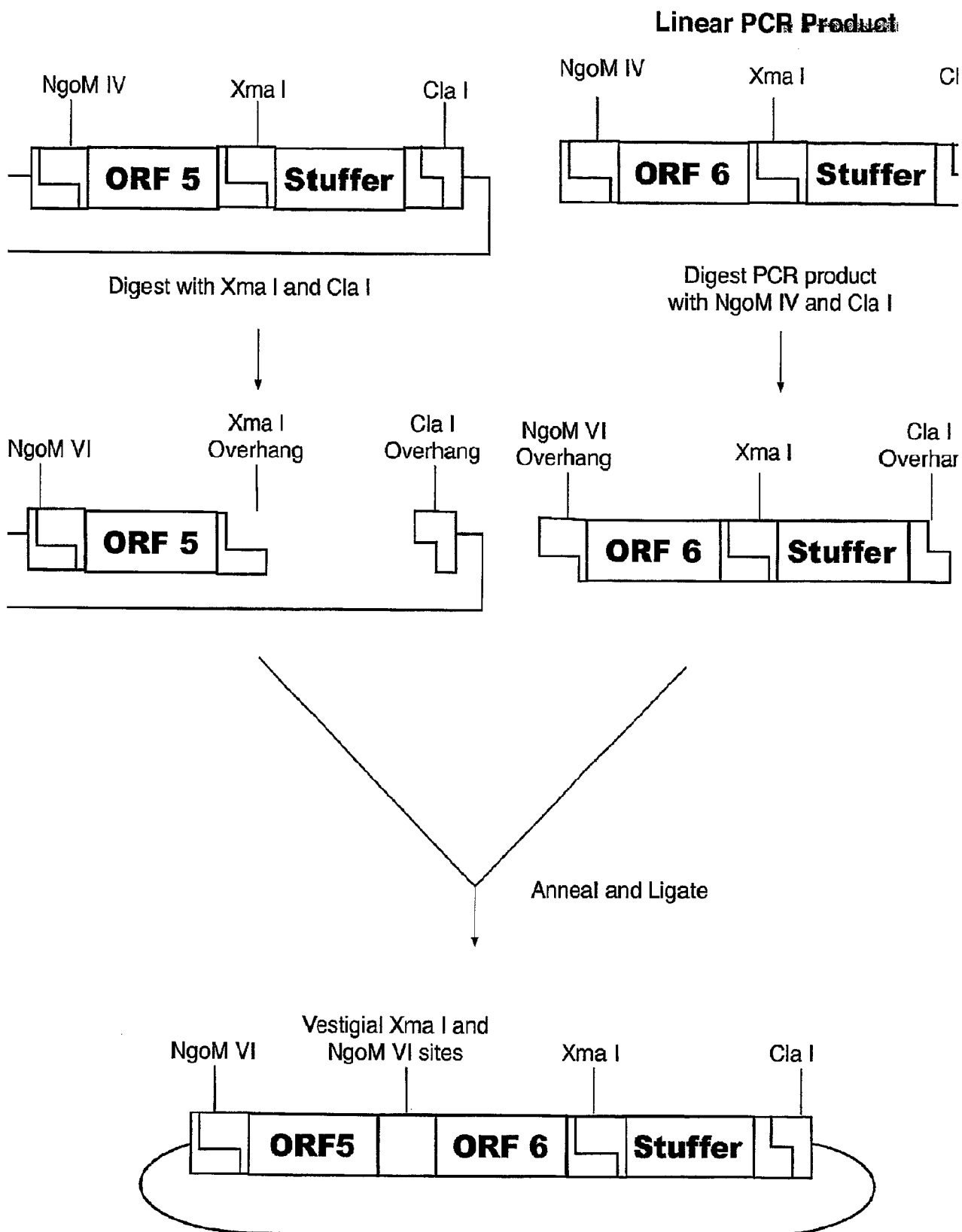
5 TITLE: METHODS OF MAKING MODULAR FUSION PROTEIN EXPRESSION PRODUCTS

A vector comprising each of the following elements arranged sequentially to form a module open reading frame, said vector comprising a) a first restriction site, b) a first open
 10 reading frame coding for a polypeptide of interest, c) a second restriction site that codes for a second group of amino acids, d) a spacer polynucleotide sequence, and e) a third restriction site that codes for a third group of amino acids, wherein elements (a) through (e) are in-frame linked to one another to form the module open reading frame, wherein the first restriction site is susceptible to a restriction enzyme that would produce
 15 a first single-stranded overhang comprising at least 2 nucleotides, wherein the second restriction site is susceptible to a restriction enzyme that would produce a second single-stranded overhang comprising at least 2 nucleotides, and wherein said first and second overhangs are complementary to one another, whereupon the annealing of the first and second overhangs, the first restriction site and the second restriction site are destroyed.
 20 The present invention also relates to a method of making a fusion polypeptide.

Fig. 1







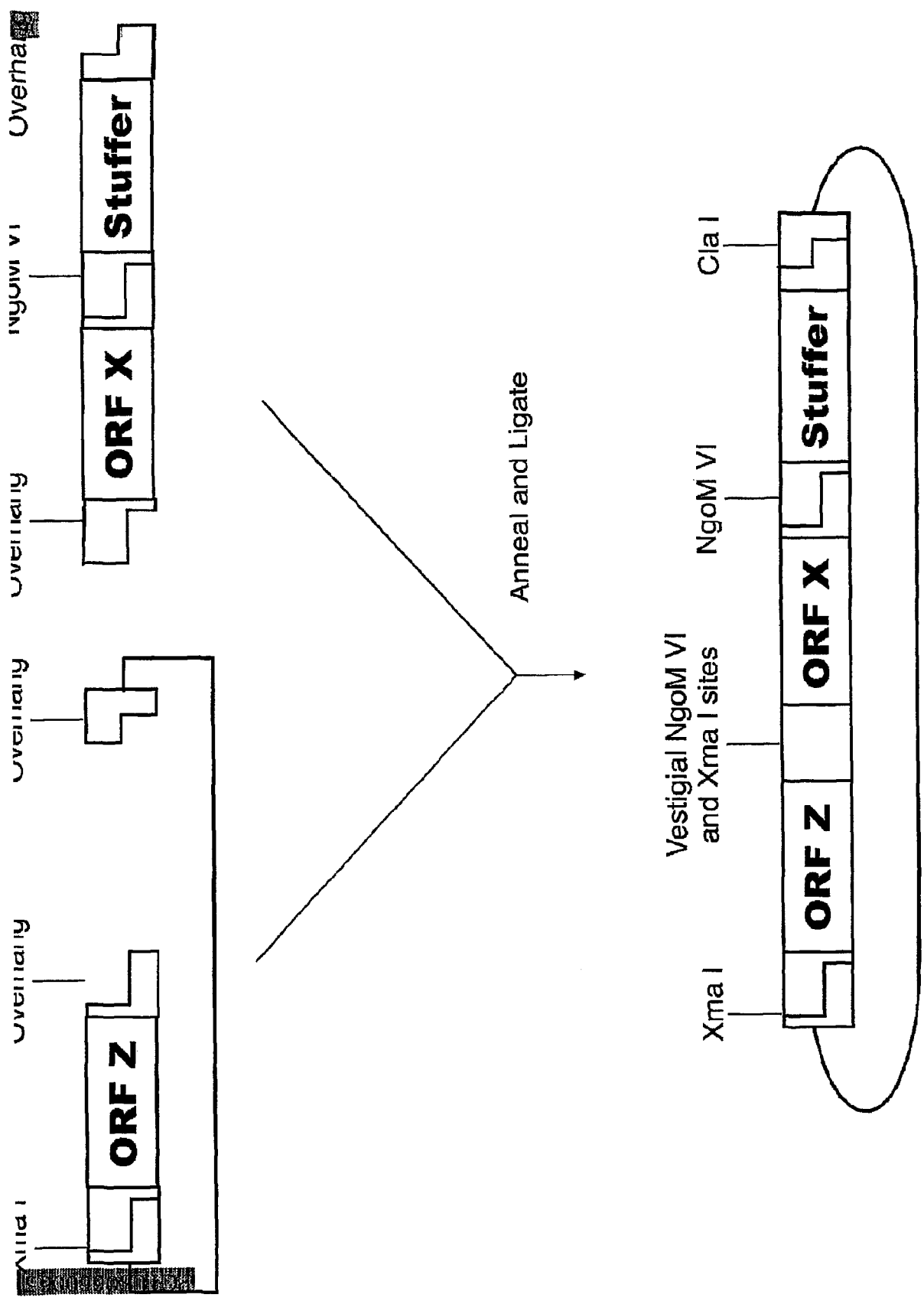
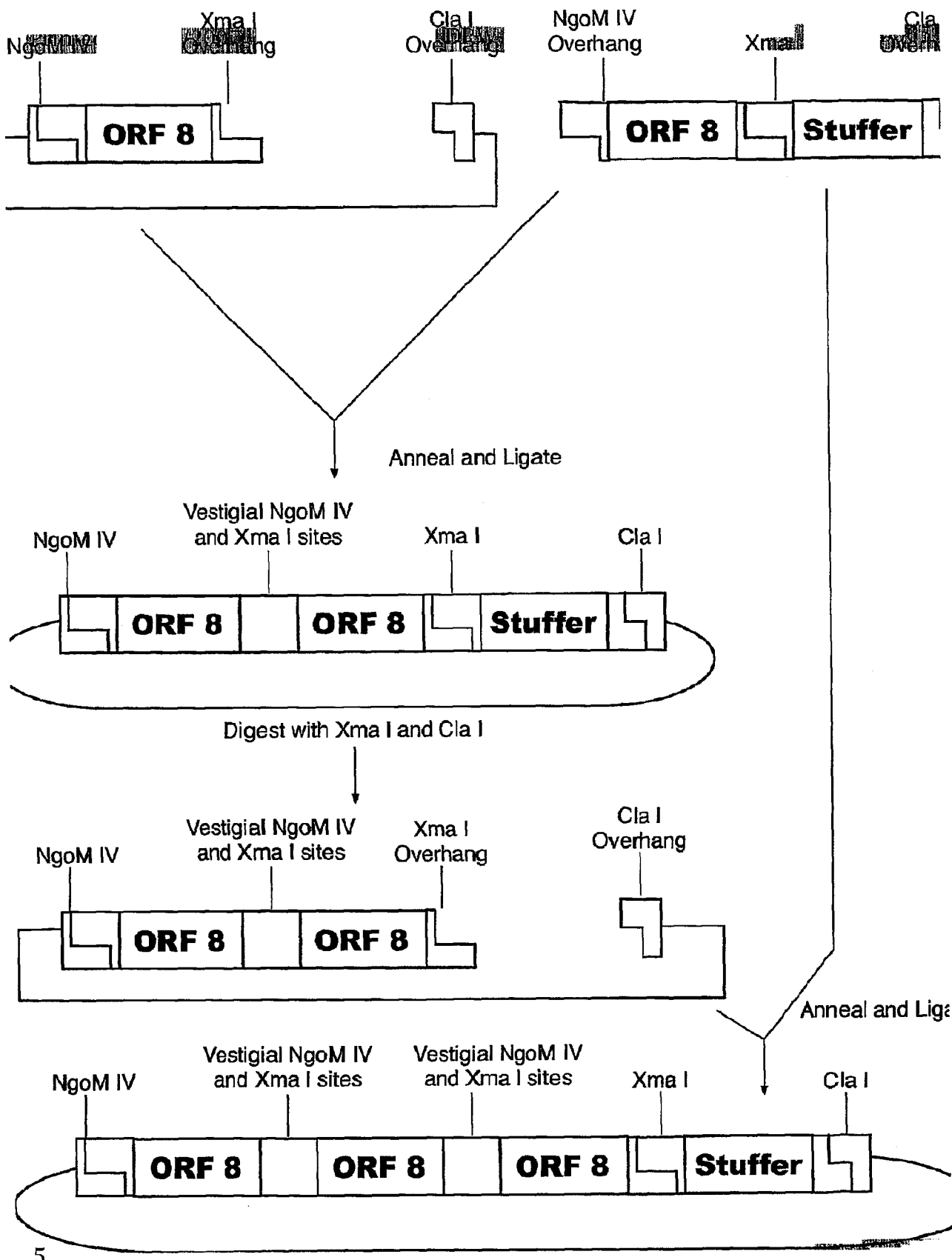


FIGURE 4



Site I	EXON R segment	Vestigial Sites	EXON T segment	Site II	stuffer	Site III
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FIGURE 6A

Site I	EXON D segment	Vestigial Sites	EXON A segment	Vestigial Sites	EXON H segment	Site II	stuffer	Site III
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FIGURE 6B

Site I	EXON A segment	Vestigial Sites	EXON P segment	Vestigial Sites	EXON L segment	Vestigial Sites	EXON C segment	Site II	stuffer	Site III
-----------	-------------------	--------------------	-------------------	--------------------	-------------------	--------------------	-------------------	------------	---------	-------------

FIGURE 6C

Site I	ORF Y	Vestigial Sites	ORF Z	Vestigial Sites	LOCALIZATION SIGNAL	Site II	stuffer	Site III
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FIGURE 7A

Site I	LOCALIZATION SIGNAL	Vestigial Sites	PEPTIDE 3	Vestigial Sites	PEPTIDE 4	Vestigial Sites	PEPTIDE 5	Site II	stuffer	Site III
-----------	------------------------	--------------------	--------------	--------------------	--------------	--------------------	--------------	------------	---------	-------------

FIGURE 7B

Site I	LIGAND X	Vestigial Sites	LIGAND X	Vestigial Sites	LIGAND X	Vestigial Sites	LOCALIZATION SIGNAL	Site II	stuffer	Site III
-----------	-------------	--------------------	-------------	--------------------	-------------	--------------------	------------------------	------------	---------	-------------

FIGURE 7C

Site I	EPITOPE	Vestigial Sites	LIGAND	Site II	stuffer	Site III
-----------	---------	--------------------	--------	------------	---------	-------------

FIGURE 8A

Site I	EXON S segment	Vestigial Sites	EXON V segment	Vestigial Sites	EPITOPE	Site II	stuffer	Site III
-----------	-------------------	--------------------	-------------------	--------------------	---------	------------	---------	-------------

FIGURE 8B

Site I	ORF 3	Vestigial Sites	ORF 9	Vestigial Sites	EPITOPE	Vestigial Sites	ORF 7	Site II	stuffer	Site III
-----------	-------	--------------------	-------	--------------------	---------	--------------------	-------	------------	---------	-------------

FIGURE 8C

Site I	CYTOPLASMIC DOMAIN	Vestigial Sites	TRANSMEMBRANE DOMAIN	Vestigial Sites	EXTRACELLULAR DOMAIN	Site II	stuffer	Site III
-----------	-----------------------	--------------------	-------------------------	--------------------	-------------------------	------------	---------	-------------

FIGURE 9A

Site I	DNA BINDING DOMAIN	Vestigial Sites	HORMONE BINDING DOMAIN	Vestigial Sites	DIMERIZATION DOMAIN	Vestigial Sites	ACTIVATION DOMAIN	Site II	stuffer	Site III
-----------	--------------------------	--------------------	------------------------------	--------------------	------------------------	--------------------	----------------------	------------	---------	-------------

FIGURE 9B

Site I	SUBSTRATE RECOGNITION DOMAIN	Vestigial Sites	CATALYTIC DOMAIN	Vestigial Sites	INHIBITION DOMAIN	Vestigial Sites	BINDING DOMAIN	Site II	stuffer	Site III
-----------	------------------------------------	--------------------	---------------------	--------------------	----------------------	--------------------	-------------------	------------	---------	-------------

FIGURE 9C

PROMOTER	CHIMERIC PROTEIN CODING SEQUENCE	STOP	POLY-A
----------	-------------------------------------	------	--------

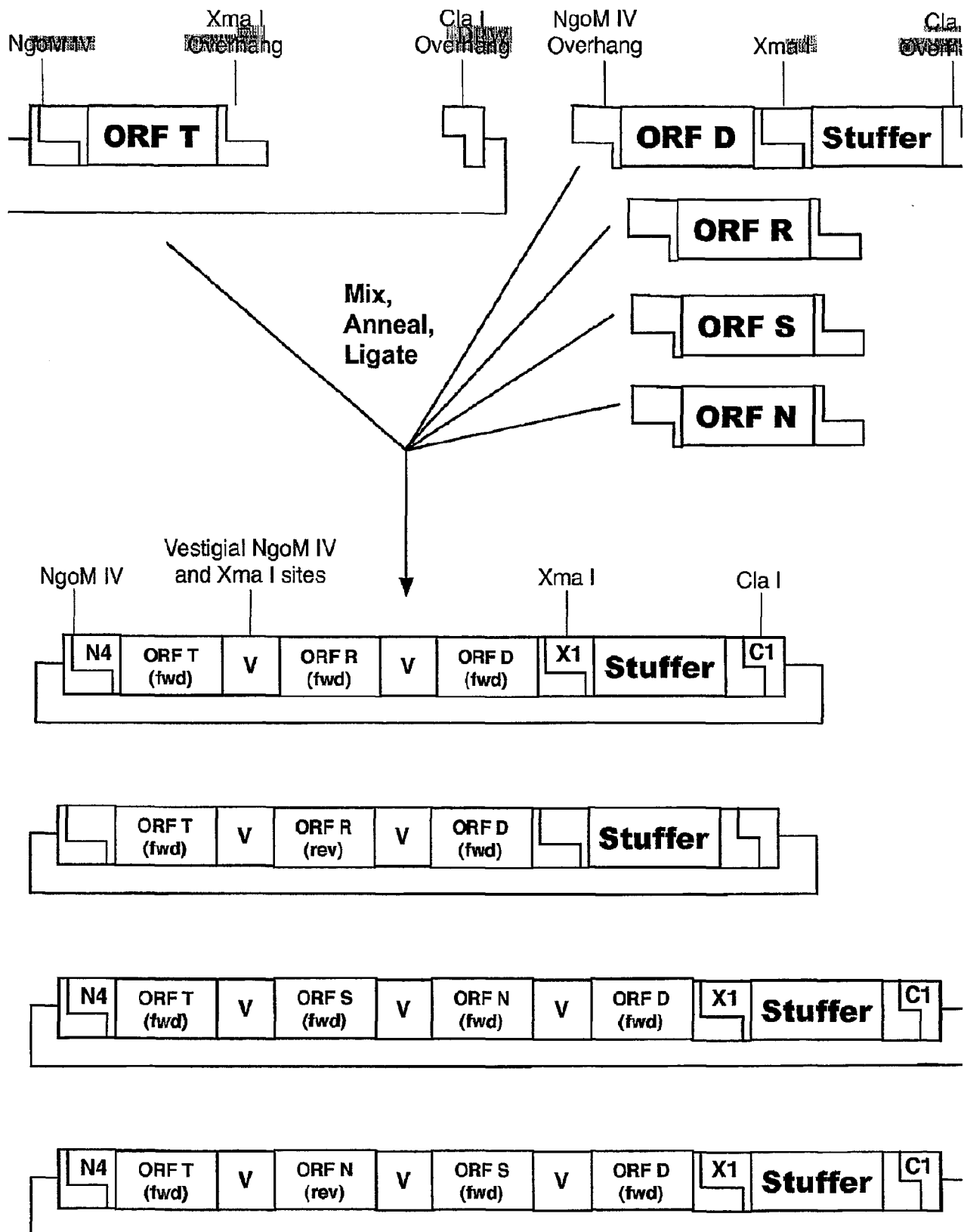
FIGURE 10

<----- Module Open Reading Frame ----->				
Ngom IV	ORF of interest	Xma I	Stuffer	Cla I
GCCGGC	AAGAAGAAAAGAAG	CCCCGG	GGCGGAGGC	ATCGAT
AlaGly	LysLysLysLysLysLys	ProGly	GlyGlyGly	IleAsp

FIGURE 11

Site I	Phosphorylation Domain	Site II	Stuffer	Site III
Site I	Zinc Finger Region	Site II	Stuffer	Site III
Site I	Peptide Inhibitor	Site II	Stuffer	Site III
Site I	Hormone Binding Domain	Site II	Stuffer	Site III
Site I	Epitope	Site II	Stuffer	Site III
Site I	Dimerization Domain	Site II	Stuffer	Site III
Site I	Lipid Binding Domain	Site II	Stuffer	Site III
Site I	Glycosylation Domain	Site II	Stuffer	Site III
Site I	Peptide Hormone	Site II	Stuffer	Site III
Site I	Ion Pore Region	Site II	Stuffer	Site III
Site I	Reporter Peptide	Site II	Stuffer	Site III
Site I	Catalytic Domain	Site II	Stuffer	Site III
Site I	DNA Binding Domain	Site II	Stuffer	Site III
Site I	Leucine Zipper Region	Site II	Stuffer	Site III
Site I	Transmembrane Domain	Site II	Stuffer	Site III
Site I	Activation Domain	Site II	Stuffer	Site III
Site I	Inhibition Domain	Site II	Stuffer	Site III
Site I	G Protein Binding Region	Site II	Stuffer	Site III
Site I	Highly Acidic Region	Site II	Stuffer	Site III
Site I	Ligand	Site II	Stuffer	Site III
Site I	Protein Subunit	Site II	Stuffer	Site III
Site I	Localization Signal	Site II	Stuffer	Site III

FIGURE 12



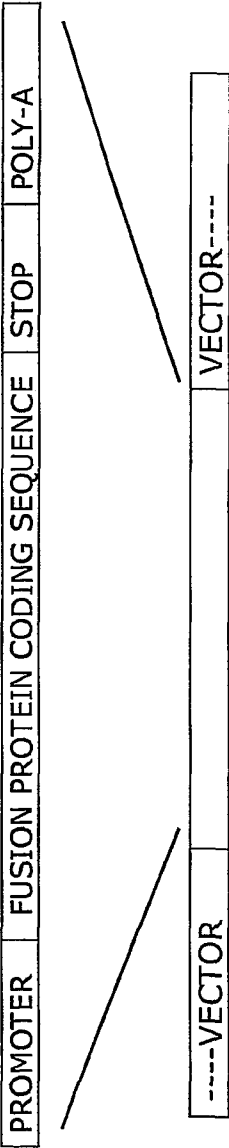


FIGURE 14A

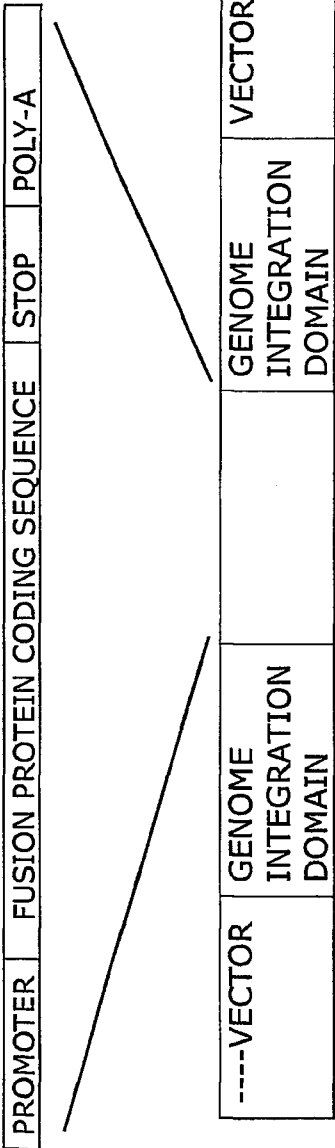


FIGURE 14B

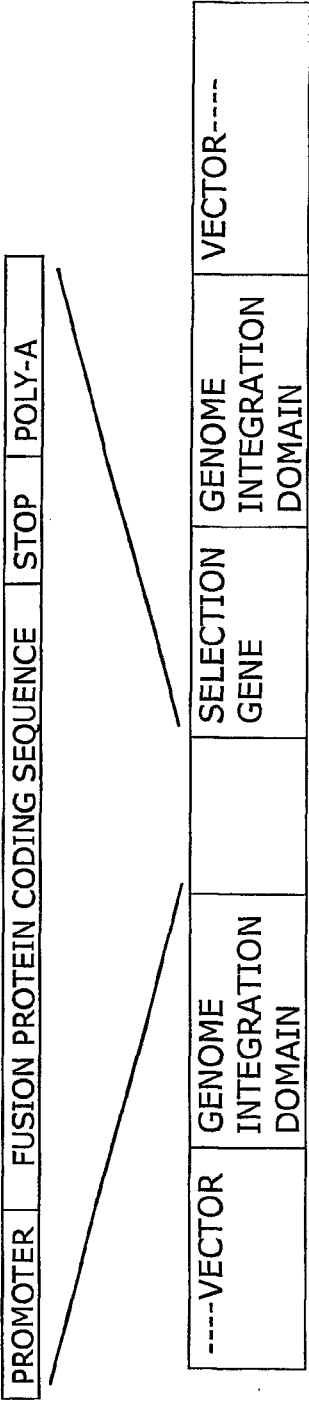


FIGURE 14C

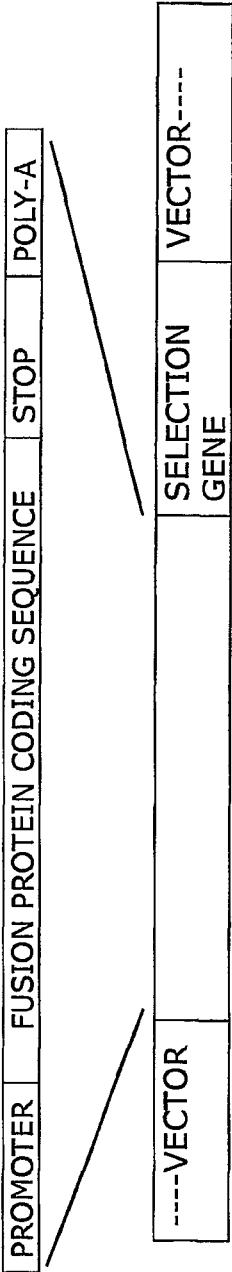


FIGURE 14D

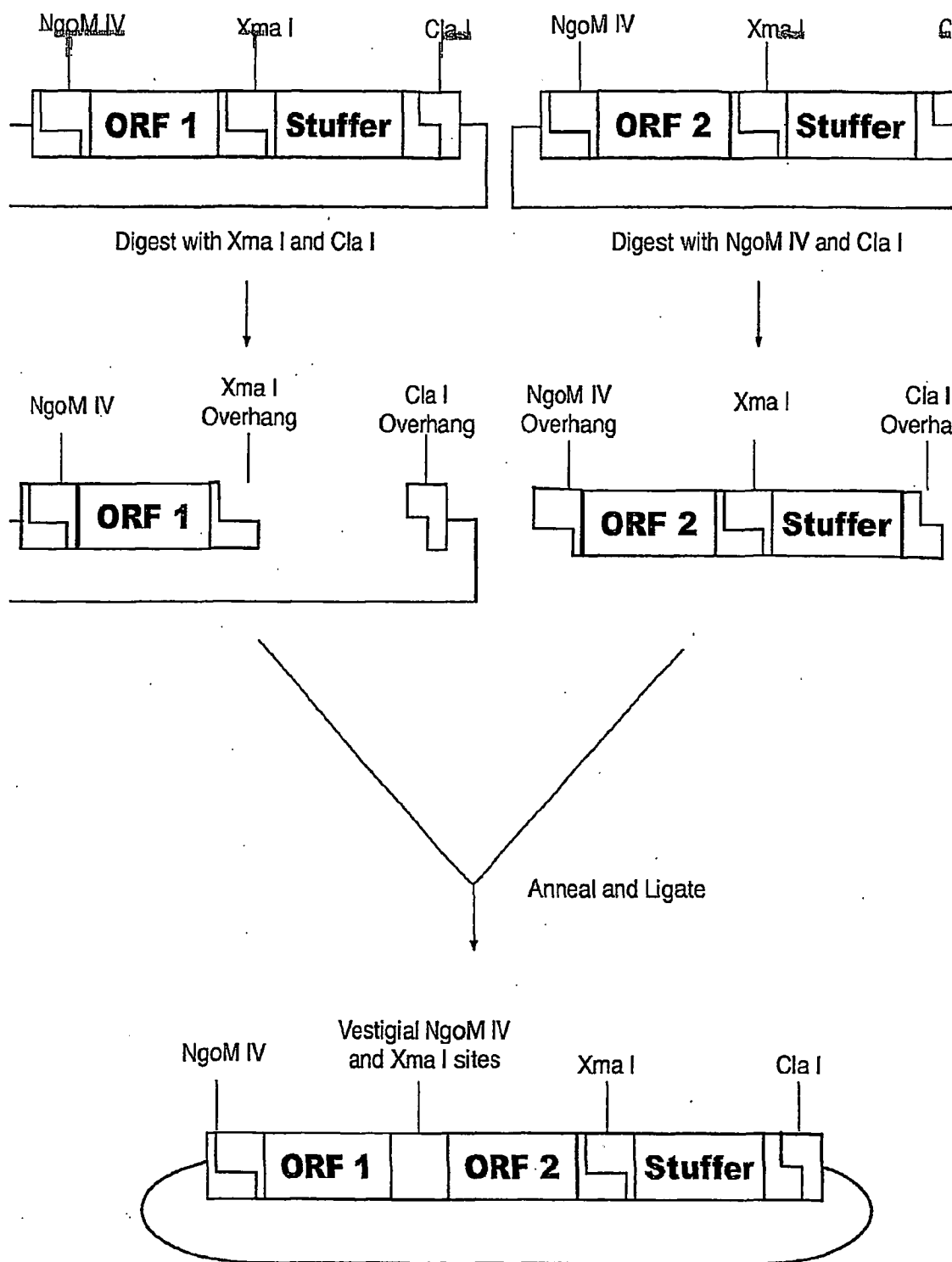


FIGURE 1

S. D. Ahuja
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of D. P. AHUJA & CO.
APPLICANT'S AGENT

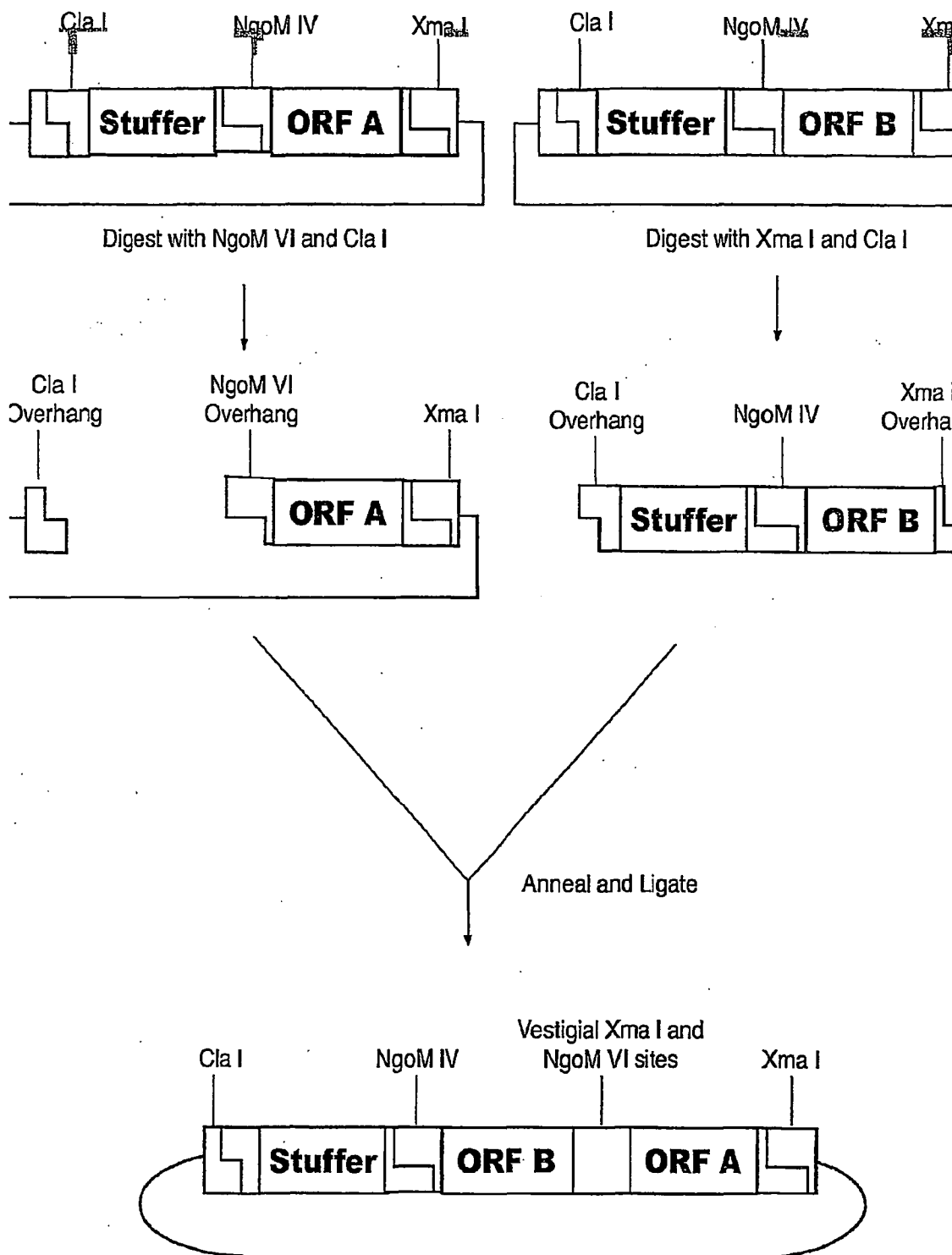


FIGURE 2

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S. D. Ahuja
 S. D. AHUJA
 of D. P. AHUJA & CO.
 APPLICANT'S AGENT

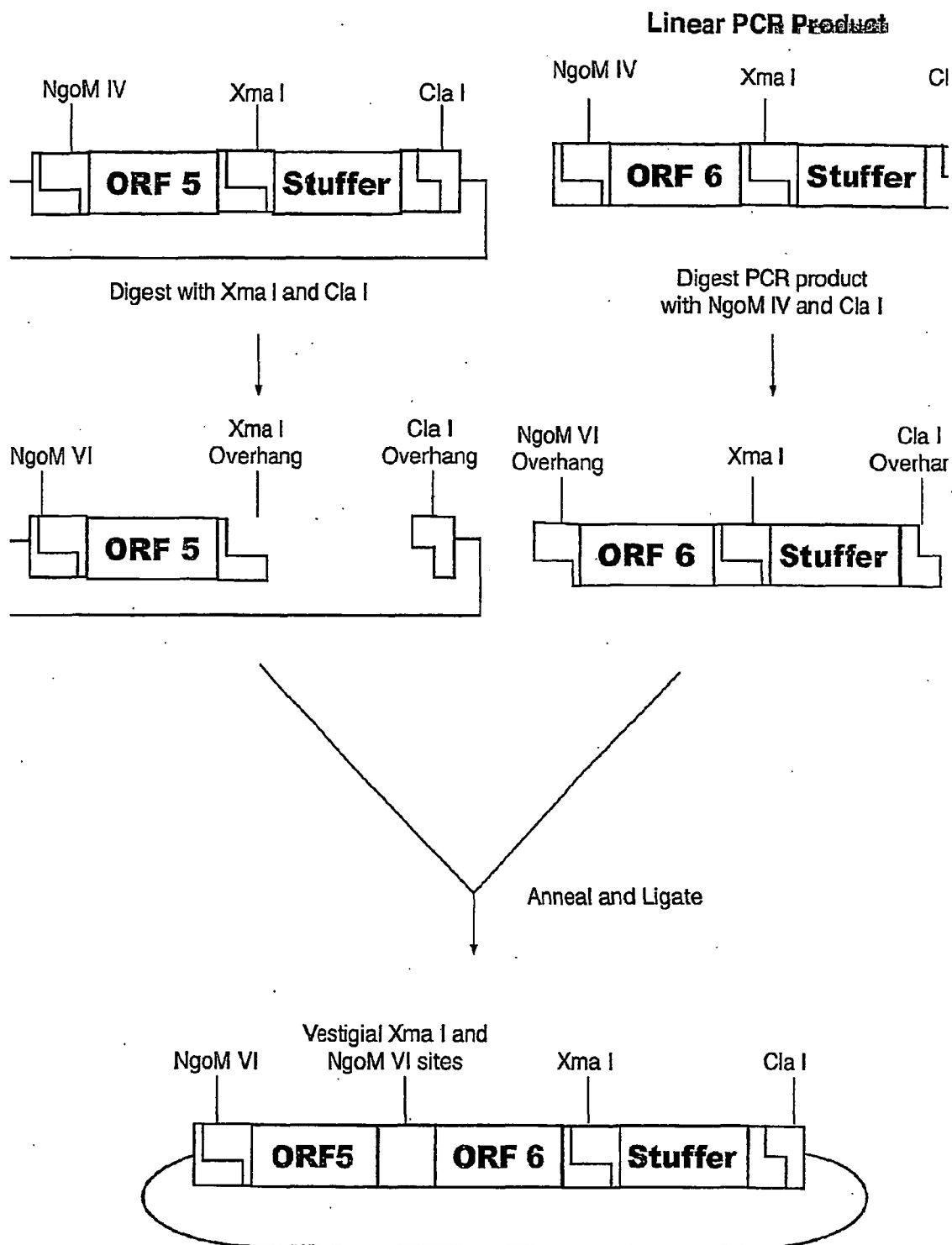


FIGURE 3

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S. D. AHUJA
of D. P. AHUJA & CO.
APPLICANT'S AGENT

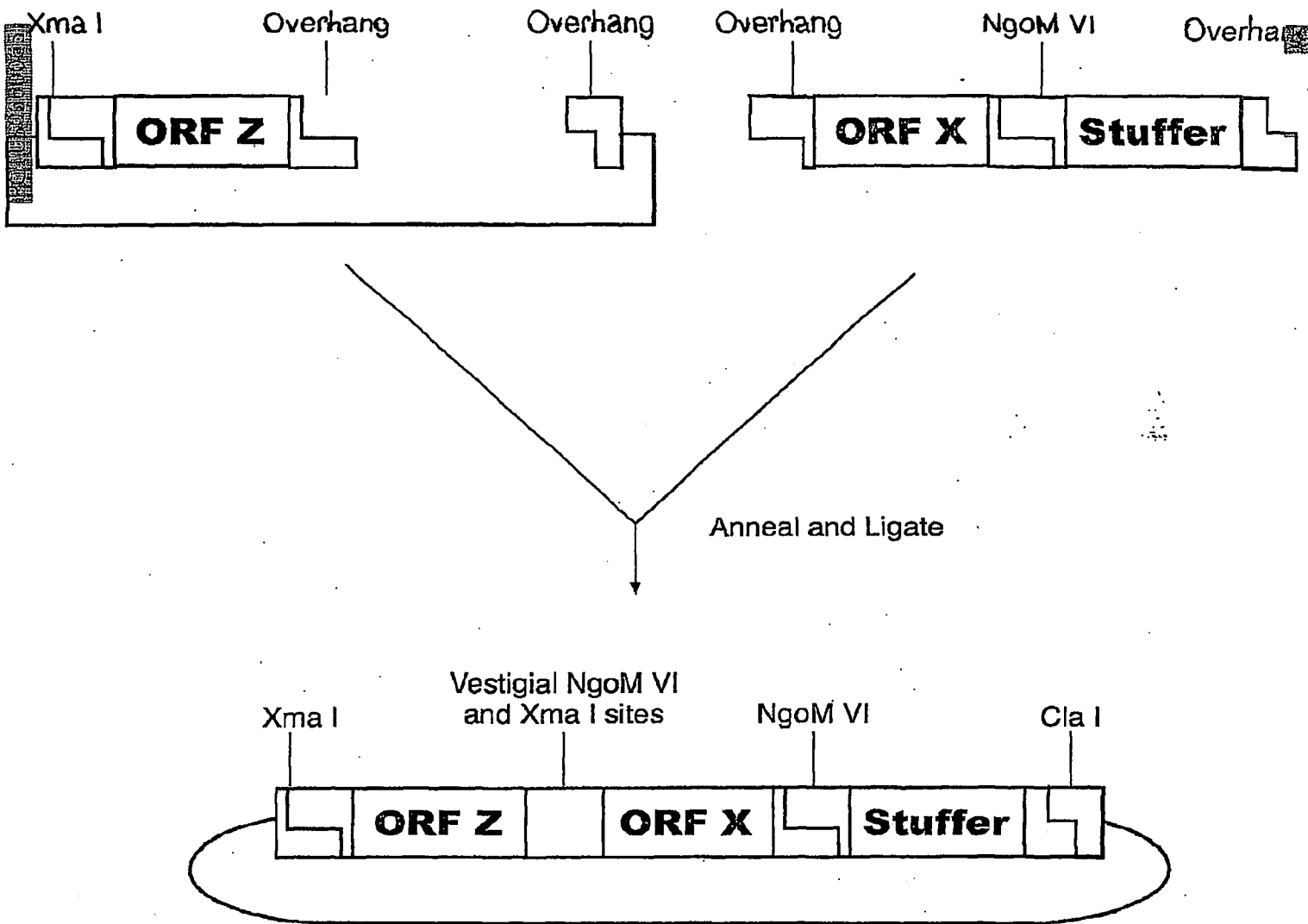


FIGURE 4

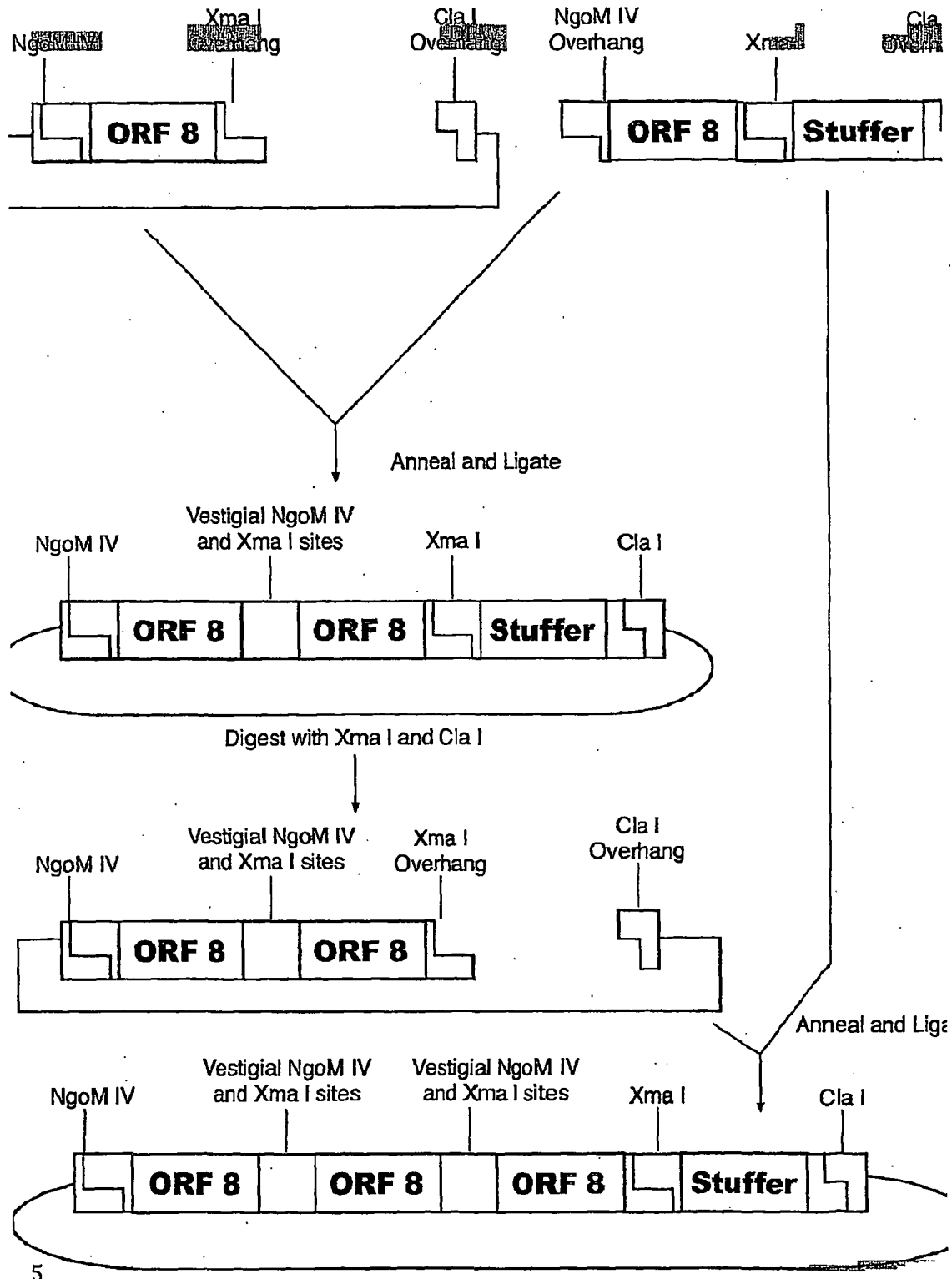


FIGURE 5

Site I	EXON R segment	Vestigial Sites	EXON T segment	Site II	stuffer	Site III
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FIGURE 6A

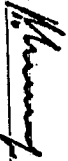
Site I	EXON D segment	Vestigial Sites	EXON A segment	Vestigial Sites	EXON H segment	Site II	stuffer	Site III
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FIGURE 6B

Site I	EXON A segment	Vestigial Sites	EXON P segment	Vestigial Sites	EXON L segment	Vestigial Sites	EXON C segment	Site II	stuffer	Site III
-----------	---------------------------	--------------------	---------------------------	--------------------	---------------------------	--------------------	---------------------------	------------	---------	-------------

FIGURE 6C

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of D. P. AHUA & CO.
APPLICANT'S AGENT

Site I	ORF Y	Vestigial Sites	ORF Z	Vestigial Sites	LOCALIZATION SIGNAL	Site II	stuffer	Site III
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FIGURE 7A

Site I	LOCALIZATION SIGNAL	Vestigial Sites	PEPTIDE 3	Vestigial Sites	PEPTIDE 4	Vestigial Sites	PEPTIDE 5	Site II	stuffer	Site III
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FIGURE 7B

Site I	LIGAND X	Vestigial Sites	LIGAND X	Vestigial Sites	LIGAND X	Vestigial Sites	LOCALIZATION SIGNAL	Site II	stuffer	Site III
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FIGURE 7C

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S. D. AHUJA

of D. P. AHUJA & CO.
APPLICANT'S AGENT

Site I	EPITOPE	Vestigial Sites	LIGAND	Site II	stuffer	Site III
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FIGURE 8A

Site I	EXON S segment	Vestigial Sites	EXON V segment	Vestigial Sites	EPITOPE	Site II	stuffer	Site III
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FIGURE 8B

Site I	ORF 3	Vestigial Sites	ORF 9	Vestigial Sites	EPITOPE	Vestigial Sites	ORF 7	Site II	stuffer	Site III
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FIGURE 8C

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S. D. AHUA
of D. P. AHUA & CO.
APPLICANTS AGENT

Site I	CYTOPLASMIC DOMAIN	Vestigial Sites	TRANSMEMBRANE DOMAIN	Vestigial Sites	EXTRACELLULAR DOMAIN	Site II	stuffer	Site III
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FIGURE 9A

Site I	DNA BINDING DOMAIN	Vestigial Sites	HORMONE BINDING DOMAIN	Vestigial Sites	DIMERIZATION DOMAIN	Vestigial Sites	ACTIVATION DOMAIN	Site II	stuffer	Site III
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FIGURE 9B

Site I	SUBSTRATE RECOGNITION DOMAIN	Vestigial Sites	CATALYTIC DOMAIN	Vestigial Sites	INHIBITION DOMAIN	Vestigial Sites	BINDING DOMAIN	Site II	stuffer	Site III
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FIGURE 9C

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[Signature]
S-D-AHUA
of D. P. AHUA & CO.
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PROMOTER	CHIMERIC PROTEIN CODING SEQUENCE	STOP	POLY-A
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FIGURE 10

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S. D. AHUA
S. D. AHUA
of D. P. AHUA & CO.
APPLICANT'S AGENT

<----- Module Open Reading Frame ----->				
NgoM IV	ORF of interest	Xma I	Stuffer	Cla I
GCCGGC	AAGAAGAAAAAGAAGAAG	CCCGGG	GGCGGAGGC	ATCGAT
AlaGly	LysLysLysLysLysLys	ProGly	GlyGlyGly	IleAsp

FIGURE 11

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S.D. AHUA

of D. P. AHUA & CO.
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Site I	Phosphorylation Domain	Site II	Stuffer	Site III	Site I	Catalytic Domain	Site II	Stuffer	Site III
Site I	Zinc Finger Region	Site II	Stuffer	Site III	Site I	DNA Binding Domain	Site II	Stuffer	Site III
Site I	Peptide Inhibitor	Site II	Stuffer	Site III	Site I	Leucine Zipper Region	Site II	Stuffer	Site III
Site I	Hormone Binding Domain	Site II	Stuffer	Site III	Site I	Transmembrane Domain	Site II	Stuffer	Site III
Site I	Epitope	Site II	Stuffer	Site III	Site I	Activation Domain	Site II	Stuffer	Site III
Site I	Dimerization Domain	Site II	Stuffer	Site III	Site I	Inhibition Domain	Site II	Stuffer	Site III
Site I	Lipid Binding Domain	Site II	Stuffer	Site III	Site I	G Protein Binding Region	Site II	Stuffer	Site III
Site I	Glycosylation Domain	Site II	Stuffer	Site III	Site I	Highly Acidic Region	Site II	Stuffer	Site III
Site I	Peptide Hormone	Site II	Stuffer	Site III	Site I	Ligand	Site II	Stuffer	Site III
Site I	Ion Pore Region	Site II	Stuffer	Site III	Site I	Protein Subunit	Site II	Stuffer	Site III
Site I	Reporter Peptide	Site II	Stuffer	Site III	Site I	Localization Signal	Site II	Stuffer	Site III

FIGURE 12

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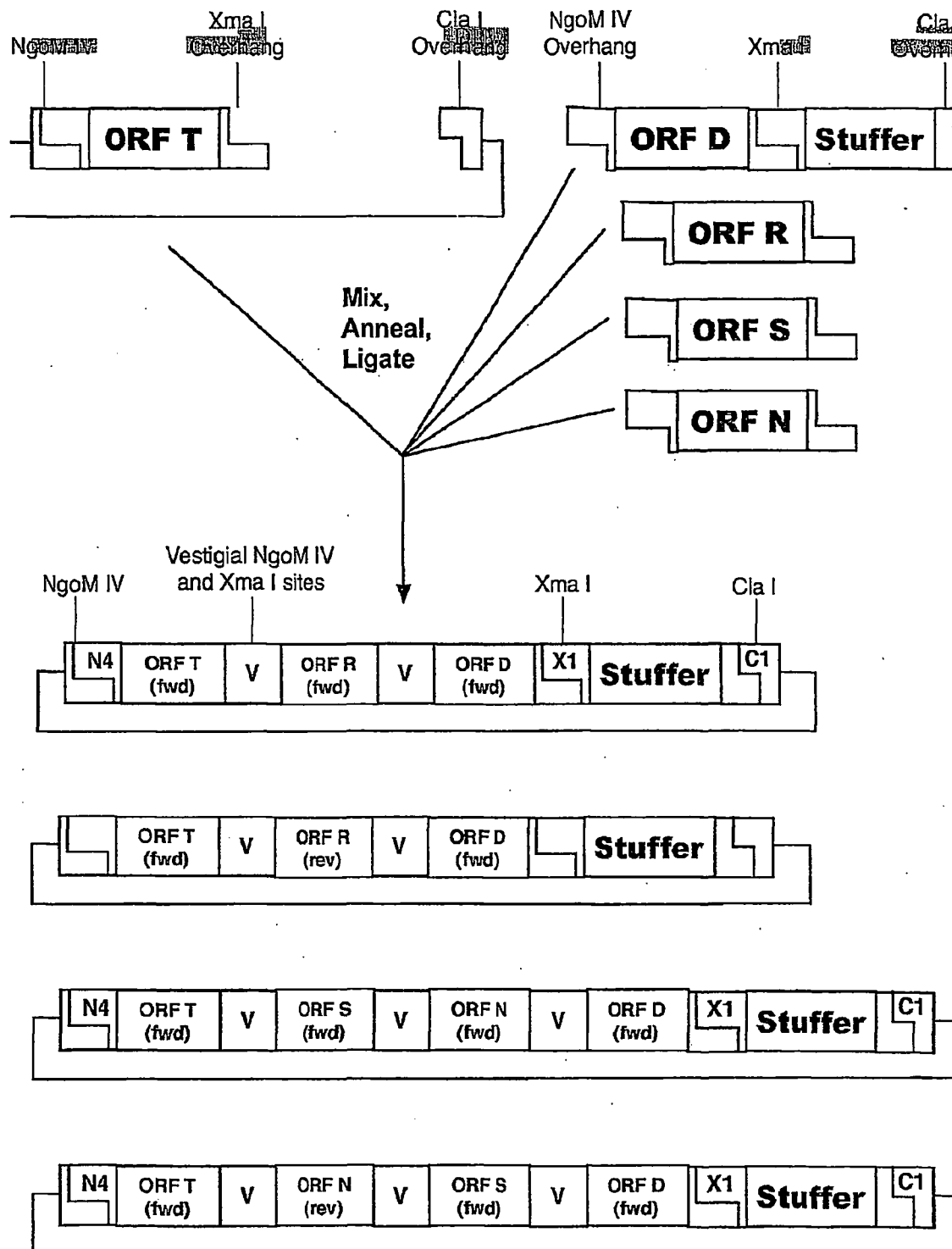


FIGURE 13

[Signature]

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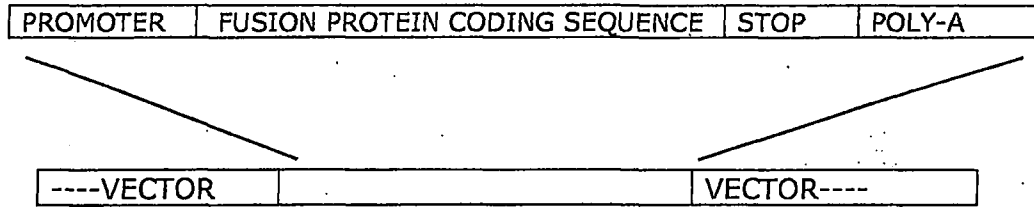


FIGURE 14A

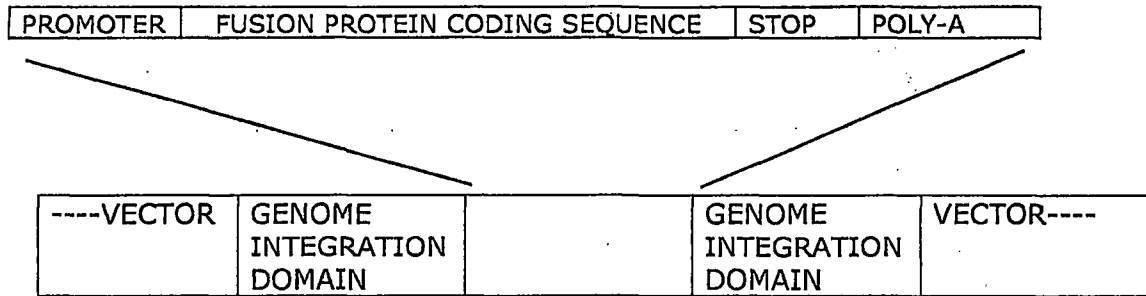


FIGURE 14B

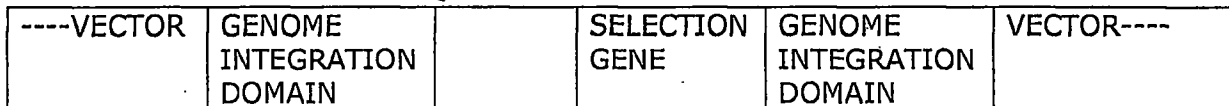


FIGURE 14C



FIGURE 14D