(12) STANDARD PATENT APPLICATION (11) Application No. **AU 2026201901 A1**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Delivery, use and therapeutic applications of the CRISPR-Cas systems and compositions for genome editing

(51) International Patent Classification(s)
A61K 48/00 (2006.01) ***C12N 15/10*** (2006.01)

(21) Application No: **2026201901** (22) Date of Filing: **2026.03.12**

(43) Publication Date: **2026.04.02**
(43) Publication Journal Date: **2026.04.02**

(62) Divisional of:
2023219828

(71) Applicant(s)
Massachusetts Institute of Technology;The Broad Institute, Inc.

(72) Inventor(s)
Cong, Le;Cox, David Benjamin Turitz;Heidenreich, Matthias;Platt, Randall Jeffrey;Swiech, Lukasz;Zhang, Feng

(74) Agent / Attorney
FPA Patent Attorneys Pty Ltd, Level 19, South Tower 80 Collins Street, Melbourne, VIC, 3000, AU

ABSTRACT

The invention provides for delivery, engineering and optimization of systems, methods, and compositions for manipulation of sequences and/or activities of target sequences. Provided are delivery systems and tissues or organ which are targeted as sites for delivery. Also provided are vectors and vector systems some of which encode one or more components of a CRISPR complex, as well as methods for the design and use of such vectors. Also provided are methods of directing CRISPR complex formation in eukaryotic cells to ensure enhanced specificity for target recognition and avoidance of toxicity and to edit or modify a target site in a genomic locus of interest to alter or improve the status of a disease or a condition.

DELIVERY, USE AND THERAPEUTIC APPLICATIONS OF THE CRISPR-CAS SYSTEMS AND COMPOSITIONS FOR GENOME EDITING

RELATED APPLICATIONS AND INCORPORATION BY REFERENCE

[0001] This application is a divisional of Australian patent application 2023219828, which in turn is a divisional application of Australian patent application 2021204395, which is a divisional of Australian patent application 2014361781 and claims priority to US provisional patent applications: 61/915,l76; 61/915,192; 61/915,215; 61/915,107, 61/915,145; 61/915,148; and 61/915,153 each filed December 12, 2013, the entire contents of all of which are incorporated herein by reference.

[0002] The foregoing applications, and all documents cited therein or during their prosecution ("appln cited documents") and all documents cited or referenced in the appln cited documents, and all documents cited or referenced herein ("herein cited documents"), and all documents cited or referenced in herein cited documents, together with any manufacturer's instructions, descriptions, product specifications, and product sheets for any products mentioned herein or in any document incorporated by reference herein, are hereby incorporated herein by reference, and may be employed in the practice of the invention. More specifically, all referenced documents are incorporated by reference to the same extent as if each individual document was specifically and individually indicated to be incorporated by reference.

FIELD OF THE INVENTION

[0003] The present invention generally relates to the delivery, engineering, optimization and therapeutic applications of systems, methods, and compositions used for the control of gene expression involving sequence targeting, such as genome perturbation or gene-editing, that relate to Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and components thereof. In particular, the present invention relates to *in vitro, ex vivo* and/or *in vivo* systems, methods, and compositions for delivery of the CRISPR-Cas system to achieve therapeutic benefits *via* genome editing in animals, including mammals.

STATEMENT AS TO FEDERALLY SPONSORED RESEARCH

[0004] This invention was made with government support under the NIH Pioneer Award (1DP1MH100706) awarded by the National Institutes of Health and grant 1DP1OD009552 also provided by National Insitutes of Health. The government has certain rights in the invention.

vitro to stimulate the expression of ATOH1 is then selected for in vivo delivery and therapeutic demonstration.

[00470] AAV or Ad viral particles or other delivery vehicle packaging the entire system are then produced, and injected using the optimal conditions as determined experimentally. The most critical parameter to optimize is the amount (i.e. dosage) of the delivery vehicle used for each individual injection.

[00471] The higher dose will give better gene therapy effectiveness but might lead to higher chance of complications due to immune response to the vehicle injection or the off-target effects of the system. Patients are monitored daily for clinical signs of procedure related complications.

Post injection procedures

[00472] Post injection, the patient are monitored for any immunological response or adverse effect. Each week post injection, ELISA or other protein measurement methods can be employed to assess the level of ATOH1 stimulation. New hair cell growth in the Cochleae can be visualized through biopsy and imaging methods. And the relief or recovery of deafness and hearing impairments is then evaluated through hearing tests on the human patients.

[00473] Key safety measures to be followed in the patients include the maximum tolerated dose of a single injection into the human Cochleae, number of treatment emergent adverse events post injection.

* * *

[00474] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention.

WHAT IS CLAIMED IS:

1. A method of modeling a disease associated with a genomic locus in a eukaryotic organism or a non-human organism comprising manipulation of a target sequence within a coding, non-coding or regulatory element of said genomic locus comprising delivering a non-naturally occurring or engineered composition comprising:

(A) – I. a CRISPR-Cas system RNA polynucleotide sequence, wherein the polynucleotide sequence comprises:

(a) a guide sequence capable of hybridizing to the target sequence,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a polynucleotide sequence encoding Cas9, optionally comprising at least one or more nuclear localization sequences,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the CRISPR complex comprises Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence and the polynucleotide sequence encoding Cas9 is DNA or RNA,

or

(B) I. polynucleotides comprising:

(a) a guide sequence capable of hybridizing to the target sequence, and

(b) at least one or more tracr mate sequences,

II. a polynucleotide sequence encoding Cas9, and

III. a polynucleotide sequence comprising a tracr sequence,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the CRISPR complex comprises the Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence, and the polynucleotide sequence encoding Cas9 is DNA or RNA.

2. The method of claim 1 wherein the Cas9 is SaCas9.

3. The method of claim 1 or 2, wherein the polynucleotides encoding the sequence

encoding Cas9, the guide sequence, tracr mate sequence or tracr sequence is/are RNA and are delivered via liposomes, nanoparticles, cell penetrating peptides, exosomes, microvesicles, or a gene-gun.

4. The method of any of claims 1 to 3, wherein the polynucleotides are comprised within a vector system comprising one or more vectors.

5. A method of modeling a disease associated with a genomic locus in a eukaryotic organism or a non-human organism comprising manipulation of a target sequence within a coding, non-coding or regulatory element of said genomic locus comprising delivering a non- naturally occurring or engineered composition comprising a viral vector system comprising one or more viral vectors operably encoding a composition for expression thereof, wherein the composition comprises:

(A) a non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to a CRISPR-Cas system RNA polynucleotide sequence, wherein the polynucleotide sequence comprises

(a) a guide sequence capable of hybridizing to the target sequence,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a second regulatory element operably linked to an enzyme-coding sequence encoding Cas9, optionally comprising at least one or more nuclear localization sequences,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein components I and II are located on the same or different vectors of the system,

wherein when transcribed, the tracr RNA sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the CRISPR complex comprises the Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence,

or

(B) a non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to

(a) a guide sequence capable of hybridizing to the target sequence, and

(b) at least one or more tracr mate sequences,

II. a second regulatory element operably linked to an enzyme-coding sequence encoding Cas9, and

III. a third regulatory element operably linked to a tracr sequence, wherein components I, II and III are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the CRISPR complex comprises the Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence; *(2)* the tracr mate sequence that is hybridized to the tracr sequence; and wherein the Cas9 is preferably SaCas9.

6. The method of claim 5, wherein one or more of the viral vectors are delivered via liposomes, nanoparticles, exosomes, microvesicles, or a gene-gun.

7. A method of treating or inhibiting a condition or a disease caused by one or more mutations in a genomic locus in a eukaryotic organism or a non-human organism comprising manipulation of a target sequence within a coding, non-coding or regulatory element of said genomic locus in a target sequence in a subject or a non-human subject *in* need thereof comprising modifying the subject or a non-human subject by manipulation of the target sequence and wherein the condition or disease is susceptible to treatment or inhibition by manipulation of the target sequence comprising providing treatment comprising:

delivering a non-naturally occurring or engineered composition comprising an AAV or lentivirus vector system, comprising one or more AAV or lentivirus vectors operably encoding a composition for expression thereof, wherein the target sequence is manipulated by the composition when expressed, wherein the composition comprises:

(A) a non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to a CRISPR-Cas system RNA polynucleotide sequence, wherein the polynucleotide sequence comprises

(a) a guide sequence capable of hybridizing to the target sequence in a eukaryotic cell,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a second regulatory element operably linked to an enzyme-coding sequence encoding Cas9 comprising at least one or more nuclear localization sequences,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,
wherein components I and II are located on the same or different vectors of the system,
wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the CRISPR complex comprises the Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence,
or

(B) a non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell, and

(b) at least one or more tracr mate sequences,

II. a second regulatory element operably linked to an enzyme-coding sequence encoding Cas9, and

III. a third regulatory element operably linked to a tracr sequence,
wherein components I, II and III are located on the same or different vectors of the system,
wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence,
wherein the CRISPR complex comprises Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence; and wherein the Cas9 is preferably SaCas9.

8. The method of any preceding claim, wherein the method is carried out *in vitro, ex vivo* or *in vivo.*

9. The method of any preceding claim including inducing expression.

10. The method of claim 1 wherein the condition or disease is an ocular disease.

11. The method of claim 10 where the ocular disease is retinitis pigmentosa or achromatopsia.

12. The method of any of claims 4 to 8 wherein the viral vector is an AAV or lentiviral vector.

13. A method of delivering the Cas9 of any preceding claim, comprising delivering to a

cell mRNA encoding the Cas9.

14. The method of any one of claims 1 to 13, wherein the polynucleotide or sequence encoding the Cas9 is delivered to the cell by delivering mRNA encoding the Cas9 to the cell.

15. A method of preparing the AAV or lentivirus vector of claim 7 comprising transfecting plasmid(s) containing or consisting essentially of nucleic acid molecule(s) coding for the AAV or lentivirus into AAV-infected or lentivirus-infected cells, and supplying AAV or lentivirus rep and/or cap and/or helper nucleic acid molecules obligatory for replication and packaging of the AAV or lentivirus.

16. A method of preparing an AAV or lentivirus vector for use in the method of claim 7, comprising transfecting plasmid(s) containing or consisting essentially of nucleic acid molecule(s) coding for the AAV or lentivirus into AAV-infected or lentivirus-infected cells, and supplying AAV or lentivirus rep and/or cap and/or helper nucleic acid molecules obligatory for replication and packaging of the AAV or lentivirus,

17. The method of claim 15 or 16 wherein the AAV or lentivirus rep and/or cap obligatory for replication and packaging of the AAV or lentivirus are supplied by transfecting the cells with helper plasmid(s) or helper virus(es).

18. The method of claim 17 wherein the helper virus is a poxvirus, adenovirus, lentivirus, herpesvirus or baculovirus.

19. The method of claim l 8 wherein the poxvirus is a vaccinia virus.

20. The method of any of claims 15 to 19 wherein the cells are mammalian cells.

21. The method of any of claims 15 to 20 wherein the cells are insect cells and the helper virus (where present) is baculovirus.

22. The method of any preceding claim wherein the Cas9 is a wild type, truncated or a chimeric Cas9.

23. A composition as defined in any of claims 1-22 for use in medicine or in therapy.

24. A composition as defined in any of claims 1-22 for use in a method of modeling a disease associated with a genetic locus in a eukaryotic organism or a non-human organism comprising manipulation of a target sequence within a coding, non-coding or regulatory element of said genetic locus.

25. Use of a composition as defined in any of claims 1-24 in *ex vivo or in vivo* gene or genome editing.

26. Use of a composition as defined in any of claims 1-24 in the manufacture of a medicament for *in vitro, ex vivo or in vivo* gene or genome editing or for use in a method of modifying

an organism or a non-human organism by manipulation of a target sequence in a genomic locus associated with a disease or in a method of treating or inhibiting a condition or disease caused by one or more mutations in a genomic locus in a eukaryotic organism or a non-human organism.

27. A composition comprising:

(A) I. a CRISPR-Cas system RNA polynucleotide sequence, wherein the polynucleotide sequence comprises:

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a polynucleotide sequence encoding Cas9, optionally comprising at least one or more nuclear localization sequences,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the CRISPR complex comprises the Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence and the polynucleotide sequence encoding SaCas9 is DNA or RNA,

or

(B) I. polynucleotides comprising:

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell, and

(b) at least one or more tracr mate sequences,

II. a polynudeotide sequence encoding Cas9, and

III. a polynucleotide sequence comprising a tracr sequence,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the CRISPR complex comprises Cas9 complexed with *(l)* the guide sequence that is hybridized to the target sequence, (2) the tracr mate sequence that is hybridized to the tracr sequence, and the polynucleotide sequence encoding Cas9 is DNA or RNA; and the Cas9 is preferably SaCas9. for use in medicine or therapy; or for use in a method of modifying an organism or a non-human organism by manipulation of a target sequence in a genomic locus associated with a disease or disorder; or for use in a method of treating or inhibiting a condition caused by one or more mutations in a genetic

locus associated with a disease in a eukaryotic organism or a non-human organism.: or for use in *in vitro, ex vivo or in vivo* gene or genome editing.

28. The composition of claim 27, wherein the polynucleotides are comprised within a vector system comprising one or more vectors.

29. The method, use or composition of any of the preceding claims, wherein the CRISPR-Cas system RNA is a chimeric RNA (chiRNA).

30. The method, use or composition of any of the preceding claims, wherein the CRISPR-Cas system is a multiplexed SaCas9 enzyme system further comprising multiple chimeras and/or multiple multiguide sequences and a single tracr sequence.

31. The method, use or composition according any of the preceding claims, wherein theCas9 is a nuclease directing cleavage ofboth strands at the location of the target sequence.

32. The method, use or composition according to any of the preceding claims, wherein the Cas9 comprises one or more mutations.

33. The method, use or composition according to claim 32, wherein the Cas9 comprises one or more mutations Dl0A, E762A, H840A, N854A, N863A or D986A.

34. The method, use or composition according to claim 32 wherein the one or more mutations is in a RuvC l domain of the Cas9.

35. The method, use or composition according to claim 30, wherein the Cas9 is a nickase directing cleavage at the location of the target sequence.

36. The method, use or composition according to claim 35, wherein the nickase is a double nickase.

37. The method, use or composition according to any preceding claim further comprising at least two or more NLS.

38. The method, use or composition according to any preceding claim, wherein the SaCas9 has one or more mutations in a catalytic domain, wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and wherein the enzyme further comprises a functional domain.

39. The method, use or composition according to claim 38, wherein the functional domain is a transcriptional activation domain.

40. The method, use or composition according to claim 39, wherein the transcriptional activation domain is VP64.

41. A therapeutic genome editing method for treating or inhibiting a condition or a disease caused by one or more mutations in a genomic locus in a eukaryotic organism or a non-human

organism comprising manipulation of a target sequence within a coding, non-coding or regulatory element of said genomic locus in a target sequence m a subject or a non-human subject in need thereof comprising modifying the subject or a non-human subject by manipulation of the target sequence and wherein the condition or disease is susceptible to treatment or inhibition by manipulation of the target sequence comprising providing treatment comprising:

delivering a non-naturally occurring or engineered composition comprising an AAV or lentivirus vector system, comprising one or more AAV or lentivirus vectors operably encoding a composition for expression thereof, wherein the target sequence is manipulated by the composition when expressed, wherein the composition comprises:

(A) a non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to a CRISPR-Cas system RNA polynucleotide sequence, wherein the polynucleotide sequence comprises

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell,

(b) a tracr mate sequence, and

(c) a tracr sequence, and

II. a second regulatory element operably linked to an enzyme-coding sequence encoding Cas9 comprising at least one or more nuclear localization sequences,

wherein (a), (b) and (c) are arranged in a 5' to 3' orientation,

wherein components I and II are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and

the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and

wherein the CRISPR complex comprises the Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence, and (2) the tracr mate sequence that is hybridized to the tracr sequence,

or

(B) a non-naturally occurring or engineered composition comprising a vector system comprising one or more vectors comprising

I. a first regulatory element operably linked to

(a) a guide sequence capable of hybridizing to a target sequence in a eukaryotic cell, and

(b) at least one or more tracr mate sequences,

II. a second regulatory element operably linked to an enzyme-coding sequence encoding Cas9, and

III. a third regulatory element operably linked to a tracr sequence,

wherein components I, II and III are located on the same or different vectors of the system,

wherein when transcribed, the tracr mate sequence hybridizes to the tracr sequence and the guide sequence directs sequence-specific binding of a CRISPR complex to the target sequence, and

wherein the CRISPR complex comprises Cas9 complexed with (1) the guide sequence that is hybridized to the target sequence, (2) the tracr mate sequence that is hybridized to the tracr; and the Cas9 is preferably SaCas9.

42. The method of claim 41, wherein the condition or disease is retinitis pigmentosa or achromatopsia.

43. The method of claim 41, wherein the AAV is AAV1, AAV2, AAV5, AAV7, AAV8, AAV DJ or any combination thereof.

44. A method of individualized or personalized treatment of a genetic disease in a subject in need of such treatment comprising:

(a) introducing multiple mutations *ex vivo* in a tissue, organ or a cell line comprising SaCas9-expressing eukaryotic cell(s), or *in vivo* in a transgenic non-human mammal having cells that express SaCas9, comprising delivering to cell(s) of the tissue, organ, cell or mammal the vector as herein-discussed, wherein the specific mutations or precise sequence substitutions are or have been correlated to the genetic disease;

(b) testing treatment(s) for the genetic disease on the cells to which the vector has been delivered that have the specific mutations or precise sequence substitutions correlated to the genetic disease; and

(c) treating the subject based on results fhm1 the testing of treatment(s) of step (b).

45. The method of claim 44, wherein the genetic disease is an ocular disease.

46. The method of claim 45, wherein the ocular disease is retinitis pigmentosa or achromatopsia.

<400> 193
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120

<210> 194
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Aminohexanoyl

<400> 194
Arg Xaa Arg Arg Arg Arg
1 5

<210> 195
<211> 66
<212> DNA
<213> Homo sapiens

<400> 195
agccaatgga gggcgcgggc aggcgcgtgc gagcagccaa tcaaagagtt tttacacccc 60

gagaaa 66

Sequence Listing

1	**Sequence Listing Information**	
1-1	File Name	Sequence listing - M53420032.xml
1-2	DTD Version	V1_3
1-3	Software Name	WIPO Sequence
1-4	Software Version	2.3.0
1-5	Production Date	2023-08-14
1-6	Original free text language code	
1-7	Non English free text language code	
2	**General Information**	
2-1	Current application: IP Office	AU
2-2	Current application: Application number	
2-3	Current application: Filing date	
2-4	Current application: Applicant file reference	M53420032
2-5	Earliest priority application: IP Office	US
2-6	Earliest priority application: Application number	61/915107
2-7	Earliest priority application: Filing date	2013-12-12
2-8en	Applicant name	The Broad Institute, Inc.
2-8	Applicant name: Name Latin	
2-9en	Inventor name	
2-9	Inventor name: Name Latin	
2-10en	Invention title	Delivery, use and therapeutic applications of the CRISPR-Cas systems and compositions for genome editing
2-11	Sequence Total Quantity	195

3-1	**Sequences**		
3-1-1	Sequence Number [ID]	1	
3-1-2	Molecule Type	DNA	
3-1-3	Length	25	
3-1-4	Features	**misc_feature 1..25**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..25	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-1-5	Residues	cctccgtgtc agcgacccat gccaa	25
3-2	**Sequences**		
3-2-1	Sequence Number [ID]	2	
3-2-2	Molecule Type	DNA	
3-2-3	Length	24	
3-2-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-2-5	Residues	ccagcgtcga acagctccag cccg	24
3-3	**Sequences**		
3-3-1	Sequence Number [ID]	3	
3-3-2	Molecule Type	DNA	
3-3-3	Length	25	
3-3-4	Features	**misc_feature 1..25**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..25	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-3-5	Residues	agagggtgcc agcgggtata tgagg	25
3-4	**Sequences**		
3-4-1	Sequence Number [ID]	4	
3-4-2	Molecule Type		
3-4-3	Length		
3-4-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-4-5	Residues	000	3
3-5	**Sequences**		
3-5-1	Sequence Number [ID]	5	
3-5-2	Molecule Type		
3-5-3	Length		
3-5-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-5-5	Residues	000	3
3-6	**Sequences**		
3-6-1	Sequence Number [ID]	6	
3-6-2	Molecule Type		
3-6-3	Length		
3-6-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-6-5	Residues	000	3
3-7	**Sequences**		
3-7-1	Sequence Number [ID]	7	
3-7-2	Molecule Type		
3-7-3	Length		
3-7-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-7-5	Residues	000	3
3-8	**Sequences**		
3-8-1	Sequence Number [ID]	8	
3-8-2	Molecule Type		

3-8-3	Length		
3-8-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-8-5	Residues	000	3
3-9	**Sequences**		
3-9-1	Sequence Number [ID]	9	
3-9-2	Molecule Type		
3-9-3	Length		
3-9-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-9-5	Residues	000	3
3-10	**Sequences**		
3-10-1	Sequence Number [ID]	10	
3-10-2	Molecule Type		
3-10-3	Length		
3-10-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-10-5	Residues	000	3
3-11	**Sequences**		
3-11-1	Sequence Number [ID]	11	
3-11-2	Molecule Type		
3-11-3	Length		
3-11-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-11-5	Residues	000	3
3-12	**Sequences**		
3-12-1	Sequence Number [ID]	12	
3-12-2	Molecule Type		
3-12-3	Length		
3-12-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-12-5	Residues	000	3
3-13	**Sequences**		
3-13-1	Sequence Number [ID]	13	
3-13-2	Molecule Type		
3-13-3	Length		
3-13-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-13-5	Residues	000	3
3-14	**Sequences**		
3-14-1	Sequence Number [ID]	14	
3-14-2	Molecule Type		
3-14-3	Length		
3-14-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-14-5	Residues	000	3
3-15	**Sequences**		
3-15-1	Sequence Number [ID]	15	
3-15-2	Molecule Type		
3-15-3	Length		
3-15-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-15-5	Residues	000	3
3-16	**Sequences**		
3-16-1	Sequence Number [ID]	16	
3-16-2	Molecule Type	DNA	
3-16-3	Length	137	
3-16-4	Features	**modified_base 1..20**	
	Location/Qualifiers	mod_base=OTHER	
		note=a, c, t, g, unknown or other	

		misc_feature 1..137
		note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..137
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-16-5	Residues	nnnnnnnnnn nnnnnnnnnn gtttttgtac tctcaagatt tagaaataaa tcttgcagaa 60 gctacaaaga taaggcttca tgccgaaatc aacaccctgt cattttatgg cagggtgttt 120 tcgttattta atttttt 137
3-17	**Sequences**	
3-17-1	Sequence Number [ID]	17
3-17-2	Molecule Type	DNA
3-17-3	Length	123
3-17-4	Features	**modified_base 1..20**
	Location/Qualifiers	mod_base=OTHER
		note=a, c, t, g, unknown or other
		misc_feature 1..123
		note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..123
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-17-5	Residues	nnnnnnnnnn nnnnnnnnnn gtttttgtac tctcagaaat gcagaagcta caaagataag 60 gcttcatgcc gaaatcaaca ccctgtcatt ttatggcagg gtgttttcgt tatttaattt 120 ttt 123
3-18	**Sequences**	
3-18-1	Sequence Number [ID]	18
3-18-2	Molecule Type	DNA
3-18-3	Length	110
3-18-4	Features	**modified_base 1..20**
	Location/Qualifiers	mod_base=OTHER
		note=a, c, t, g, unknown or other
		misc_feature 1..110
		note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..110
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-18-5	Residues	nnnnnnnnnn nnnnnnnnnn gtttttgtac tctcagaaat gcagaagcta caaagataag 60 gcttcatgcc gaaatcaaca ccctgtcatt ttatggcagg gtgtttttt 110
3-19	**Sequences**	
3-19-1	Sequence Number [ID]	19
3-19-2	Molecule Type	DNA
3-19-3	Length	102
3-19-4	Features	**modified_base 1..20**
	Location/Qualifiers	mod_base=OTHER
		note=a, c, t, g, unknown or other
		misc_feature 1..102
		note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..102
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-19-5	Residues	nnnnnnnnnn nnnnnnnnnn gttttagagc tagaaatagc aagttaaaat aaggctagtc 60 cgttatcaac ttgaaaaagt ggcaccgagt cggtgctttt tt 102
3-20	**Sequences**	
3-20-1	Sequence Number [ID]	20
3-20-2	Molecule Type	DNA
3-20-3	Length	88
3-20-4	Features	**modified_base 1..20**
	Location/Qualifiers	mod_base=OTHER
		note=a, c, t, g, unknown or other
		misc_feature 1..88
		note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"
		source 1..88
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-20-5	Residues	nnnnnnnnnn nnnnnnnnnn gttttagagc tagaaatagc aagttaaaat aaggctagtc 60

		cgttatcaac ttgaaaaagt gttttttt	88
3-21	**Sequences**		
3-21-1	Sequence Number [ID]	21	
3-21-2	Molecule Type	DNA	
3-21-3	Length	76	
3-21-4	Features	**modified_base 1..20**	
	Location/Qualifiers	mod_base=OTHER	
		note=a, c, t, g, unknown or other	
		misc_feature 1..76	
		note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..76	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-21-5	Residues	nnnnnnnnnn nnnnnnnnnn gttttagagc tagaaatagc aagttaaaat aaggctagtc	60
		cgttatcatt tttttt	76
3-22	**Sequences**		
3-22-1	Sequence Number [ID]	22	
3-22-2	Molecule Type	DNA	
3-22-3	Length	20	
3-22-4	Features	**source 1..20**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-22-5	Residues	gagtccgagc agaagaagaa	20
3-23	**Sequences**		
3-23-1	Sequence Number [ID]	23	
3-23-2	Molecule Type	DNA	
3-23-3	Length	20	
3-23-4	Features	**source 1..20**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-23-5	Residues	gagtcctagc aggagaagaa	20
3-24	**Sequences**		
3-24-1	Sequence Number [ID]	24	
3-24-2	Molecule Type	DNA	
3-24-3	Length	20	
3-24-4	Features	**source 1..20**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-24-5	Residues	gagtctaagc agaagaagaa	20
3-25	**Sequences**		
3-25-1	Sequence Number [ID]	25	
3-25-2	Molecule Type	AA	
3-25-3	Length	7	
3-25-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Simian virus 40	
	NonEnglishQualifier Value		
3-25-5	Residues	PKKKRKV	7
3-26	**Sequences**		
3-26-1	Sequence Number [ID]	26	
3-26-2	Molecule Type	AA	
3-26-3	Length	16	
3-26-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=source = /note="Description of Unknown: Nucleoplasmin bipartite NLS sequence"	
		source 1..16	
		mol_type=protein	
		organism=unidentified	
	NonEnglishQualifier Value		
3-26-5	Residues	KRPAATKKAG QAKKKK	16
3-27	**Sequences**		
3-27-1	Sequence Number [ID]	27	
3-27-2	Molecule Type	AA	
3-27-3	Length	9	
3-27-4	Features	**REGION 1..9**	

	Location/Qualifiers	note=source = /note="Description of Unknown: C-myc NLS sequence"	
		source 1..9	
		mol_type=protein	
		organism=unidentified	
	NonEnglishQualifier Value		
3-27-5	Residues	PAAKRVKLD	9
3-28	**Sequences**		
3-28-1	Sequence Number [ID]	28	
3-28-2	Molecule Type	AA	
3-28-3	Length	11	
3-28-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=source = /note="Description of Unknown: C-myc NLS sequence"	
		source 1..11	
		mol_type=protein	
		organism=unidentified	
	NonEnglishQualifier Value		
3-28-5	Residues	RQRRNELKRS P	11
3-29	**Sequences**		
3-29-1	Sequence Number [ID]	29	
3-29-2	Molecule Type	AA	
3-29-3	Length	38	
3-29-4	Features	**source 1..38**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-29-5	Residues	NQSSNFGPMK GGNFGGRSSG PYGGGGQYFA KPRNQGGY	38
3-30	**Sequences**		
3-30-1	Sequence Number [ID]	30	
3-30-2	Molecule Type	AA	
3-30-3	Length	42	
3-30-4	Features	**REGION 1..42**	
	Location/Qualifiers	note=source = /note="Description of Unknown: IBB domain from importin -alpha sequence"	
		source 1..42	
		mol_type=protein	
		organism=unidentified	
	NonEnglishQualifier Value		
3-30-5	Residues	RMRIZFKNKG KDTAELRRRR VEVSVELRKA KKDEQILKRR NV	42
3-31	**Sequences**		
3-31-1	Sequence Number [ID]	31	
3-31-2	Molecule Type	AA	
3-31-3	Length	8	
3-31-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=source = /note="Description of Unknown: Myoma T protein sequence "	
		source 1..8	
		mol_type=protein	
		organism=unidentified	
	NonEnglishQualifier Value		
3-31-5	Residues	VSRKRPRP	8
3-32	**Sequences**		
3-32-1	Sequence Number [ID]	32	
3-32-2	Molecule Type	AA	
3-32-3	Length	8	
3-32-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=source = /note="Description of Unknown: Myoma T protein sequence "	
		source 1..8	
		mol_type=protein	
		organism=unidentified	
	NonEnglishQualifier Value		
3-32-5	Residues	PPKKARED	8
3-33	**Sequences**		
3-33-1	Sequence Number [ID]	33	
3-33-2	Molecule Type	AA	
3-33-3	Length	8	
3-33-4	Features	**source 1..8**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-33-5	Residues	PQPKKKPL	8

3-34	**Sequences**		
3-34-1	Sequence Number [ID]	34	
3-34-2	Molecule Type	AA	
3-34-3	Length	12	
3-34-4	Features	**source 1..12**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-34-5	Residues	SALIKKKKKM AP	12
3-35	**Sequences**		
3-35-1	Sequence Number [ID]	35	
3-35-2	Molecule Type	AA	
3-35-3	Length	5	
3-35-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Influenza virus	
	NonEnglishQualifier Value		
3-35-5	Residues	DRLRR	5
3-36	**Sequences**		
3-36-1	Sequence Number [ID]	36	
3-36-2	Molecule Type	AA	
3-36-3	Length	7	
3-36-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Influenza virus	
	NonEnglishQualifier Value		
3-36-5	Residues	PKQKKRK	7
3-37	**Sequences**		
3-37-1	Sequence Number [ID]	37	
3-37-2	Molecule Type	AA	
3-37-3	Length	10	
3-37-4	Features	**source 1..10**	
	Location/Qualifiers	mol_type=protein	
		organism=Hepatitis delta virus	
	NonEnglishQualifier Value		
3-37-5	Residues	RKLKKKIKKL	10
3-38	**Sequences**		
3-38-1	Sequence Number [ID]	38	
3-38-2	Molecule Type	AA	
3-38-3	Length	10	
3-38-4	Features	**source 1..10**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-38-5	Residues	REKKKFLKRR	10
3-39	**Sequences**		
3-39-1	Sequence Number [ID]	39	
3-39-2	Molecule Type	AA	
3-39-3	Length	20	
3-39-4	Features	**source 1..20**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-39-5	Residues	KRKGDEVDGV DEVAKKKSKK	20
3-40	**Sequences**		
3-40-1	Sequence Number [ID]	40	
3-40-2	Molecule Type	AA	
3-40-3	Length	17	
3-40-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-40-5	Residues	RKCLQAGMNL EARKTKK	17
3-41	**Sequences**		
3-41-1	Sequence Number [ID]	41	
3-41-2	Molecule Type	AA	
3-41-3	Length	9	
3-41-4	Features	**source 1..9**	

	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-41-5	Residues	LAGLIDADG	9
3-42	**Sequences**		
3-42-1	Sequence Number [ID]	42	
3-42-2	Molecule Type	RNA	
3-42-3	Length	12	
3-42-4	Features	**misc_feature 1..12**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..12	
		mol_type=other RNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-42-5	Residues	gttttagagc ta	12
3-43	**Sequences**		
3-43-1	Sequence Number [ID]	43	
3-43-2	Molecule Type	DNA	
3-43-3	Length	30	
3-43-4	Features	**misc_feature 1..30**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..30	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-43-5	Residues	cgcacgcgta attcgaacgc tgacgtcatc	30
3-44	**Sequences**		
3-44-1	Sequence Number [ID]	44	
3-44-2	Molecule Type	DNA	
3-44-3	Length	130	
3-44-4	Features	**modified_base 92..110**	
	Location/Qualifiers	mod_base=OTHER	
		note=a, c, t, g, unknown or other	
		misc_feature 1..130	
		note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..130	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-44-5	Residues	cacacgcgta aaaaagcacc gactcggtgc cacttttca agttgataac ggactagcct 60 tattttaact tgctatttct agctctaaaa cnnnnnnnnn nnnnnnnnn cggtgtttcg 120 tcctttccac 130	
3-45	**Sequences**		
3-45-1	Sequence Number [ID]	45	
3-45-2	Molecule Type	DNA	
3-45-3	Length	23	
3-45-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-45-5	Residues	tgcgaatacg cccacgcgat ggg	23
3-46	**Sequences**		
3-46-1	Sequence Number [ID]	46	
3-46-2	Molecule Type	DNA	
3-46-3	Length	24	
3-46-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-46-5	Residues	gtgtctagac tgcagagggc cctg	24
3-47	**Sequences**		
3-47-1	Sequence Number [ID]	47	
3-47-2	Molecule Type	DNA	
3-47-3	Length	28	

3-47-4	Features	**misc_feature 1..28**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..28	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-47-5	Residues	gtgtcgtgcc tgagagcgca gtcgagaa	28
3-48	**Sequences**		
3-48-1	Sequence Number [ID]	48	
3-48-2	Molecule Type	DNA	
3-48-3	Length	29	
3-48-4	Features	**misc_feature 1..29**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..29	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-48-5	Residues	gagaagctta gctgaatggg gtccgcctc	29
3-49	**Sequences**		
3-49-1	Sequence Number [ID]	49	
3-49-2	Molecule Type	DNA	
3-49-3	Length	31	
3-49-4	Features	**misc_feature 1..31**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..31	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-49-5	Residues	ctcaccggtg cgcgcaaccg atgccgggac c	31
3-50	**Sequences**		
3-50-1	Sequence Number [ID]	50	
3-50-2	Molecule Type	DNA	
3-50-3	Length	32	
3-50-4	Features	**misc_feature 1..32**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..32	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-50-5	Residues	gagaagcttg gcgaaatgat ttgctgcaga tg	32
3-51	**Sequences**		
3-51-1	Sequence Number [ID]	51	
3-51-2	Molecule Type	DNA	
3-51-3	Length	32	
3-51-4	Features	**misc_feature 1..32**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..32	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-51-5	Residues	ctcaccggtg cgcgcgtcgc ctccccctcc gc	32
3-52	**Sequences**		
3-52-1	Sequence Number [ID]	52	
3-52-2	Molecule Type	DNA	
3-52-3	Length	134	
3-52-4	Features	**misc_feature 1..134**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..134	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-52-5	Residues	agcttcgcgc cgggaggagg ggggacgcag tgggcggagc ggagacagca ccttcggaga	60
		taatcctttc tcctgccgca gagcagagga gcggcgggag aggaacactt ctcccaggct	120
		ttagcagagc cgga	134
3-53	**Sequences**		
3-53-1	Sequence Number [ID]	53	
3-53-2	Molecule Type	DNA	
3-53-3	Length	134	

3-53-4	Features	**misc_feature 1..134**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"	
		source 1..134	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-53-5	Residues	ccggtccggc tctgctaaag cctgggagaa gtgttcctct cccgccgctc ctctgctctg	60
		cggcaggaga aaggattatc tccgaaggtg ctgtctccgc tccgcccact gcgtcccccc	120
		tcctcccggc gcga	134
3-54	**Sequences**		
3-54-1	Sequence Number [ID]	54	
3-54-2	Molecule Type	DNA	
3-54-3	Length	55	
3-54-4	Features	**misc_feature 1..55**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..55	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-54-5	Residues	aattcaataa aagatcttta ttttcattag atctgtgtgt tggttttttg tgtgc	55
3-55	**Sequences**		
3-55-1	Sequence Number [ID]	55	
3-55-2	Molecule Type	DNA	
3-55-3	Length	55	
3-55-4	Features	**misc_feature 1..55**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..55	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-55-5	Residues	ggccgcacac aaaaaaccaa cacacagatc taatgaaaat aaagatcttt tattg	55
3-56	**Sequences**		
3-56-1	Sequence Number [ID]	56	
3-56-2	Molecule Type	DNA	
3-56-3	Length	23	
3-56-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-56-5	Residues	ggagctggag ctgttcacgt tgg	23
3-57	**Sequences**		
3-57-1	Sequence Number [ID]	57	
3-57-2	Molecule Type	DNA	
3-57-3	Length	23	
3-57-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-57-5	Residues	cgggcagcag atgttcgcgt agg	23
3-58	**Sequences**		
3-58-1	Sequence Number [ID]	58	
3-58-2	Molecule Type	DNA	
3-58-3	Length	23	
3-58-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-58-5	Residues	agggcttgag atgttcgggc tgg	23
3-59	**Sequences**		
3-59-1	Sequence Number [ID]	59	
3-59-2	Molecule Type	DNA	
3-59-3	Length	23	
3-59-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-59-5	Residues	ccggctgggg ctgtcctcgc tag	23
3-60	**Sequences**		

3-60-1	Sequence Number [ID]	60	
3-60-2	Molecule Type	DNA	
3-60-3	Length	23	
3-60-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-60-5	Residues	cggggtgcag ctgctcacgc cag	23
3-61	**Sequences**		
3-61-1	Sequence Number [ID]	61	
3-61-2	Molecule Type	DNA	
3-61-3	Length	23	
3-61-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-61-5	Residues	ctggcgggag ctggtcgcgt gag	23
3-62	**Sequences**		
3-62-1	Sequence Number [ID]	62	
3-62-2	Molecule Type	DNA	
3-62-3	Length	23	
3-62-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-62-5	Residues	tgagcatggg ccgctggcgg tgg	23
3-63	**Sequences**		
3-63-1	Sequence Number [ID]	63	
3-63-2	Molecule Type	DNA	
3-63-3	Length	23	
3-63-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-63-5	Residues	atggcatagg ccgctgacag agg	23
3-64	**Sequences**		
3-64-1	Sequence Number [ID]	64	
3-64-2	Molecule Type	DNA	
3-64-3	Length	23	
3-64-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-64-5	Residues	ttggcatggt gagctggcgg ggg	23
3-65	**Sequences**		
3-65-1	Sequence Number [ID]	65	
3-65-2	Molecule Type	DNA	
3-65-3	Length	23	
3-65-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-65-5	Residues	tgggcagggg tctctgaggg cag	23
3-66	**Sequences**		
3-66-1	Sequence Number [ID]	66	
3-66-2	Molecule Type	DNA	
3-66-3	Length	23	
3-66-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-66-5	Residues	ttggcatggg tctcttacca agg	23
3-67	**Sequences**		
3-67-1	Sequence Number [ID]	67	
3-67-2	Molecule Type	DNA	
3-67-3	Length	23	
3-67-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	

		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-67-5	Residues	acatggttcc agtgggtatg tag	23
3-68	**Sequences**		
3-68-1	Sequence Number [ID]	68	
3-68-2	Molecule Type	DNA	
3-68-3	Length	23	
3-68-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-68-5	Residues	ggaggtgggc agcgggtatg tag	23
3-69	**Sequences**		
3-69-1	Sequence Number [ID]	69	
3-69-2	Molecule Type	DNA	
3-69-3	Length	23	
3-69-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-69-5	Residues	agaaggtccc cgcgggcatg gag	23
3-70	**Sequences**		
3-70-1	Sequence Number [ID]	70	
3-70-2	Molecule Type	DNA	
3-70-3	Length	23	
3-70-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-70-5	Residues	ggagggaacc agccggtatg ggg	23
3-71	**Sequences**		
3-71-1	Sequence Number [ID]	71	
3-71-2	Molecule Type	DNA	
3-71-3	Length	23	
3-71-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-71-5	Residues	agagagtggc agtgggtaag cag	23
3-72	**Sequences**		
3-72-1	Sequence Number [ID]	72	
3-72-2	Molecule Type	DNA	
3-72-3	Length	23	
3-72-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-72-5	Residues	agaggtggcc agcgggcagg aag	23
3-73	**Sequences**		
3-73-1	Sequence Number [ID]	73	
3-73-2	Molecule Type	DNA	
3-73-3	Length	23	
3-73-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-73-5	Residues	tgaggggcc agctgggatg cag	23
3-74	**Sequences**		
3-74-1	Sequence Number [ID]	74	
3-74-2	Molecule Type	DNA	
3-74-3	Length	20	
3-74-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..20	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-74-5	Residues	ggtctcatgt gtggcactca	20

3-75	**Sequences**		
3-75-1	Sequence Number [ID]	75	
3-75-2	Molecule Type	DNA	
3-75-3	Length	20	
3-75-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..20	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-75-5	Residues	tgtccaacct tcaggcaagg	20
3-76	**Sequences**		
3-76-1	Sequence Number [ID]	76	
3-76-2	Molecule Type	DNA	
3-76-3	Length	21	
3-76-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-76-5	Residues	atccctcctc agagggtcag c	21
3-77	**Sequences**		
3-77-1	Sequence Number [ID]	77	
3-77-2	Molecule Type	DNA	
3-77-3	Length	22	
3-77-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-77-5	Residues	tacctcatgc acagctagca cc	22
3-78	**Sequences**		
3-78-1	Sequence Number [ID]	78	
3-78-2	Molecule Type	DNA	
3-78-3	Length	22	
3-78-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-78-5	Residues	ttcgggcata gcatggtctt cc	22
3-79	**Sequences**		
3-79-1	Sequence Number [ID]	79	
3-79-2	Molecule Type	DNA	
3-79-3	Length	24	
3-79-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-79-5	Residues	gttctatttc agagggctga tccc	24
3-80	**Sequences**		
3-80-1	Sequence Number [ID]	80	
3-80-2	Molecule Type	DNA	
3-80-3	Length	21	
3-80-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-80-5	Residues	gttctgagcc gcacagtttg g	21
3-81	**Sequences**		
3-81-1	Sequence Number [ID]	81	

3-81-2	Molecule Type	DNA	
3-81-3	Length	22	
3-81-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-81-5	Residues	ggataagaag ggacaataca gg	22
3-82	**Sequences**		
3-82-1	Sequence Number [ID]	82	
3-82-2	Molecule Type	DNA	
3-82-3	Length	21	
3-82-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-82-5	Residues	gccggggtct cgttcagagc t	21
3-83	**Sequences**		
3-83-1	Sequence Number [ID]	83	
3-83-2	Molecule Type	DNA	
3-83-3	Length	20	
3-83-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..20	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-83-5	Residues	ctaccgcctg cggacatggt	20
3-84	**Sequences**		
3-84-1	Sequence Number [ID]	84	
3-84-2	Molecule Type	DNA	
3-84-3	Length	24	
3-84-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-84-5	Residues	cctgtctctc tgtcctaggg ctcc	24
3-85	**Sequences**		
3-85-1	Sequence Number [ID]	85	
3-85-2	Molecule Type	DNA	
3-85-3	Length	25	
3-85-4	Features	**misc_feature 1..25**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..25	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-85-5	Residues	ccgtttgctg atgtagtagg ggtcc	25
3-86	**Sequences**		
3-86-1	Sequence Number [ID]	86	
3-86-2	Molecule Type	DNA	
3-86-3	Length	25	
3-86-4	Features	**misc_feature 1..25**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..25	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-86-5	Residues	cccacaggaa acaatgaagg gagac	25
3-87	**Sequences**		
3-87-1	Sequence Number [ID]	87	
3-87-2	Molecule Type	DNA	
3-87-3	Length	25	

3-87-4	Features	**misc_feature 1..25**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..25	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-87-5	Residues	catccttcgt gtctgaggac tggtc	25
3-88	**Sequences**		
3-88-1	Sequence Number [ID]	88	
3-88-2	Molecule Type	DNA	
3-88-3	Length	23	
3-88-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-88-5	Residues	ccctgacacc agctgttcag cac	23
3-89	**Sequences**		
3-89-1	Sequence Number [ID]	89	
3-89-2	Molecule Type	DNA	
3-89-3	Length	23	
3-89-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-89-5	Residues	ctctgggtga ccacacacga tgc	23
3-90	**Sequences**		
3-90-1	Sequence Number [ID]	90	
3-90-2	Molecule Type	DNA	
3-90-3	Length	21	
3-90-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-90-5	Residues	gagcaggcag agccgagcaa g	21
3-91	**Sequences**		
3-91-1	Sequence Number [ID]	91	
3-91-2	Molecule Type	DNA	
3-91-3	Length	19	
3-91-4	Features	**misc_feature 1..19**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..19	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-91-5	Residues	ggagagcgtc cgccaggag	19
3-92	**Sequences**		
3-92-1	Sequence Number [ID]	92	
3-92-2	Molecule Type	DNA	
3-92-3	Length	24	
3-92-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-92-5	Residues	gggtcttgtt gtgagtaggg tgtg	24
3-93	**Sequences**		
3-93-1	Sequence Number [ID]	93	
3-93-2	Molecule Type	DNA	
3-93-3	Length	22	
3-93-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	

		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-93-5	Residues	gaagctctct taactactgt tc	22
3-94	**Sequences**		
3-94-1	Sequence Number [ID]	94	
3-94-2	Molecule Type	DNA	
3-94-3	Length	23	
3-94-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-94-5	Residues	cctggaatac tatttccacg ccg	23
3-95	**Sequences**		
3-95-1	Sequence Number [ID]	95	
3-95-2	Molecule Type	DNA	
3-95-3	Length	20	
3-95-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..20	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-95-5	Residues	caggccctag cagcgagcag	20
3-96	**Sequences**		
3-96-1	Sequence Number [ID]	96	
3-96-2	Molecule Type	DNA	
3-96-3	Length	22	
3-96-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-96-5	Residues	gcagcacact ccaccctcac at	22
3-97	**Sequences**		
3-97-1	Sequence Number [ID]	97	
3-97-2	Molecule Type	DNA	
3-97-3	Length	21	
3-97-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-97-5	Residues	ggaaggggct ttcctccgag c	21
3-98	**Sequences**		
3-98-1	Sequence Number [ID]	98	
3-98-2	Molecule Type	DNA	
3-98-3	Length	23	
3-98-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-98-5	Residues	cggcgtcacg tgacctgagt aac	23
3-99	**Sequences**		
3-99-1	Sequence Number [ID]	99	
3-99-2	Molecule Type	DNA	
3-99-3	Length	20	
3-99-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..20	
		mol_type=other DNA	

		organism=synthetic construct	
	NonEnglishQualifier Value		
3-99-5	Residues	gctccgaccc tgctctccca	20
3-100	**Sequences**		
3-100-1	Sequence Number [ID]	100	
3-100-2	Molecule Type	DNA	
3-100-3	Length	21	
3-100-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-100-5	Residues	gtgtctgcct cgctctgctg c	21
3-101	**Sequences**		
3-101-1	Sequence Number [ID]	101	
3-101-2	Molecule Type	DNA	
3-101-3	Length	23	
3-101-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-101-5	Residues	cctgttcatc aggctcgtag ccc	23
3-102	**Sequences**		
3-102-1	Sequence Number [ID]	102	
3-102-2	Molecule Type	DNA	
3-102-3	Length	27	
3-102-4	Features	**misc_feature 1..27**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..27	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-102-5	Residues	ctatctgaaa tccaccacct tagacgc	27
3-103	**Sequences**		
3-103-1	Sequence Number [ID]	103	
3-103-2	Molecule Type	DNA	
3-103-3	Length	21	
3-103-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-103-5	Residues	cgattgctgg cttgccttga g	21
3-104	**Sequences**		
3-104-1	Sequence Number [ID]	104	
3-104-2	Molecule Type	DNA	
3-104-3	Length	19	
3-104-4	Features	**misc_feature 1..19**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..19	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-104-5	Residues	gcctgagggg gccagaggt	19
3-105	**Sequences**		
3-105-1	Sequence Number [ID]	105	
3-105-2	Molecule Type	DNA	
3-105-3	Length	22	
3-105-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		

3-105-5	Residues	ggttcgcgtc cgcccgcgtg at	22
3-106	**Sequences**		
3-106-1	Sequence Number [ID]	106	
3-106-2	Molecule Type	DNA	
3-106-3	Length	18	
3-106-4	Features	**misc_feature 1..18**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..18	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-106-5	Residues	gggactcccc gggtggtg	18
3-107	**Sequences**		
3-107-1	Sequence Number [ID]	107	
3-107-2	Molecule Type	DNA	
3-107-3	Length	23	
3-107-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-107-5	Residues	gagaggtggt cctgtcgcct atg	23
3-108	**Sequences**		
3-108-1	Sequence Number [ID]	108	
3-108-2	Molecule Type	DNA	
3-108-3	Length	24	
3-108-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-108-5	Residues	gaccctgtgt ttcaagtctc tctg	24
3-109	**Sequences**		
3-109-1	Sequence Number [ID]	109	
3-109-2	Molecule Type	DNA	
3-109-3	Length	23	
3-109-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-109-5	Residues	cccagcaggt cacagctgac atc	23
3-110	**Sequences**		
3-110-1	Sequence Number [ID]	110	
3-110-2	Molecule Type	DNA	
3-110-3	Length	23	
3-110-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-110-5	Residues	ggccatccag tacattcaat acg	23
3-111	**Sequences**		
3-111-1	Sequence Number [ID]	111	
3-111-2	Molecule Type	DNA	
3-111-3	Length	32	
3-111-4	Features	**misc_feature 1..32**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..32	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-111-5	Residues	agcacagtat gtattctata aaataatacg ac	32
3-112	**Sequences**		

3-112-1	Sequence Number [ID]	112	
3-112-2	Molecule Type	DNA	
3-112-3	Length	22	
3-112-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-112-5	Residues	gcagaagccg tgactcacag ca	22
3-113	**Sequences**		
3-113-1	Sequence Number [ID]	113	
3-113-2	Molecule Type	DNA	
3-113-3	Length	22	
3-113-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-113-5	Residues	gtgggagggg acagagacca tg	22
3-114	**Sequences**		
3-114-1	Sequence Number [ID]	114	
3-114-2	Molecule Type	DNA	
3-114-3	Length	28	
3-114-4	Features	**misc_feature 1..28**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..28	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-114-5	Residues	cttgtgcttg tgattctgtc cttactgc	28
3-115	**Sequences**		
3-115-1	Sequence Number [ID]	115	
3-115-2	Molecule Type	DNA	
3-115-3	Length	28	
3-115-4	Features	**misc_feature 1..28**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..28	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-115-5	Residues	ccttacctgt tcctcttcct tatccagc	28
3-116	**Sequences**		
3-116-1	Sequence Number [ID]	116	
3-116-2	Molecule Type	DNA	
3-116-3	Length	25	
3-116-4	Features	**misc_feature 1..25**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..25	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-116-5	Residues	cgagaagtcg atgcagacac ttcaa	25
3-117	**Sequences**		
3-117-1	Sequence Number [ID]	117	
3-117-2	Molecule Type	DNA	
3-117-3	Length	22	
3-117-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-117-5	Residues	atacccagtc cacatccctg cc	22
3-118	**Sequences**		
3-118-1	Sequence Number [ID]	118	
3-118-2	Molecule Type	DNA	

3-118-3	Length	23	
3-118-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-118-5	Residues	gctgaagact ggcgagcaca gct	23
3-119	**Sequences**		
3-119-1	Sequence Number [ID]	119	
3-119-2	Molecule Type	DNA	
3-119-3	Length	26	
3-119-4	Features	**misc_feature 1..26**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..26	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-119-5	Residues	cctctgcatc tccctcagga agtatt	26
3-120	**Sequences**		
3-120-1	Sequence Number [ID]	120	
3-120-2	Molecule Type	DNA	
3-120-3	Length	26	
3-120-4	Features	**misc_feature 1..26**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..26	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-120-5	Residues	gacctgaatg ttgtggctga gagtcc	26
3-121	**Sequences**		
3-121-1	Sequence Number [ID]	121	
3-121-2	Molecule Type	DNA	
3-121-3	Length	20	
3-121-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..20	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-121-5	Residues	gcctcctgtc cccaggtccc	20
3-122	**Sequences**		
3-122-1	Sequence Number [ID]	122	
3-122-2	Molecule Type	DNA	
3-122-3	Length	22	
3-122-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-122-5	Residues	ccctcacgtt cctgtccagc aa	22
3-123	**Sequences**		
3-123-1	Sequence Number [ID]	123	
3-123-2	Molecule Type	DNA	
3-123-3	Length	22	
3-123-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic pr imer"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-123-5	Residues	cactaggctt gggctgccct ct	22
3-124	**Sequences**		
3-124-1	Sequence Number [ID]	124	
3-124-2	Molecule Type	DNA	
3-124-3	Length	2503	
3-124-4	Features	**misc_feature 1..2503**	

	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..2503
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-124-5	Residues	accagaaagt ctctagctgt ccagaggaca tagcacagag gcccatggtc cctatttcaa 60 acccaggcca ccagactgag ctgggacctt gggacagaca agtcatgcag aagttagggg 120 accttctcct ccctttttcct ggatcctgag tacctctcct ccctgacctc aggcttcctc 180 ctagtgtcac cttggcccct cttagaagcc aattaggccc tcagtttctg cagcggggat 240 taatatgatt atgaacaccc ccaatctccc agatgctgat tcagccagga gcttaggagg 300 gggaggtcac tttataaggg tctgggggggg tcagaaccca gagtcatcca gctggagccc 360 tgagtggctg agctcaggcc ttcgcagcat tcttgggtgg gagcagccac gggtcagcca 420 caagggccac agccatgaat ggcacagaag gccctaactt ctacgtgccc ttctccaatg 480 cgacgggtgt ggtacgcagc cccttcgagt acccacagta ctacctggct gagccatggc 540 agttctccat gctggccgcc tacatgtttc tgctgatcgt gctgggcttc cccatcaact 600 tcctcacgct ctacgtcacc gtccagcaca agaagctgcg cacgcctctc aactacatcc 660 tgctcaacct agccgtggct gacctcttca tggtcctagg tggcttcacc agcaccctct 720 acacctctct gcatggatac ttcgtcttcg ggcccacagg atgcaatttg gagggcttct 780 ttgccaccct gggcggtatg agccgggtgt gggtggggtg tgcaggagcc cgggagcatg 840 gaggggtctg ggagagtccc gggcttggcg gtggtggctg agaggccttc tcccttctcc 900 tgtcctgtca atgttatcca aagccctcat atattcagtc aacaaacacc attcatggtg 960 atagccgggc tgctgtttgt gcagggctgg cactgaacac tgccttgatc ttatttggag 1020 caatatgcgc ttgtctaatt tcacagcaag aaaactgagc tgaggctcaa agaagtcaag 1080 cgccctgctg gggcgtcaca cagggacggg tgcagagttg agttggaagc ccgcatctat 1140 ctcgggccat gtttgcagca ccaagcctct gtttcccttg gagcagctgt gctgagtcag 1200 acccaggctg ggcactgagg gagagctggg caagccagac ccctcctctc tgggggccca 1260 agctcagggt gggaagtgga ttttccattc tccagtcatt gggtcttccc tgtgctgggc 1320 aatgggctcg gtcccctctg gcatcctctg cctcccctct cagcccctgt cctcaggtgc 1380 ccctccagcc tccctgccgc gttccaagtc tcctggtgtt gagaaccgca agcagccgct 1440 ctgaagcagt tccttttttgc tttagaataa tgtcttgcat ttaacaggaa aacagatggg 1500 gtgctgcagg gataacagat cccacttaac agagaggaaa actgaggcag ggagagggga 1560 agagactcat ttagggatgt ggccaggcag caacaagagc ctaggtctcc tggctgtgat 1620 ccaggaatat ctctgctgag atgcaggagg agacgctaga agcagccatt gcaaagctgg 1680 gtgacgggga gagcttaccg ccagccacaa gcgtctctct gccagccttg ccctgtctcc 1740 cccatgtcca ggctgctgcc tcggtcccat tctcagggaa tctctggcca ttgttgggtg 1800 tttgttgcat tcaataatca cagatcactc agttctggcc agaaggtggg tgtgccactt 1860 acgggtggtt gttctctgca gggtcagtcc cagtttacaa atattgtccc tttcactgtt 1920 aggaatgtcc cagtttggtt gattaactat atggccactc tccctatgga acttcatggg 1980 gtggtgagca ggacagatgt ctgaattcca tcatttcctt cttcttcctc tgggcaaaac 2040 attgcacatt gcttcatggc tcctaggaga ggcccccaca tgtccgggtt atttcatttc 2100 ccgagaaggg agagggagga aggactgcca attctgggtt tccaccacct ctgcattcct 2160 tcccaacaag gaactctgcc ccacattagg atgcattctt ctgctaaaca cacacacaca 2220 cacacacaca cacaacacac acacacacac acacacacac acacacacaa aactccctac 2280 cgggttccca gttcaatcct gacccctga tctgattcgt gtcccttatg ggcccagagc 2340 gctaagcaaa taacttcccc cattccctgg aatttctttg cccagctctc ctcagcgtgt 2400 ggtccctctg ccccttcccc ctcctcccag caccaagctc tctccttccc caaggcctcc 2460 tcaaatccct ctcccactcc tggttgcctt cctagctacc ctc 2503
3-125	**Sequences**	
3-125-1	Sequence Number [ID]	125
3-125-2	Molecule Type	DNA
3-125-3	Length	2500
3-125-4	Features	**misc_feature 1..2500**
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..2500
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-125-5	Residues	ctgctgcctg ctctgtcccc tttaagtatt gacatcctca aaaccctctt tggaaaaagc 60 acaggccaca gatcttactg tgacttgtgt ttctttctcc taggtgtacc ttcaaccttg 120 ataaaaataa acctctaaat caattgagat ctgcctccgt cacttttttt ttttcaaaga 180 ctcagagtct cactctgttg cccaggctgg agtgtagtgg tgcgatcttg gctcattgca 240 ccctccacct cctgggttca agtggttctc gtgcctcagc ttcctgagta gctgggatta 300 caggggtgca ccaccacatc tggctaattt ttgtatttttt agtagagaca gggtttcacc 360 atgttgccca ggctggtctc aaaccccttga cctcaggtga tccacccgcc tcggcctctc 420 aaagtactgg gattataggc atgagccacg gcacccggcc ctctgtcact ttttgattta 480 caacatgtat ctctaatttt aaaggatcct tttttaaaat atgtatataa tttccattta 540 tcttttaaaa tttaataatc attctttgtt atcatgtaat acccaattta tatttaaatt 600 tactcaatca acctatgttt taaaaaaatt caatagaata gattagaacc tcatagaata 660 gaaaatatca gagtgcattt cctgtagtaa tggtaagtgt tgtttttgaa atcatttcta 720 ttatatatgt atcactgcat actgtgtagc cgtgaggtaa aatatgtttc tttgtactat 780 ggtcaaaaaa agtcagcctc tgtgatgccc aatgacctcc atcttcttct ttaggttttc 840 tcgagcaagg cttaatggtc agtgatacca acaggctgtg gcagcattac aagacgacca 900 cgcagttcaa gctggatgtg ttgtccctgg tccccaccga cctggcttac ttaaaggtgg 960 gcacaaacta cccagaagtg aggttcaacc gcctactgaa gttttcccgg ctctttgaat 1020

		tctttgaccg cacagagaca aggaccaact accccaatat gttcaggatt gggaacttgg 1080 tcttgtacat tctcatcatc atccactgga atgcctgcat ctactttgcc atttccaagt 1140 tcattggttt tgggacagac tcctgggtct acccaaacat ctcaatccca gagcatgggc 1200 gcctctccag gaagtacatt tacagtctct actggtccac cttgaccctt accaccattg 1260 gtgagacccc acccccgtg aaagatgagg agtatctctt tgtggtcgta gacttcttgg 1320 tgggtgttct gatttttgcc accattgtgg gcaatgtggg ctccatgatc tcgaatatga 1380 atgcctcacg ggcagagttc caggccaaga ttgattccat caagcagtac atgcagttcc 1440 gcaaggtcac caaggacttg gagacgcggg ttatccggtg gtttgactac ctgtgggcca 1500 acaagaagac ggtggatgag aaggaggtgc tcaagagcct cccagacaag ctgaaggctg 1560 agatcgccat caacgtgcac ctggacacgc tgaagaaggt tcgcatcttc caggactgtg 1620 aggcagggct gctggtggag ctggtgctga agctgcgacc cactgtgttc agccctgggg 1680 attatatctg caagaaggga gatattggga aggagatgta catcatcaac gagggcaagc 1740 tggccgtggt ggctgatgat ggggtcaccc agttcgtggt cctcagcgat ggcagctact 1800 tcggggagat cagcattctg aacatcaagg ggagcaagtc ggggaaccgc aggacggcca 1860 acatccgcag cattggctac tcagacctgt tctgcctctc aaaggacgat ctcatggagg 1920 ccctcaccga gtaccccgaa gccaagaagg ccctggagga gaaaggacgg cagatcctga 1980 tgaaagacaa cctgatcgat gaggagctgg ccagggcggg cgcggacccc aaggaccttg 2040 aggagaaagt ggagcagctg gggtcctccc tggacaccct gcagaccagg tttgcacgcc 2100 tcctggctga gtacaacgcc acccagatga agatgaagca gcgtctcagc caactggaaa 2160 gccaggtgaa gggtggtggg gacaagcccc tggctgatgg ggaagttccc ggggatgcta 2220 caaaaacaga ggacaaacaa cagtgaaaat gcagcatctg tctcctgctt cacagggtcg 2280 actgtcaggg tgaccgtatg tggccgcagc tgtgtggcat ggaacttggt cagggttgaa 2340 ttccagctct actcaccctt tgaaagctgt gtgactgcct gagagaacct gtttcttcac 2400 ctaaaaaatg ggacttttg tctcagtccc agtgaagtgc caggtttgat tgtgaagtcc 2460 gcatgaaaca ctgcaccagg cagggctttg caaagtgcaa 2500
3-126	**Sequences**	
3-126-1	Sequence Number [ID]	126
3-126-2	Molecule Type	DNA
3-126-3	Length	2500
3-126-4	Features	**misc_feature 1..2500**
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..2500
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-126-5	Residues	actttgaggc aattttactg tagctggtat tttagtcaat ttttagataa attagttgtt 60 tatatcaaag taaataattc acattctaaa gggaattatt tatttagtaa attttctgga 120 aattgagtgt ctgtgtgtgt gtgtttccca atcagtggtc cttctgactt taaattcttt 180 aaaatcggtt ctggttgtta taatccctta tacatatcca actcactcta ggtagtatgt 240 aattttgtaa gttattttcc ctctctttgc tctatcctat aattgctctc catcccaagg 300 ctgcagtgag ttgcccttca aagtaatgct gggacctgct ttttttccag tttggacatt 360 gccttattat atgttcaatg tcatttcact ggagcagaaa gttagtgaag tcaactttat 420 gccaggtctt tgtattttac caaaaggaaa tttcactatt aaataaccca gttgccattt 480 ctgagtcctg attctactgt tctaaatttt tcaagtgatc tttttttatt tctgggacac 540 ttgcatacct aattgtcaag tttaatttat gatcctcgtt actctctaag tgtttaattg 600 agttagtggt tatagctgac tcataaaccc ataaaaccct tcactggtaa actaattagc 660 cactgcacct gccctttaaa taattaacat tgttcattac taacaatcgg catcggagtt 720 attaaaagtt accttactgc tcagttgtct agaggctttc aaacttttt gatcatgatc 780 cagagtaaaa aatgcatttc acaggccaac tcaggataca cacacacaca cacacactcc 840 cctactatct atcagactct gatattttct attctattat tctctatctt ctttcattta 900 aaaatgtatt gacttactaa agaggttttt cagcttaaaa atttttattt agaccaattc 960 atggggtact catgcaattt tgttacatgt atacaatgca tagtgatcaa gtcagggtgt 1020 ttagggtgtt tattactcga gtacaataca tgttttgaaa ctatagtcac cctactctgt 1080 tgcaaacgtt gaatatattc ttactgtatg tttgtatcct ttaatccact tttctttatg 1140 cgctcctctc cccaccactc acccttccca gtctctgtta tctttccact ctctgtctct 1200 atgtgatcaa aatttttagc tcccacatat atgtgagaac gtgtgatatt tatcgttttg 1260 ggtctggctt atttcactaa gataatgacc ttcagtccca tccattttgg tgcaaatgac 1320 atgattttat cctttttttat ggccaaatag catttaccag ccattgaatg ggttatgaca 1380 gcttcaaaaa cactggctct cataaattca tacaatgaaa cagaatgtta aaaataatca 1440 ataaaggttt ctttcaaaat cagaacttac tcgtttcctt ccccatcata cacccatcta 1500 gtagtgccaa ttccttcata gtttgaagcc cagtaataaa cacaggcatt aatgtgcaga 1560 ataaacagca agtatccagt tgttcgaata actctgtcag agagaataga tgcaaagtaa 1620 gattcatgtt gtttctgaaa tacagcctat tttaacattt tcttttcctt aaagtcacca 1680 gcgaacccct tgctttggat ttgtgaactg ttaactctca ttagtacagt acaaagtgat 1740 ggtgccattg catgttttct gatggcaatg tcttgactgg gattgacaga gtgtaaagaa 1800 aaaaaaaaga aaaagaaaac ttcctctctt ttcacagatg ttgtgagtca actccgtgaa 1860 agacatgcct caaaggtcac ttcttcagtt taagtcccat aaaatacact atgctaattt 1920 aactggatat ctctgaaaag ctcatgagac tttatgctac gatgaatggc aactagaggt 1980 ttcggtgcaa gtaaaattta gaacaacaaa cgaatgaaat tcagattagg aatgaattat 2040 catgagaaag gtttaaagtt aacttgcaaa agagtatgtt tttctgtact tgttttgaca 2100 gaggcagata ataagtccta ttttcttagt ccagtattct aaaatctgat atgattttca 2160 tactcttatt tcacttaaaa tatccacatc tgttctagaa catagtccta tattttatat 2220 agccaaagct gaaattatat ccttttttg aagaggggg tcatatccct gccaaattcc 2280 gtctaaaatg ttgtaccatt gctttttccc cttcccccaa gtatactgag ttatacttta 2340 cctgtagata tatgctttgt ccattataga ctctaggtga tgattaaatt caaaaaatga 2400

		agtgtactat atagaaaagc aaaagaaatc caaaagcatg ttagtcttaa atatatatat ttaaataaaa ctatatgaaa tagattttat tactgaaaat	2460 2500
3-127	**Sequences**		
3-127-1	Sequence Number [ID]	127	
3-127-2	Molecule Type	DNA	
3-127-3	Length	30	
3-127-4	Features	**source 1..30**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-127-5	Residues	ccaccattct gcagagccag cagaggcagg	30
3-128	**Sequences**		
3-128-1	Sequence Number [ID]	128	
3-128-2	Molecule Type	RNA	
3-128-3	Length	20	
3-128-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..20	
		mol_type=other RNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-128-5	Residues	ccattctgca gagccagcag	20
3-129	**Sequences**		
3-129-1	Sequence Number [ID]	129	
3-129-2	Molecule Type	DNA	
3-129-3	Length	23	
3-129-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-129-5	Residues	ccattctgca gagccagcag agg	23
3-130	**Sequences**		
3-130-1	Sequence Number [ID]	130	
3-130-2	Molecule Type	DNA	
3-130-3	Length	24	
3-130-4	Features	**source 1..24**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-130-5	Residues	ccattctgca gagccagagg cagg	24
3-131	**Sequences**		
3-131-1	Sequence Number [ID]	131	
3-131-2	Molecule Type	DNA	
3-131-3	Length	21	
3-131-4	Features	**source 1..21**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-131-5	Residues	ccattctgca gagcccagag g	21
3-132	**Sequences**		
3-132-1	Sequence Number [ID]	132	
3-132-2	Molecule Type	DNA	
3-132-3	Length	22	
3-132-4	Features	**source 1..22**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-132-5	Residues	ccattctgca gagccagaga gg	22
3-133	**Sequences**		
3-133-1	Sequence Number [ID]	133	
3-133-2	Molecule Type	DNA	
3-133-3	Length	19	
3-133-4	Features	**source 1..19**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-133-5	Residues	ccattctgca gagcagagg	19
3-134	**Sequences**		

3-134-1	Sequence Number [ID]	134	
3-134-2	Molecule Type	DNA	
3-134-3	Length	22	
3-134-4	Features	**source 1..22**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-134-5	Residues	ccattctgca gagccccaga gg	22
3-135	**Sequences**		
3-135-1	Sequence Number [ID]	135	
3-135-2	Molecule Type	DNA	
3-135-3	Length	25	
3-135-4	Features	**source 1..25**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-135-5	Residues	ccattctgca gagccaggag gcagg	25
3-136	**Sequences**		
3-136-1	Sequence Number [ID]	136	
3-136-2	Molecule Type	DNA	
3-136-3	Length	67	
3-136-4	Features	**modified_base 18..61**	
	Location/Qualifiers	mod_base=OTHER	
		note=a, c, t, g, unknown or other	
		source 1..67	
		mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-136-5	Residues	ccattctgca gagccagnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn ncagagg	60 67
3-137	**Sequences**		
3-137-1	Sequence Number [ID]	137	
3-137-2	Molecule Type	DNA	
3-137-3	Length	55	
3-137-4	Features	**modified_base 18..52**	
	Location/Qualifiers	mod_base=OTHER	
		note=a, c, t, g, unknown or other	
		source 1..55	
		mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-137-5	Residues	ccattctgca gagccagnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnagg	55
3-138	**Sequences**		
3-138-1	Sequence Number [ID]	138	
3-138-2	Molecule Type	DNA	
3-138-3	Length	23	
3-138-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-138-5	Residues	ccattctgca gagccagaag agg	23
3-139	**Sequences**		
3-139-1	Sequence Number [ID]	139	
3-139-2	Molecule Type	DNA	
3-139-3	Length	25	
3-139-4	Features	**source 1..25**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-139-5	Residues	ccattctgca gagccagcac agagg	25
3-140	**Sequences**		
3-140-1	Sequence Number [ID]	140	
3-140-2	Molecule Type	DNA	
3-140-3	Length	22	
3-140-4	Features	**source 1..22**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		

3-140-5	Residues	ccattctgca gagccacaga gg	22
3-141	**Sequences**		
3-141-1	Sequence Number [ID]	141	
3-141-2	Molecule Type	DNA	
3-141-3	Length	24	
3-141-4	Features	**source 1..24**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-141-5	Residues	ccattctgca gagccagtca gagg	24
3-142	**Sequences**		
3-142-1	Sequence Number [ID]	142	
3-142-2	Molecule Type	RNA	
3-142-3	Length	18	
3-142-4	Features	**misc_feature 1..18**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..18	
		mol_type=other RNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-142-5	Residues	ttggcatggt gctgacgg	18
3-143	**Sequences**		
3-143-1	Sequence Number [ID]	143	
3-143-2	Molecule Type	DNA	
3-143-3	Length	30	
3-143-4	Features	**source 1..30**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-143-5	Residues	ccagcctccg tcagcgaccc atgccaagac	30
3-144	**Sequences**		
3-144-1	Sequence Number [ID]	144	
3-144-2	Molecule Type	RNA	
3-144-3	Length	20	
3-144-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..20	
		mol_type=other RNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-144-5	Residues	cgggctggag ctgttcgcgc	20
3-145	**Sequences**		
3-145-1	Sequence Number [ID]	145	
3-145-2	Molecule Type	DNA	
3-145-3	Length	30	
3-145-4	Features	**source 1..30**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-145-5	Residues	gatgccagcg cgaacagctc cagcccgagt	30
3-146	**Sequences**		
3-146-1	Sequence Number [ID]	146	
3-146-2	Molecule Type	DNA	
3-146-3	Length	30	
3-146-4	Features	**source 1..30**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-146-5	Residues	agaagagggt gccagcgggt atgaggagtg	30
3-147	**Sequences**		
3-147-1	Sequence Number [ID]	147	
3-147-2	Molecule Type	RNA	
3-147-3	Length	20	
3-147-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..20	
		mol_type=other RNA	
		organism=synthetic construct	

	NonEnglishQualifier Value		
3-147-5	Residues	agagggtgcc agcgggtatg	20
3-148	**Sequences**		
3-148-1	Sequence Number [ID]	148	
3-148-2	Molecule Type	DNA	
3-148-3	Length	23	
3-148-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-148-5	Residues	ctgggagagg gagcccctcc agg	23
3-149	**Sequences**		
3-149-1	Sequence Number [ID]	149	
3-149-2	Molecule Type	DNA	
3-149-3	Length	23	
3-149-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-149-5	Residues	aaaggtggga gacacctcct tgg	23
3-150	**Sequences**		
3-150-1	Sequence Number [ID]	150	
3-150-2	Molecule Type	DNA	
3-150-3	Length	23	
3-150-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-150-5	Residues	tccaaccttc aggcaaggtg ggg	23
3-151	**Sequences**		
3-151-1	Sequence Number [ID]	151	
3-151-2	Molecule Type	DNA	
3-151-3	Length	23	
3-151-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-151-5	Residues	aggaagtctg gccgatctgc tgg	23
3-152	**Sequences**		
3-152-1	Sequence Number [ID]	152	
3-152-2	Molecule Type	DNA	
3-152-3	Length	23	
3-152-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-152-5	Residues	ctctgaggcc ctggagatcc tgg	23
3-153	**Sequences**		
3-153-1	Sequence Number [ID]	153	
3-153-2	Molecule Type	DNA	
3-153-3	Length	23	
3-153-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-153-5	Residues	ttggcatggg tcgctgacgg agg	23
3-154	**Sequences**		
3-154-1	Sequence Number [ID]	154	
3-154-2	Molecule Type	DNA	
3-154-3	Length	23	
3-154-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-154-5	Residues	cgggctggag ctgttcgcgc tgg	23
3-155	**Sequences**		
3-155-1	Sequence Number [ID]	155	
3-155-2	Molecule Type	DNA	

3-155-3	Length	23	
3-155-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-155-5	Residues	agagggtgcc agcgggtatg agg	23
3-156	**Sequences**		
3-156-1	Sequence Number [ID]	156	
3-156-2	Molecule Type	DNA	
3-156-3	Length	23	
3-156-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-156-5	Residues	cctccgtcag cgacccatgc caa	23
3-157	**Sequences**		
3-157-1	Sequence Number [ID]	157	
3-157-2	Molecule Type	DNA	
3-157-3	Length	24	
3-157-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-157-5	Residues	cctccgatca gcgacccatg ccaa	24
3-158	**Sequences**		
3-158-1	Sequence Number [ID]	158	
3-158-2	Molecule Type	DNA	
3-158-3	Length	25	
3-158-4	Features	**misc_feature 1..25**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..25	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-158-5	Residues	cctccgtgtc agcgacccat gccaa	25
3-159	**Sequences**		
3-159-1	Sequence Number [ID]	159	
3-159-2	Molecule Type	DNA	
3-159-3	Length	24	
3-159-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-159-5	Residues	cctccgttca gcgacccatg ccaa	24
3-160	**Sequences**		
3-160-1	Sequence Number [ID]	160	
3-160-2	Molecule Type	DNA	
3-160-3	Length	24	
3-160-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-160-5	Residues	cctccgctca gcgacccatg ccaa	24
3-161	**Sequences**		
3-161-1	Sequence Number [ID]	161	
3-161-2	Molecule Type	DNA	
3-161-3	Length	22	
3-161-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..22	

		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-161-5	Residues	cctcctcagc gacccatgcc aa	22
3-162	**Sequences**		
3-162-1	Sequence Number [ID]	162	
3-162-2	Molecule Type	DNA	
3-162-3	Length	22	
3-162-4	Features	**misc_feature 1..22**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..22	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-162-5	Residues	cctccgcagc gacccatgcc aa	22
3-163	**Sequences**		
3-163-1	Sequence Number [ID]	163	
3-163-2	Molecule Type	DNA	
3-163-3	Length	21	
3-163-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-163-5	Residues	cctctcagcg acccatgcca a	21
3-164	**Sequences**		
3-164-1	Sequence Number [ID]	164	
3-164-2	Molecule Type	DNA	
3-164-3	Length	19	
3-164-4	Features	**misc_feature 1..19**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..19	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-164-5	Residues	cctccgcgac ccatgccaa	19
3-165	**Sequences**		
3-165-1	Sequence Number [ID]	165	
3-165-2	Molecule Type	DNA	
3-165-3	Length	19	
3-165-4	Features	**misc_feature 1..19**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..19	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-165-5	Residues	cctcagcgac ccatgccaa	19
3-166	**Sequences**		
3-166-1	Sequence Number [ID]	166	
3-166-2	Molecule Type	DNA	
3-166-3	Length	18	
3-166-4	Features	**misc_feature 1..18**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..18	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-166-5	Residues	ctcagcgacc catgccaa	18
3-167	**Sequences**		
3-167-1	Sequence Number [ID]	167	
3-167-2	Molecule Type	DNA	
3-167-3	Length	23	
3-167-4	Features	**misc_feature 1..23**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..23	
		mol_type=other DNA	
		organism=synthetic construct	

	NonEnglishQualifier Value		
3-167-5	Residues	ccagcgcgaa cagctccagc ccg	23
3-168	**Sequences**		
3-168-1	Sequence Number [ID]	168	
3-168-2	Molecule Type	DNA	
3-168-3	Length	24	
3-168-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-168-5	Residues	ccagcgccga acagctccag cccg	24
3-169	**Sequences**		
3-169-1	Sequence Number [ID]	169	
3-169-2	Molecule Type	DNA	
3-169-3	Length	24	
3-169-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-169-5	Residues	ccagcgtcga acagctccag cccg	24
3-170	**Sequences**		
3-170-1	Sequence Number [ID]	170	
3-170-2	Molecule Type	DNA	
3-170-3	Length	21	
3-170-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-170-5	Residues	ccagcgaaca gctccagccc g	21
3-171	**Sequences**		
3-171-1	Sequence Number [ID]	171	
3-171-2	Molecule Type	DNA	
3-171-3	Length	21	
3-171-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-171-5	Residues	ccagcggaca gctccagccc g	21
3-172	**Sequences**		
3-172-1	Sequence Number [ID]	172	
3-172-2	Molecule Type	DNA	
3-172-3	Length	19	
3-172-4	Features	**misc_feature 1..19**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..19	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-172-5	Residues	ccagaacagc tccagcccg	19
3-173	**Sequences**		
3-173-1	Sequence Number [ID]	173	
3-173-2	Molecule Type	DNA	
3-173-3	Length	18	
3-173-4	Features	**misc_feature 1..18**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..18	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-173-5	Residues	ccagcgagct ccagcccg	18

3-174	**Sequences**		
3-174-1	Sequence Number [ID]	174	
3-174-2	Molecule Type	DNA	
3-174-3	Length	21	
3-174-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-174-5	Residues	ccagcgcaca gctccagccc g	21
3-175	**Sequences**		
3-175-1	Sequence Number [ID]	175	
3-175-2	Molecule Type	DNA	
3-175-3	Length	16	
3-175-4	Features	**misc_feature 1..16**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..16	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-175-5	Residues	ccagcgctcc agcccg	16
3-176	**Sequences**		
3-176-1	Sequence Number [ID]	176	
3-176-2	Molecule Type	DNA	
3-176-3	Length	24	
3-176-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-176-5	Residues	agagggtgcc agcgggttat gagg	24
3-177	**Sequences**		
3-177-1	Sequence Number [ID]	177	
3-177-2	Molecule Type	DNA	
3-177-3	Length	25	
3-177-4	Features	**misc_feature 1..25**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..25	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-177-5	Residues	agagggtgcc agcgggtata tgagg	25
3-178	**Sequences**		
3-178-1	Sequence Number [ID]	178	
3-178-2	Molecule Type	DNA	
3-178-3	Length	24	
3-178-4	Features	**misc_feature 1..24**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..24	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-178-5	Residues	agagggtgcc agcgggtaat gagg	24
3-179	**Sequences**		
3-179-1	Sequence Number [ID]	179	
3-179-2	Molecule Type	DNA	
3-179-3	Length	36	
3-179-4	Features	**modified_base 18..36**	
	Location/Qualifiers	mod_base=OTHER	
		note=a, c, t, g, unknown or other	
		misc_feature 1..36	
		note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..36	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		

3-179-5	Residues	agagggtgcc agcgggtnnn nnnnnnnnnn nnnnnn	36
3-180	**Sequences**		
3-180-1	Sequence Number [ID]	180	
3-180-2	Molecule Type	DNA	
3-180-3	Length	19	
3-180-4	Features	**misc_feature 1..19**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..19	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-180-5	Residues	agagggtgcc agtatgagg	19
3-181	**Sequences**		
3-181-1	Sequence Number [ID]	181	
3-181-2	Molecule Type	DNA	
3-181-3	Length	21	
3-181-4	Features	**misc_feature 1..21**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..21	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-181-5	Residues	agagggtgcc agcgggtgag g	21
3-182	**Sequences**		
3-182-1	Sequence Number [ID]	182	
3-182-2	Molecule Type	DNA	
3-182-3	Length	17	
3-182-4	Features	**misc_feature 1..17**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..17	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-182-5	Residues	agagggtgcc agcgagg	17
3-183	**Sequences**		
3-183-1	Sequence Number [ID]	183	
3-183-2	Molecule Type	DNA	
3-183-3	Length	20	
3-183-4	Features	**misc_feature 1..20**	
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic ol igonucleotide"	
		source 1..20	
		mol_type=other DNA	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-183-5	Residues	agagggtgcc agcggggagg	20
3-184	**Sequences**		
3-184-1	Sequence Number [ID]	184	
3-184-2	Molecule Type	DNA	
3-184-3	Length	79	
3-184-4	Features	**source 1..79**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-184-5	Residues	ctacgtgccc ttctccaatg cgacgggtgt ggtacgcagc cccttcgagt acccacagta	60
		ctacctggct gagccatgg	79
3-185	**Sequences**		
3-185-1	Sequence Number [ID]	185	
3-185-2	Molecule Type	DNA	
3-185-3	Length	79	
3-185-4	Features	**source 1..79**	
	Location/Qualifiers	mol_type=genomic DNA	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-185-5	Residues	gggcacaaac tacccagaag tgaggttcaa ccgcctactg aagttttccc ggctctttga	60
		attctttgac cgcacagag	79
3-186	**Sequences**		
3-186-1	Sequence Number [ID]	186	
3-186-2	Molecule Type	DNA	

3-186-3	Length	79
3-186-4	Features	**source 1..79**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-186-5	Residues	atgcctgtgt ttattactgg gcttcaaact atgaaggaat tggcactact agatgggtgt 60 atgatgggga aggaaacga 79
3-187	**Sequences**	
3-187-1	Sequence Number [ID]	187
3-187-2	Molecule Type	DNA
3-187-3	Length	79
3-187-4	Features	**source 1..79**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-187-5	Residues	cggcgagccg cgggcagggg ccggagcccg cgcccggagg cggggtggag ggggtcgggg 60 ctcgcggcgt cgcactgaa 79
3-188	**Sequences**	
3-188-1	Sequence Number [ID]	188
3-188-2	Molecule Type	DNA
3-188-3	Length	79
3-188-4	Features	**source 1..79**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-188-5	Residues	tcgggcctcc gaaaccatga actttctgct gtcttgggtg cattggagcc ttgccttgct 60 gctctacctc caccatgcc 79
3-189	**Sequences**	
3-189-1	Sequence Number [ID]	189
3-189-2	Molecule Type	DNA
3-189-3	Length	64
3-189-4	Features	**source 1..64**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-189-5	Residues	tttctggggt gtaaaaactc tttgattggc tgctgcacgc gcctgcccgc gccctccatt 60 ggct 64
3-190	**Sequences**	
3-190-1	Sequence Number [ID]	190
3-190-2	Molecule Type	DNA
3-190-3	Length	66
3-190-4	Features	**source 1..66**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-190-5	Residues	gagaagacac gcgaccggcg cgaggagggg gttgggagag gagcgggggg agactgagtg 60 gcgcgt 66
3-191	**Sequences**	
3-191-1	Sequence Number [ID]	191
3-191-2	Molecule Type	DNA
3-191-3	Length	66
3-191-4	Features	**source 1..66**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-191-5	Residues	agagagcatc ccgtctaccc gcctgagctg tccctcctgg acagcaccga cccacgcgcc 60 tggctg 66
3-192	**Sequences**	
3-192-1	Sequence Number [ID]	192
3-192-2	Molecule Type	DNA
3-192-3	Length	57
3-192-4	Features	**source 1..57**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-192-5	Residues	cgcgccgccc agtatttgct acattccccg gagctgggtg cctcagaggc cgctgcg 57
3-193	**Sequences**	
3-193-1	Sequence Number [ID]	193
3-193-2	Molecule Type	DNA

3-193-3	Length	120
3-193-4	Features	**misc_feature 1..120**
	Location/Qualifiers	note=source = /note="Description of Artificial Sequence: Synthetic po lynucleotide"
		source 1..120
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-193-5	Residues	aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120
3-194	**Sequences**	
3-194-1	Sequence Number [ID]	194
3-194-2	Molecule Type	AA
3-194-3	Length	6
3-194-4	Features	**MOD_RES 2**
	Location/Qualifiers	note=Aminohexanoyl
		REGION 1..6
		note=source = /note="Description of Artificial Sequence: Synthetic pe ptide"
		source 1..6
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-194-5	Residues	RXRRRR 6
3-195	**Sequences**	
3-195-1	Sequence Number [ID]	195
3-195-2	Molecule Type	DNA
3-195-3	Length	66
3-195-4	Features	**source 1..66**
	Location/Qualifiers	mol_type=genomic DNA
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-195-5	Residues	agccaatgga gggcgcgggc aggcgcgtgc gagcagccaa tcaaagagtt tttacacccc 60 gagaaa 66