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(54) **COMPOSITIONS AND METHODS FOR ANALYTE DETECTION USING BIOLUMINESCENCE**

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**Related U.S. Application Data**

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(60) Provisional application No. 62/832,052, filed on Apr. 10, 2019.

**Publication Classification**

(51) **Int. Cl.**

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*C12Q 1/66* (2006.01)

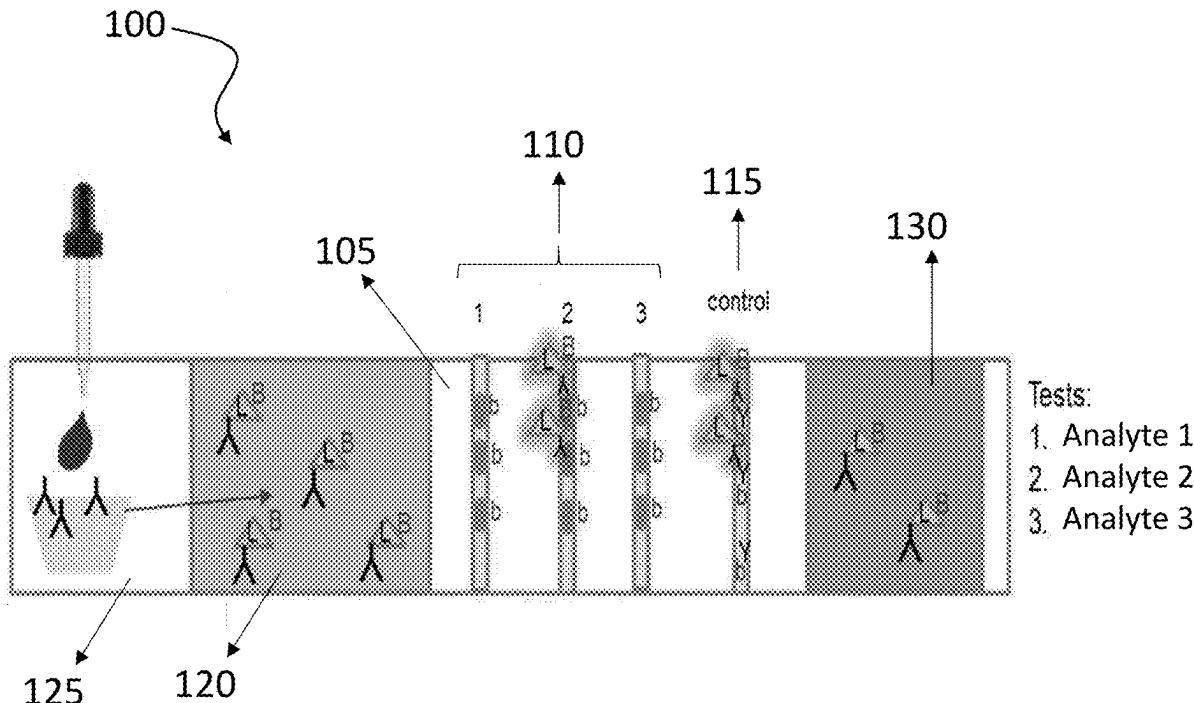
(52) **U.S. Cl.**

CPC . *G01N 33/54388* (2021.08); *G01N 33/54306* (2013.01); *G01N 33/54366* (2013.01); *C12Q 1/66* (2013.01); *C12Q 2563/103* (2013.01)

(57) **ABSTRACT**

Provided herein are systems and methods for the detection of an analyte or analytes in a sample. In particular, the present disclosure provides compositions, assays, and methods for detecting and/or quantifying a target analyte using a bioluminescent complex comprising substrates, peptides, and/or polypeptides capable of generating a bioluminescent signal that correlates to the presence, absence, or amount of the target analyte.

**Specification includes a Sequence Listing.**



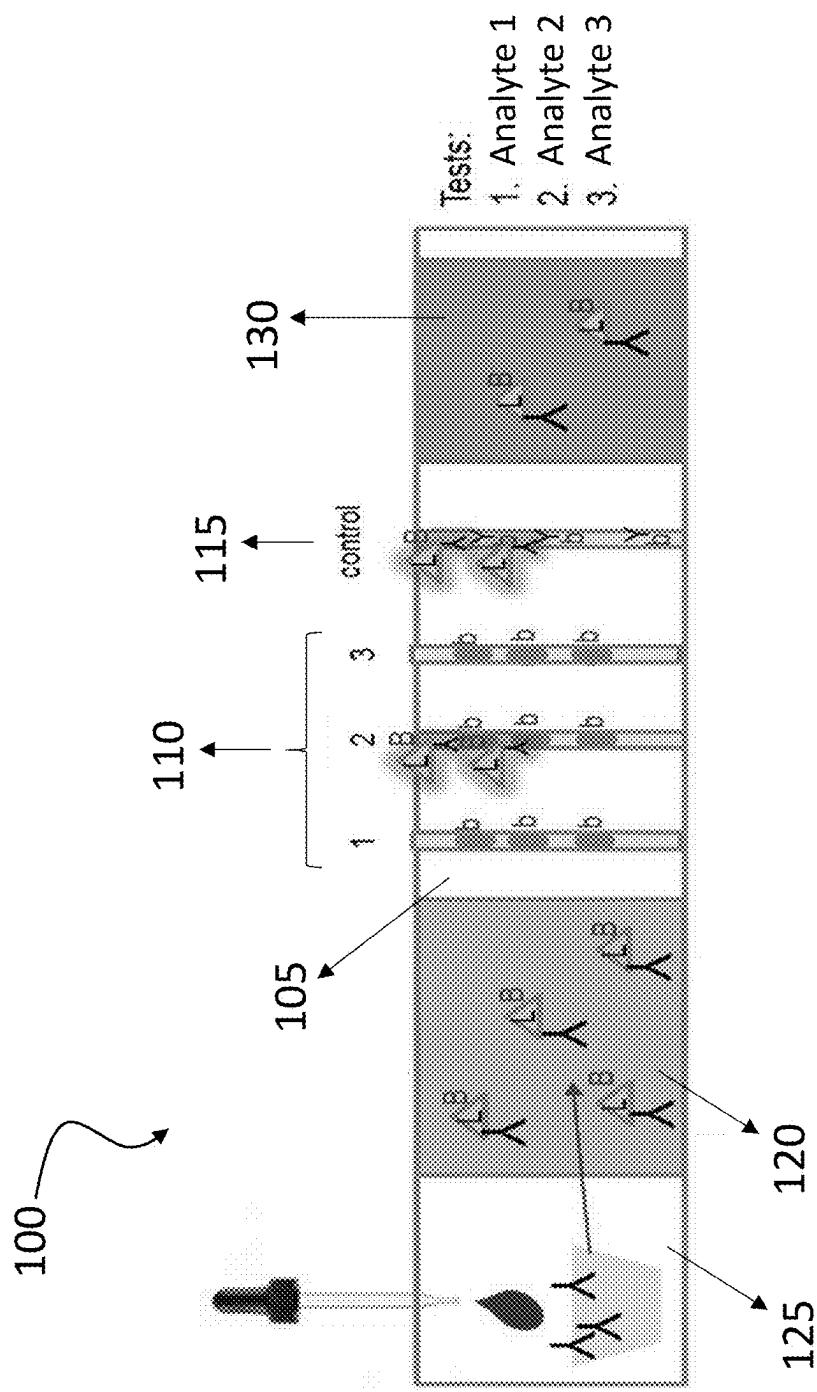


FIG. 1

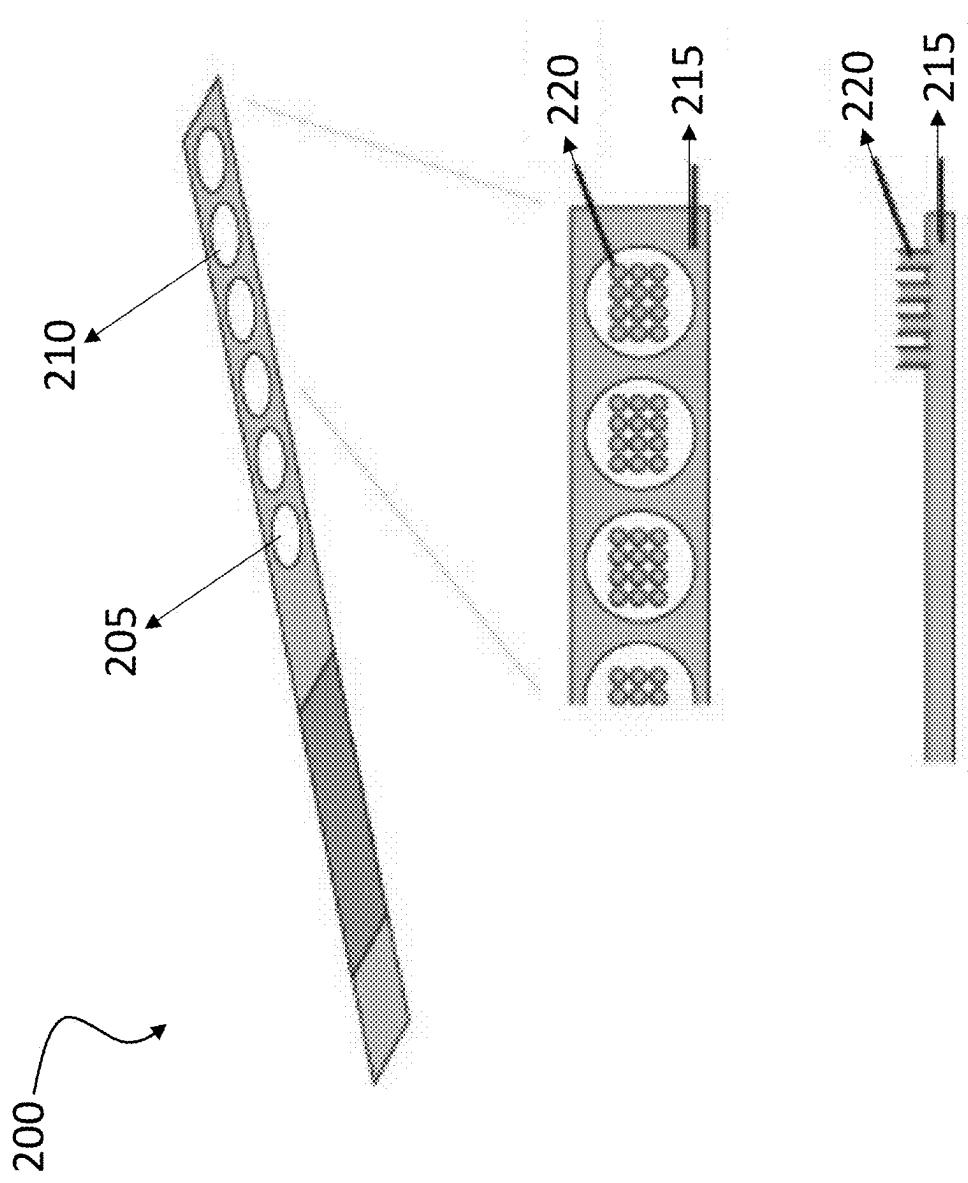


FIG. 2

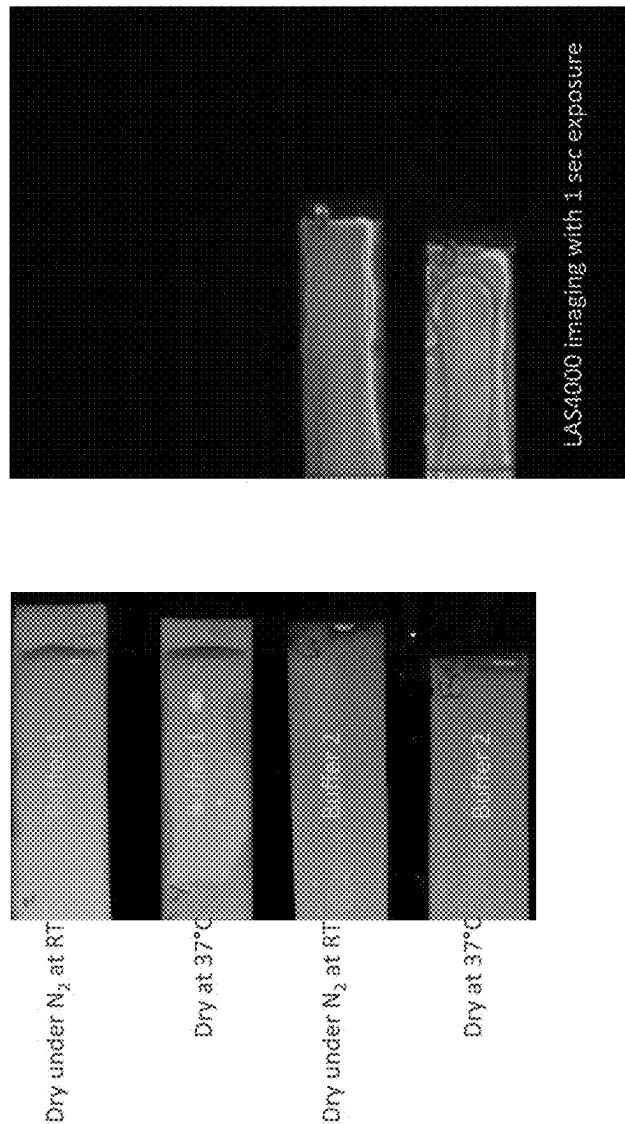


FIG. 3

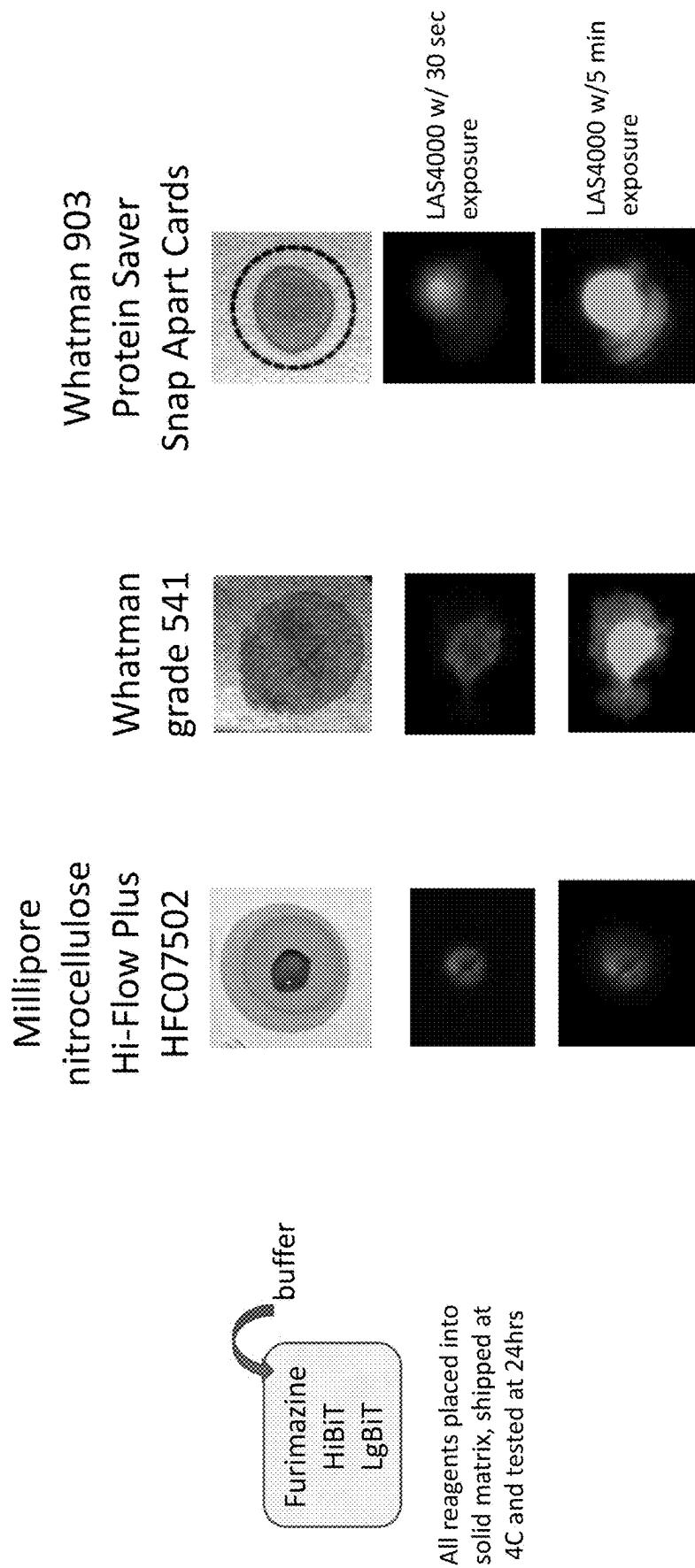
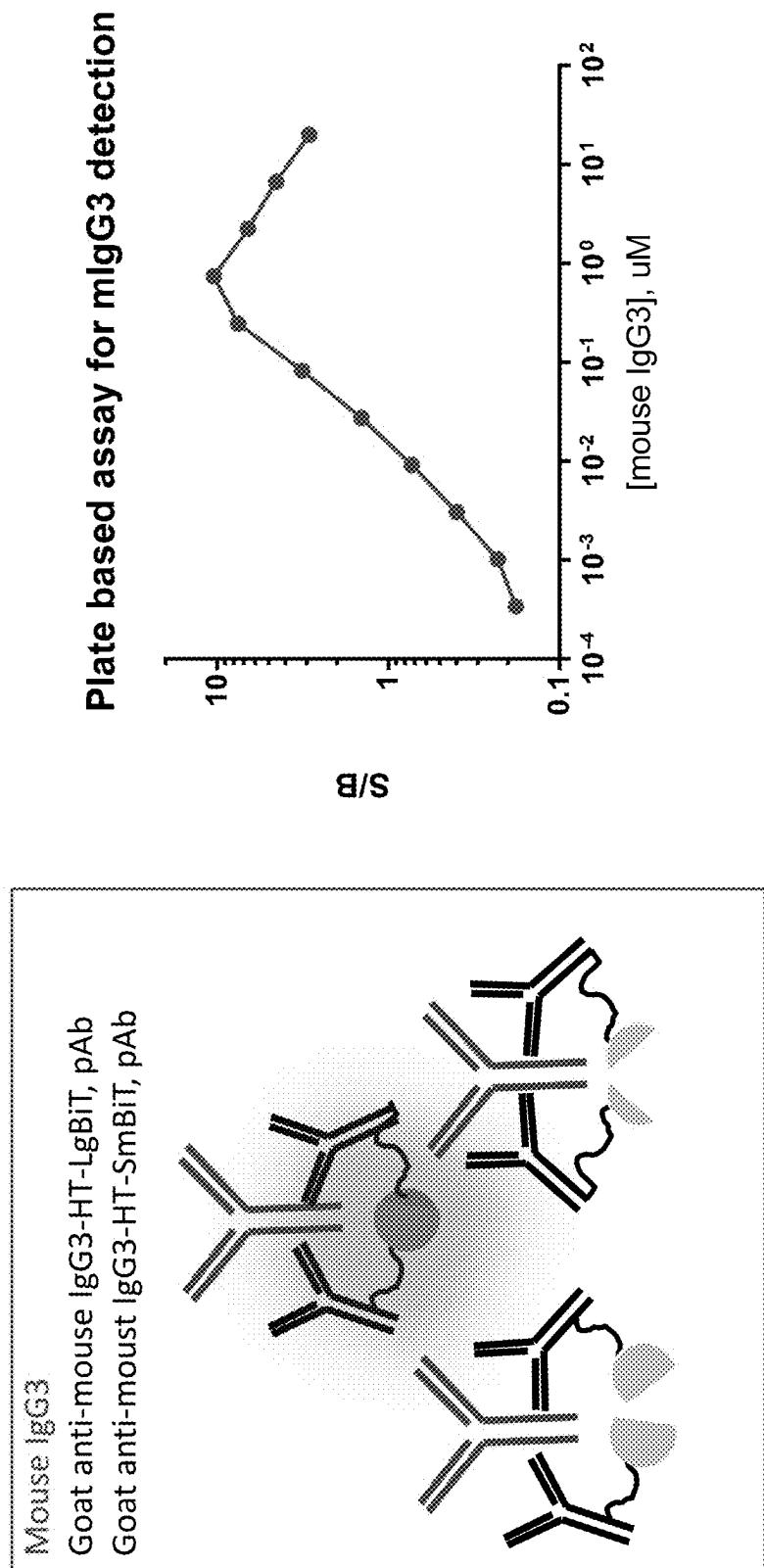


FIG. 4



**FIG. 5**

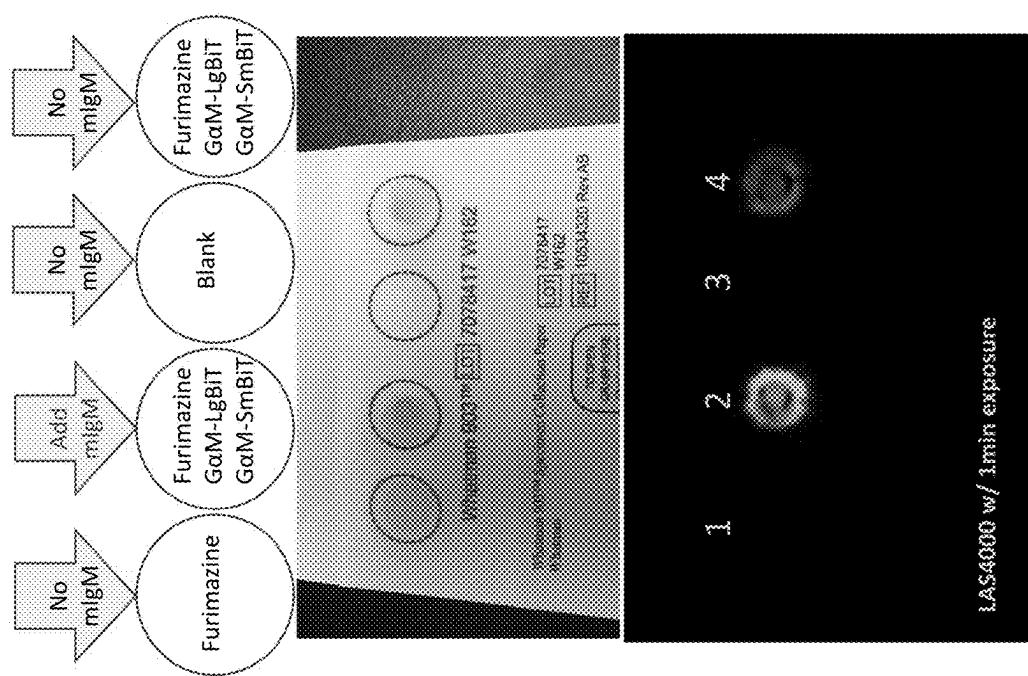


FIG. 6

6/93

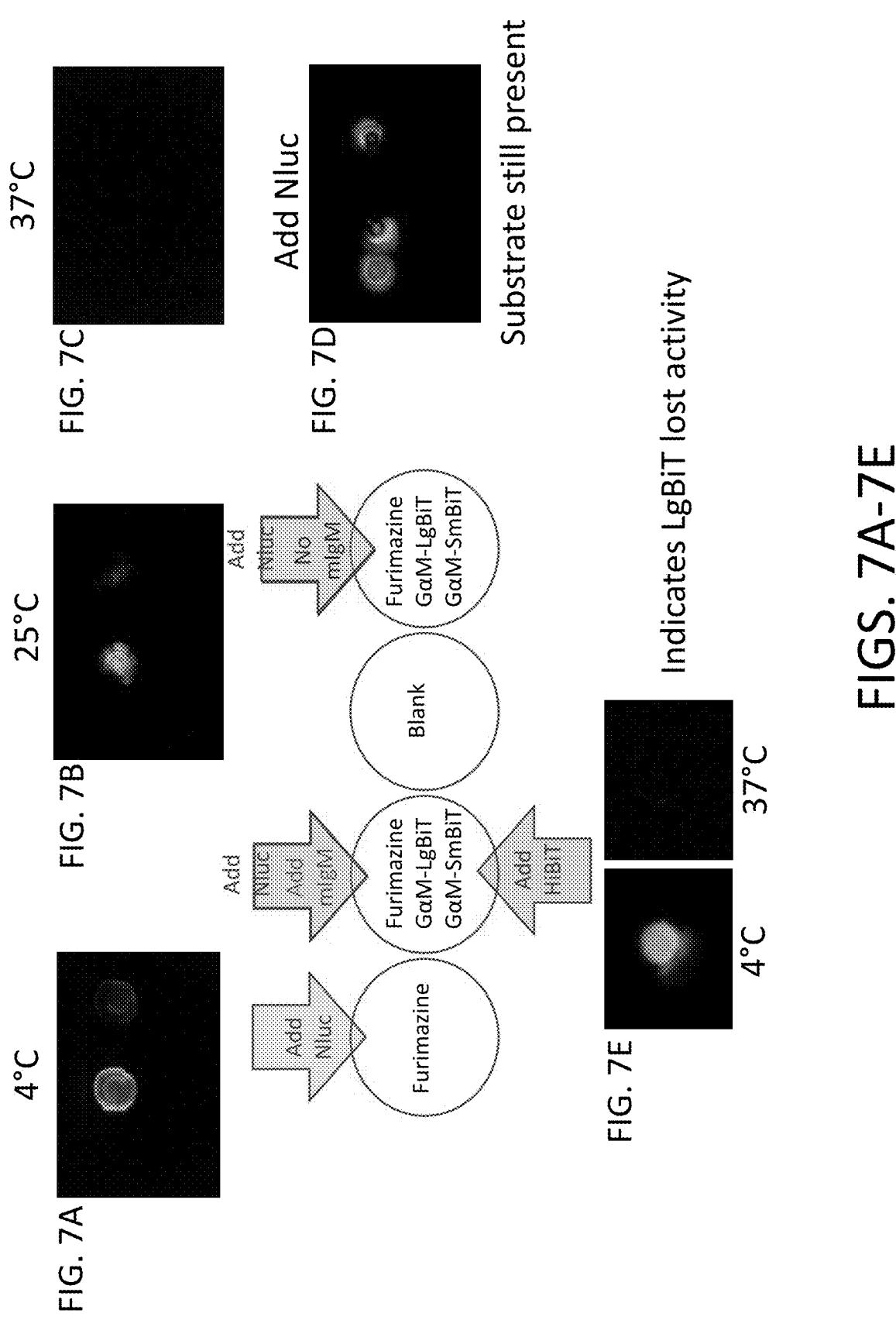


FIG. 8A

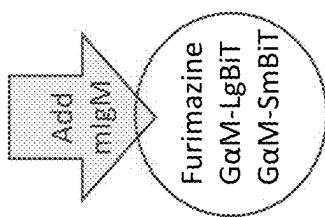


FIG. 8C

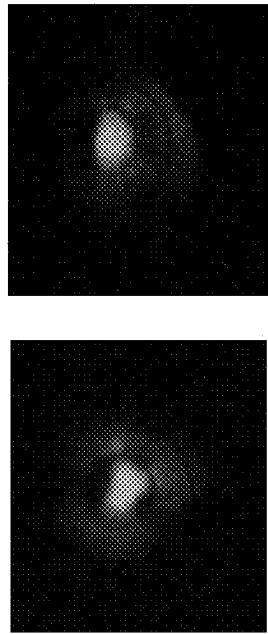
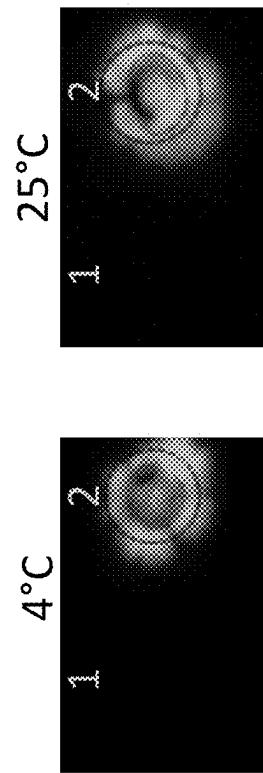
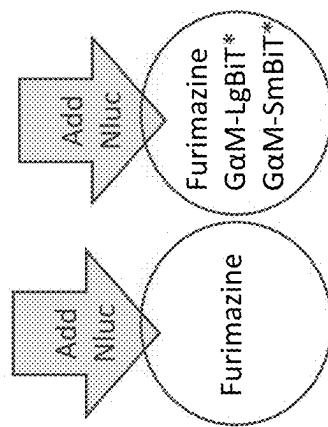


FIG. 8B



\*Conjugation buffer: 20mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 10% w/v sucrose

FIGS. 8A-8B

FIG. 9A

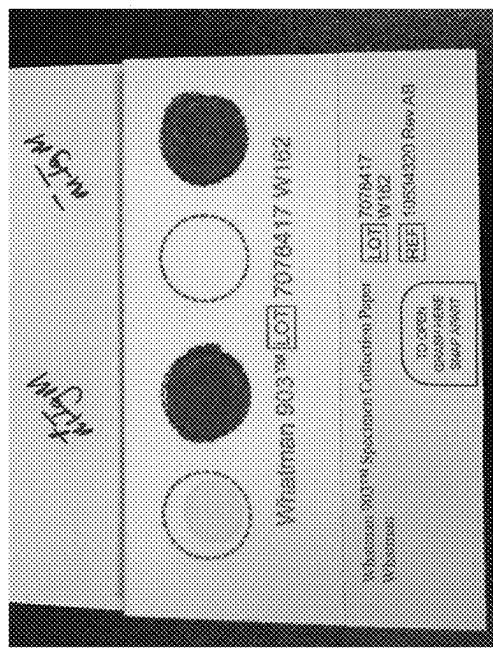


FIG. 9B

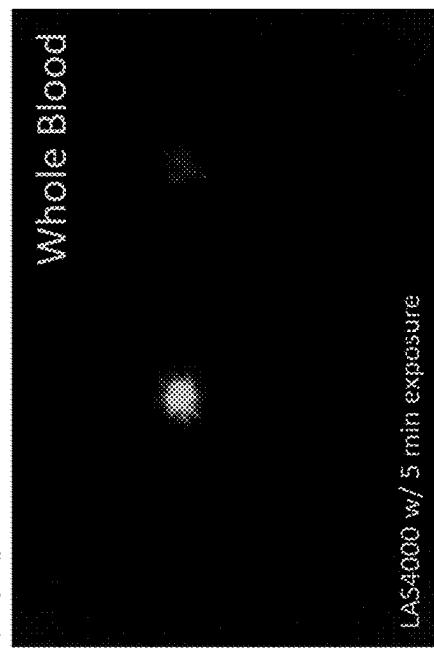
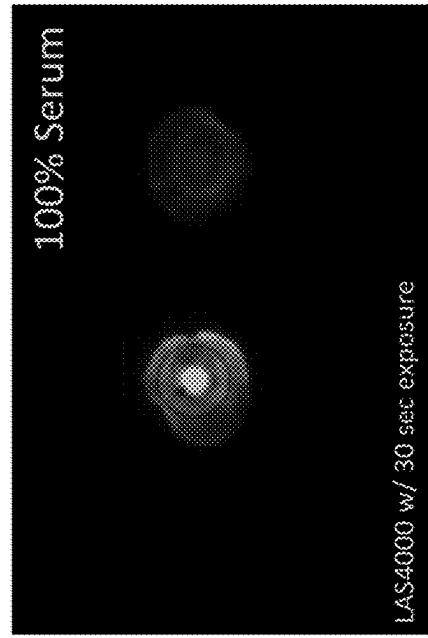


FIG. 9C



FIGS. 9A-9C

FIG. 10A

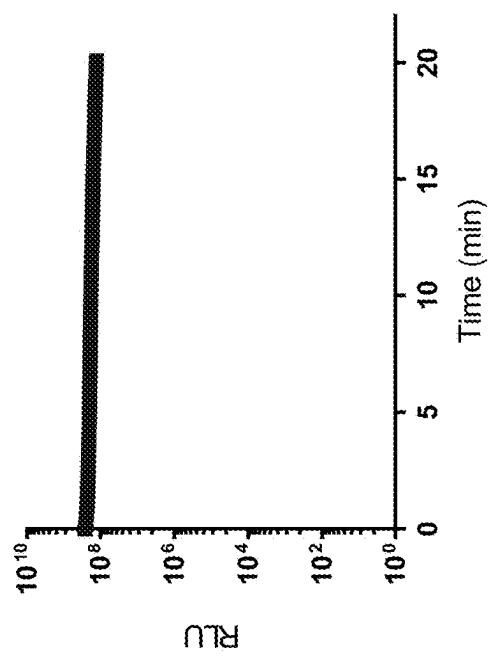
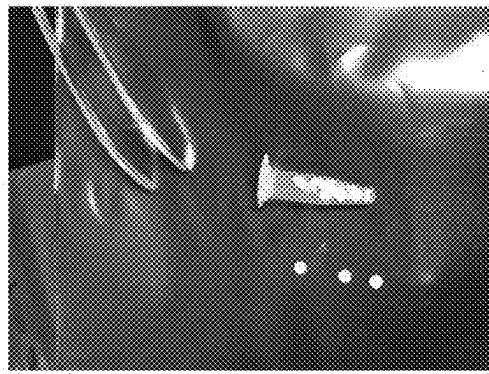
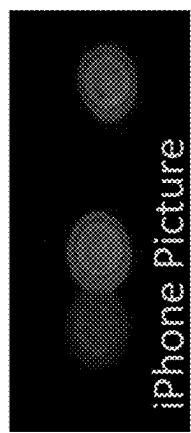
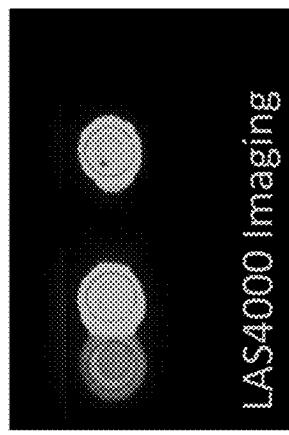


FIG. 10B



LAS4000 imaging

FIGS. 10A-10B

FIG. 11A

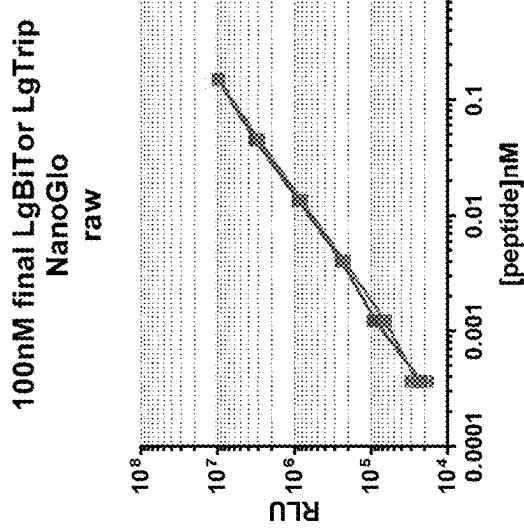
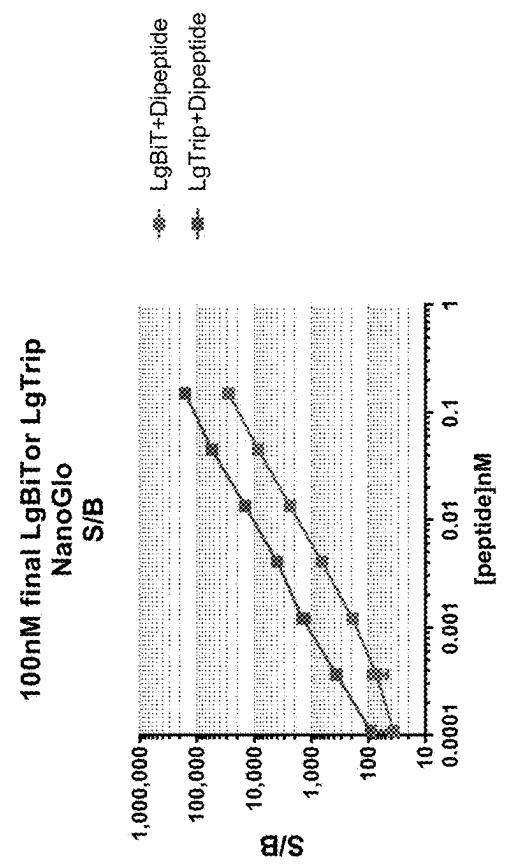


FIG. 11B



FIGS. 11A-11B

Paper punches  
containing purified  
protein in  
conjugation buffer

+/- dipeptide  
+ 50uM substrate

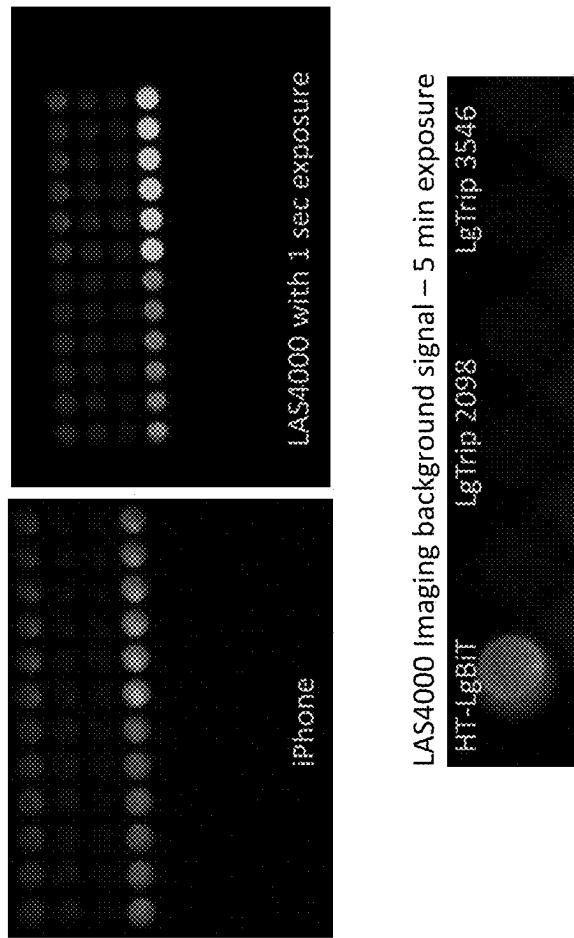
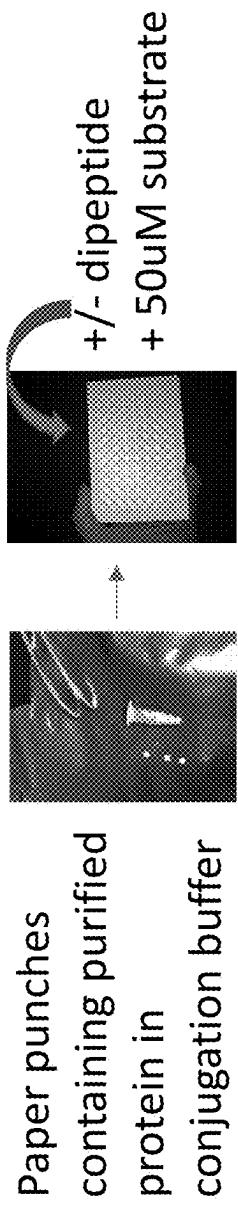
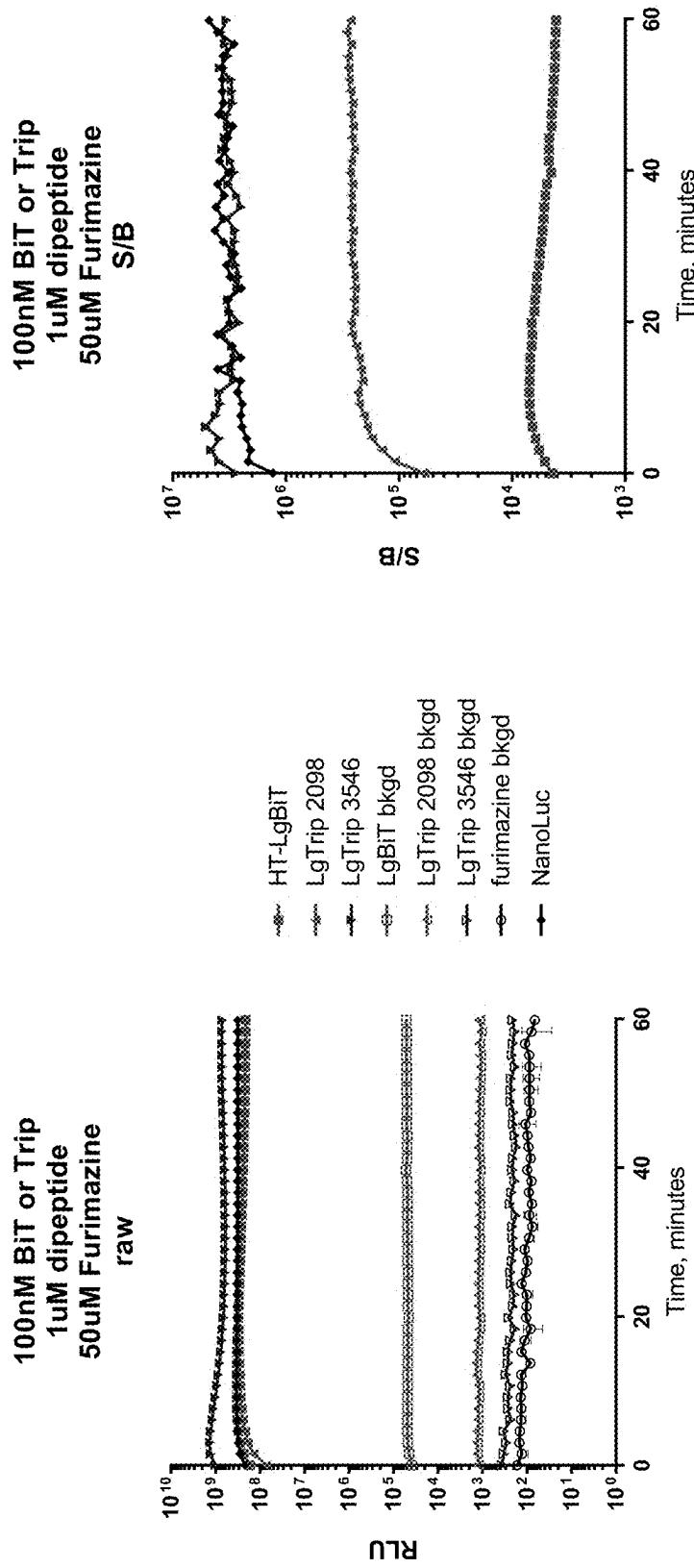


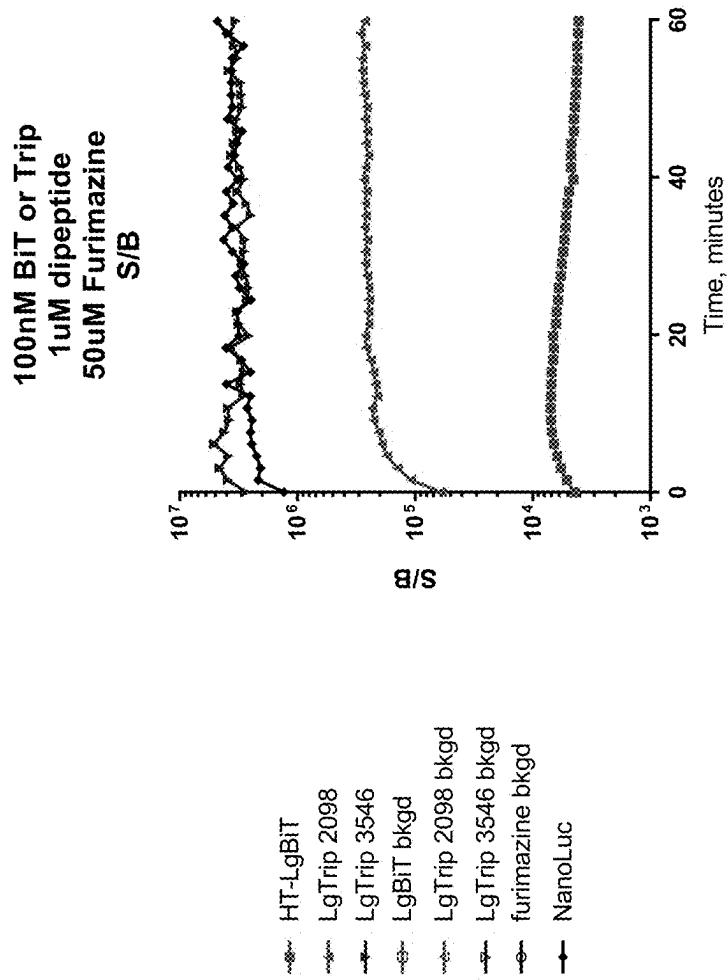
FIG. 12

FIG. 13A



Day 3 at 25°C

FIG. 13B



FIGS. 13A-13B

FIG. 14A

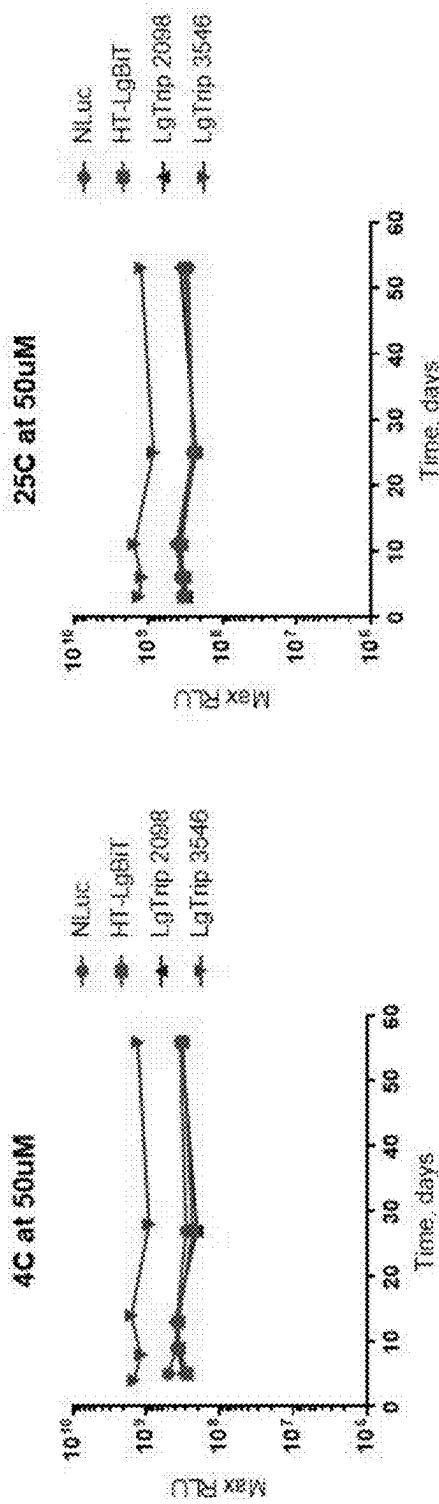
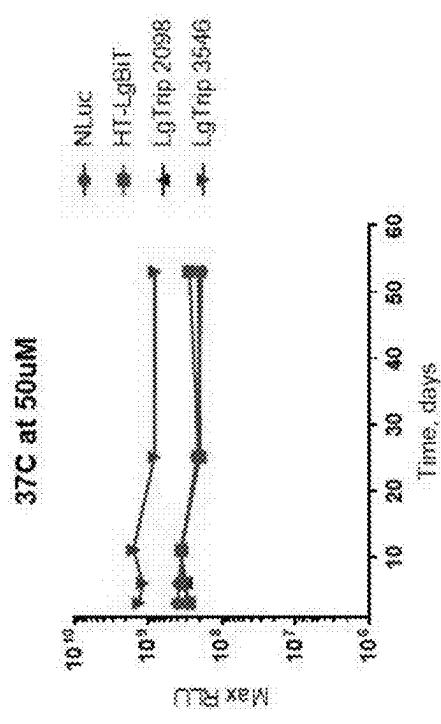
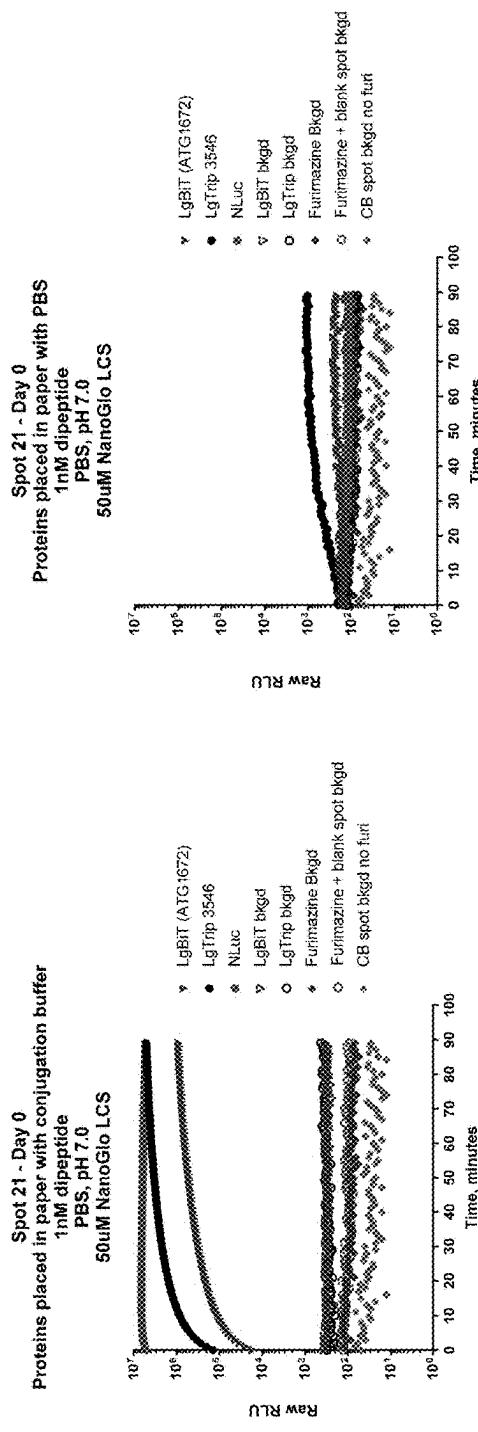


FIG. 14C

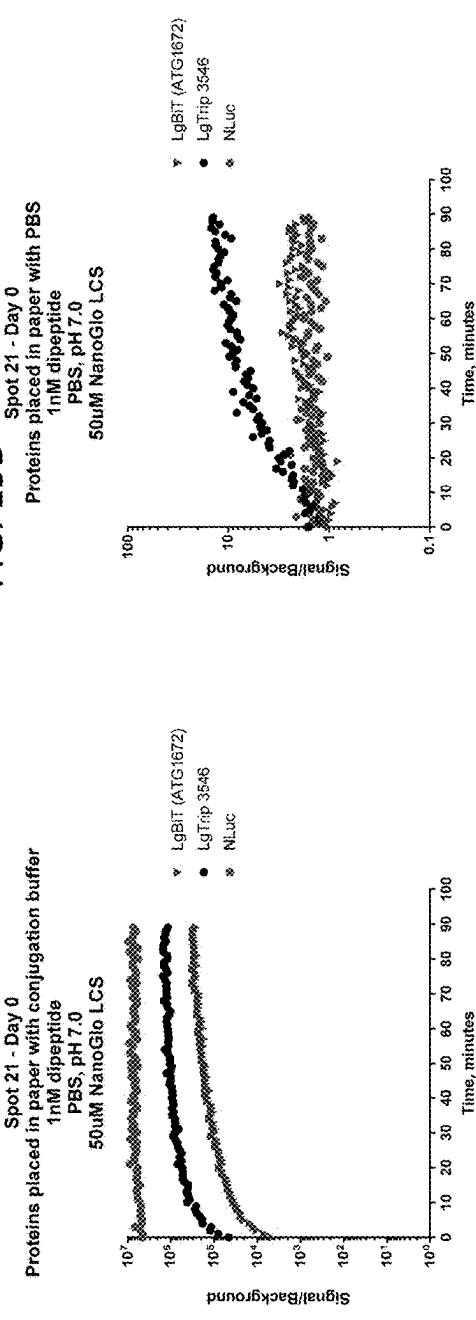


FIGS. 14A-14C

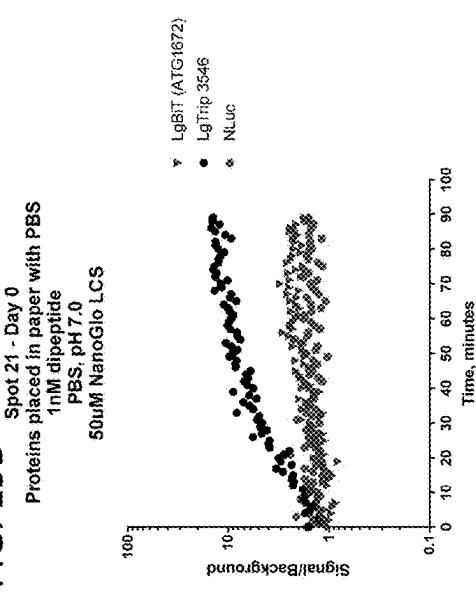
**FIG. 15A**



**FIG. 15C**



**FIG. 15D**



**FIGS. 15A-15D**

FIG. 16A

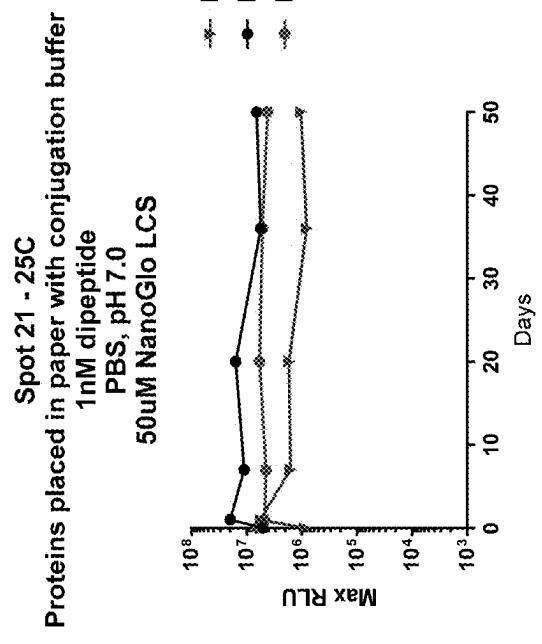
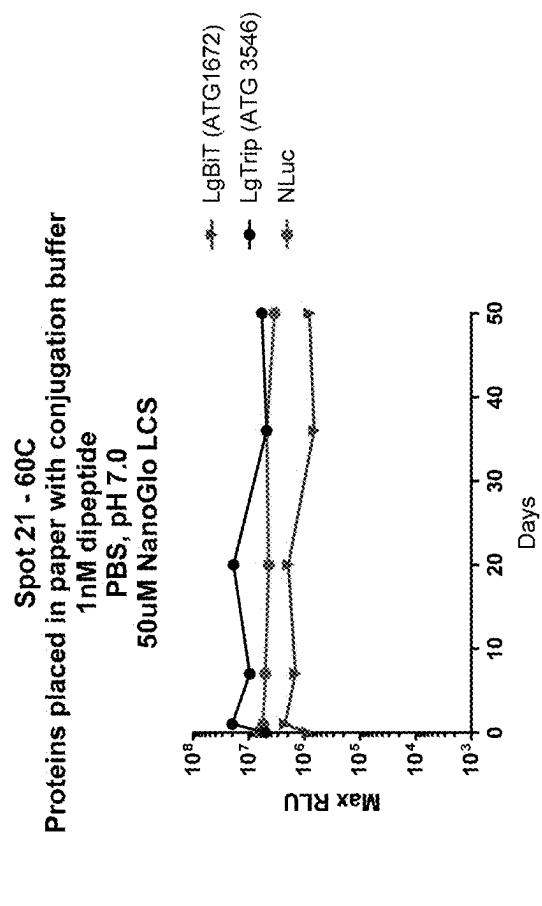


FIG. 16B



FIGS. 16A-16B

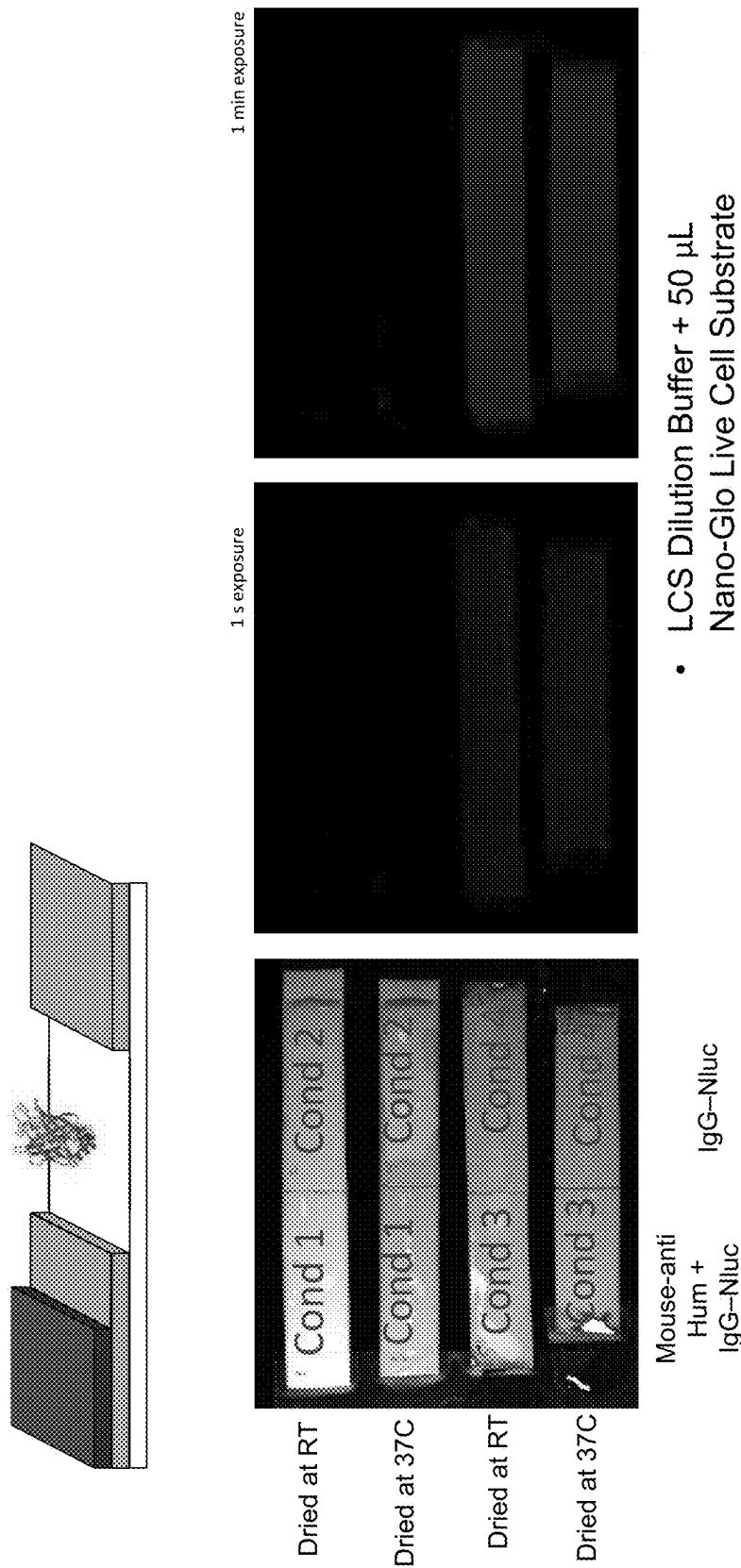
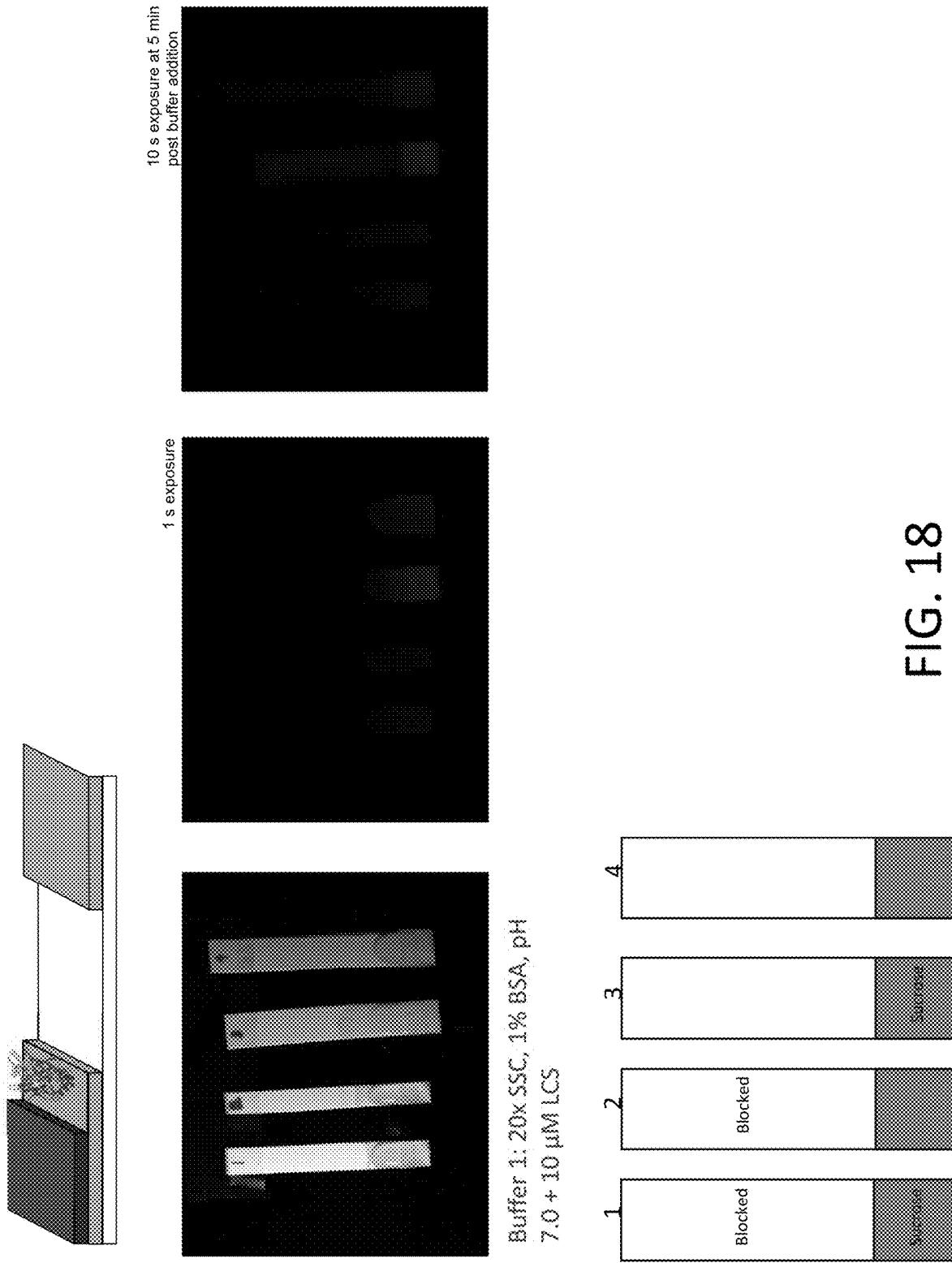


FIG. 17



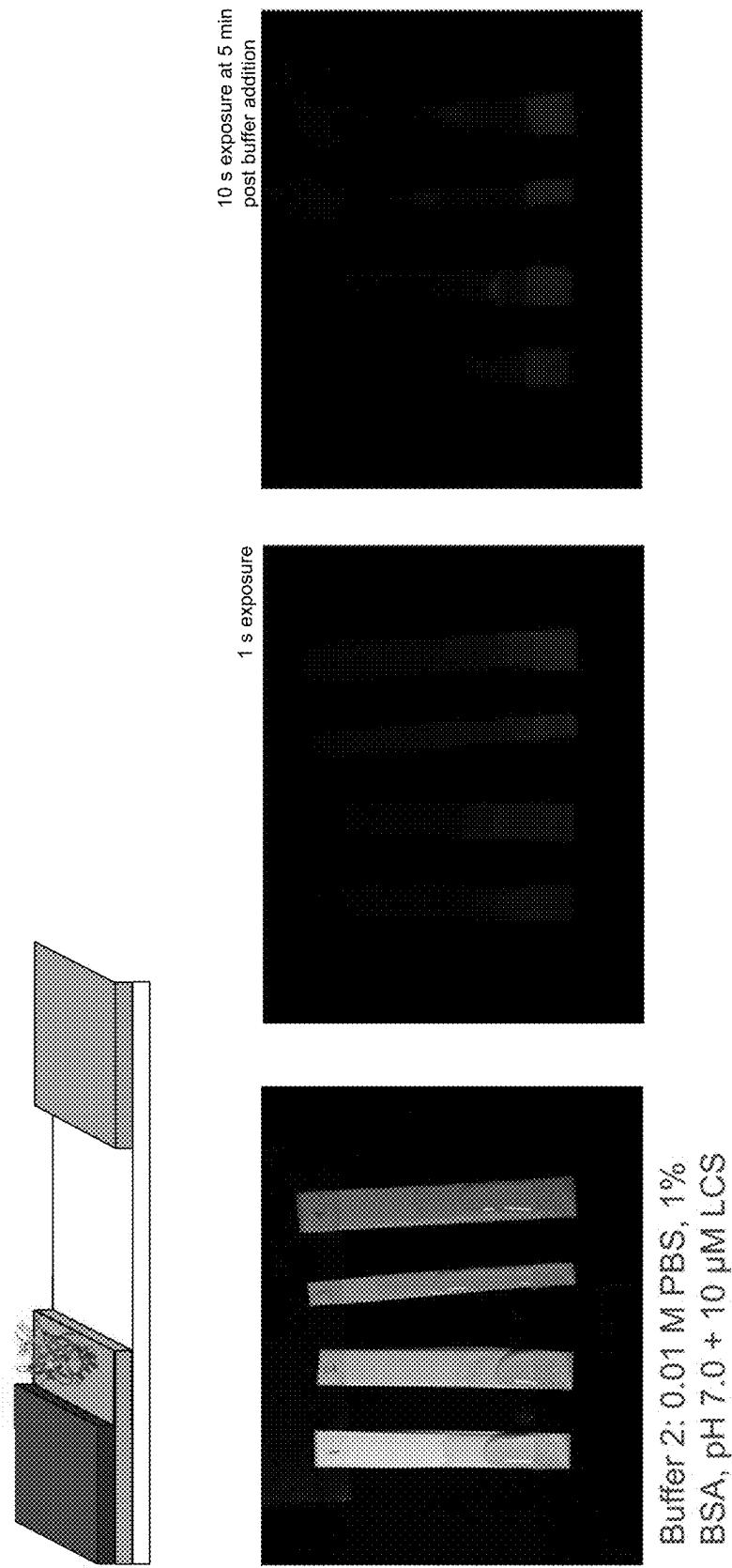


FIG. 19

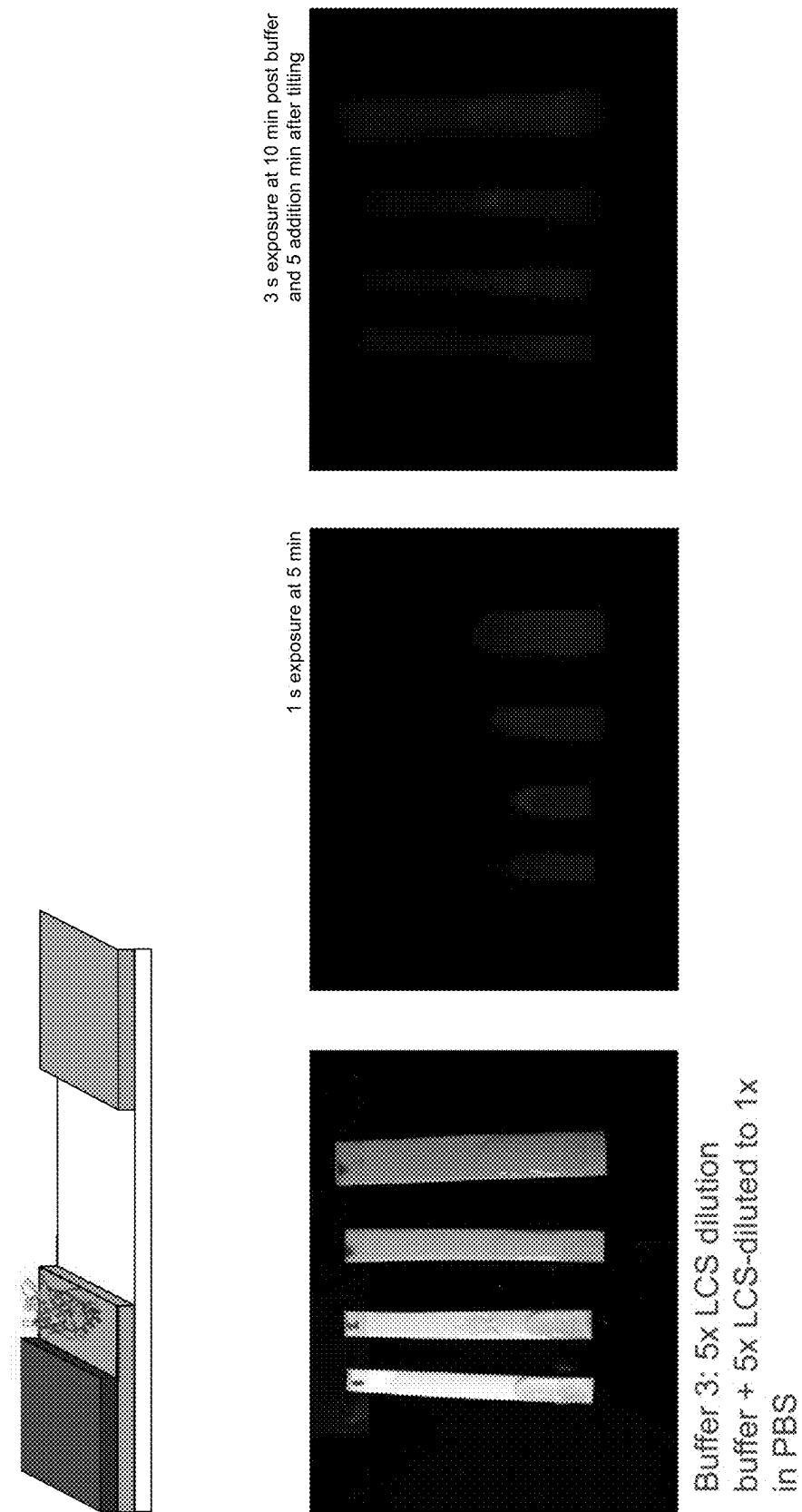


FIG. 20

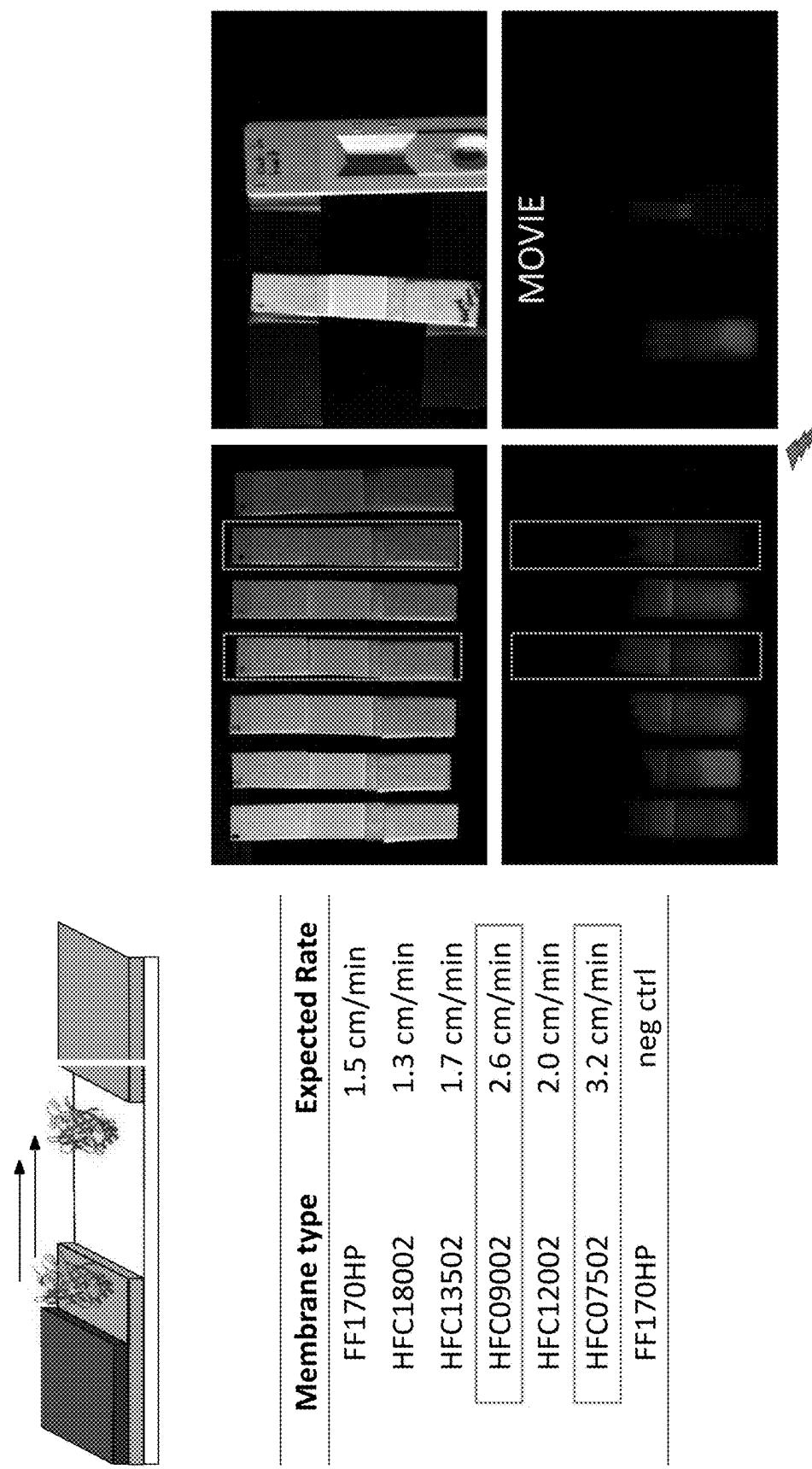


FIG. 21

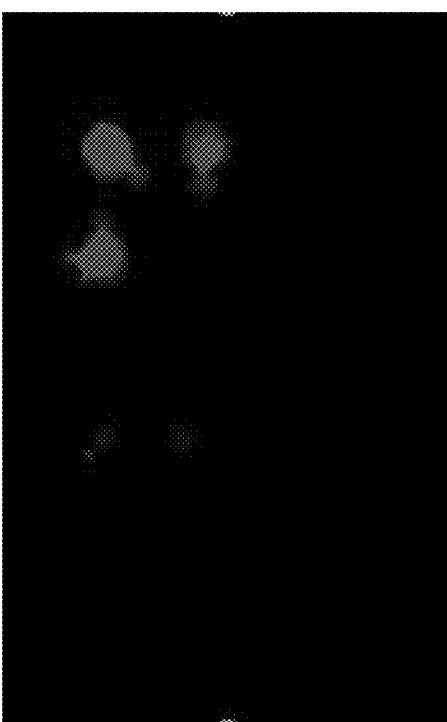
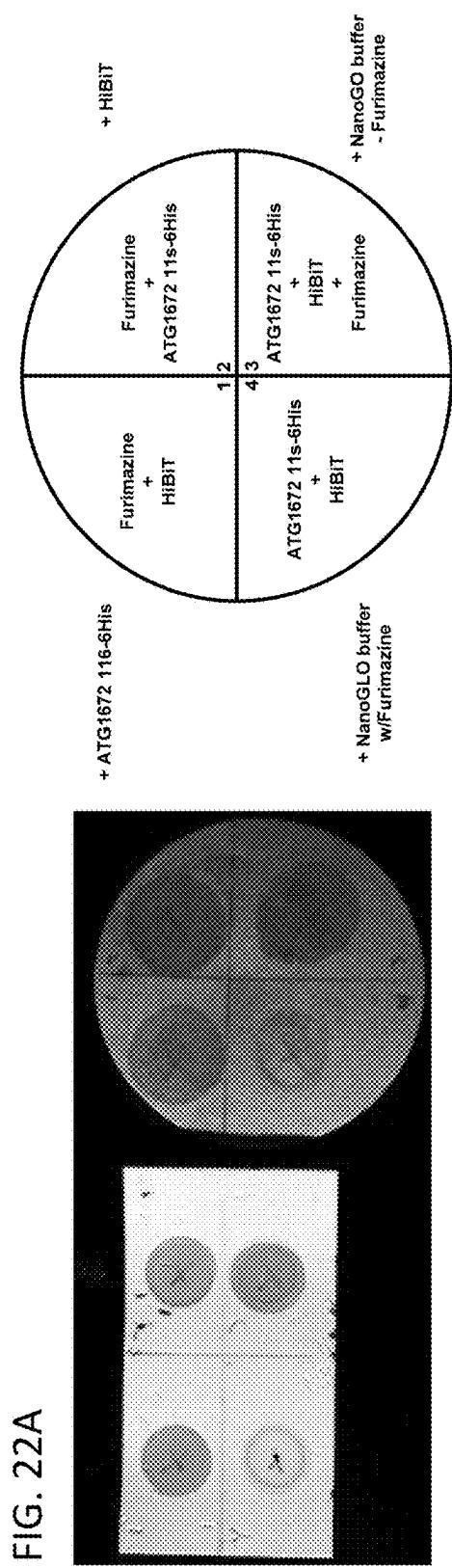


FIG. 22B

FIGS. 22A-22B

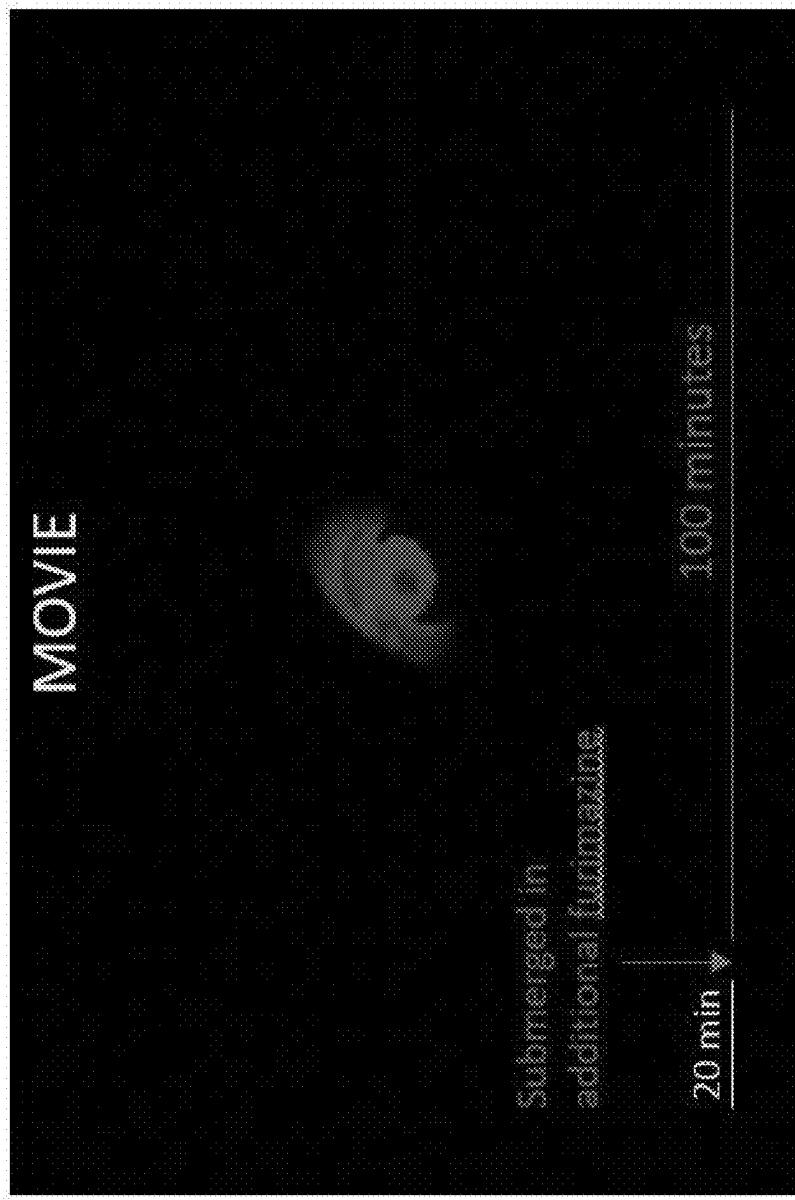


FIG. 23

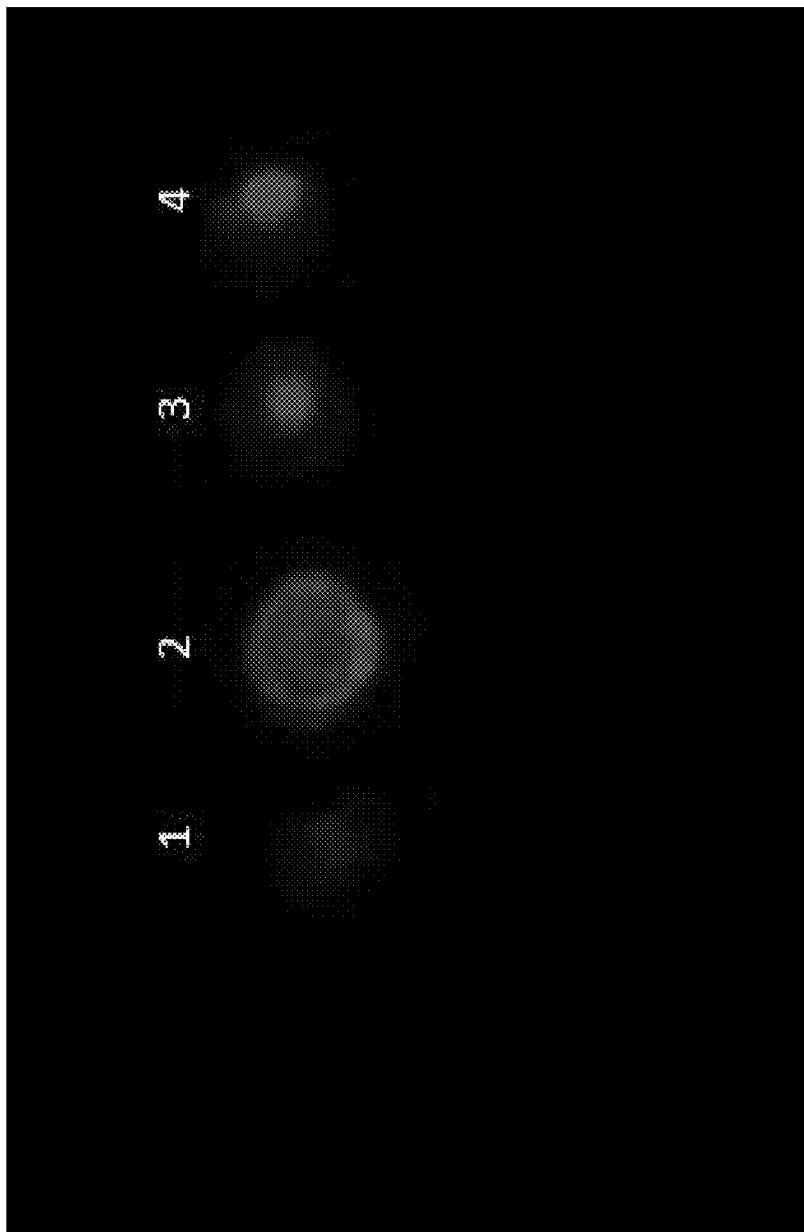
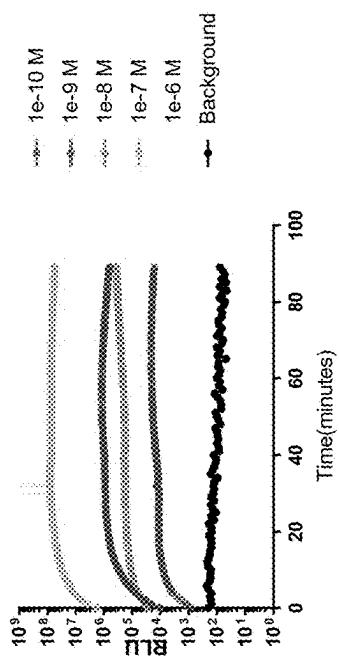
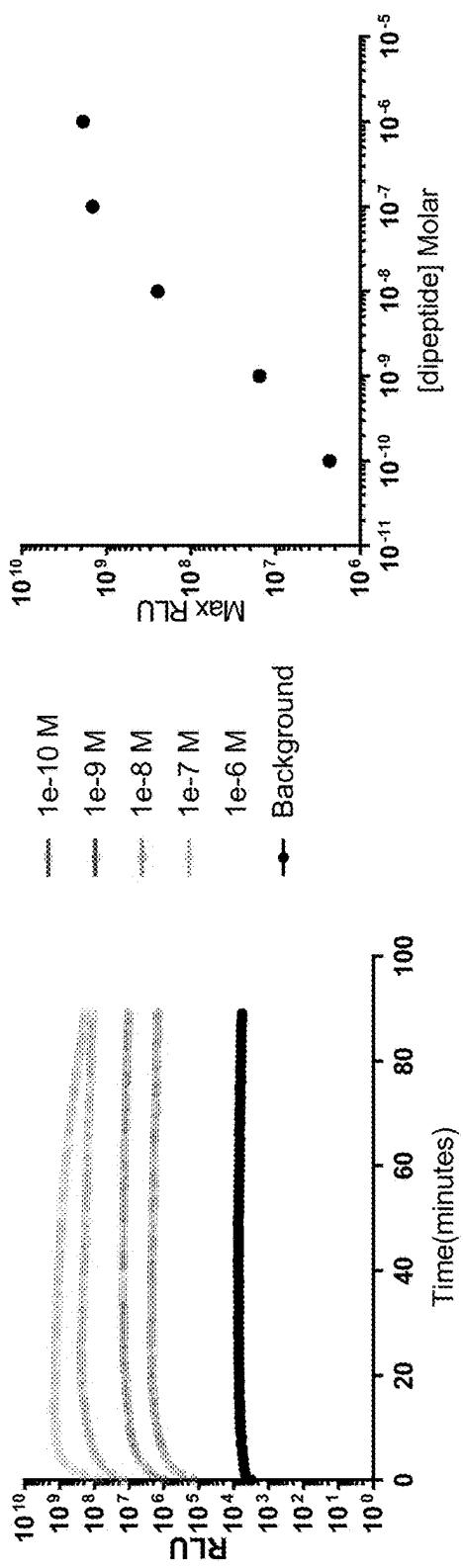


FIG. 24

**FIG. 25A**  
reconstitution of LgTrip + substrate spots: No BSA

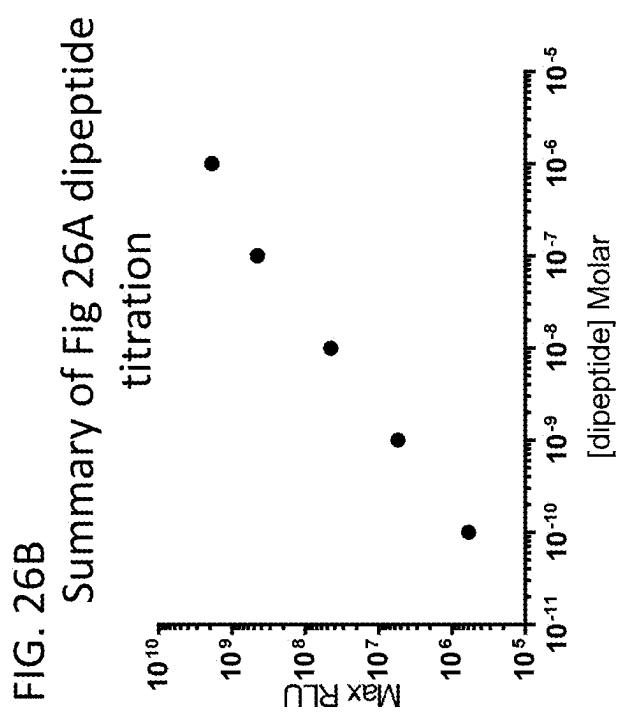
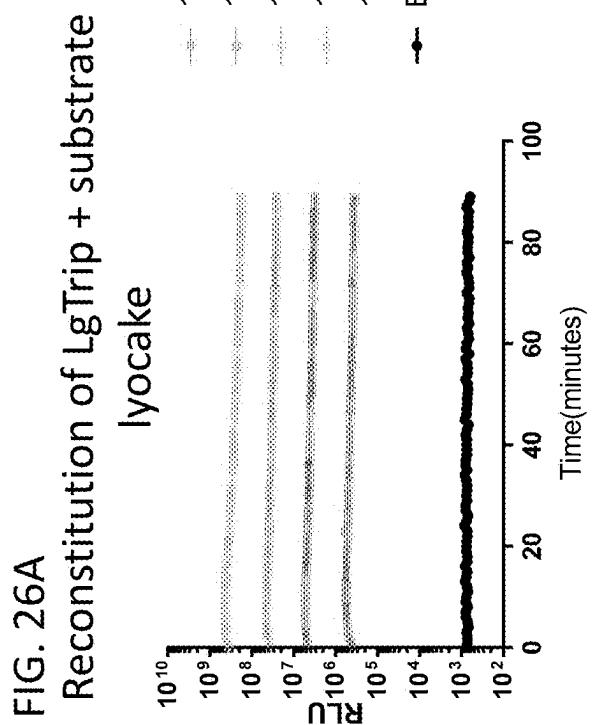


**FIG. 25B**  
reconstitution of LgTrip + substrate spots: BSA



**FIG. 25C**  
Summary of Fig 25B

**FIGS. 25A-25C**



FIGS. 26A-26B

## Summary

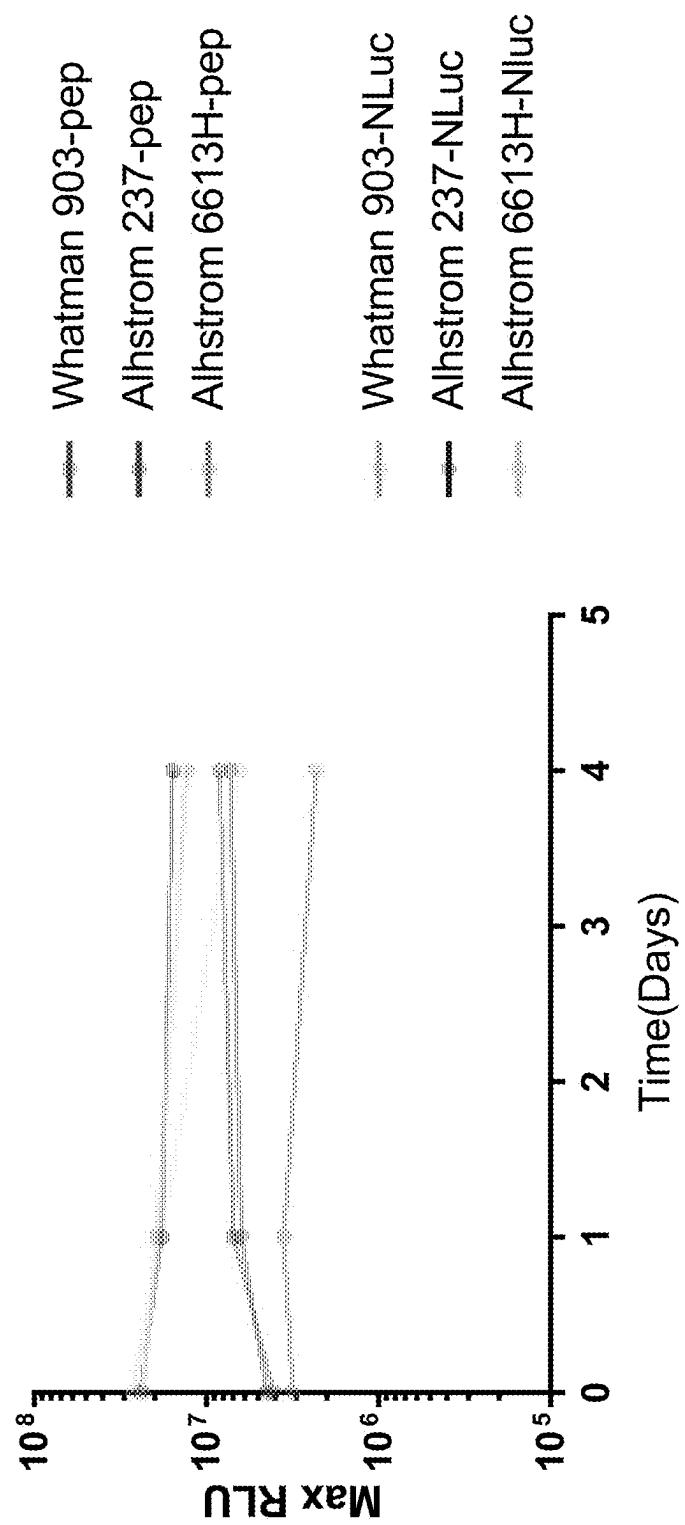


FIG. 27

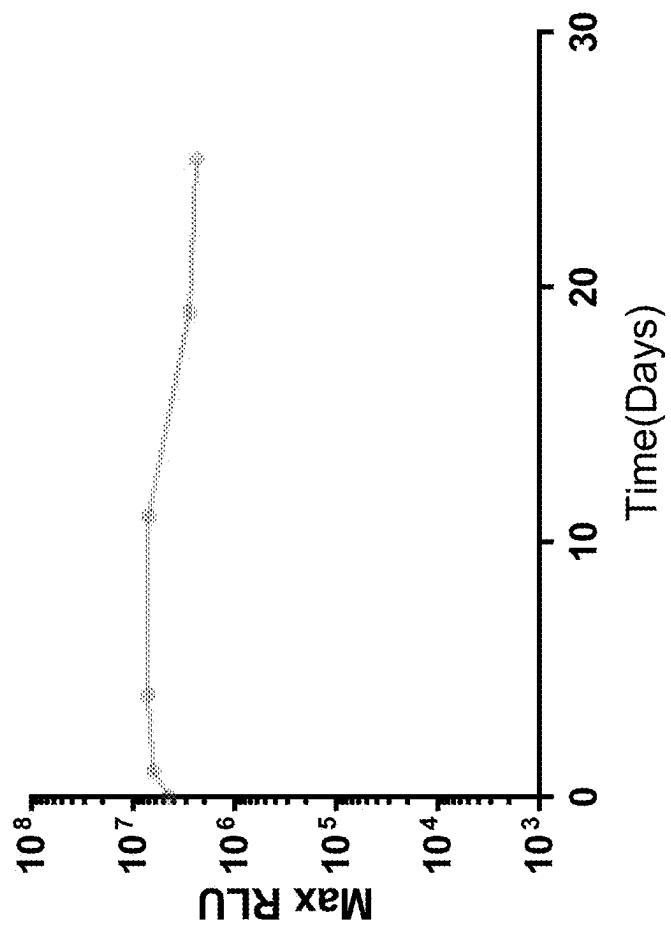


FIG. 28

FIG. 29A

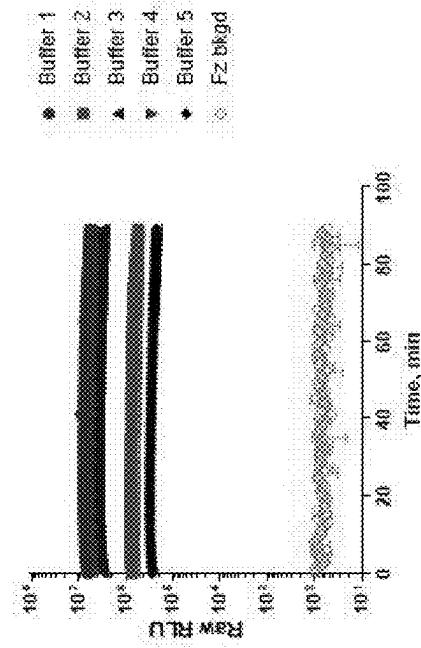


FIG. 29B

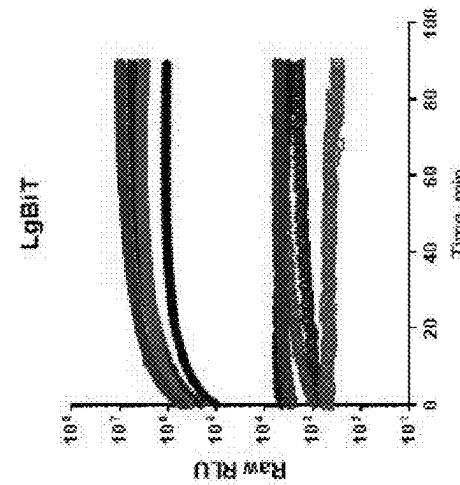
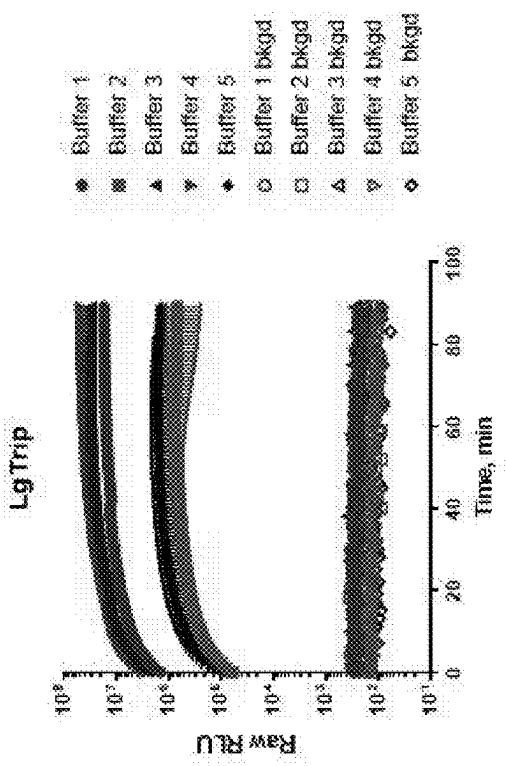


FIG. 29C



FIGS. 29A-29C

FIG. 30A

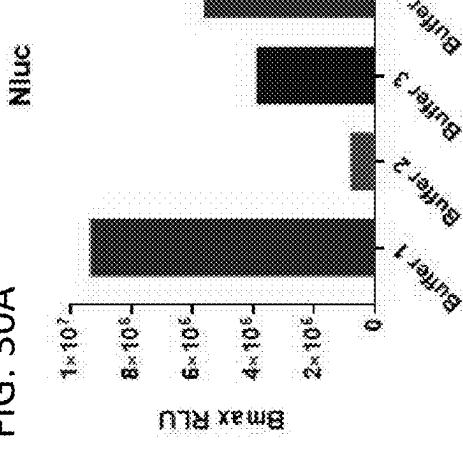


FIG. 30B

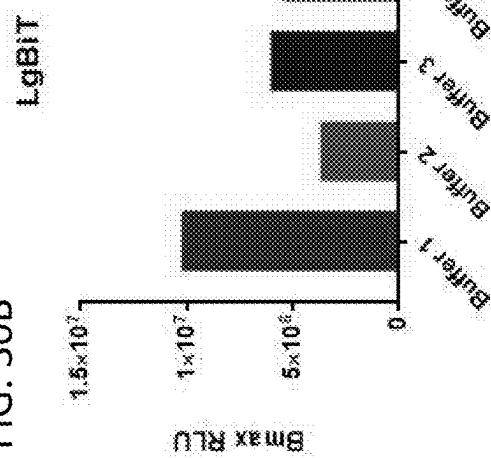
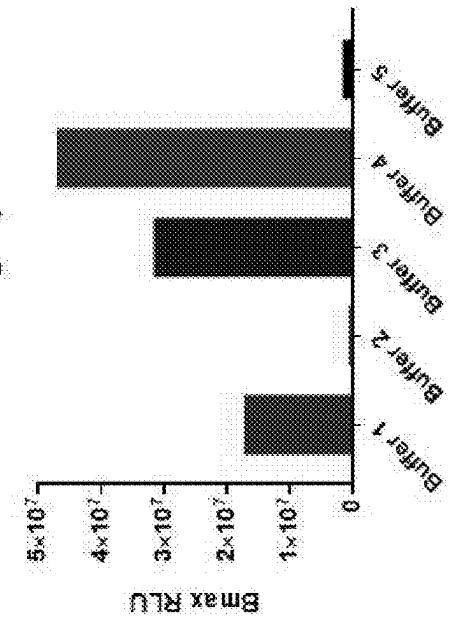
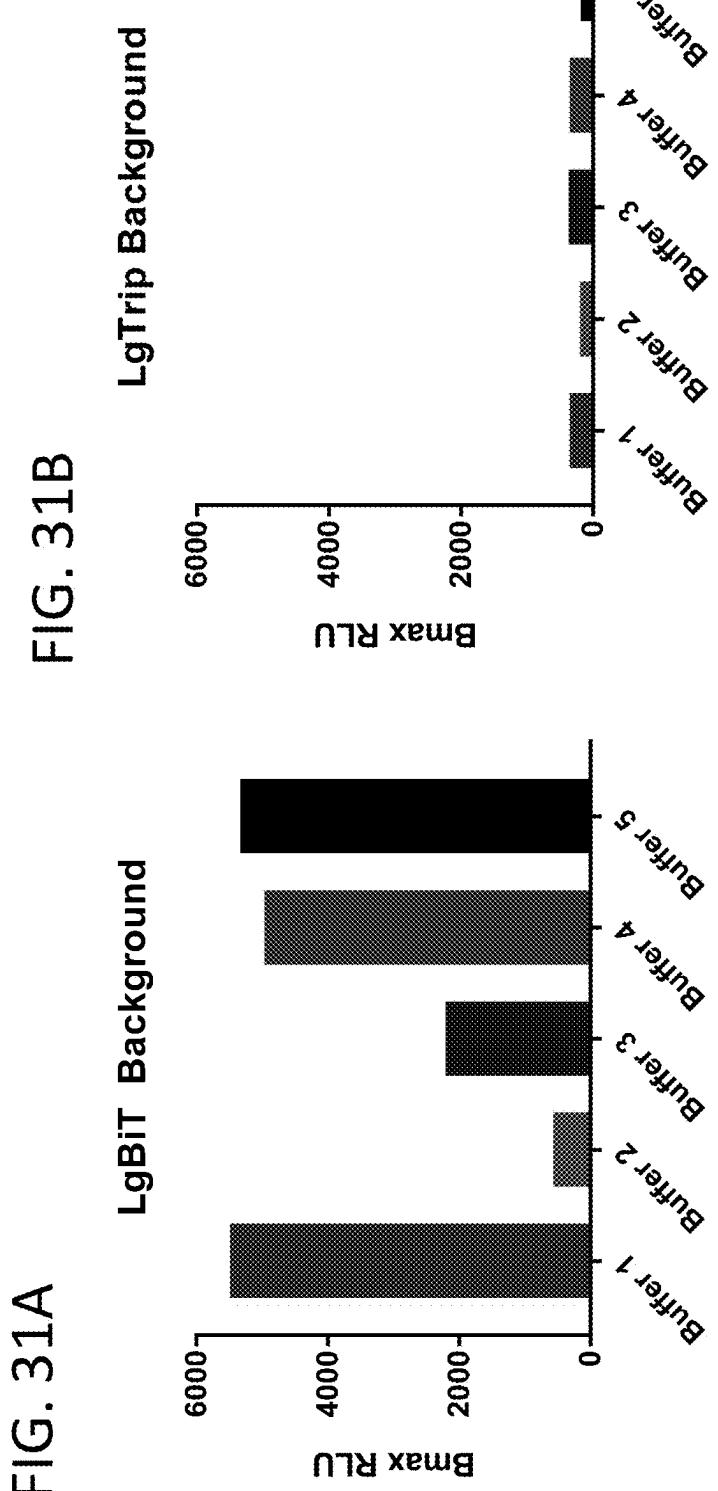


FIG. 30C



FIGS. 30A-30C



FIGS. 31A-31B

FIG. 32A

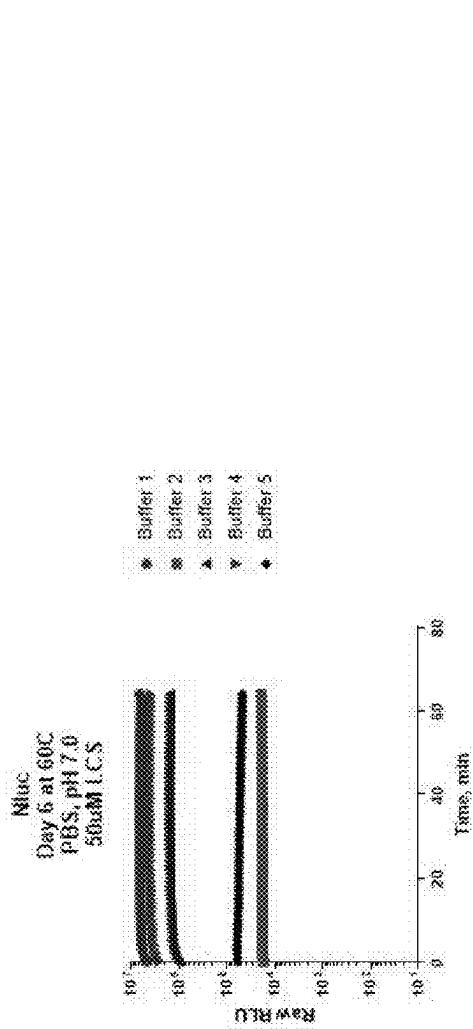


FIG. 32B

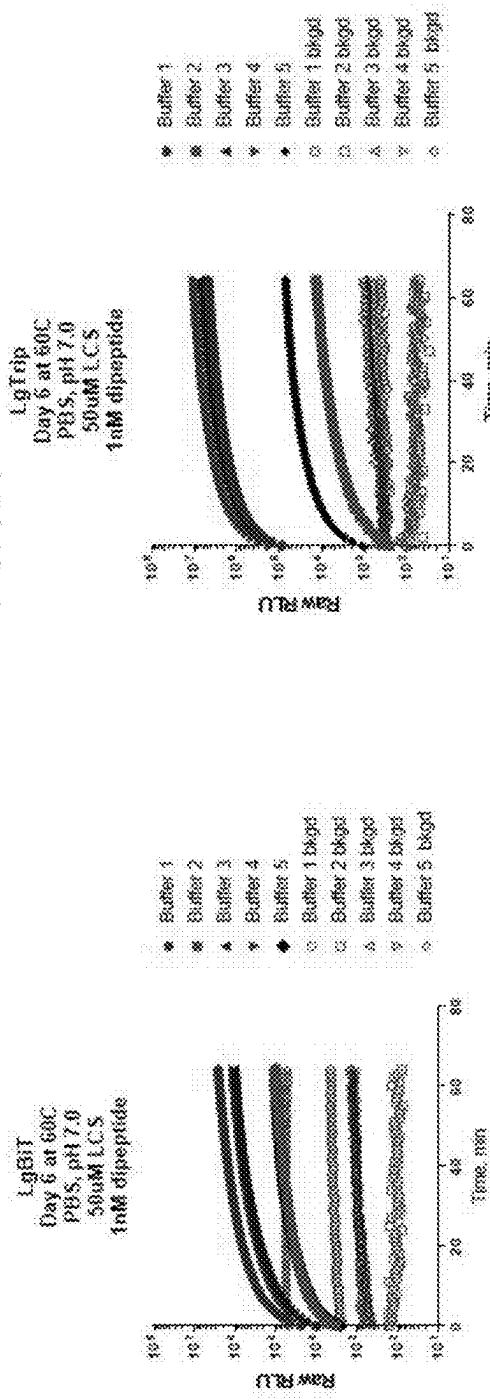
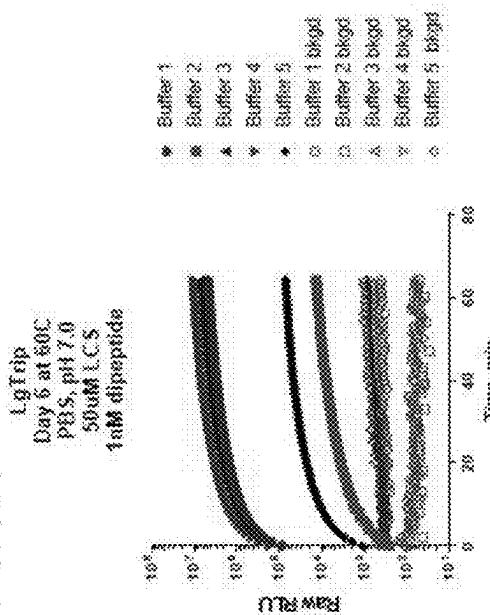


FIG. 32C



FIGS. 32A-32F

FIG. 32D

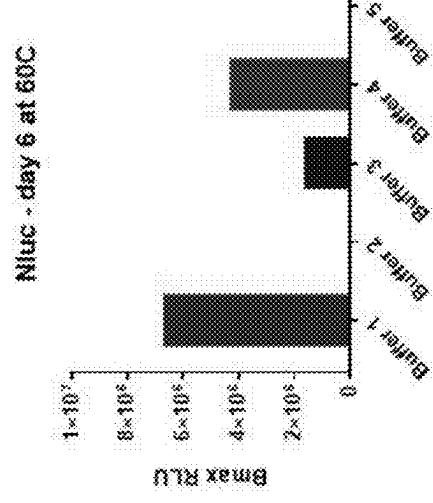


FIG. 32E

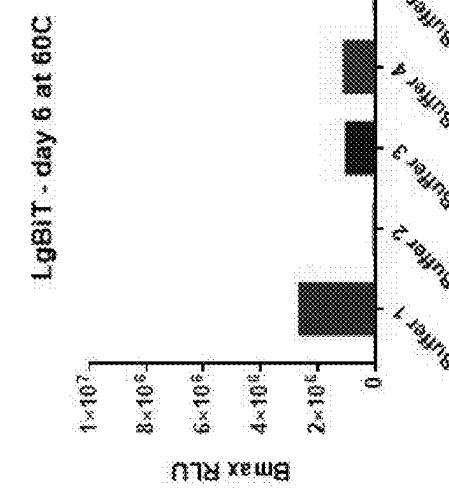
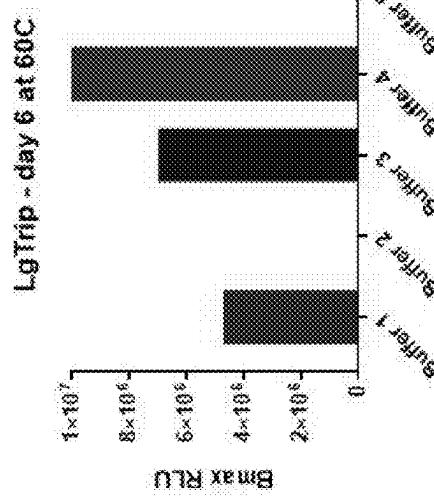
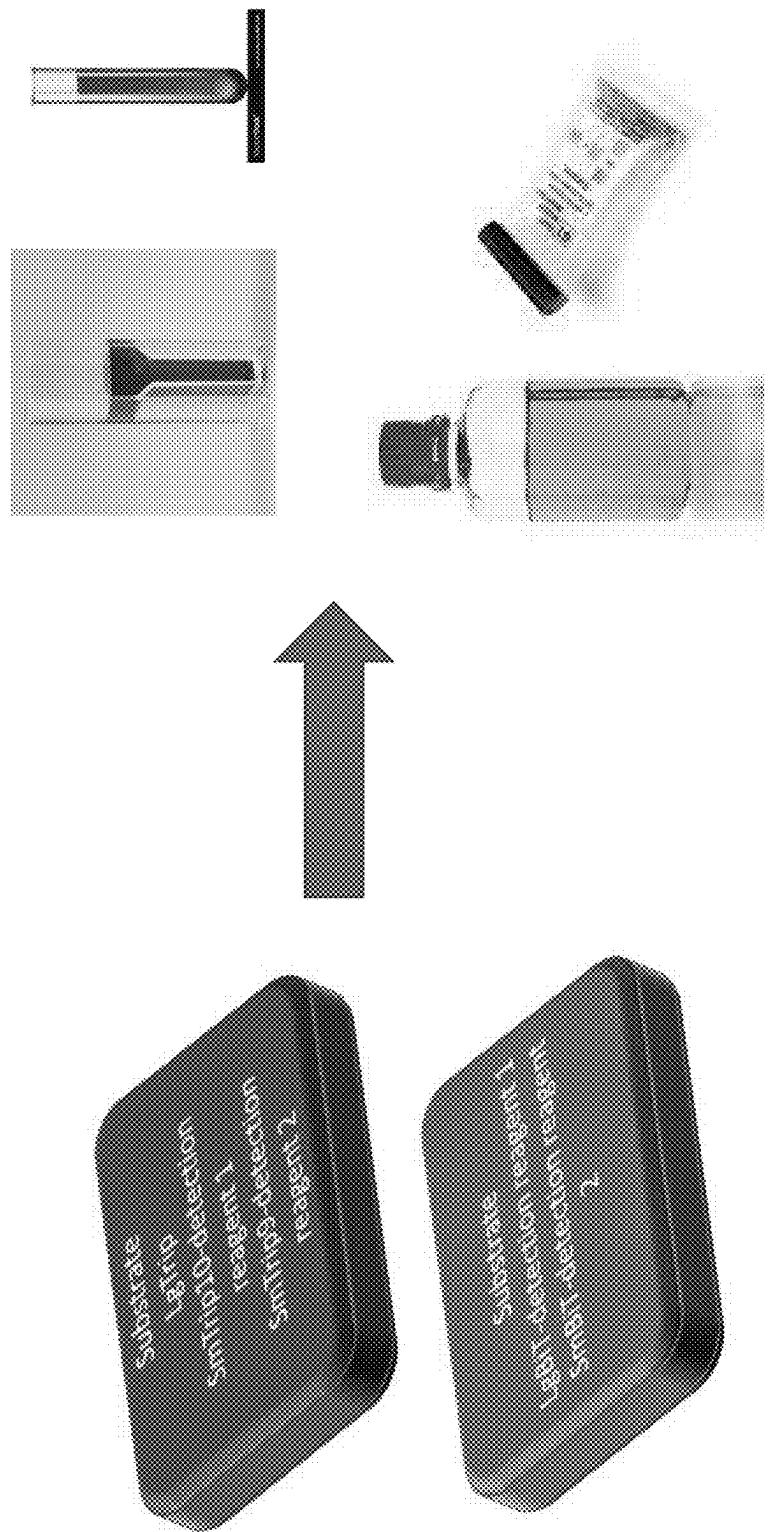


FIG. 32F



FIGS. 32A-32F



Tablet or lyocake embodiments containing all assay components that can be used in cuvettes, test tubes, bottles, snap test type formats, etc.

FIG. 33

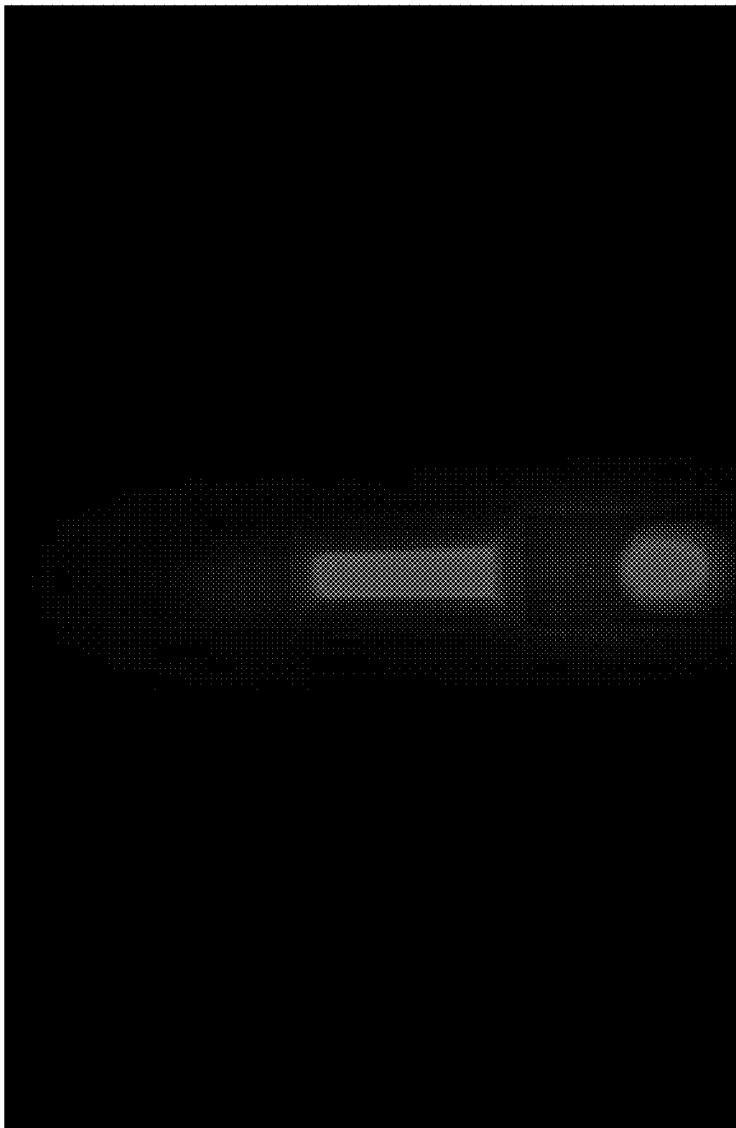


FIG. 34

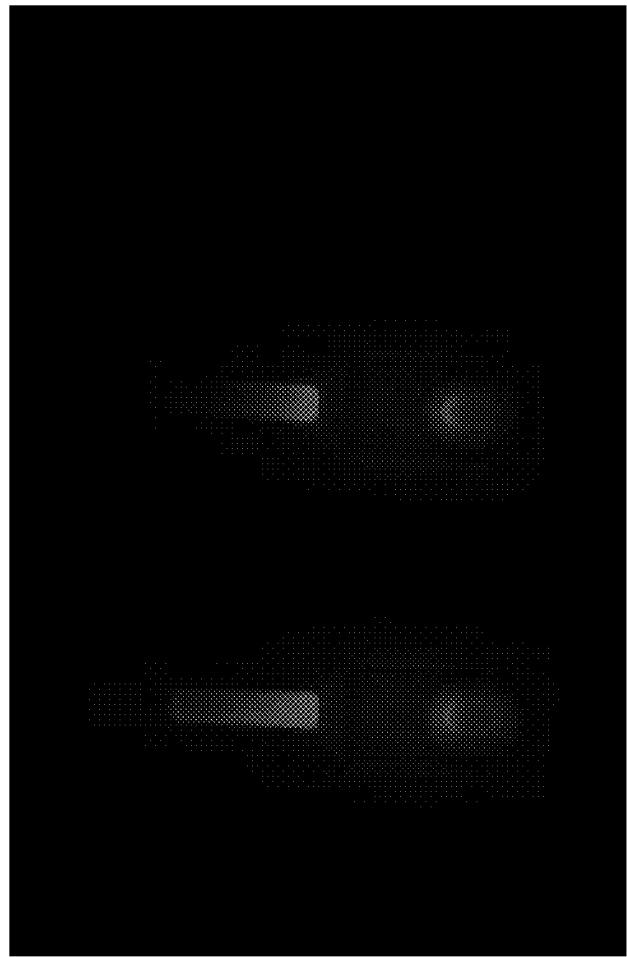
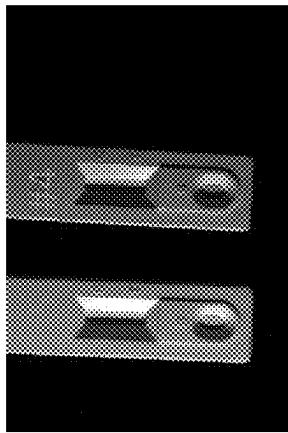


FIG. 35

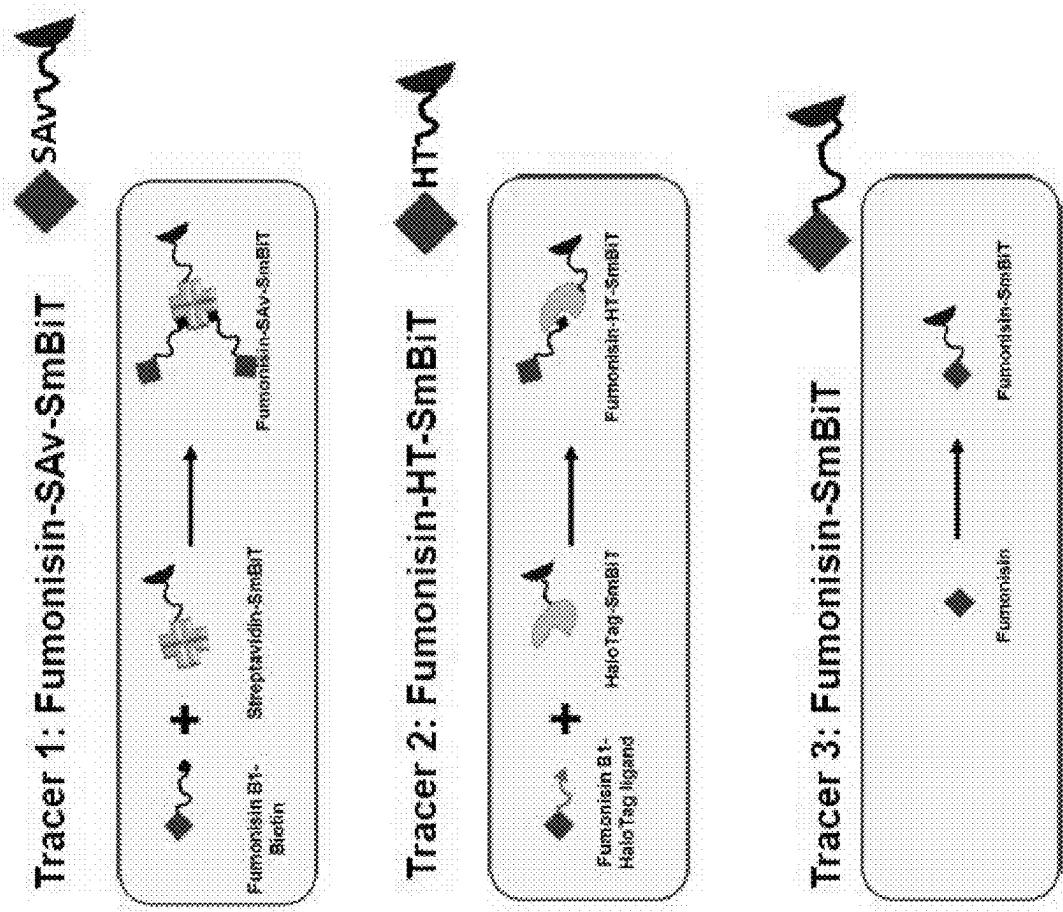


FIG. 36

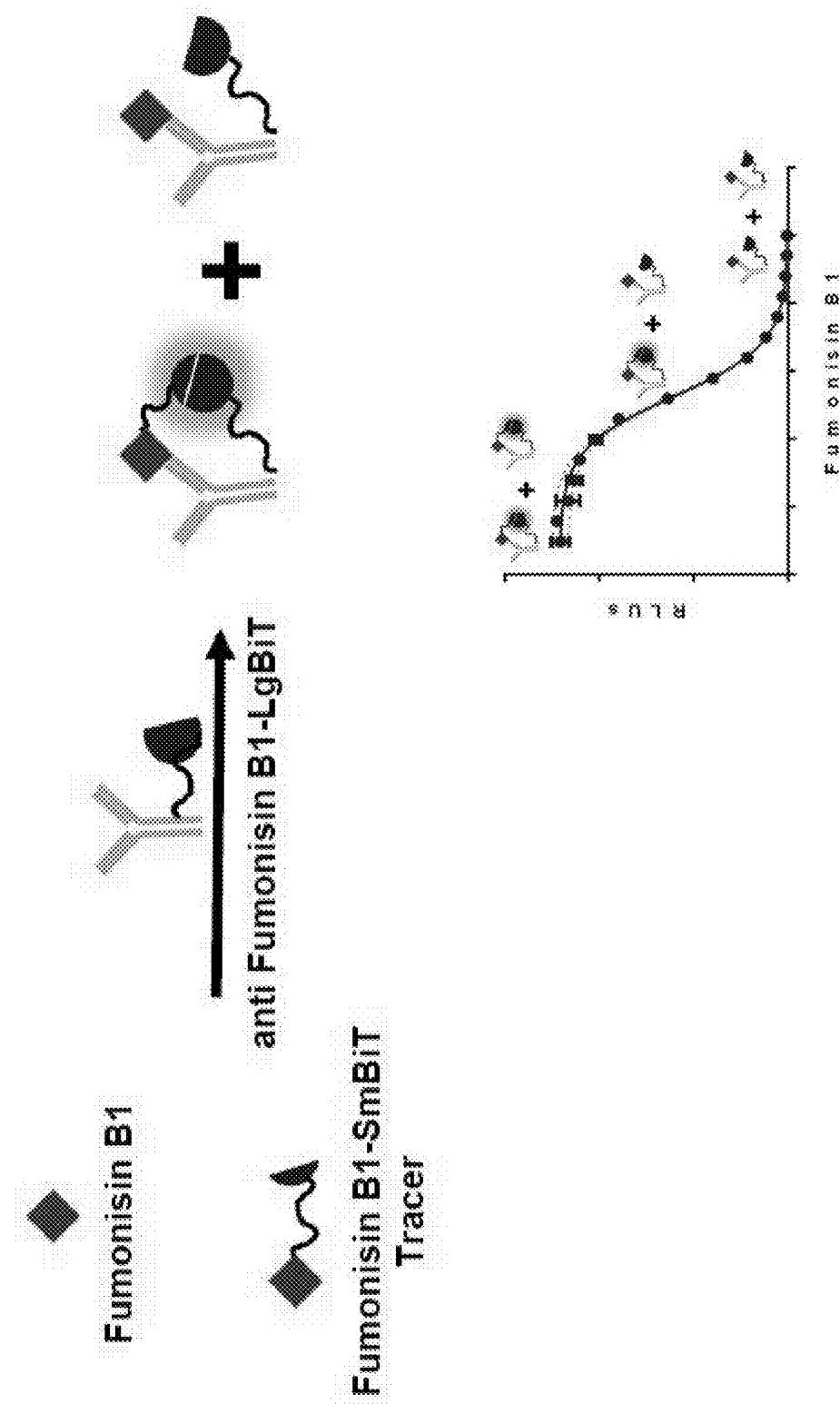


FIG. 37

FIG. 38A

LgBiT + Furimazine lyocake

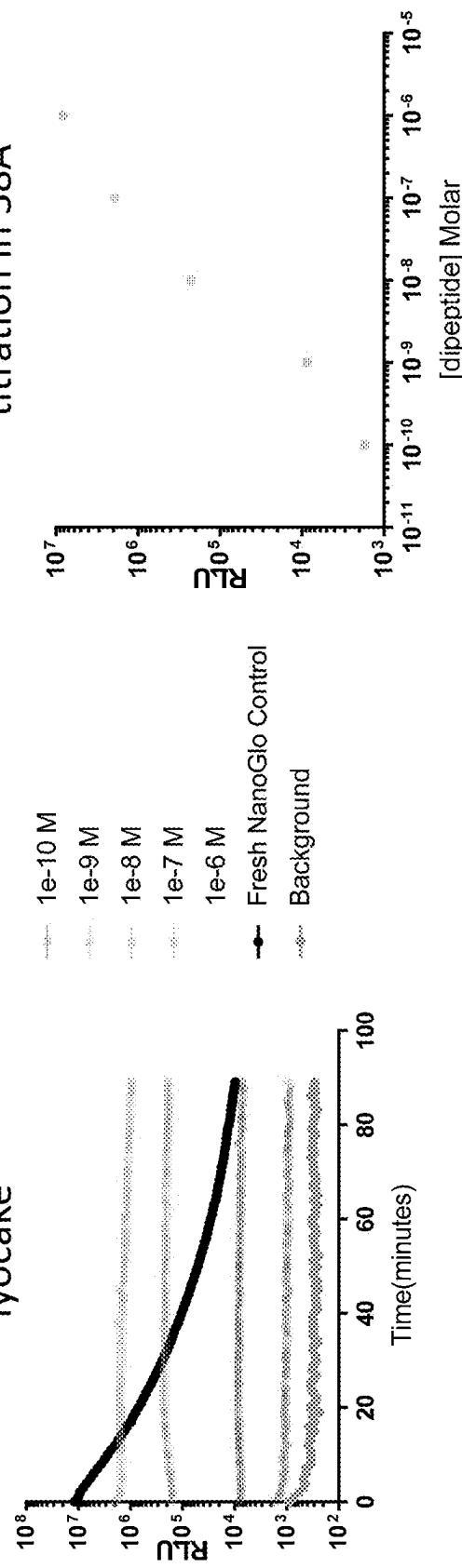
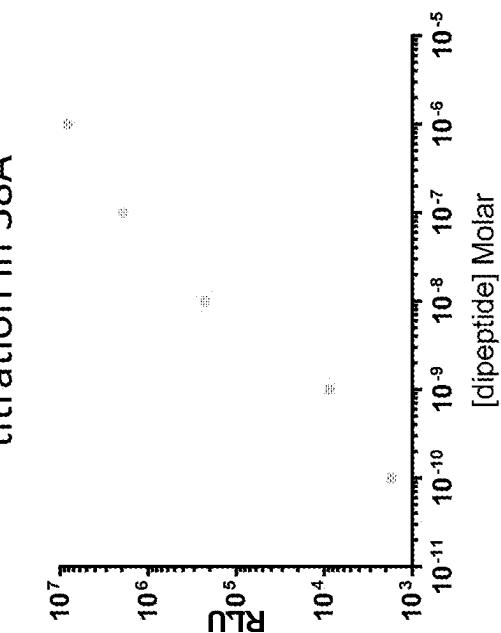


FIG. 38B

B<sub>max</sub> from dipeptide titration in 38A



FIGS. 38A-38B

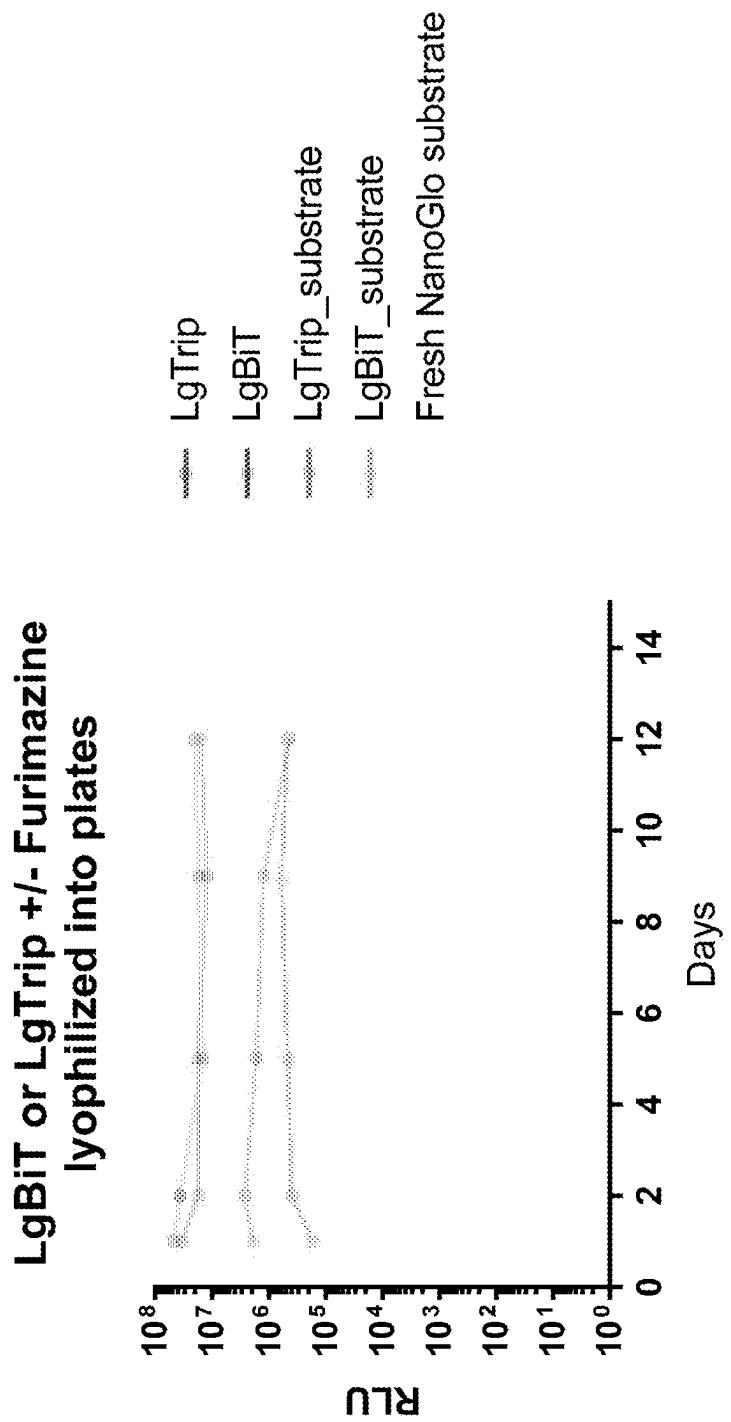


FIG. 39

FIG. 40A Paper based assay for Remicade NanoBiT

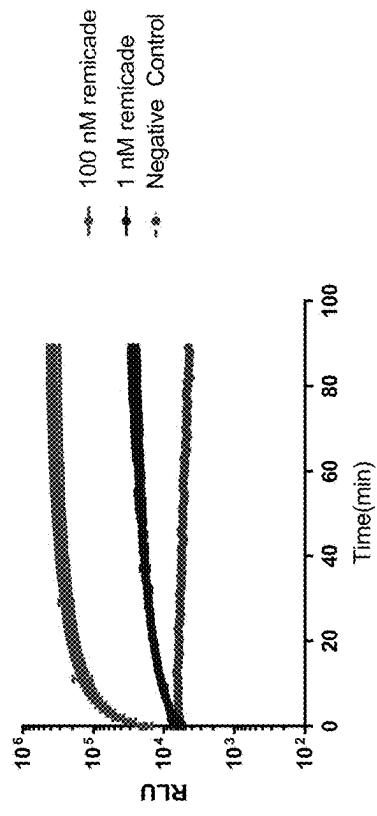
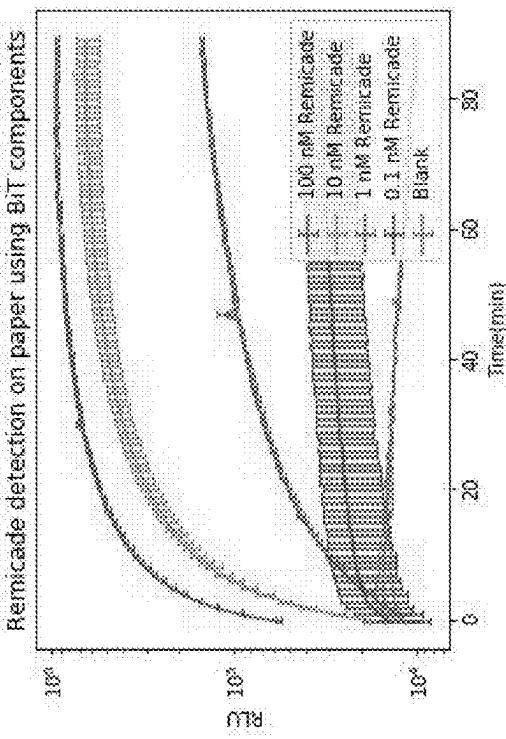
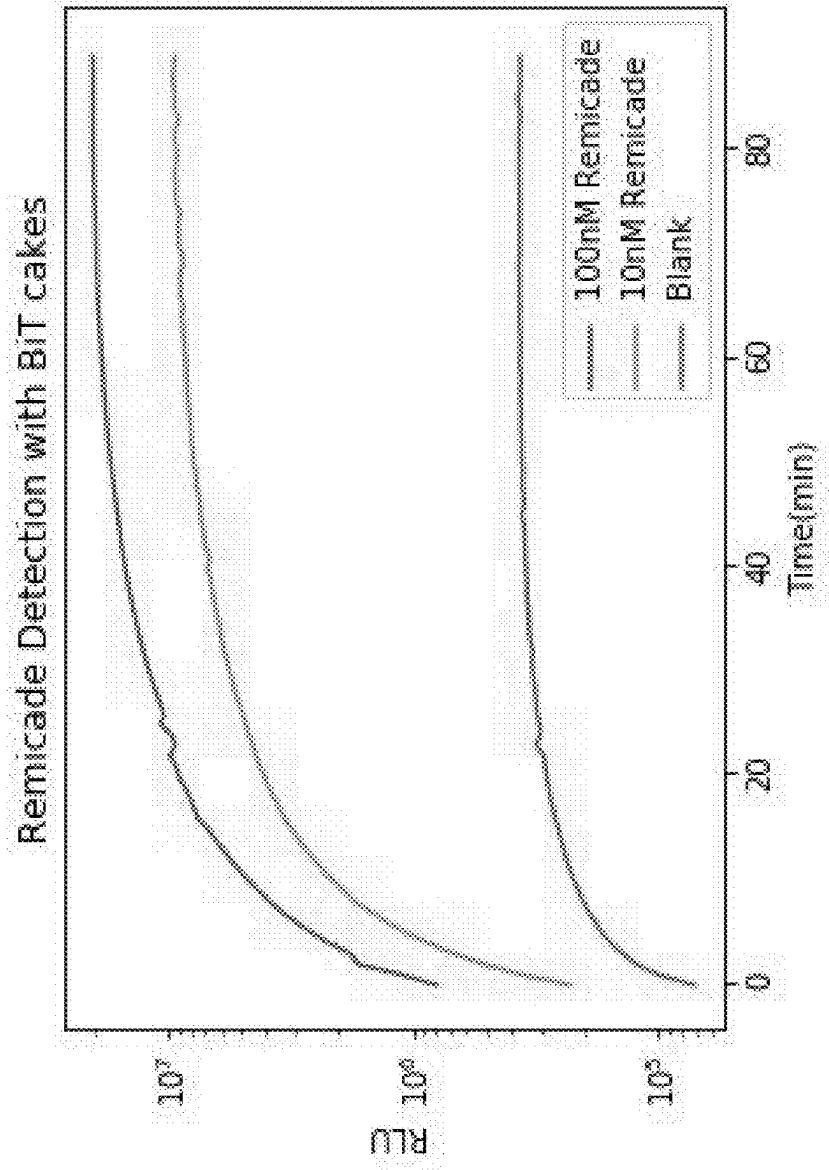


FIG. 40B



FIGS. 40A-40C

FIG. 40C



FIGS. 40A-40C

FIG. 41A

Paper based assay for Remicade  
NanoTrip

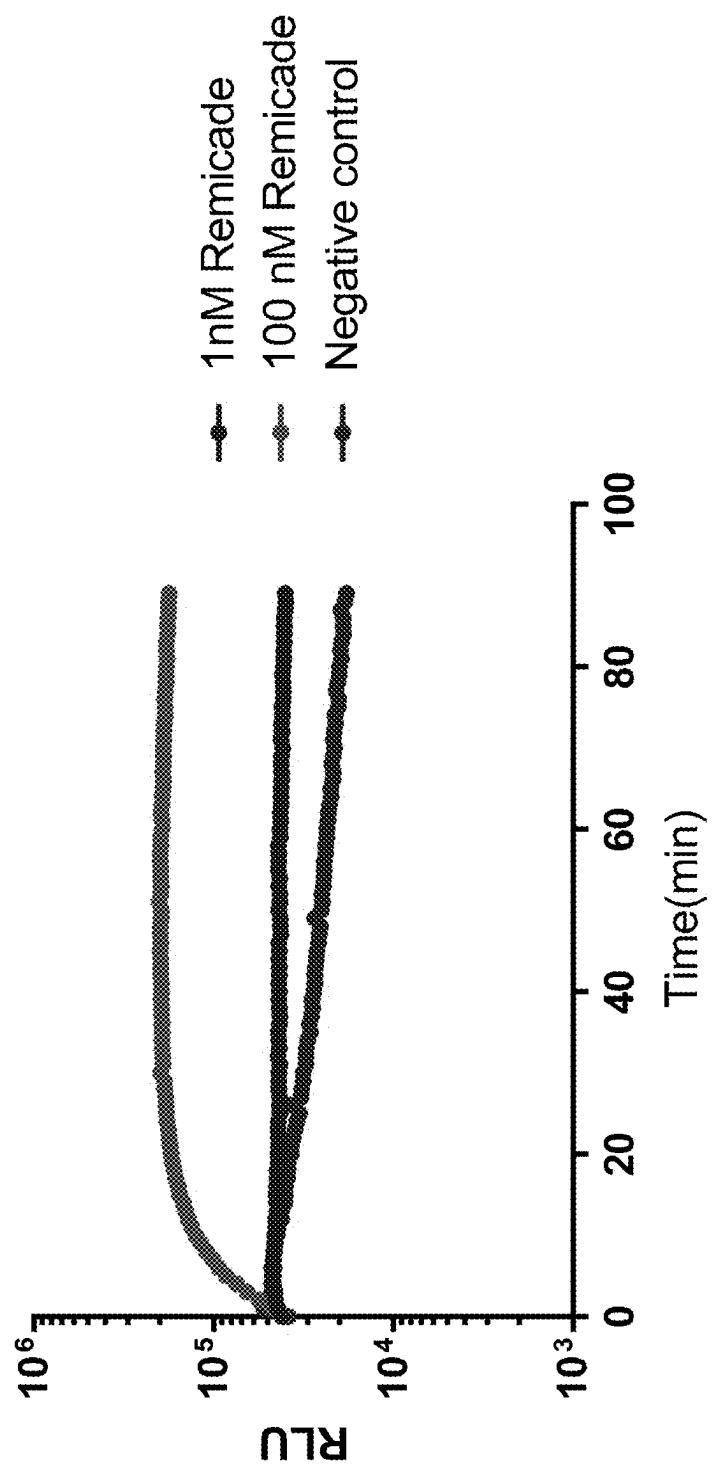


FIG. 41B

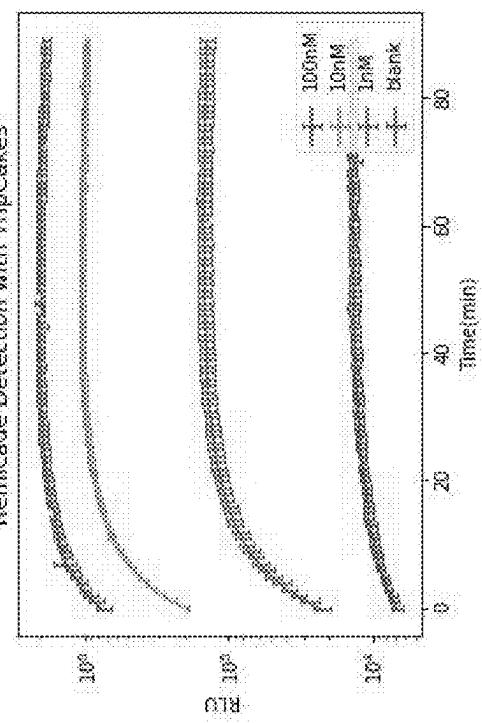
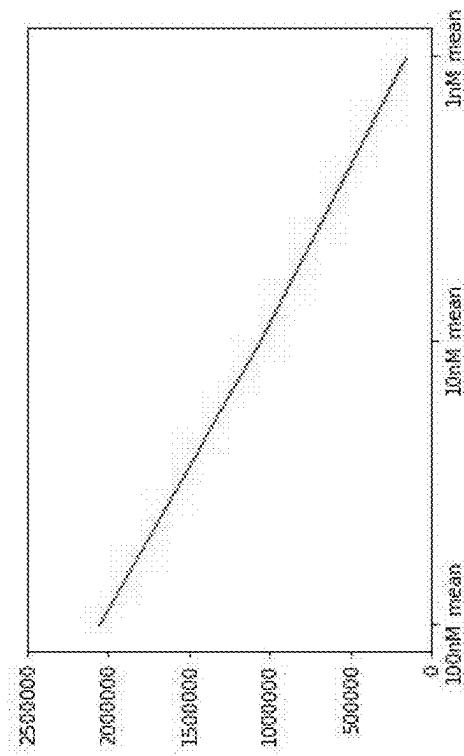
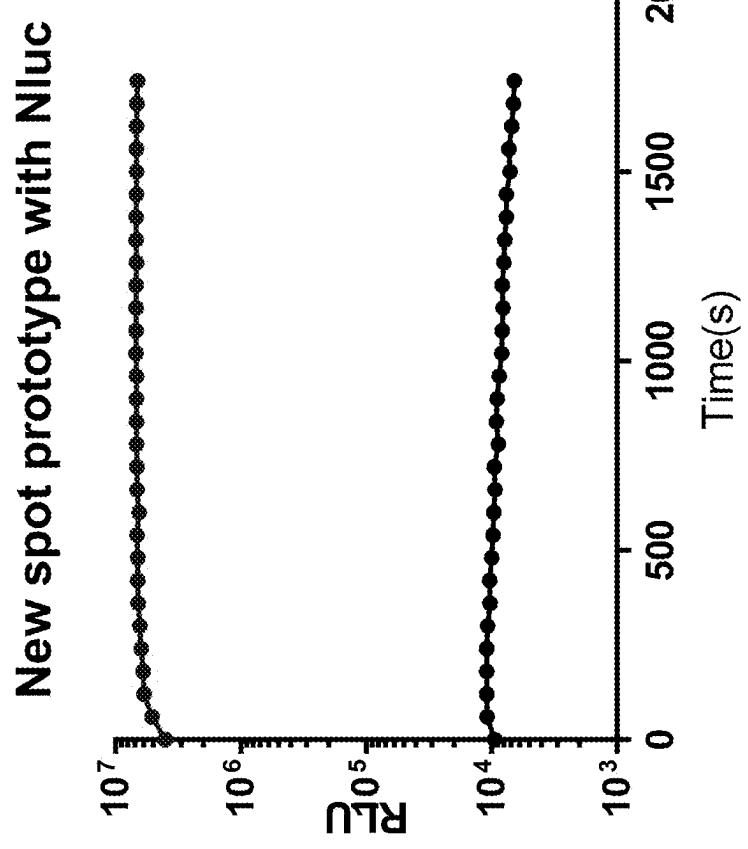


FIG. 41C

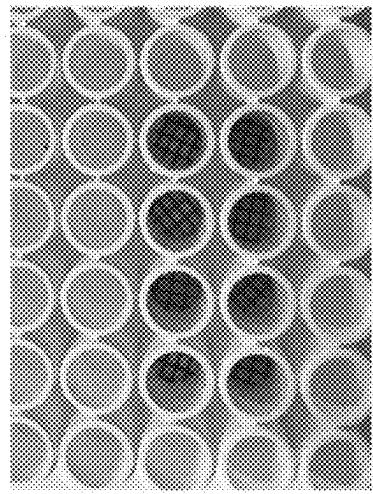


FIGS. 41A-41C

FIG. 42A



— Surface  
● Blank



FIGS. 42A-42E

FIG. 42B

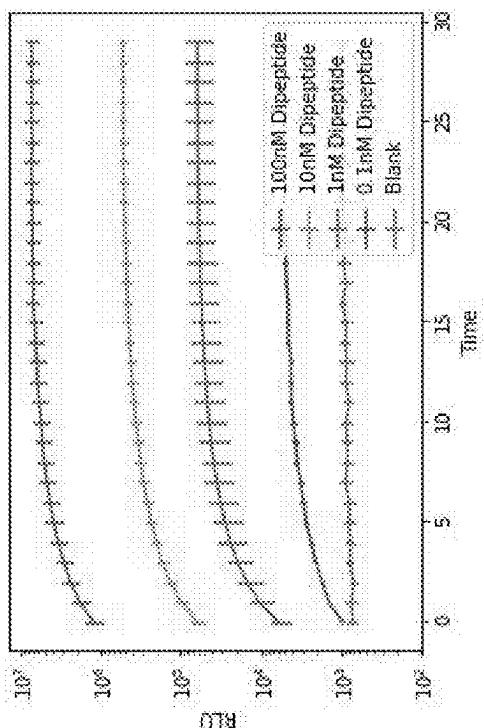
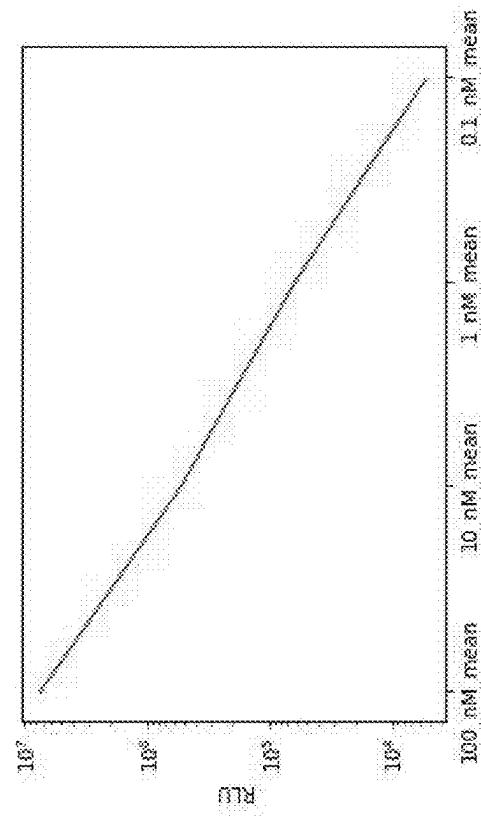


FIG. 42C



FIGS. 42A-42E

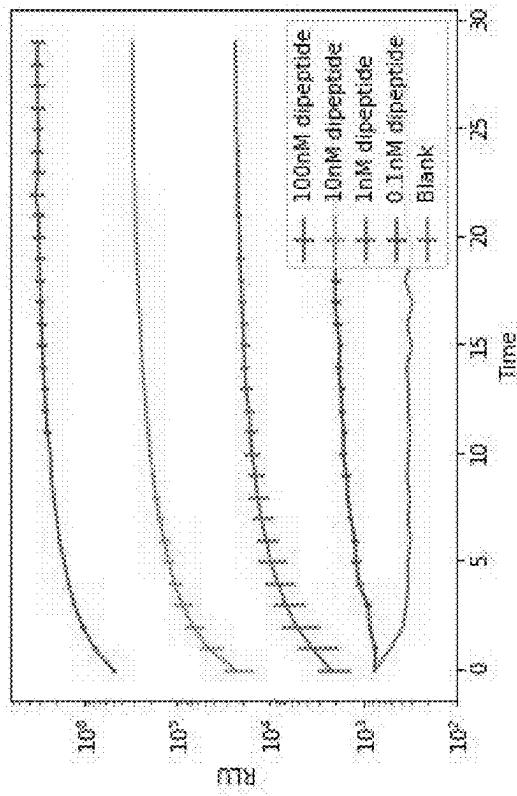
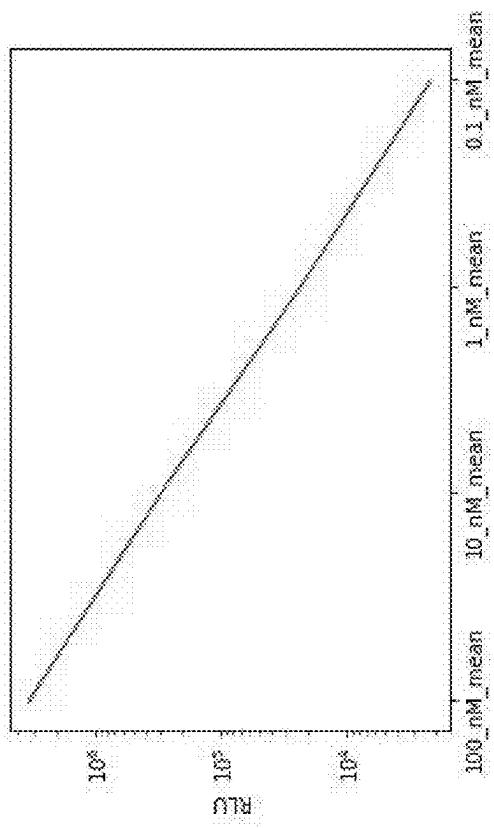


FIG. 42E



FIGS. 42A-42E

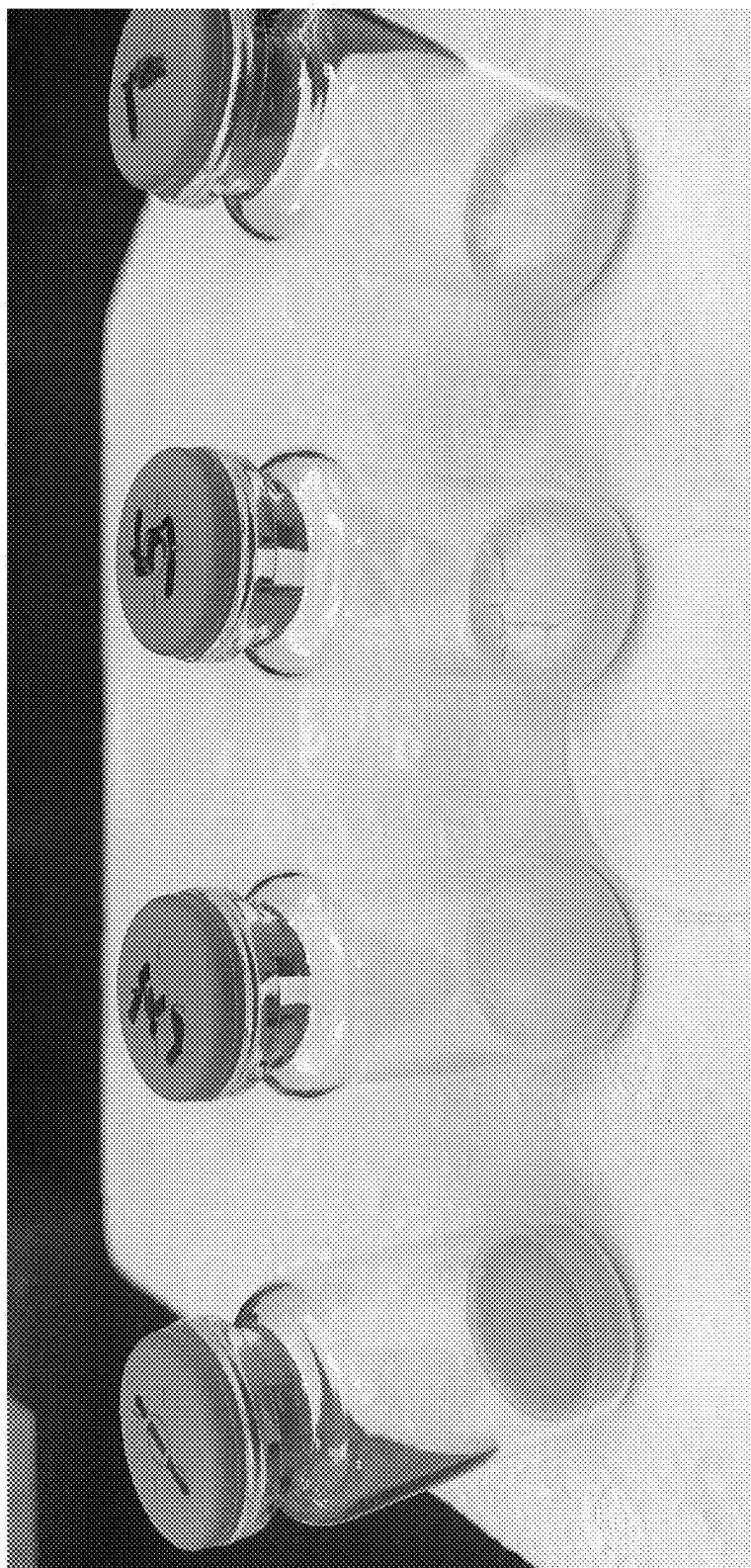


FIG. 43

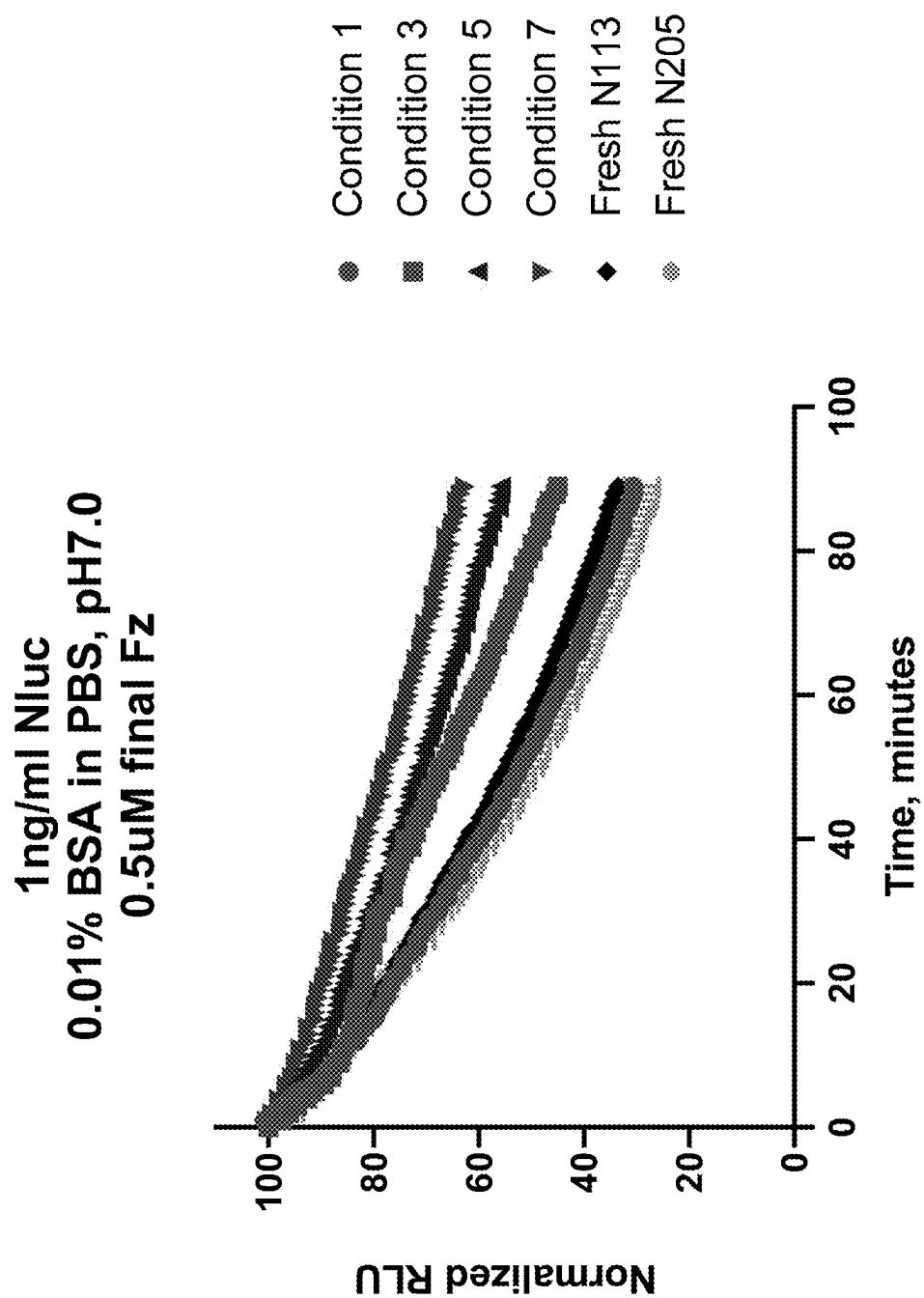


FIG. 44

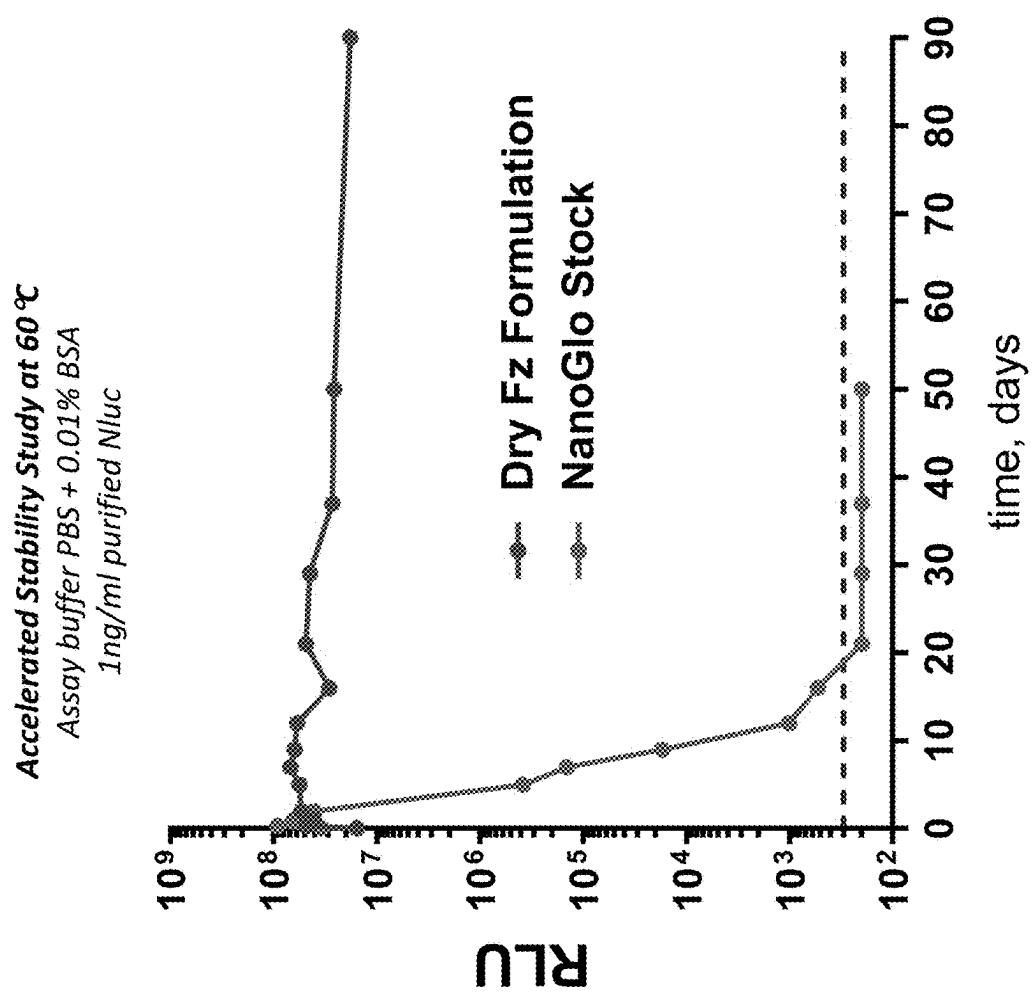


FIG. 45

Absolute [furimazine] remaining

FIG. 46A

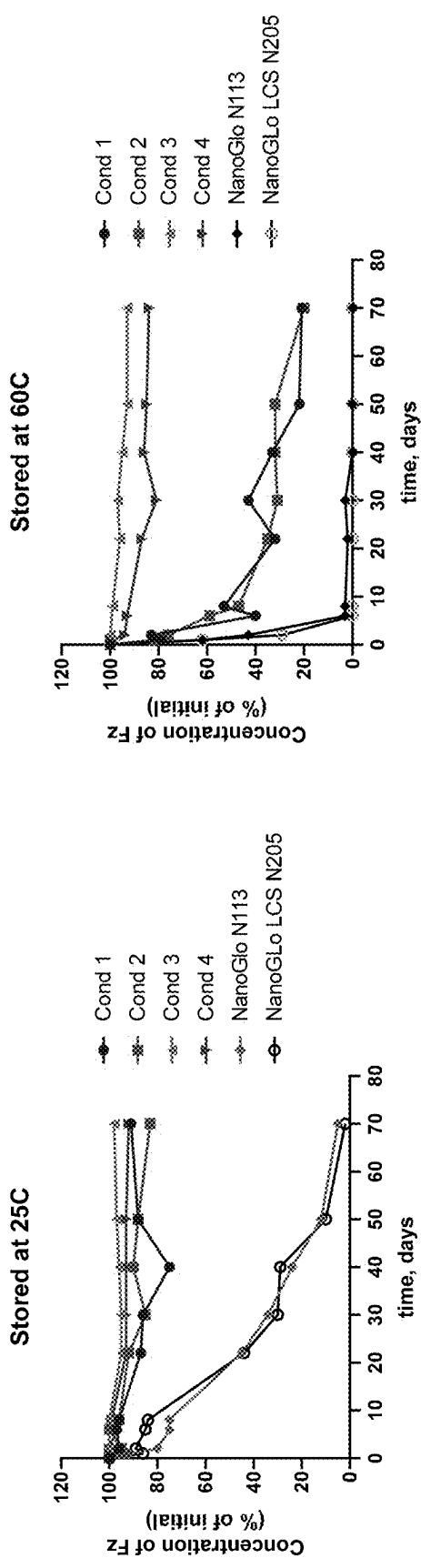
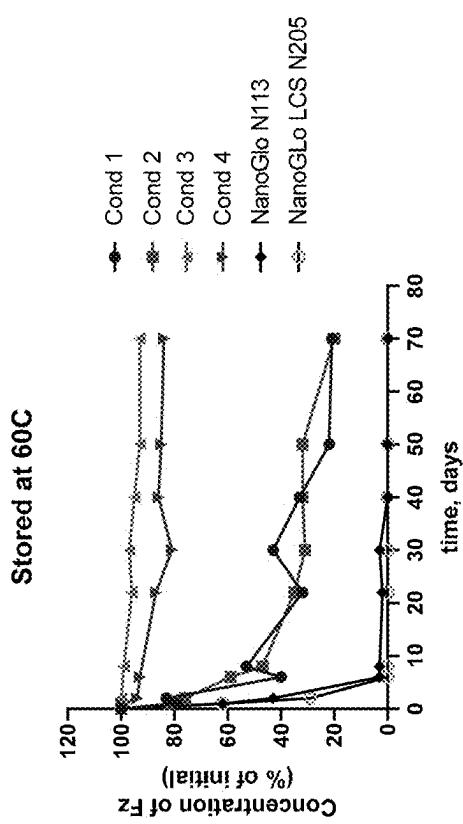


FIG. 46B



FIGS. 46A-46B

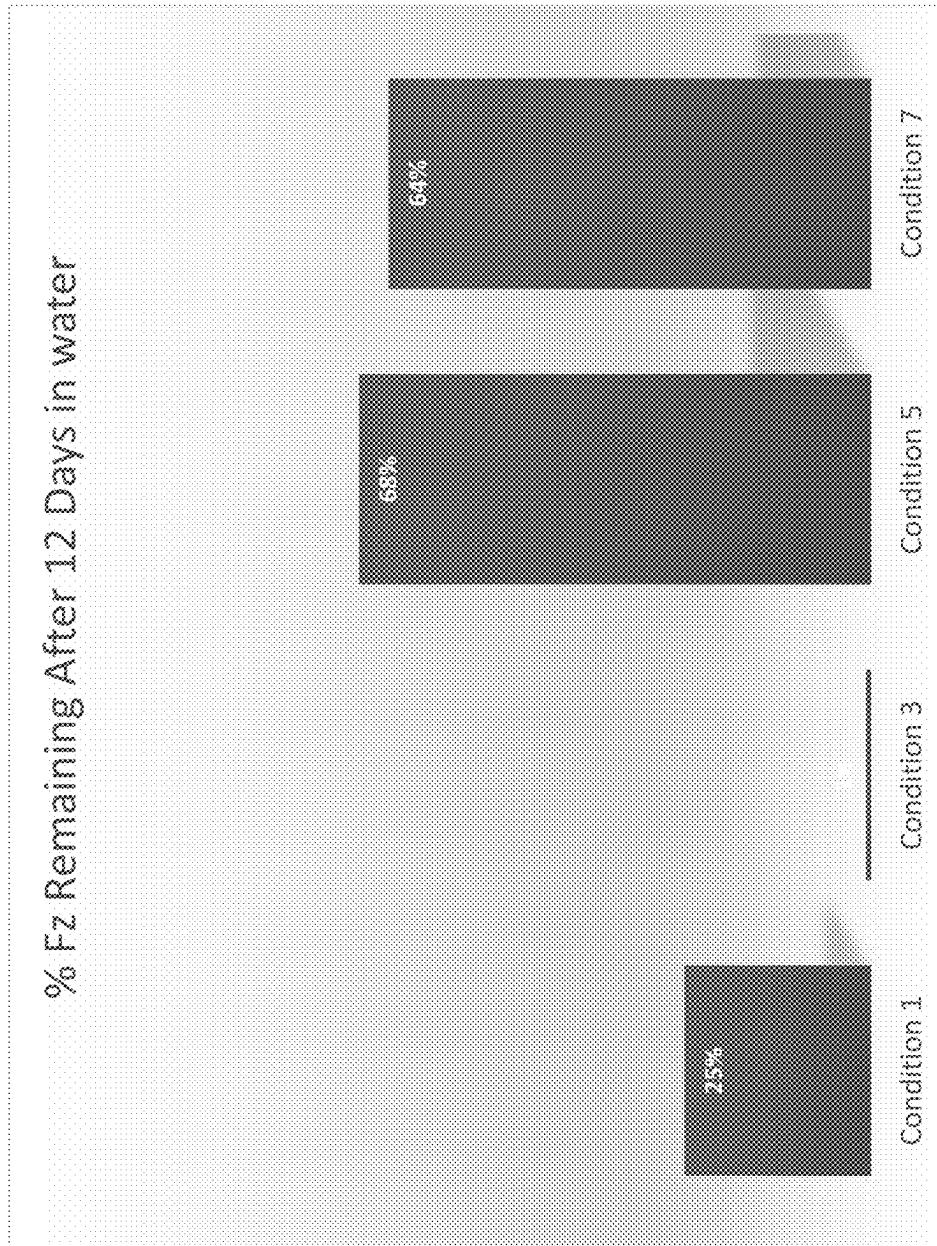


FIG. 47

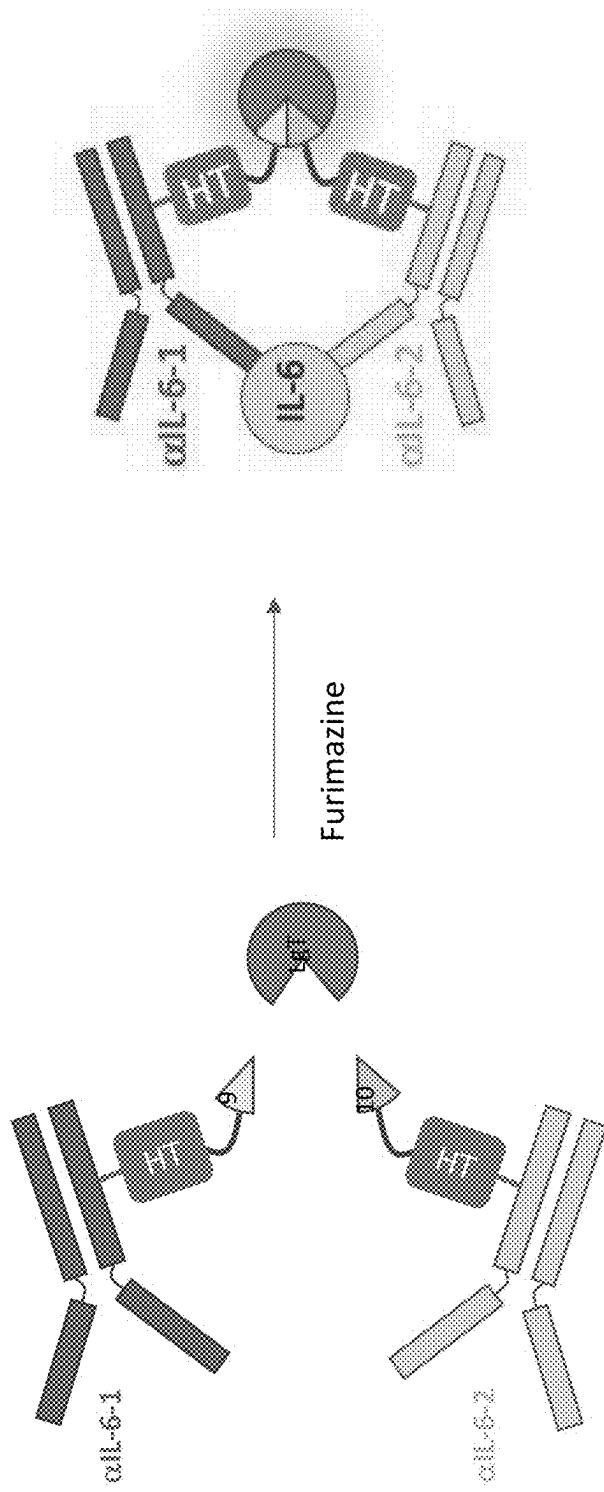


FIG. 48

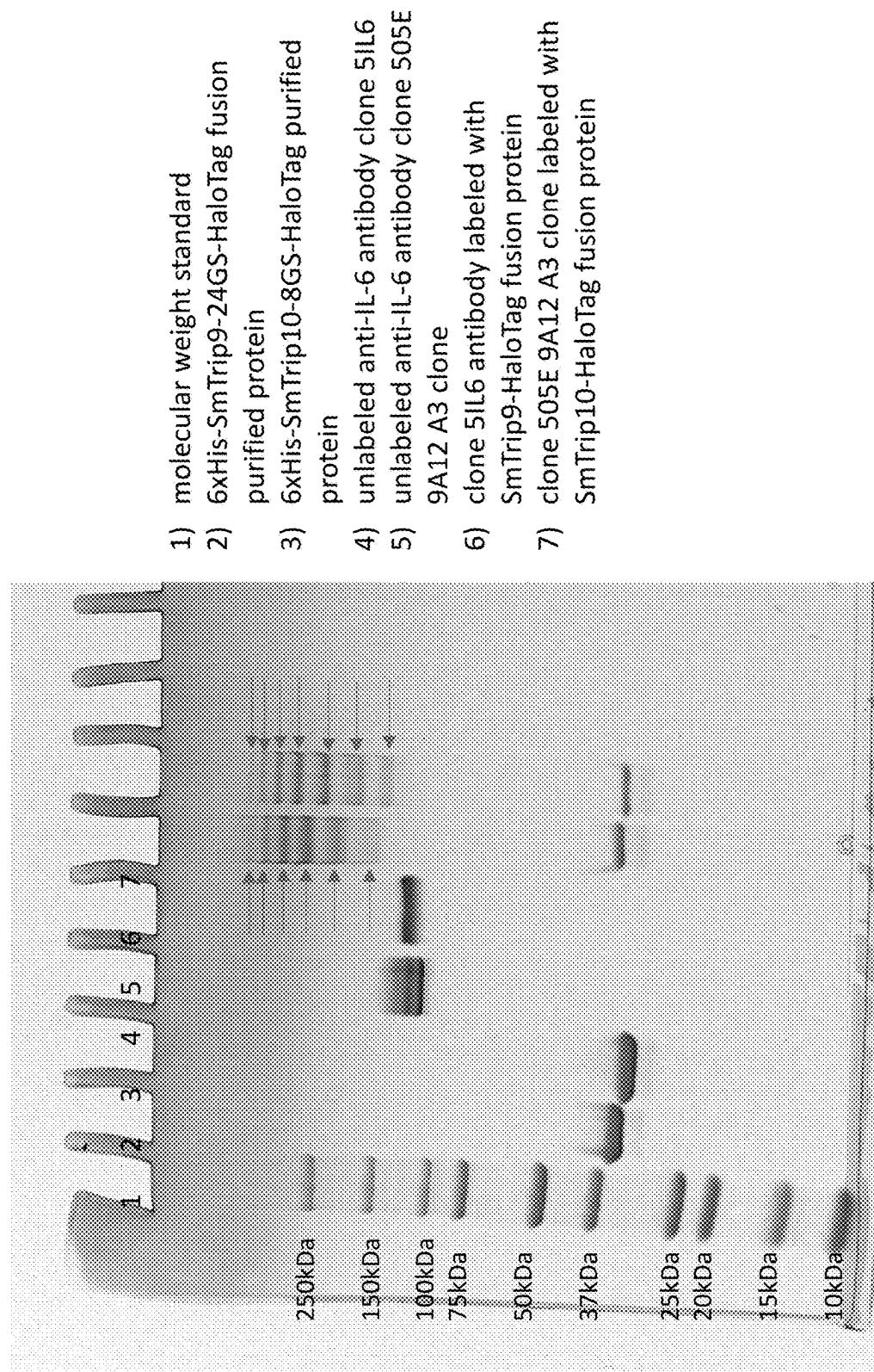


FIG. 49

FIG. 50A

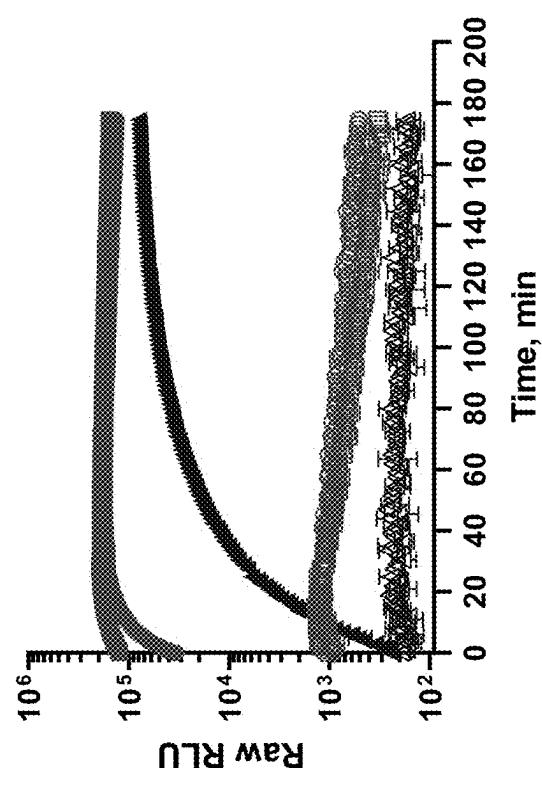
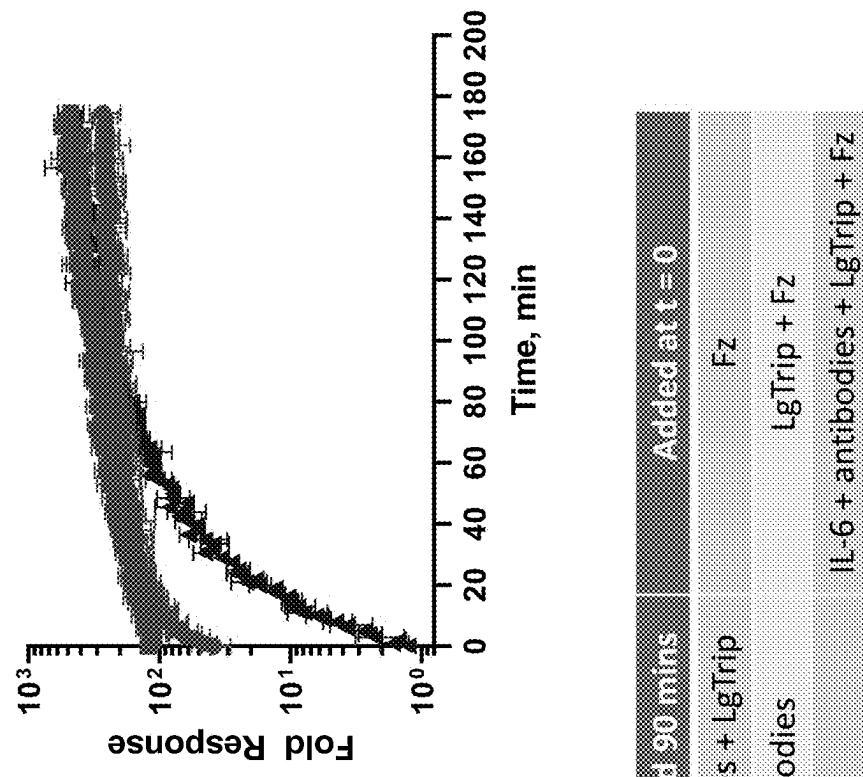
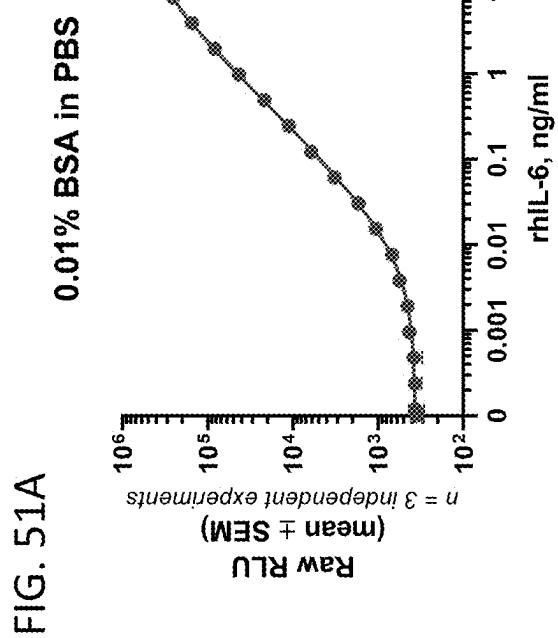


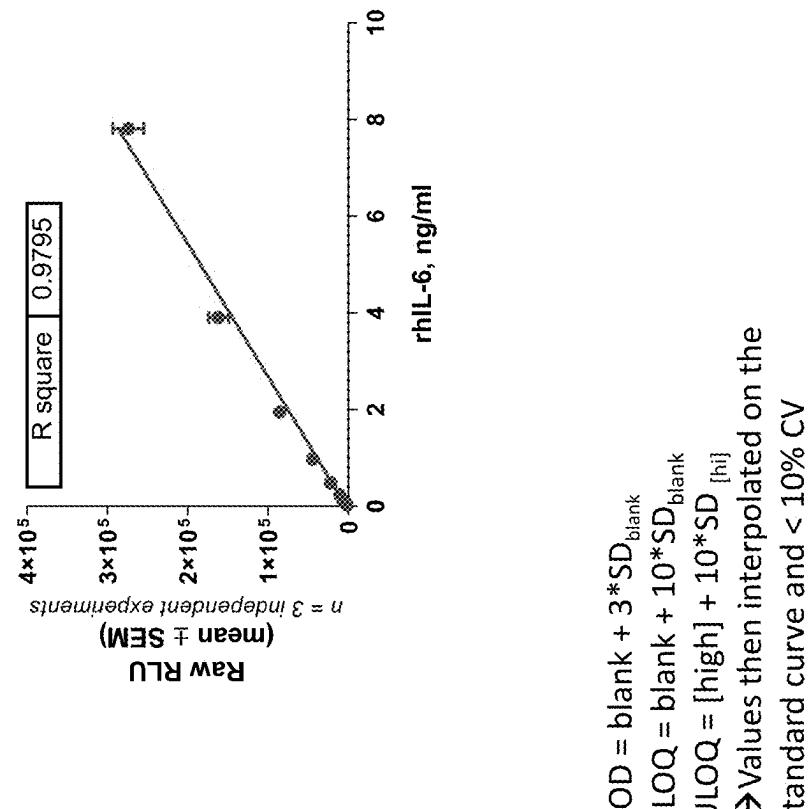
FIG. 50B



FIGS. 50A-50B



**FIG. 51B**



LOD	blank + 3 * SD <sub>blank</sub>
LLQ	blank + 10 * SD <sub>blank</sub>
ULOQ	[high] + 10 * SD <sub>[hi]</sub>
	→ Values then interpolated on the standard curve and < 10% CV

LOD = blank + 3 \* SD<sub>blank</sub>  
LLQ = blank + 10 \* SD<sub>blank</sub>  
ULOQ = [high] + 10 \* SD<sub>[hi]</sub>  
→ Values then interpolated on the standard curve and < 10% CV

**FIGS. 51A-51B**

FIG. 52A

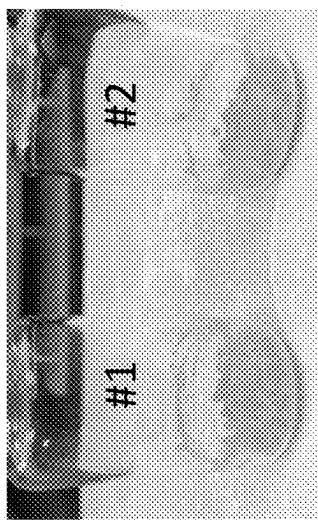


FIG. 52B

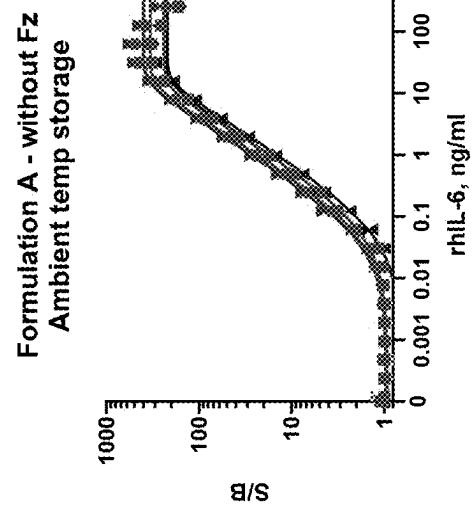
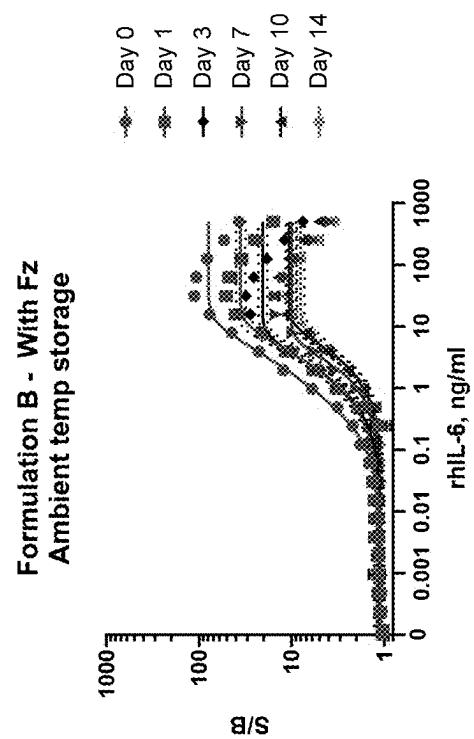


FIG. 52C



FIGS. 52A-52C

FIG. 53A

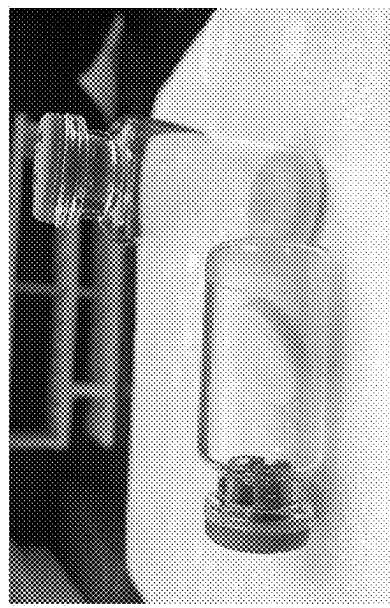
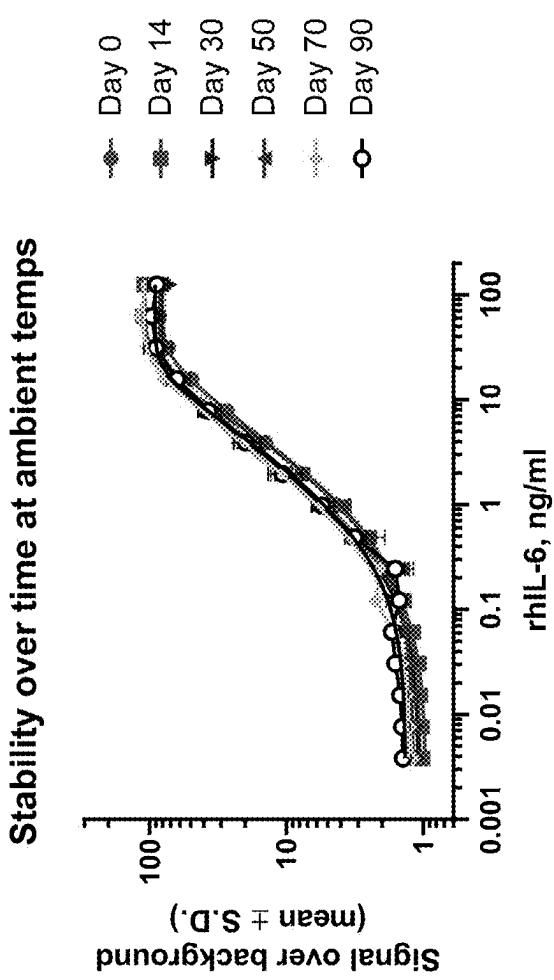


FIG. 53B



FIGS. 53A-53B

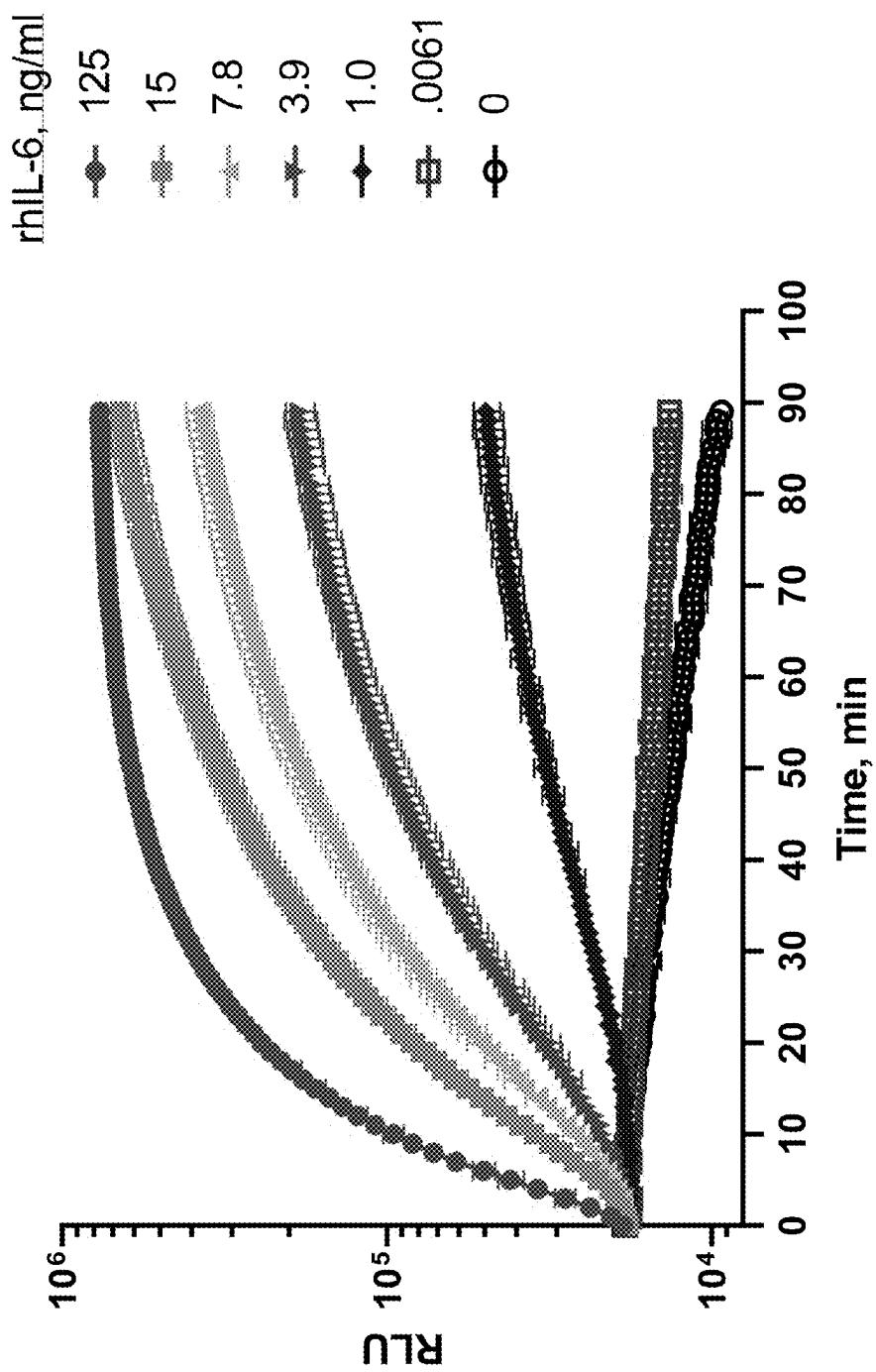


FIG. 54

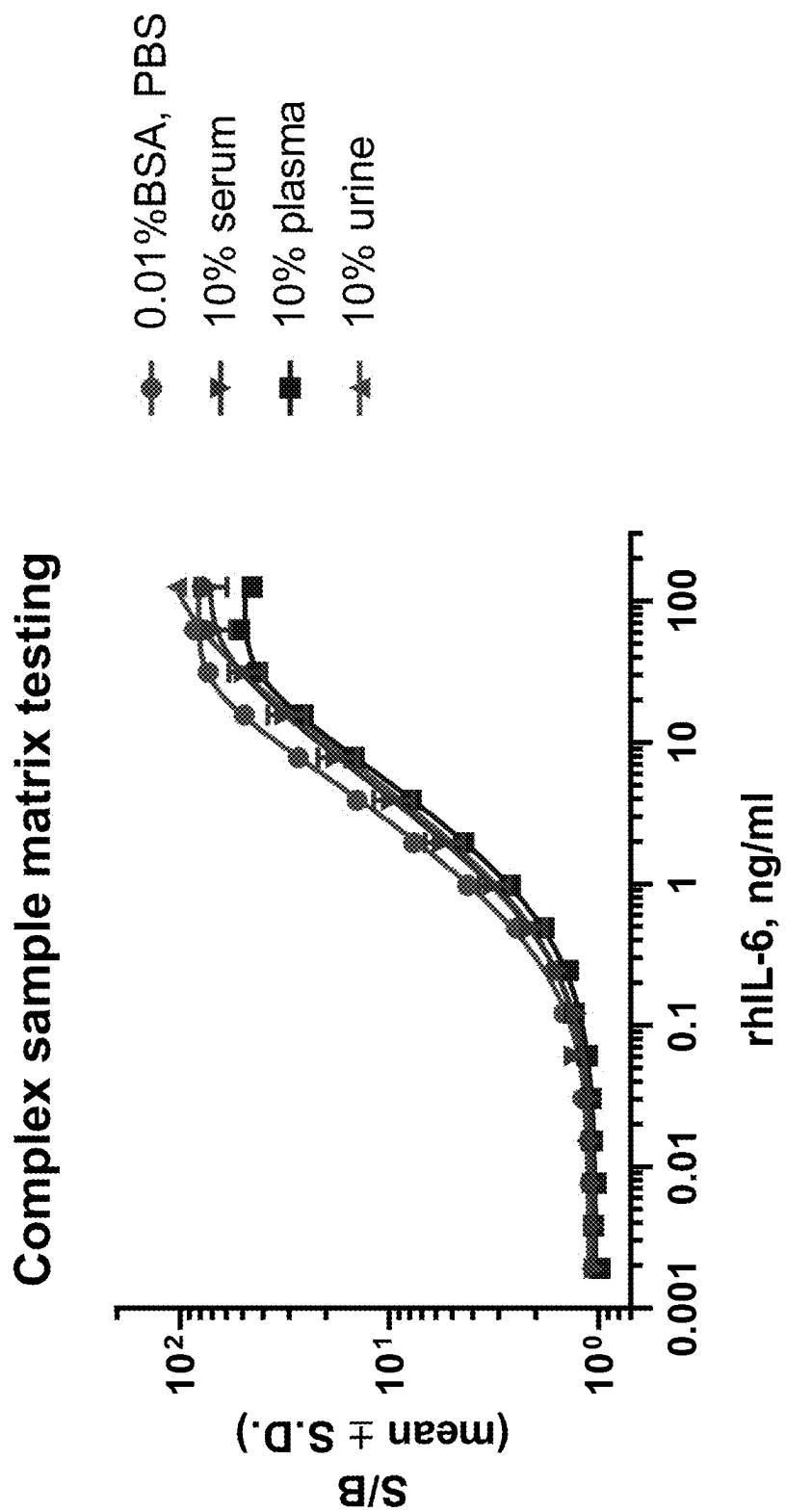


FIG. 55

FIG. 56A

Add sample and read

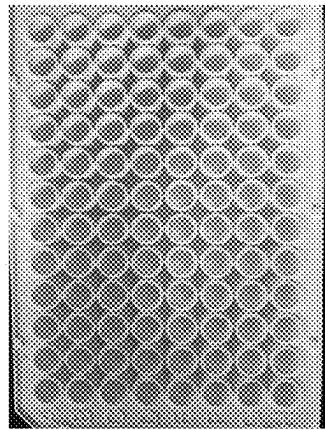
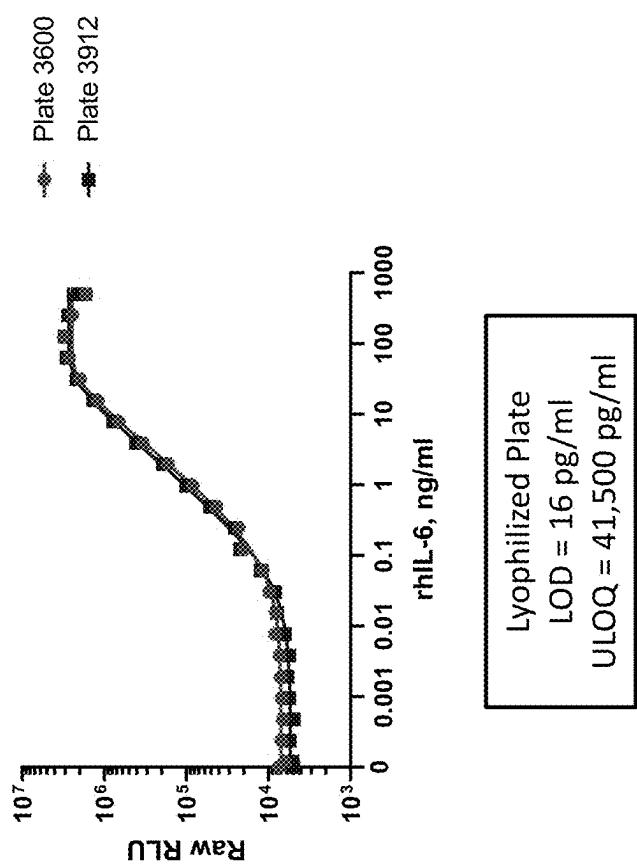


FIG. 56B

Single reagent lyophilized 96-well plate  
0.01% BSA in PBS assay buffer



FIGS. 56A-56B

FIG. 57A

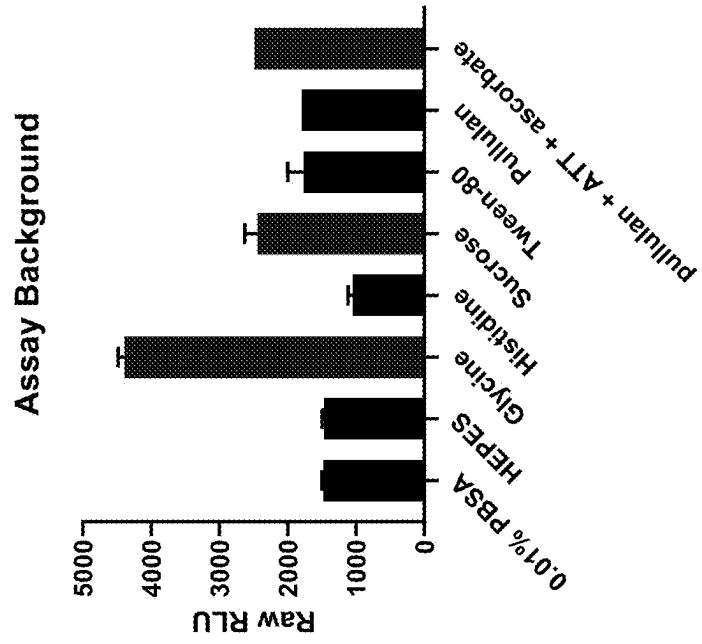
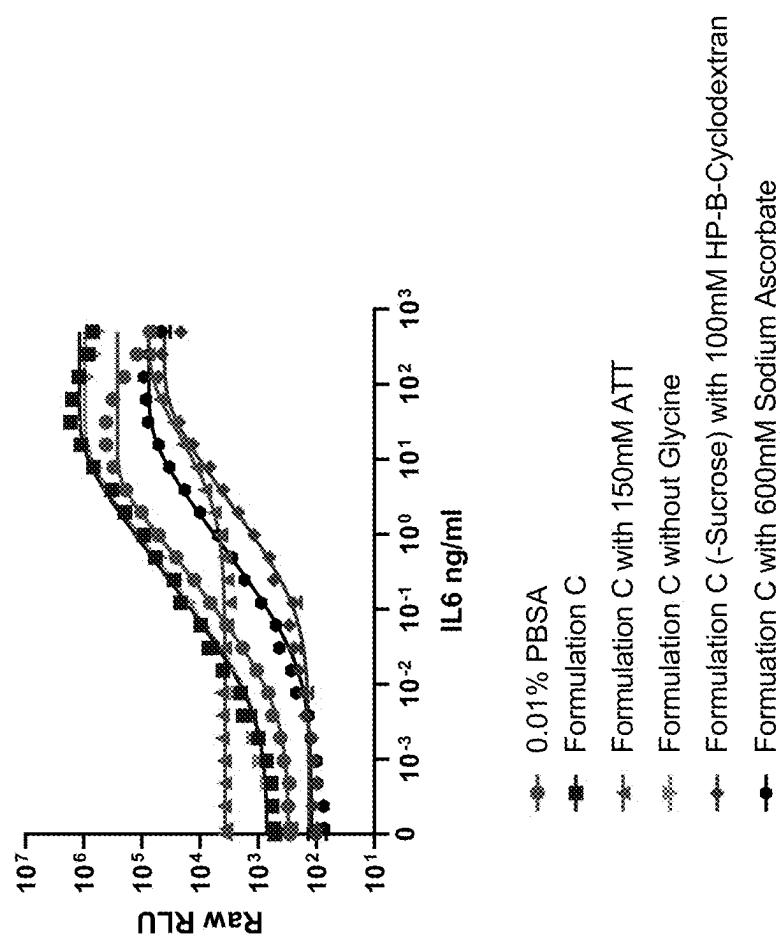


FIG. 57B

Solution-based assay formulations testing



FIGS. 57A-57B

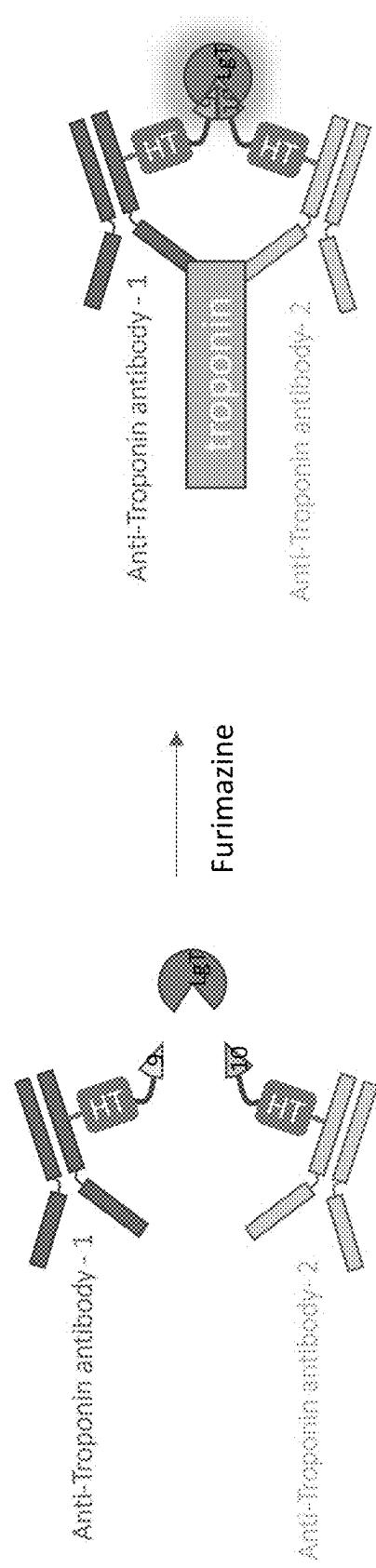


FIG. 58

FIG. 59A

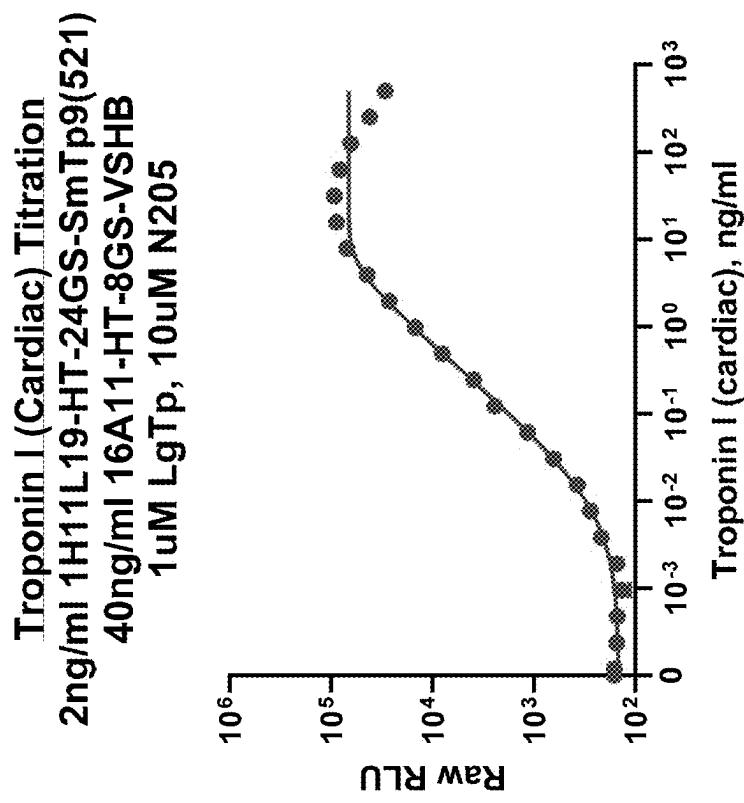
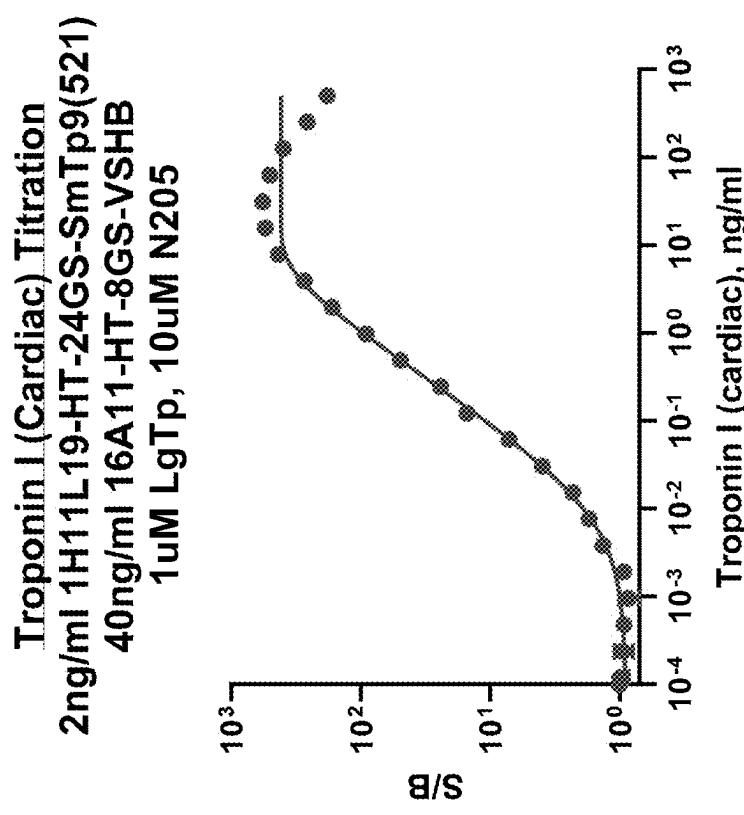


FIG. 59B



FIGS. 59A-59B

**Condition 12 of Lyo Run 4 Day 0**  
2ng/ml 1H11L19-HT-24GS-SmTp9(521)  
40ng/ml 16A11-HT-8GS-VSHB  
1uM LgTp, 10uM N113

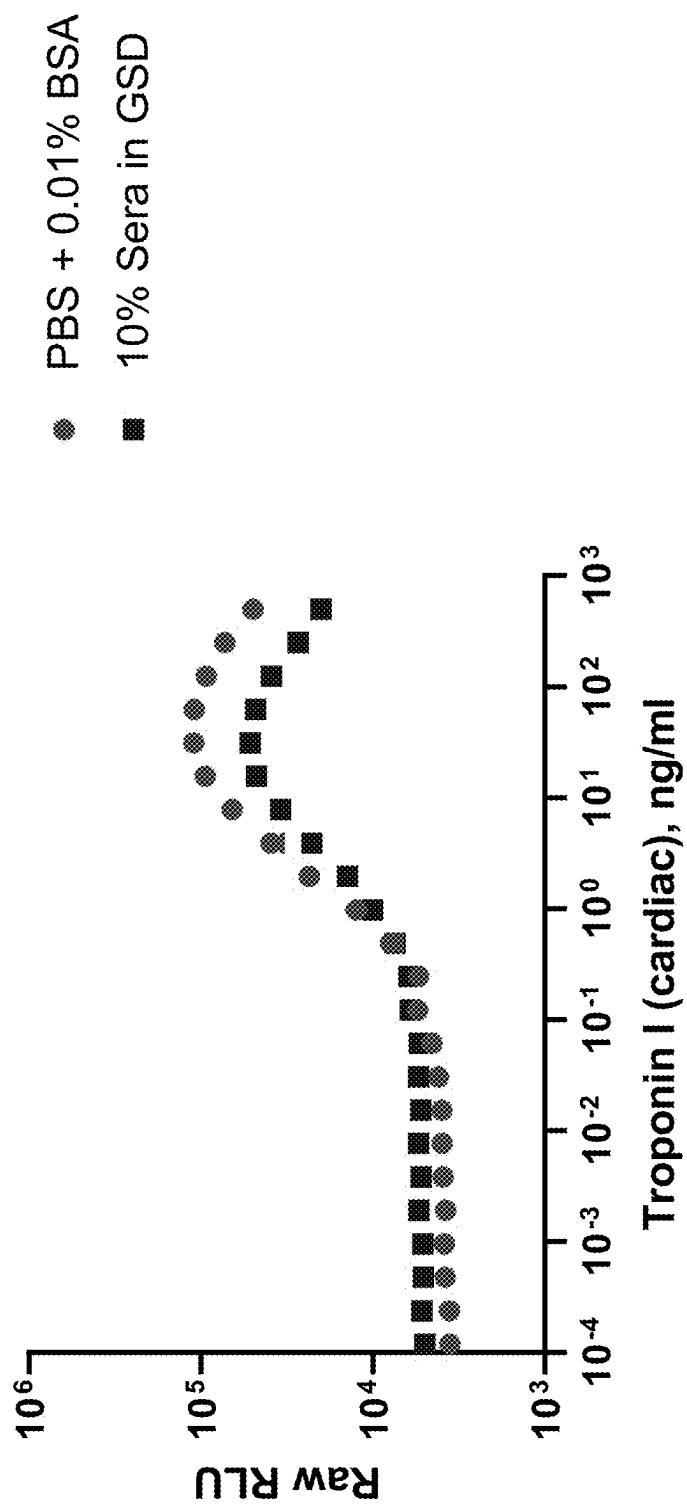


FIG. 60

FIG. 61A

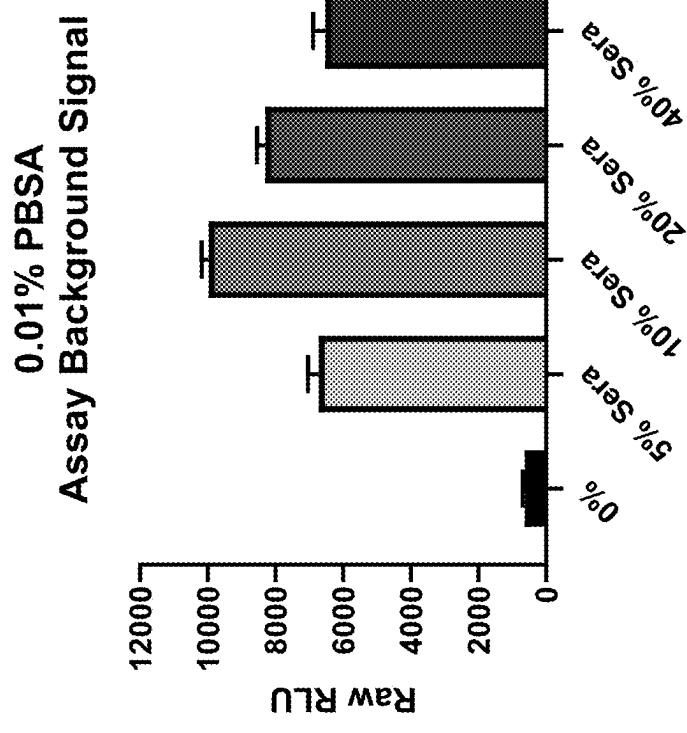
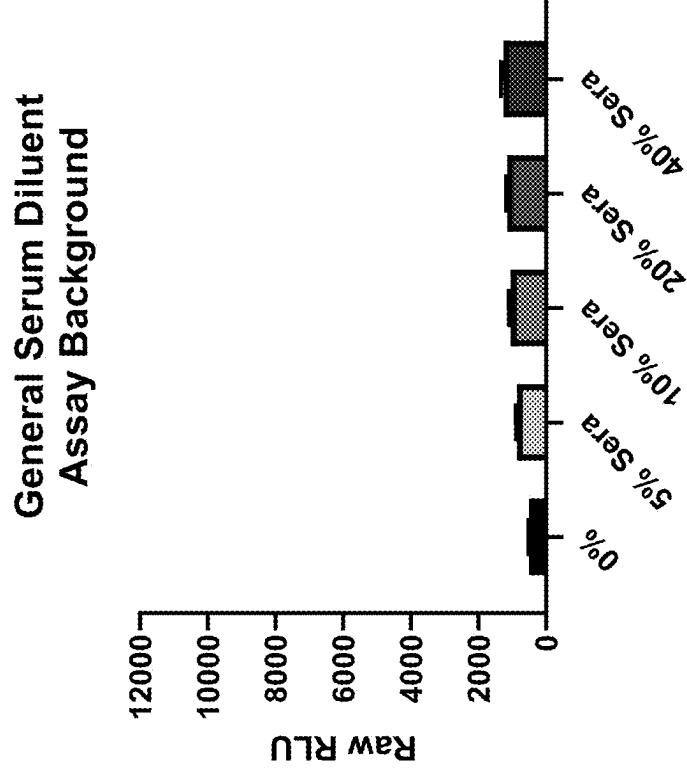


FIG. 61B



*Diluting samples with general serum diluent (GSD) preferred over PBSA. GSD mitigates non-specific IgG effects  
Using N205 as substrate*

FIGS. 61A-61B

FIG. 62A

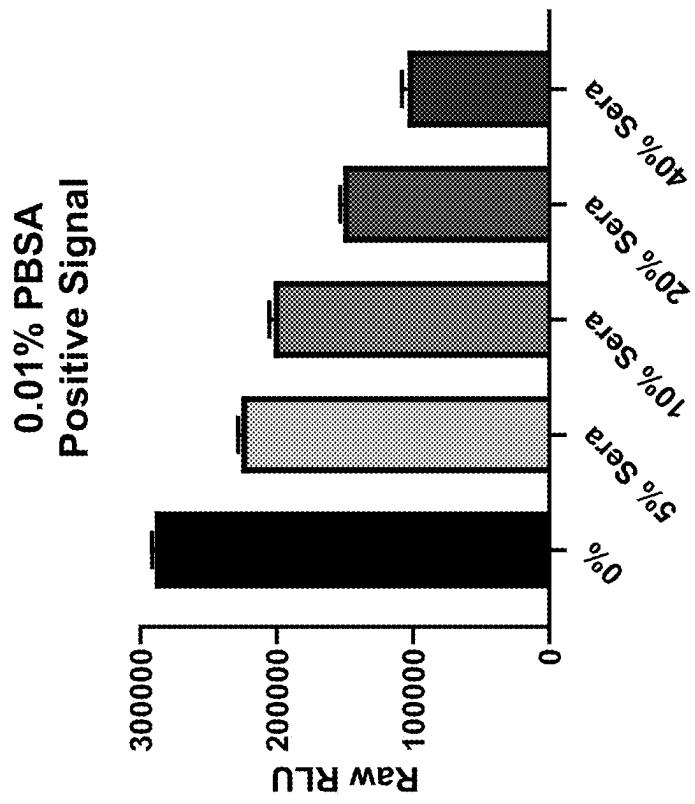


FIG. 62B

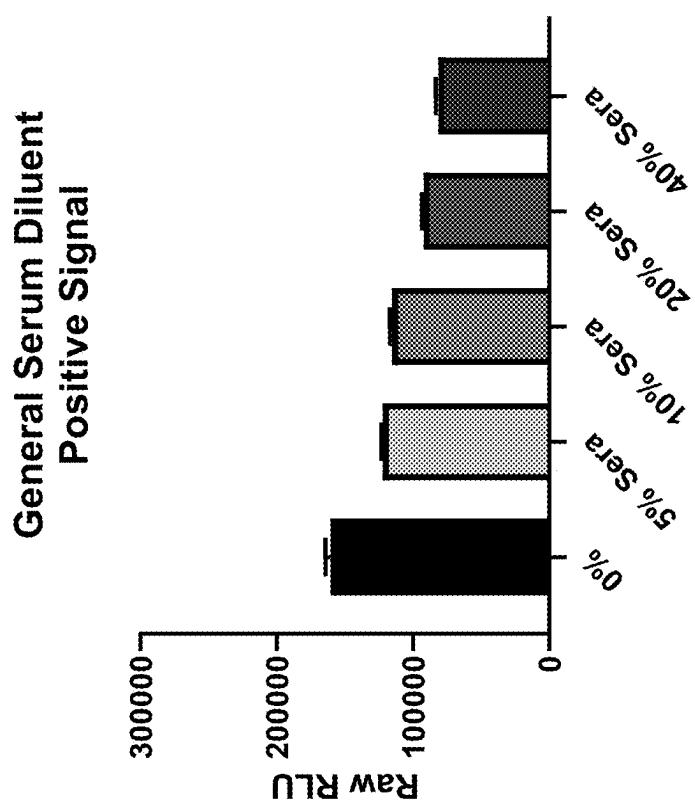


FIG. 63A

N205 (with ATT)

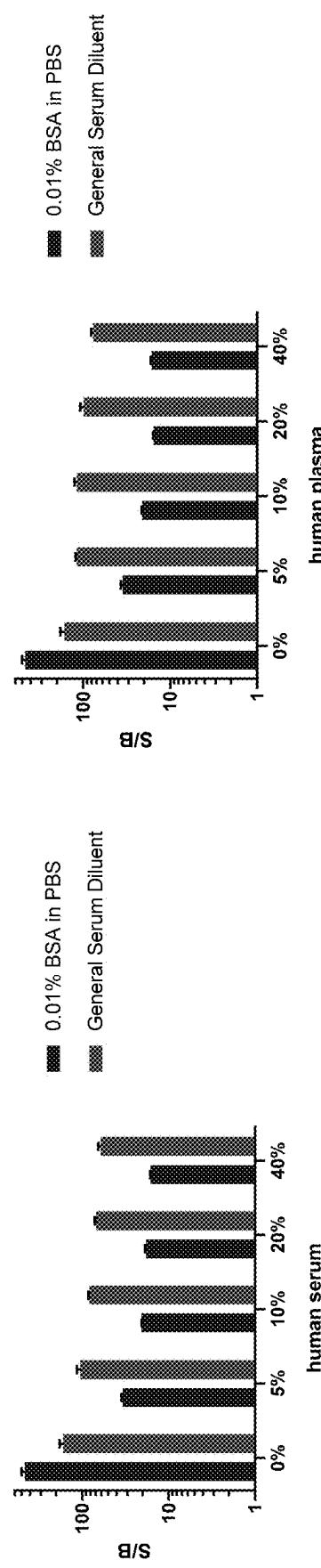


FIG. 63B

N205 (with ATT)

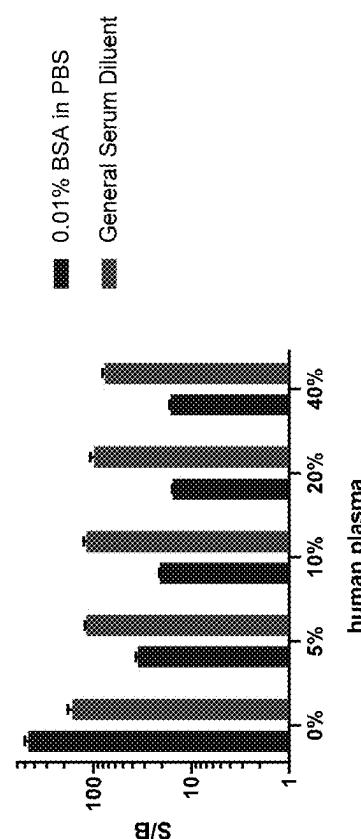


FIG. 63C

N113

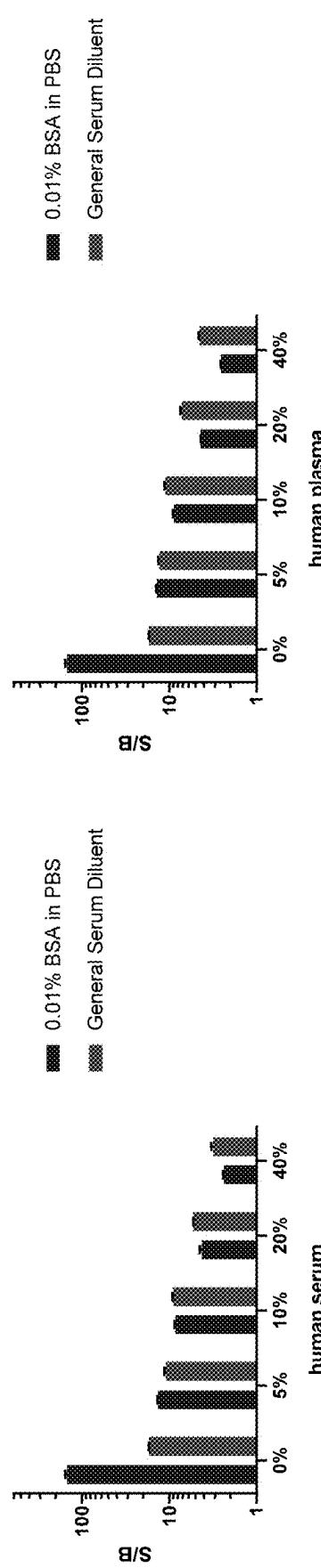
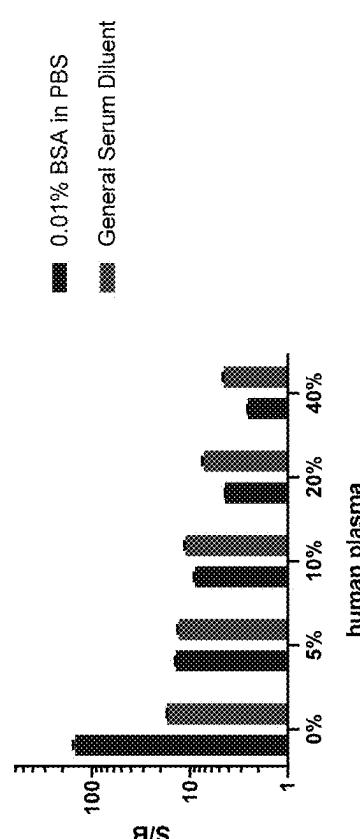


FIG. 63D

N113



FIGS. 63A-63D

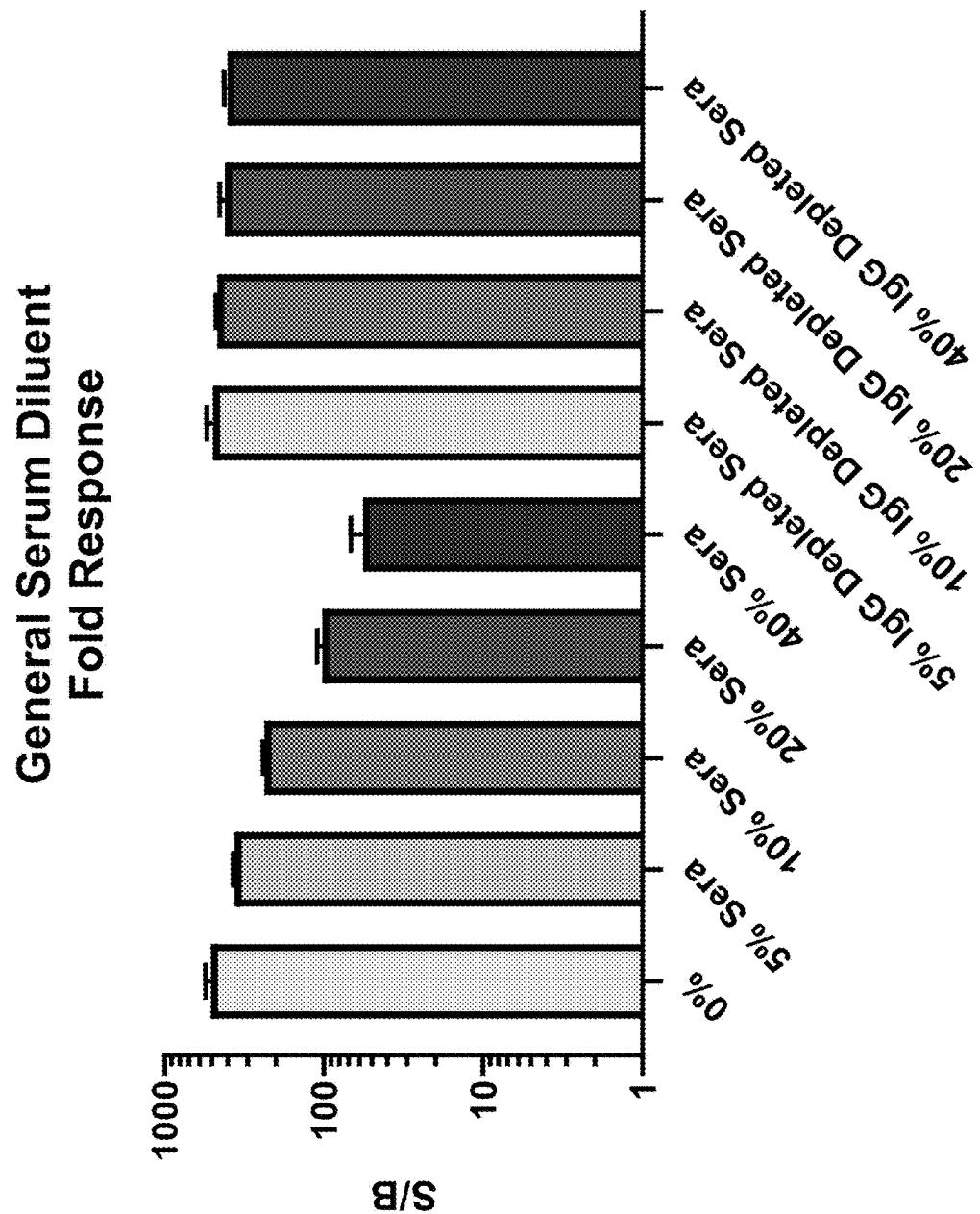


FIG. 64

FIG. 65A

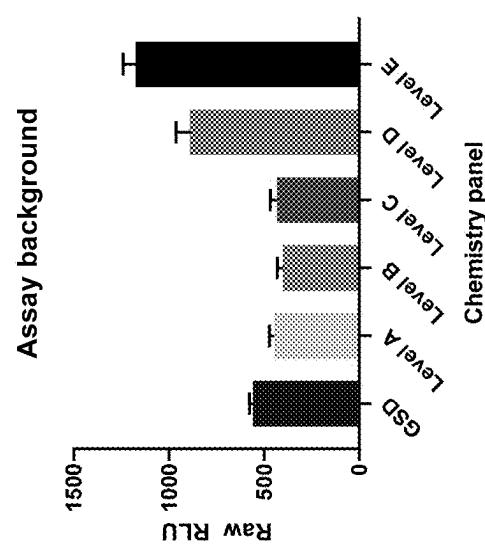


FIG. 65B

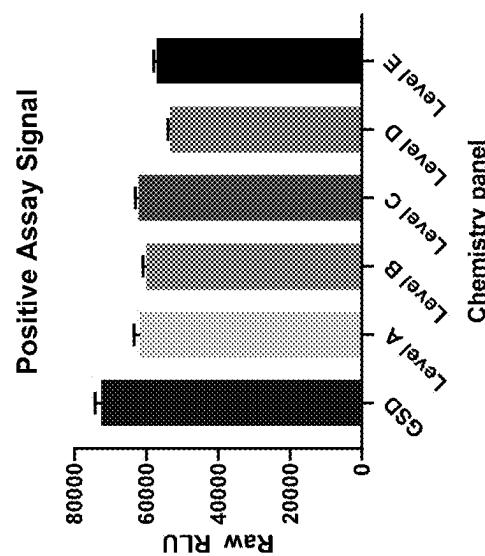
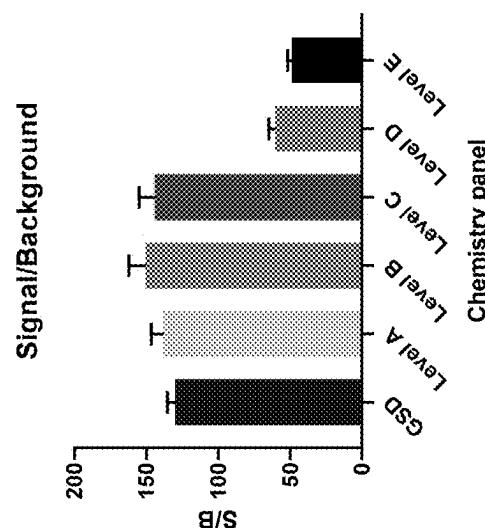


FIG. 65C



FIGS. 65A-65C

FIG. 66A

Assay Background

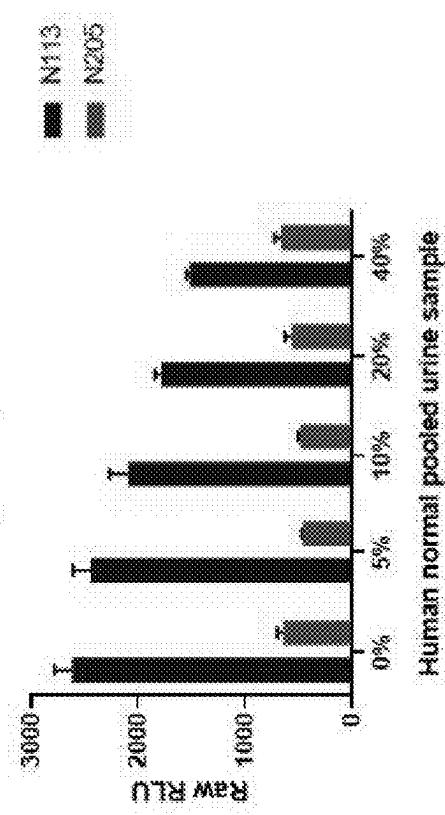


FIG. 66B

Positive Signal

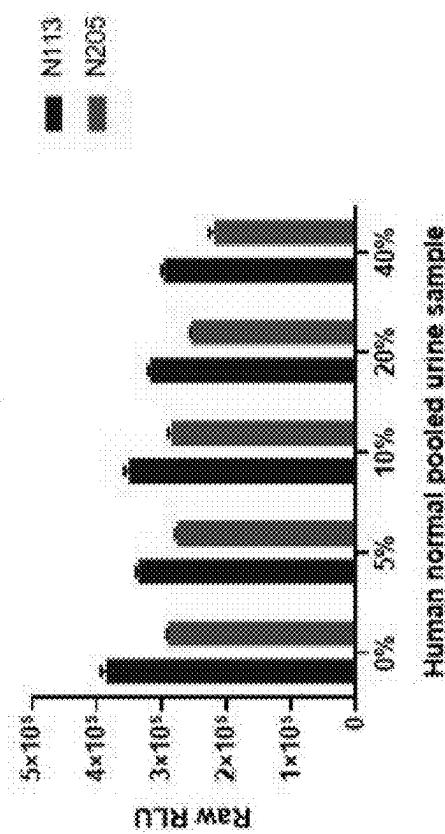
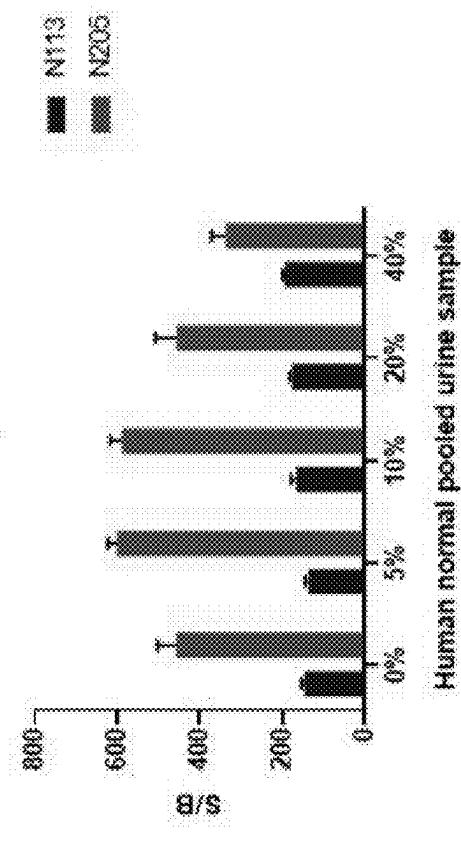


FIG. 66C

Fold Response



FIGS. 66A-66C

FIG. 67A

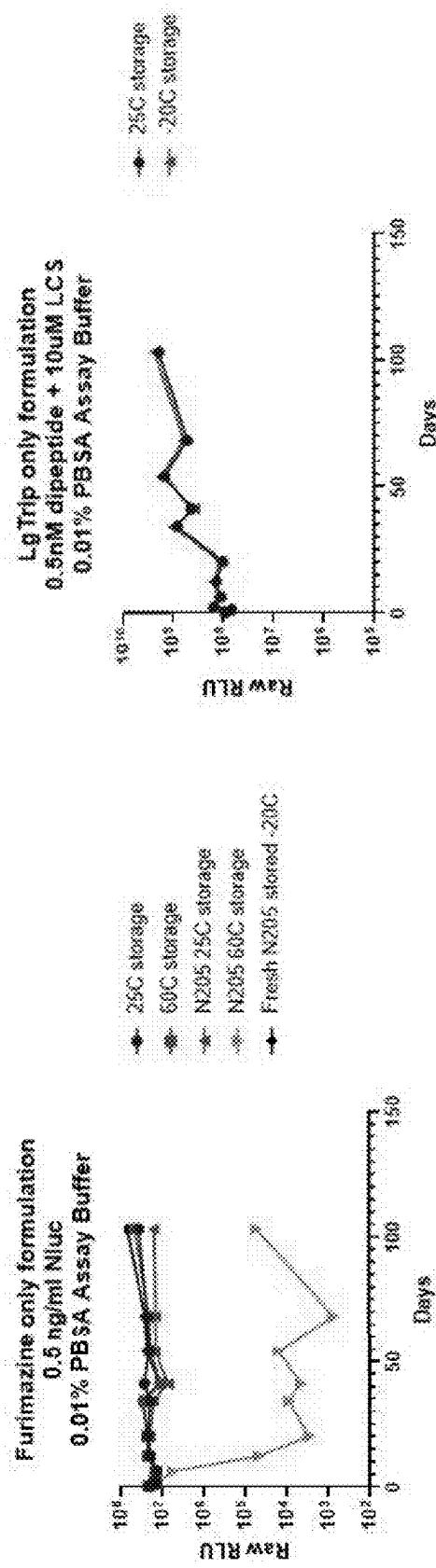


FIG. 67B

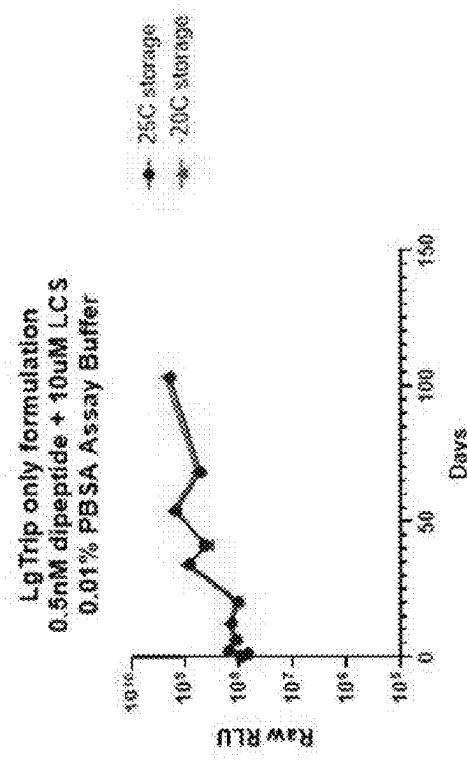
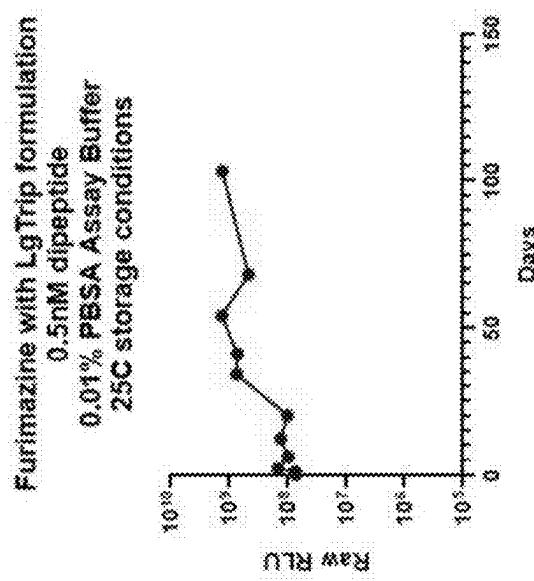


FIG. 67C



FIGS. 67A-76C

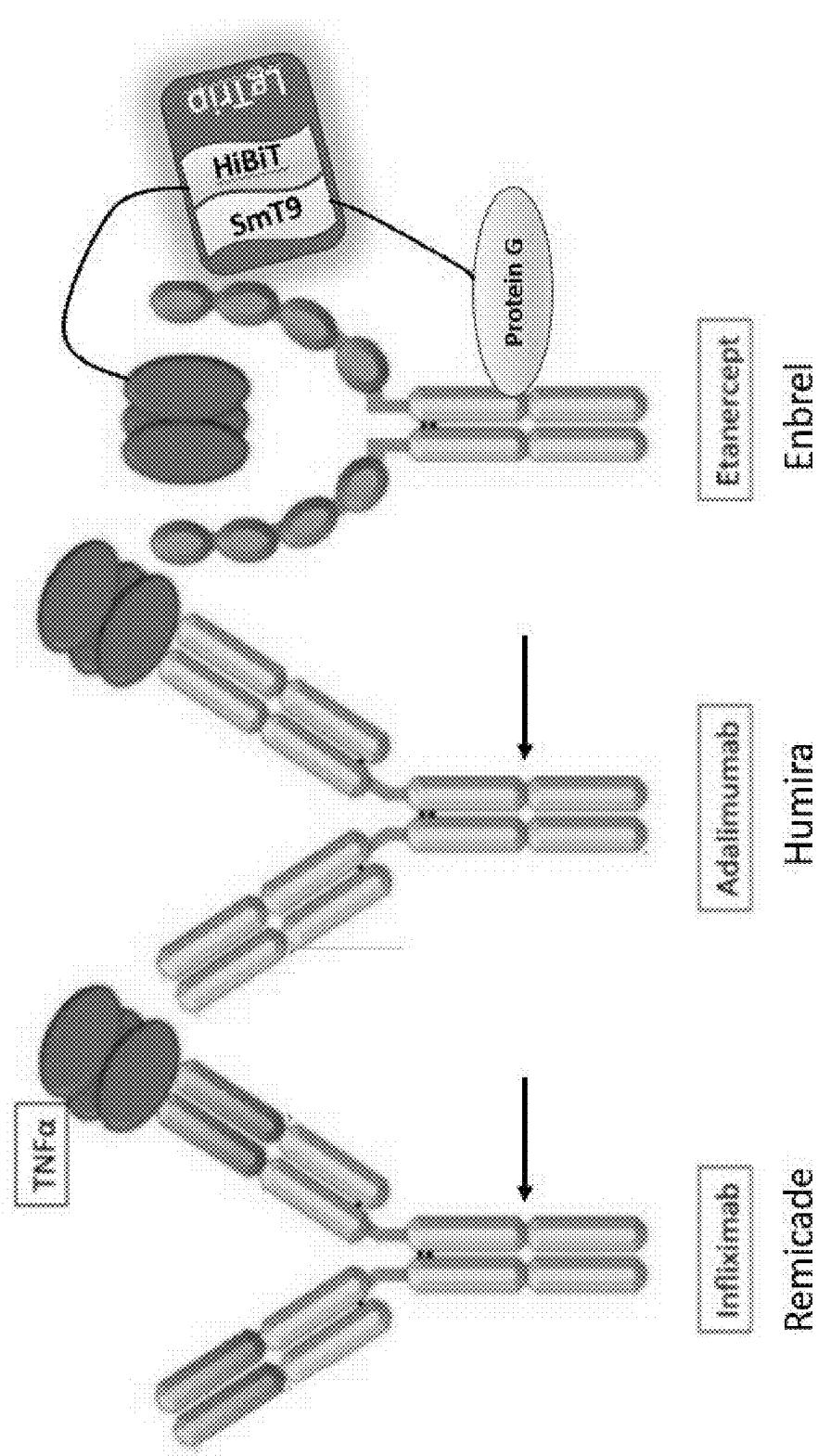
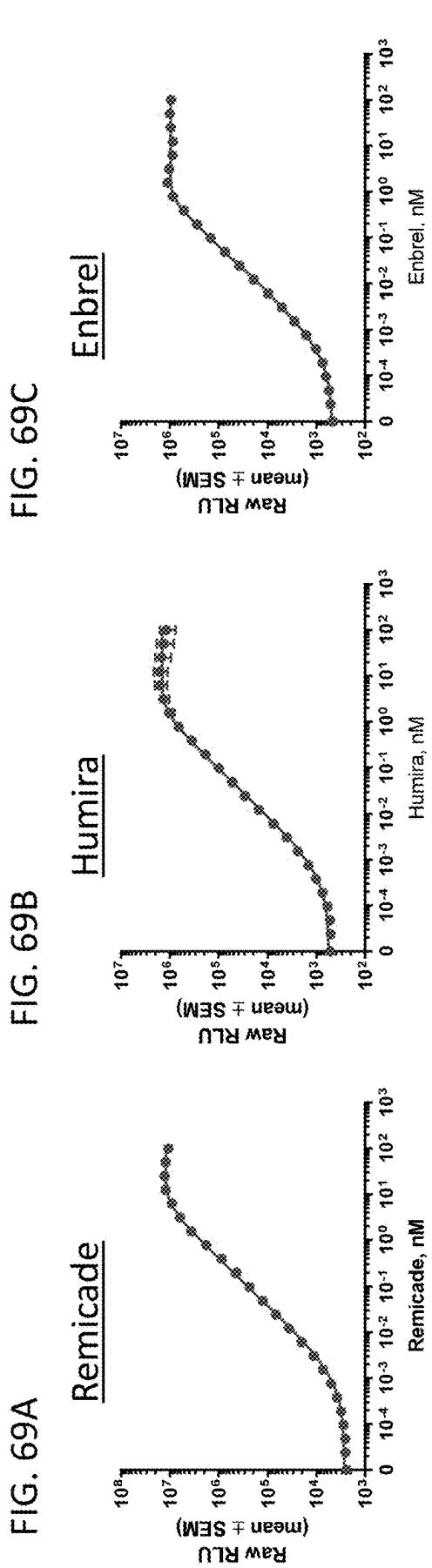


FIG. 68



**FIGS. 69A-69C**

FIG. 70A

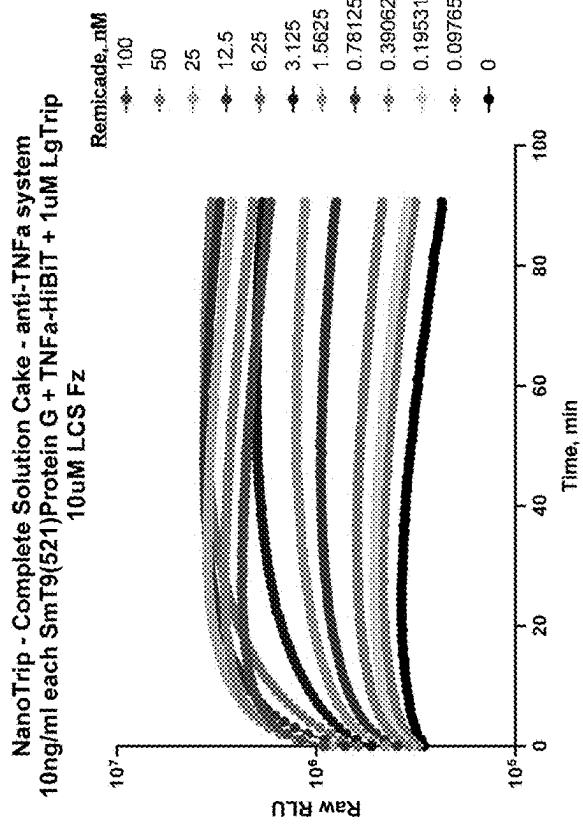
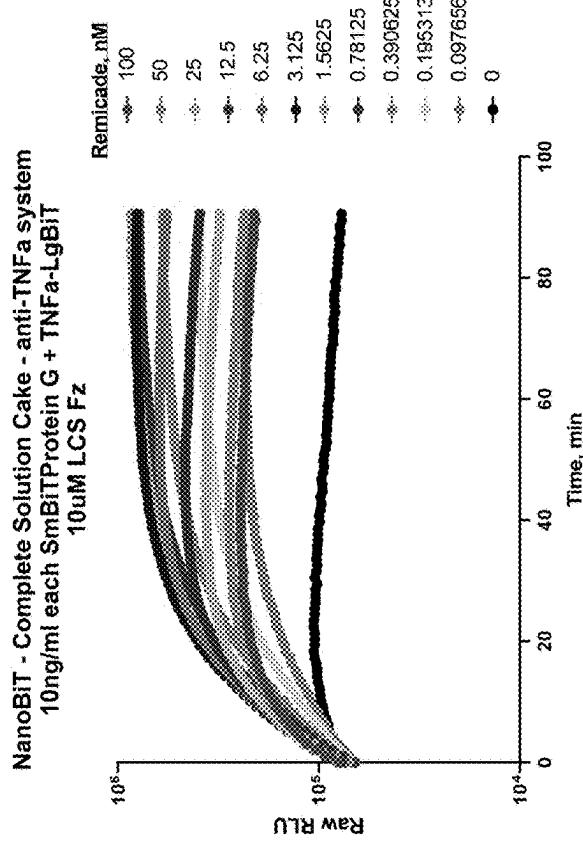


FIG. 70B



FIGS. 70A-70B

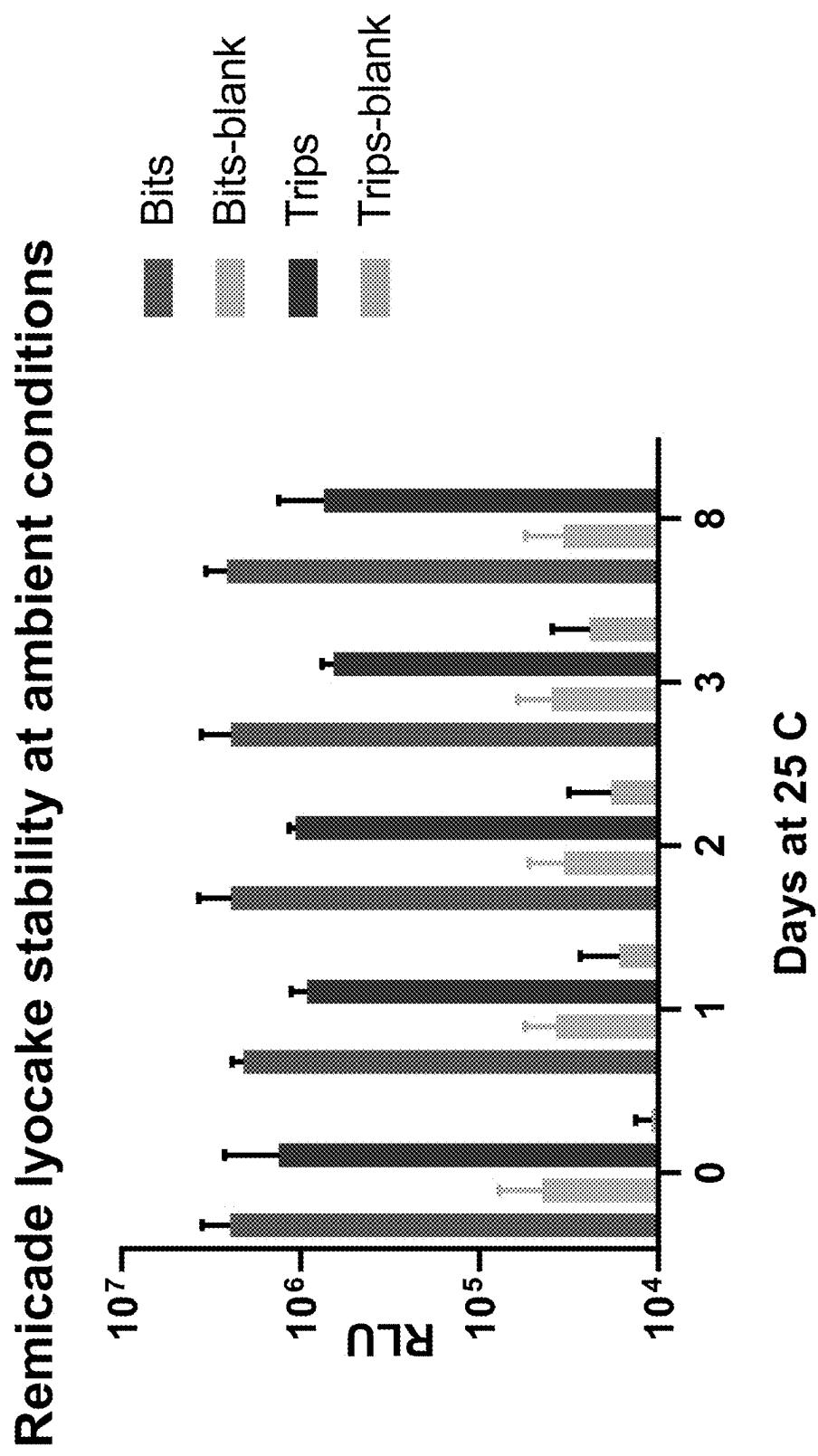
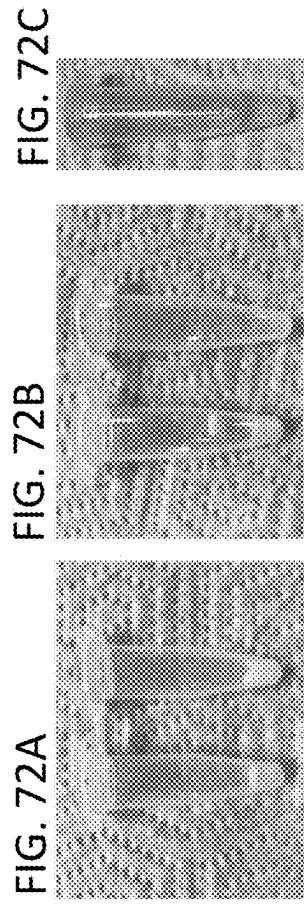
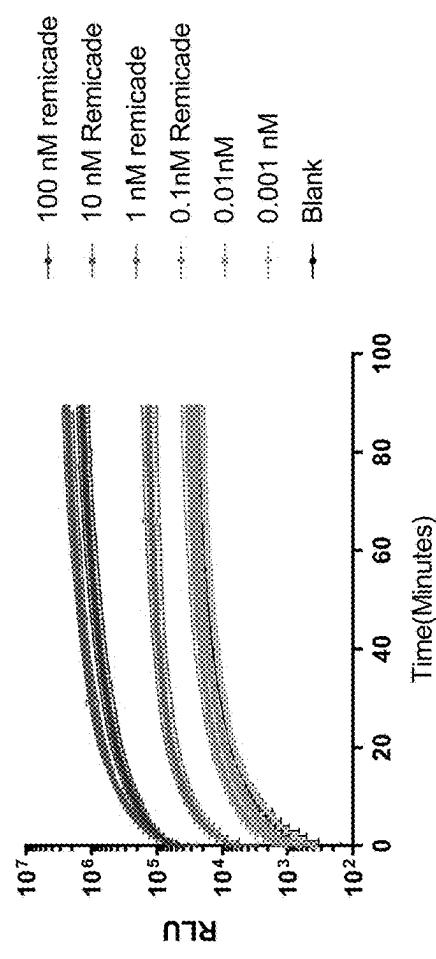


FIG. 71



**FIG. 72D**  
Dual-BIT Cake format / remicade detection



**FIG. 72A:**  
Formulated, split-cakes  
Yellow Vial: LgBIT-TNF $\alpha$  and furimazine  
White Vial: SmBIT – Protein G

**FIG. 72B:**  
Combining separate cakes manually

**FIG. 72C:**  
Reconstituted cakes in opti-mem  
buffer containing analyte of interest

**FIG. 72D:**  
Light output of Split NanoBIT cakes  
after reconstitution in the presence of  
increasing amounts of Remicade

**FIGS. 72A-72D**

Dual-Trip cake format/ remicade detection

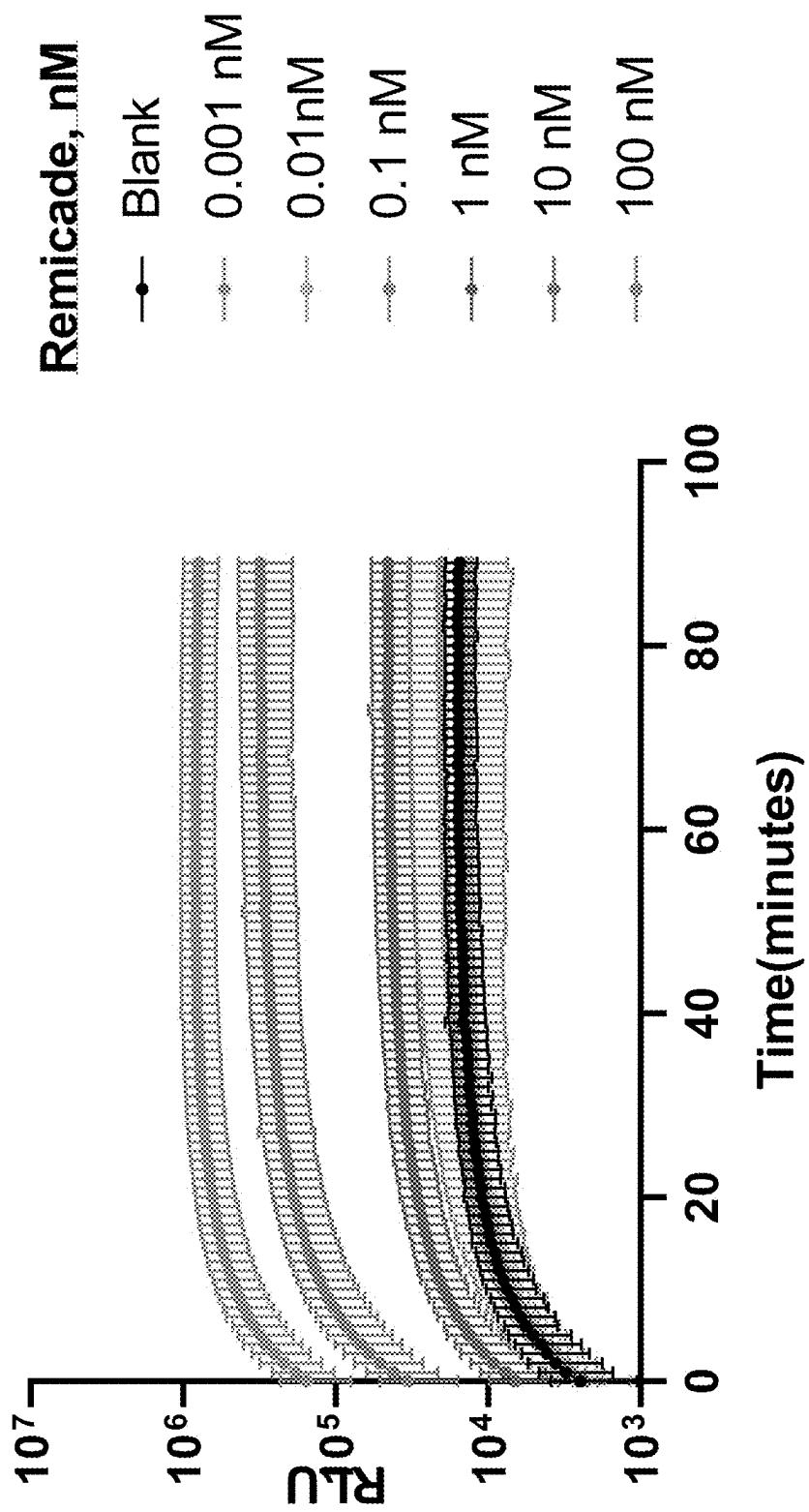


FIG. 73

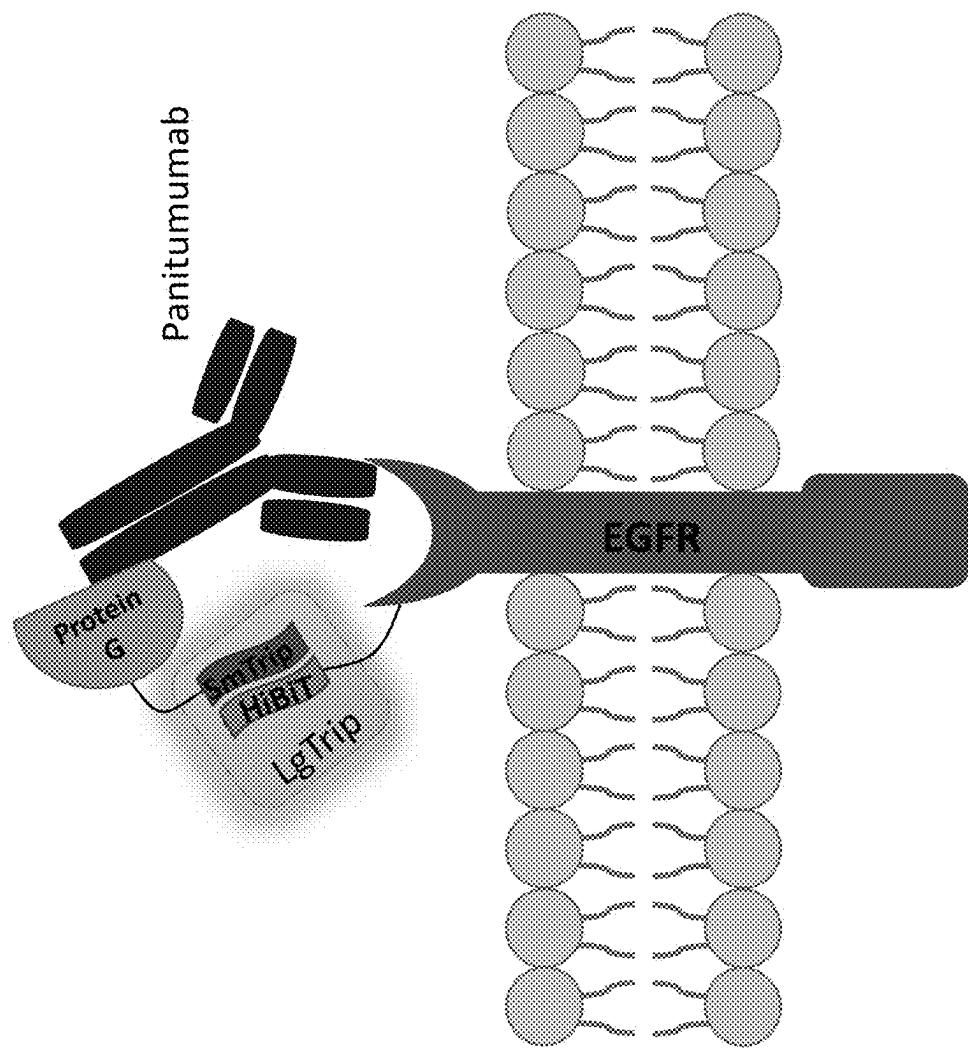


FIG. 74

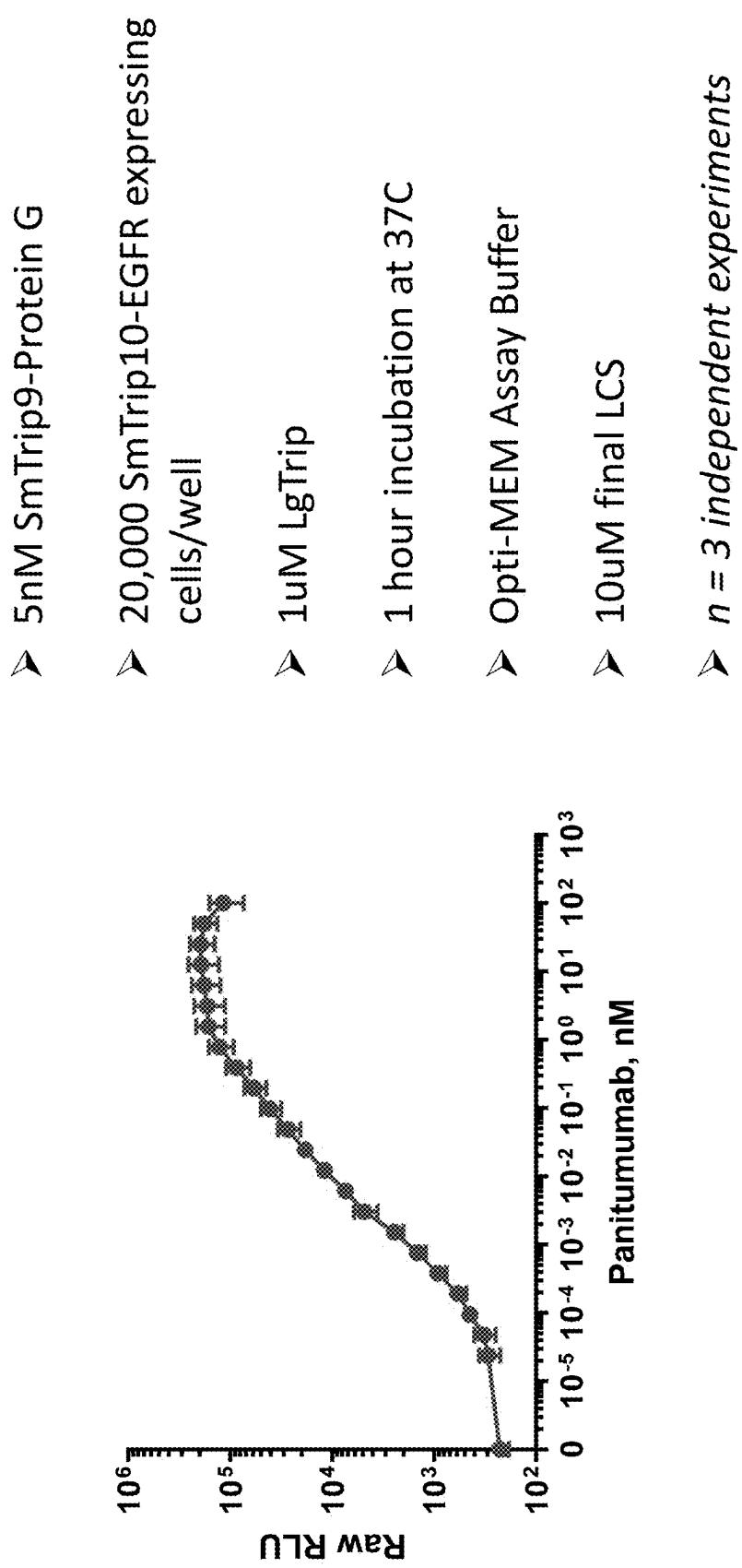


FIG. 75

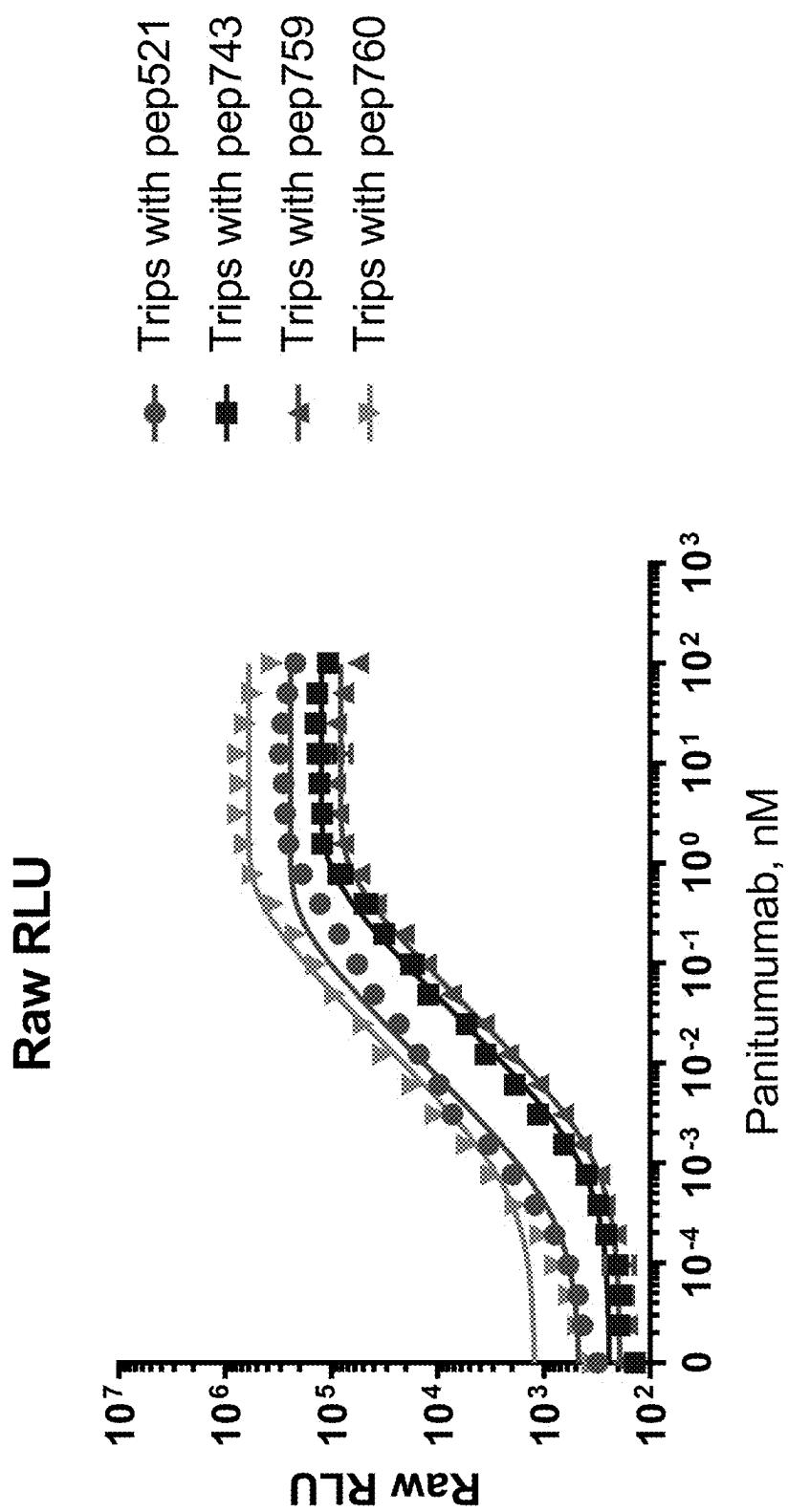
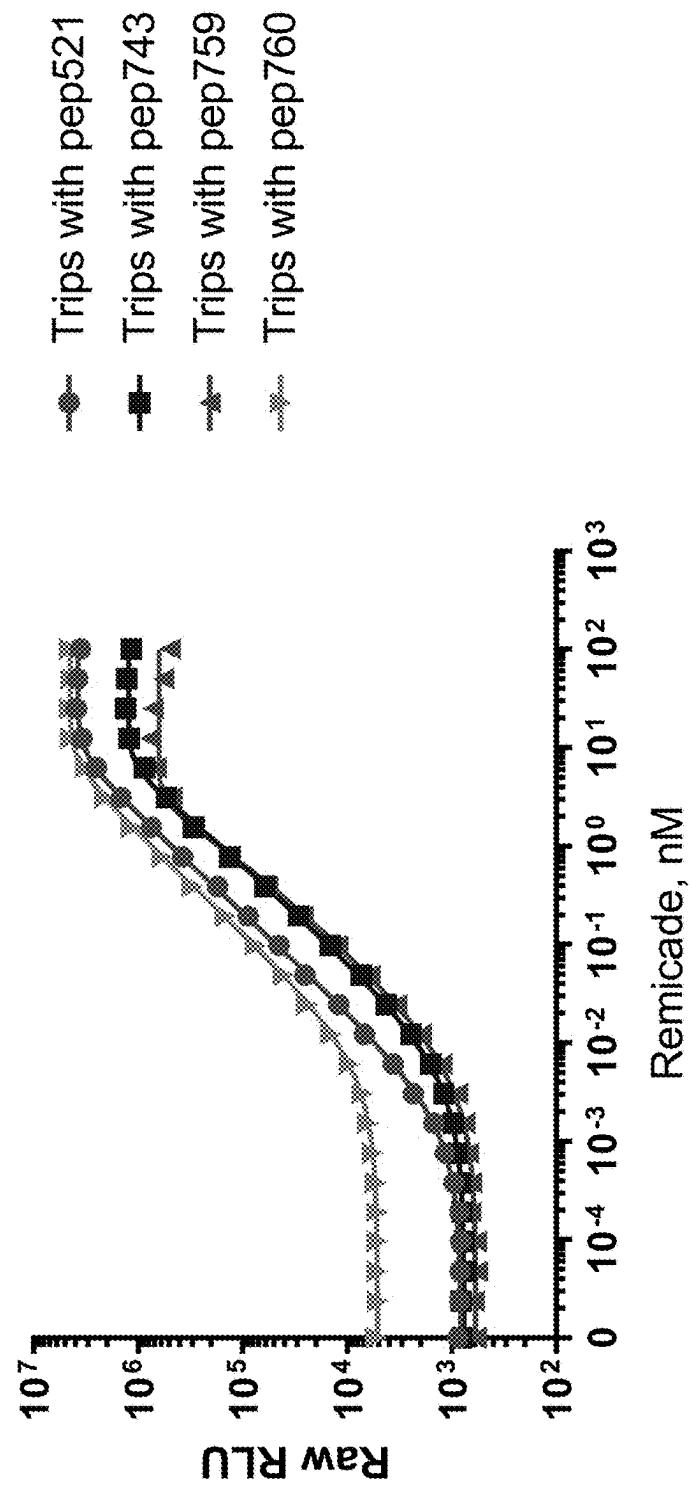


FIG. 76

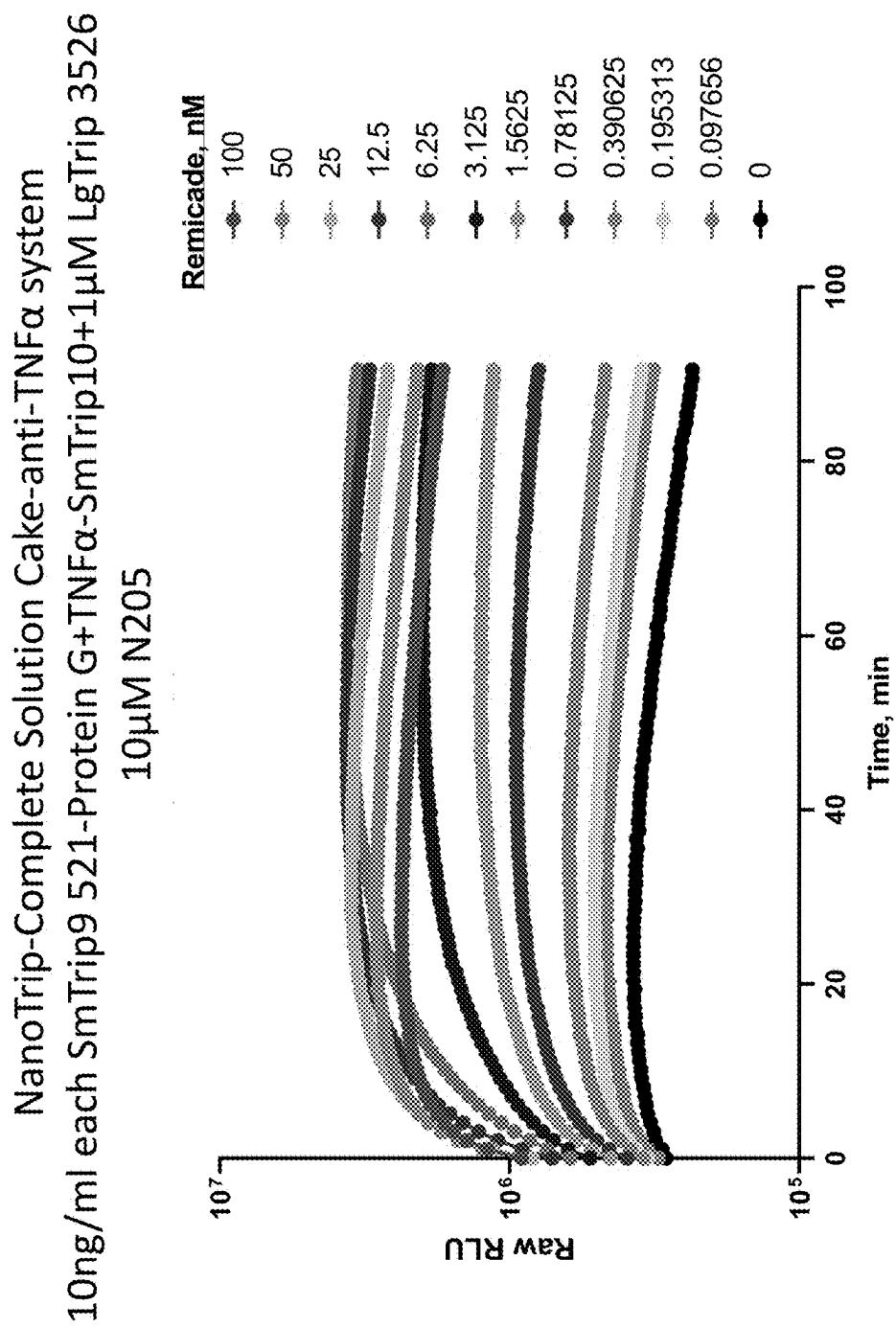
FIG. 77A

**Remicade Titration (anti-TNF $\alpha$  Model)**  
**10nM components, 1 $\mu$ M Lg Trip**  
**90minute 37C Incubation, 10 $\mu$ M LGS**



FIGS. 77A-77B

FIG. 77B



FIGS. 77A-77B

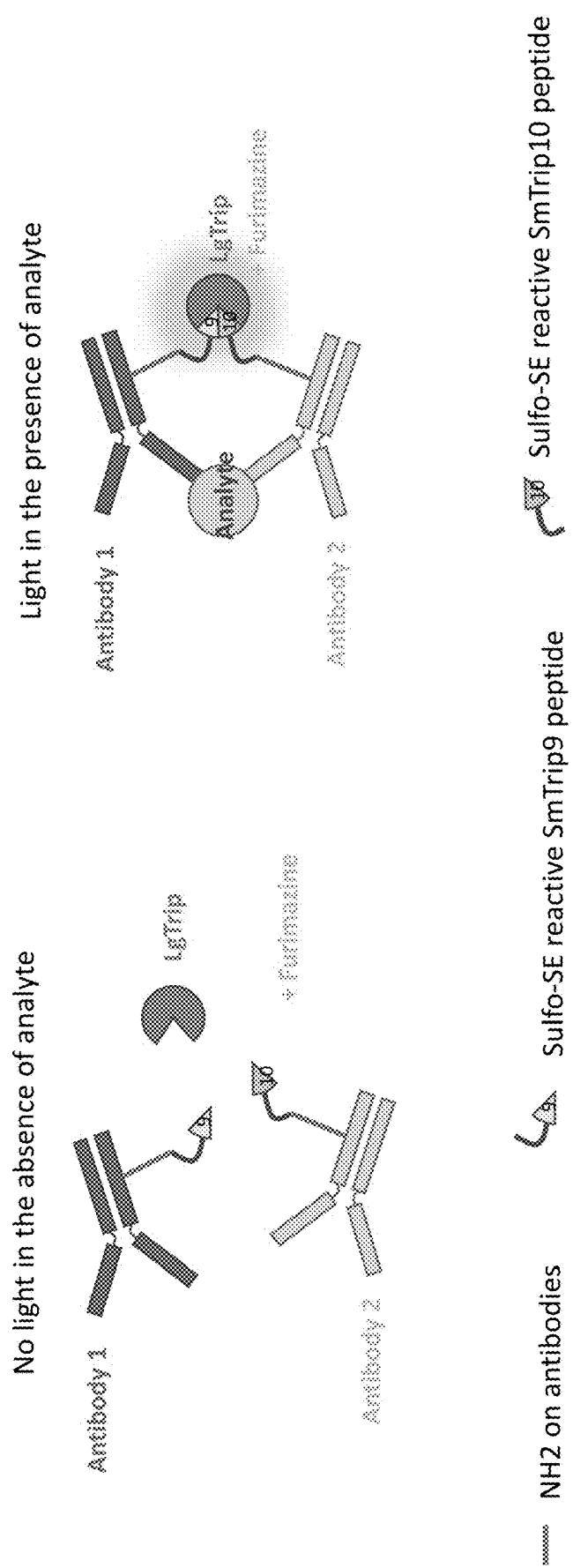
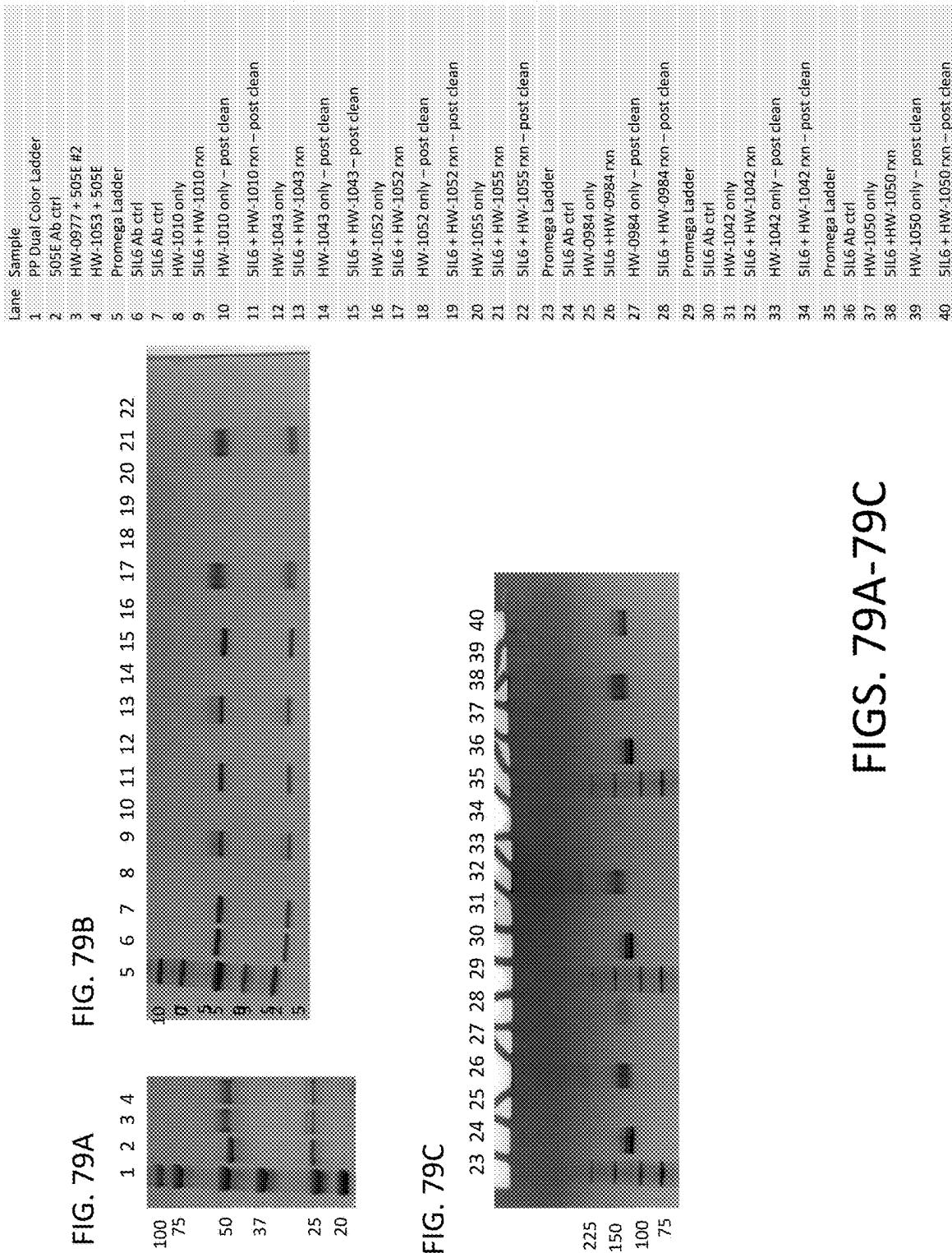


FIG. 78



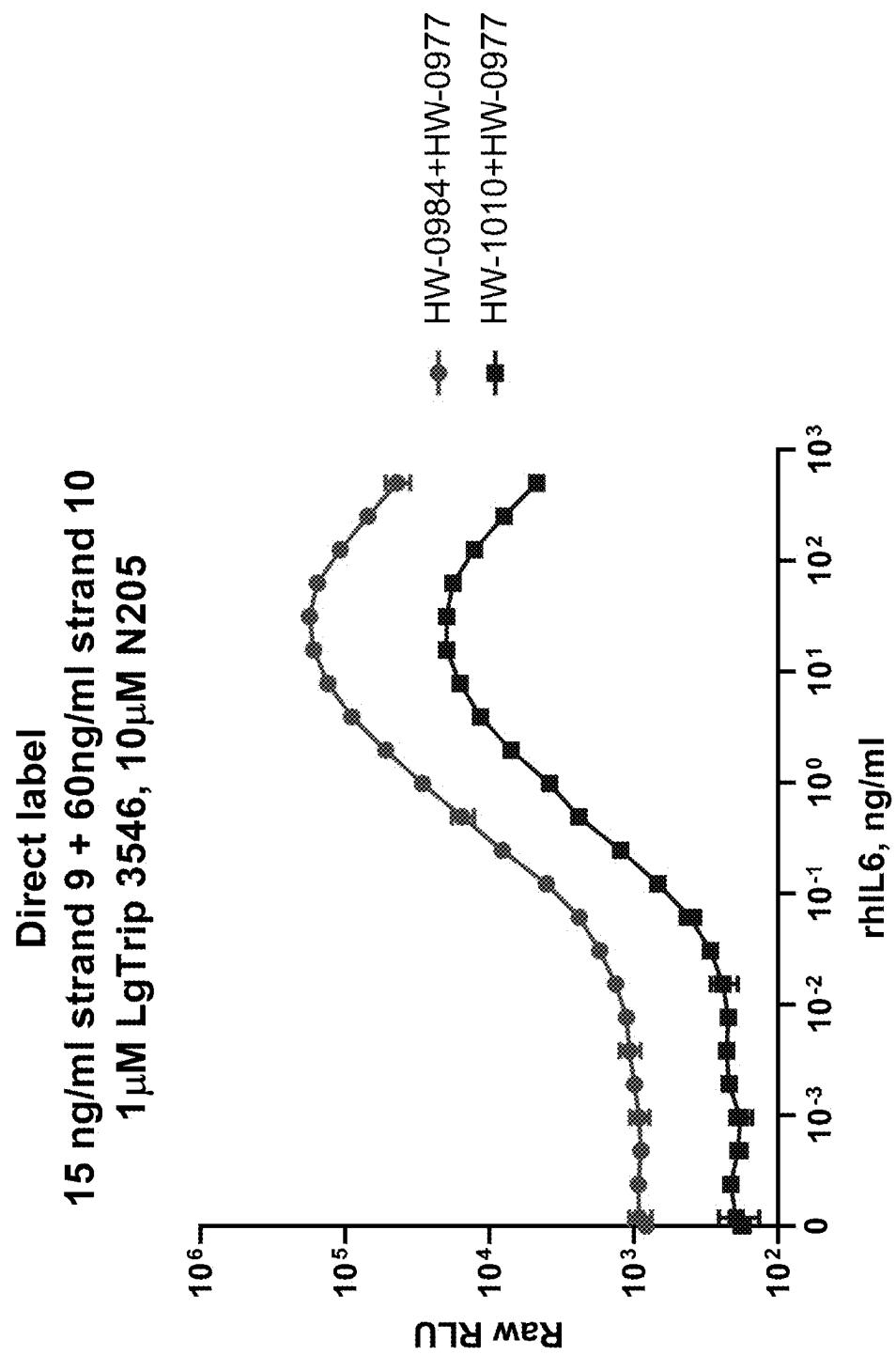


FIG. 80

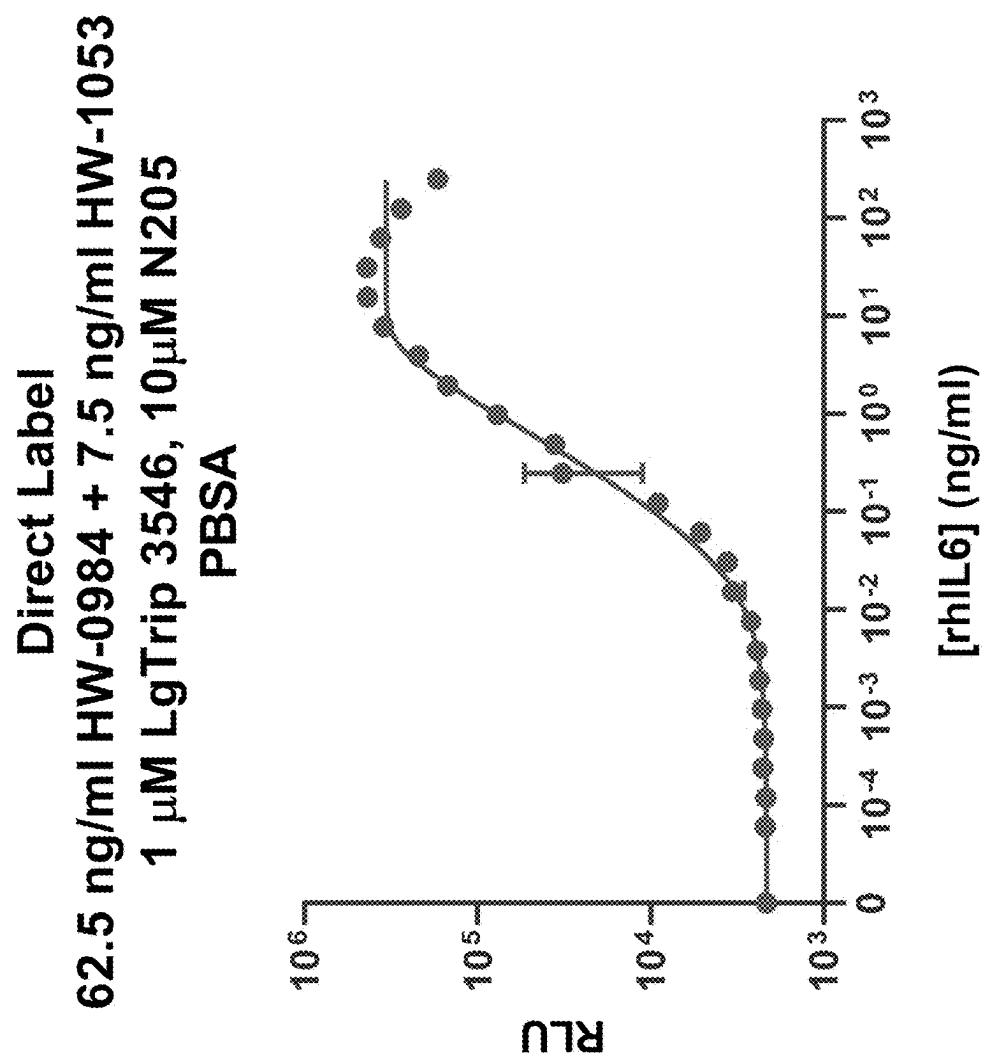


FIG. 81

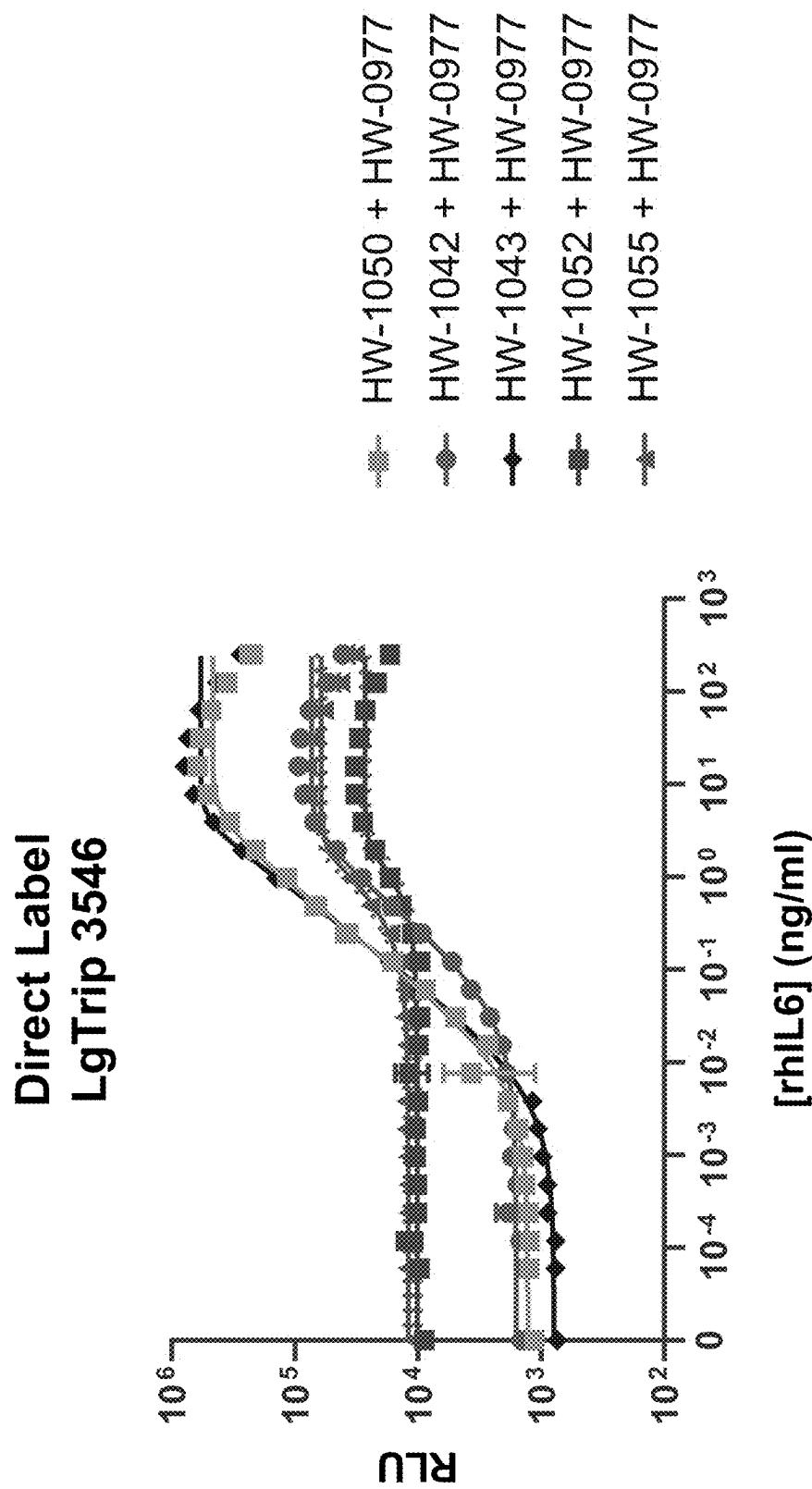


FIG. 82

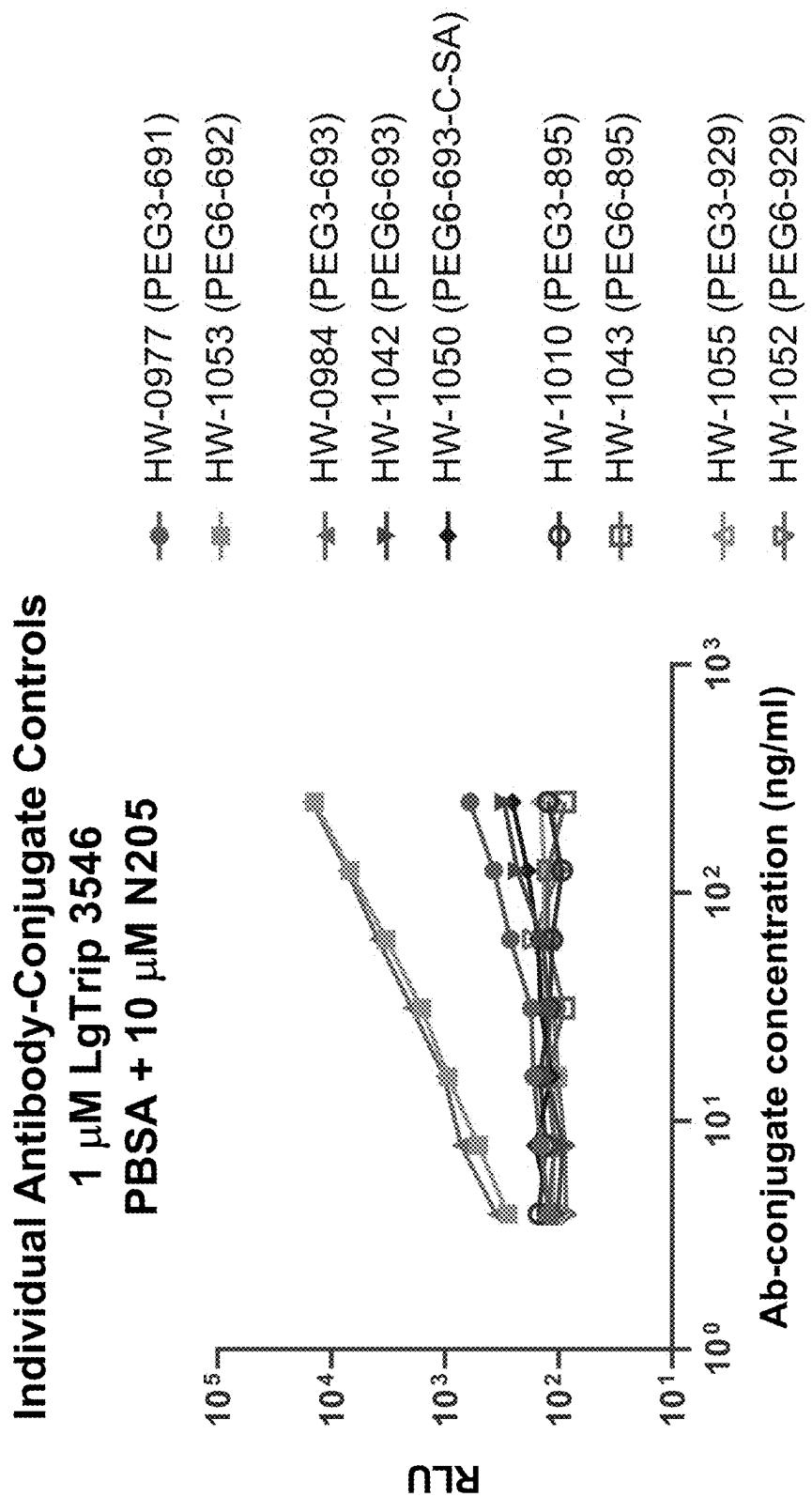
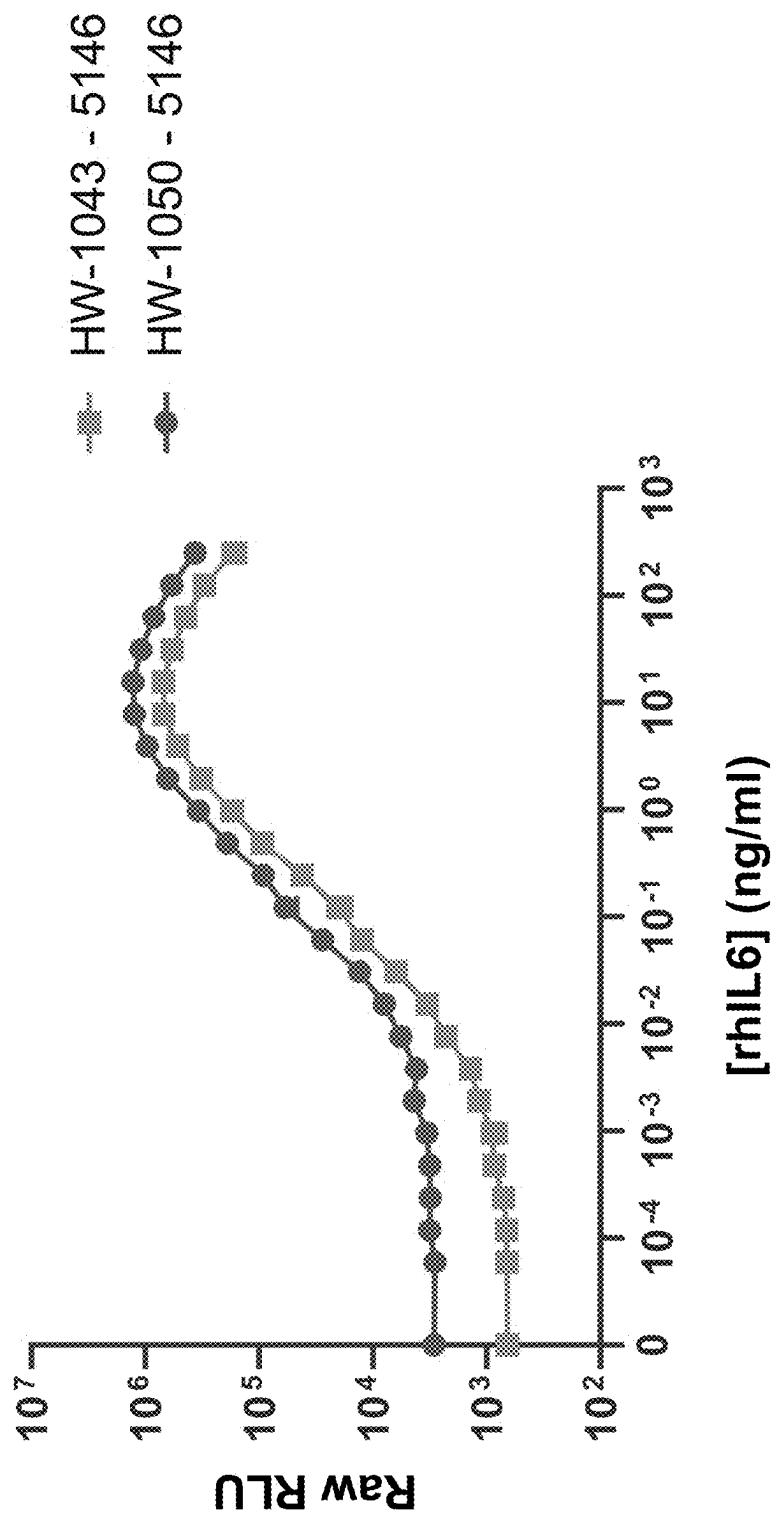


FIG. 83

**Direct Label  
LgTrip 5146**



**FIG. 84**

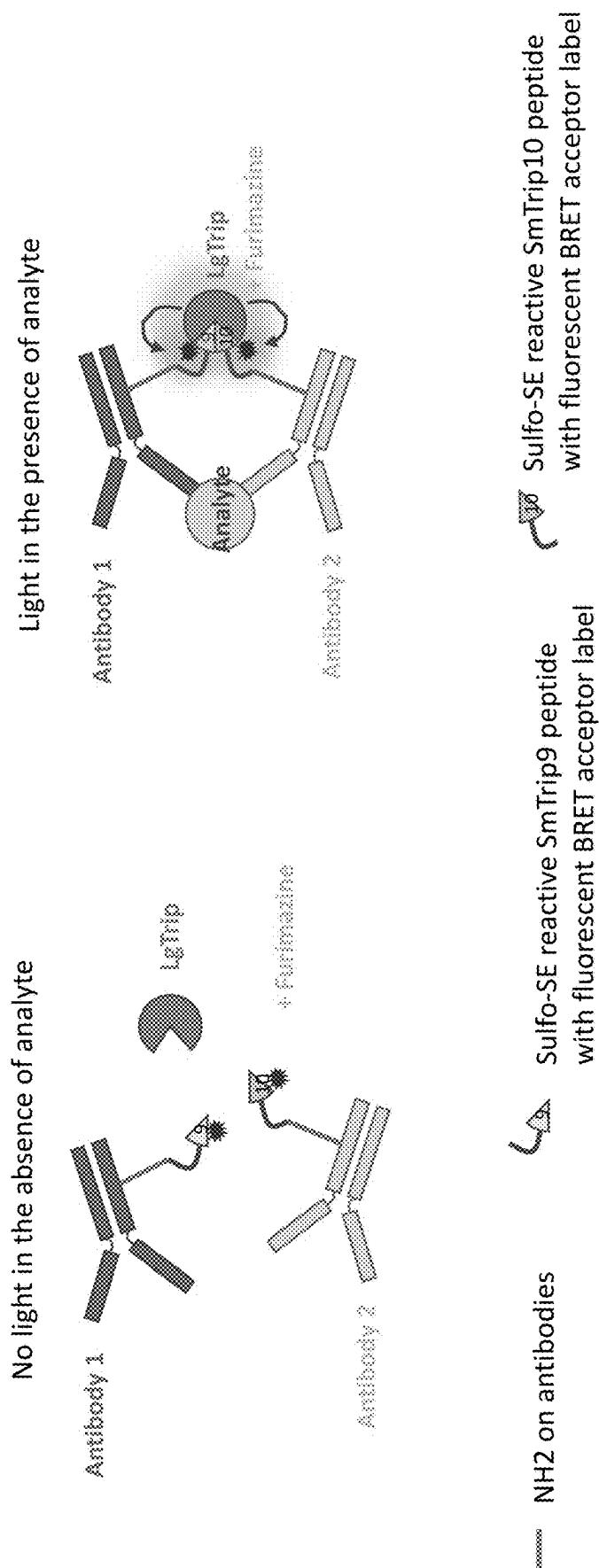


FIG. 85

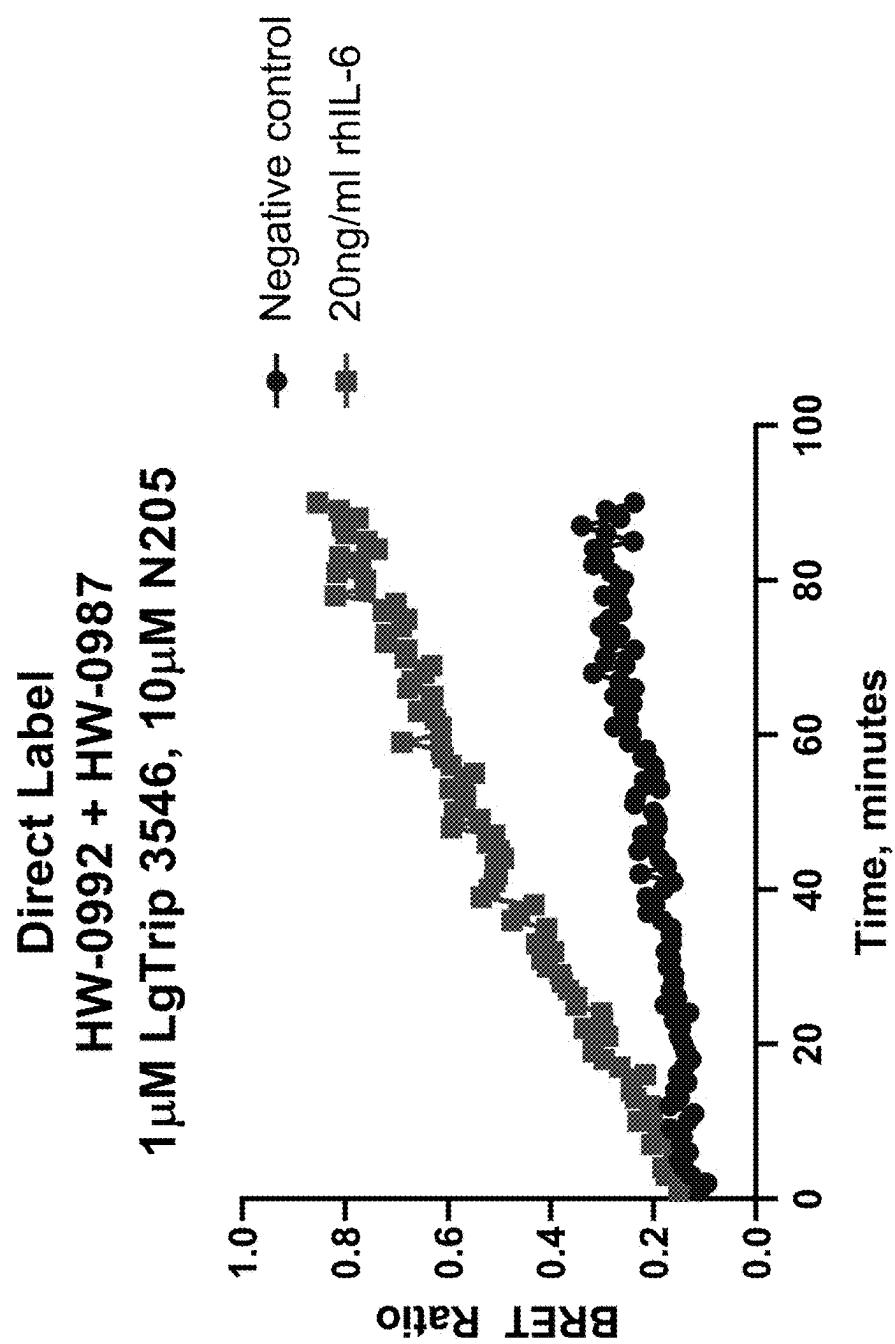


FIG. 86

FIG. 87A

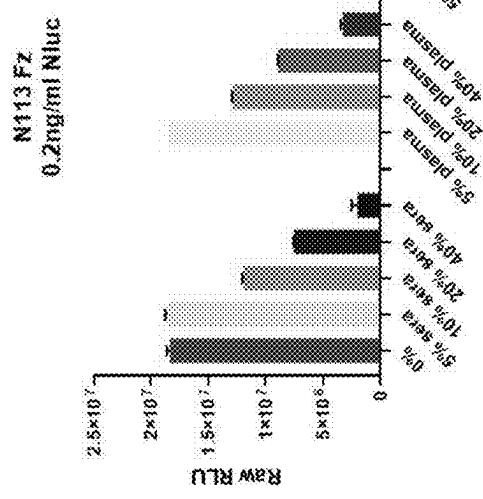


FIG. 87B

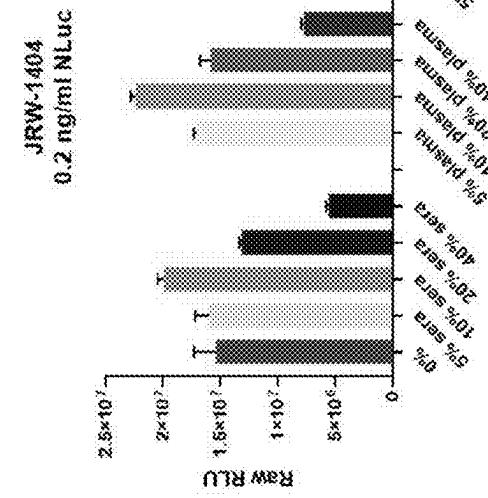
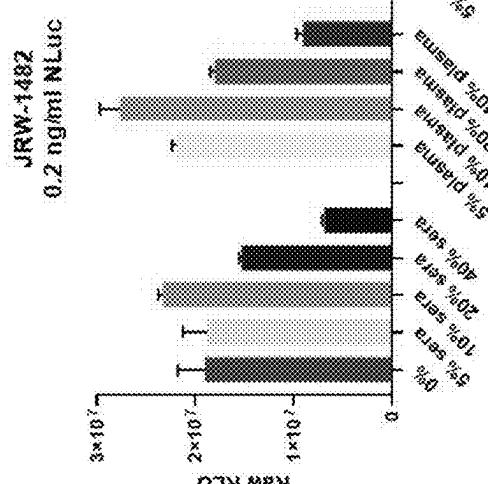


FIG. 87C



FIGS. 87A-87C

## COMPOSITIONS AND METHODS FOR ANALYTE DETECTION USING BIOLUMINESCENCE

### CROSS REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a continuation of U.S. patent application Ser. No. 16/845,802, filed Apr. 10, 2020, which claims priority to and the benefit of U.S. Provisional Patent Application No. 62/832,052, filed Apr. 10, 2019, which is incorporated herein by reference in its entirety and for all purposes.

### SEQUENCE LISTING

[0002] The text of the computer readable sequence listing filed herewith, titled "PRMG-35851\_303\_SequenceListing.xml", created Mar. 6, 2025, having a file size of 993,616 bytes, is hereby incorporated by reference in its entirety.

### FIELD

[0003] Provided herein are systems and methods for the detection of an analyte or analytes in a sample. In particular, the present disclosure provides compositions, assays, and methods for detecting and/or quantifying a target analyte using a bioluminescent complex comprising substrates, peptides, and/or polypeptides capable of generating a bioluminescent signal that correlates to the presence, absence, or amount of the target analyte.

### BACKGROUND

[0004] Biological processes rely on covalent and non-covalent interactions between molecules, macromolecules, and molecular complexes. In order to understand such processes, and to develop techniques and compounds to manipulate them for research and clinical and other practical applications, it is necessary to have tools available to detect and monitor these interactions and/or components involved in such interactions. The study of these interactions, particularly under physiological conditions (e.g., at normal expression levels for monitoring protein interactions), requires high sensitivity.

[0005] Creation of better assays for use in the field and in clinical settings is an ongoing area of urgent need. Speed, sensitivity, selectivity, robustness, simplicity, quantitative versus qualitative capabilities, and cost are all critical factors affecting the relevance of a diagnostic bioassays, and thus their utility to and adoption by the relevant community. Rapid diagnostic tests are not only relevant to clinical settings, but also can be applied to environmental, industrial, and direct to consumer contexts.

### SUMMARY

[0006] Provided herein are compositions and formulations comprising a luminogenic substrate and a target analyte binding agent comprising a target analyte binding element and one of a polypeptide component of a bioluminescent complex, or a peptide component of a bioluminescent complex.

[0007] In accordance with these embodiments, the polypeptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 5; at

least 60% sequence identity with SEQ ID NO: 9; or at least 60% sequence identity with SEQ ID NO: 12.

[0008] In some embodiments, the peptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 10; at least 60% sequence identity with SEQ ID NO: 11; at least 60% sequence identity with SEQ ID NO: 13; or at least 60% sequence identity with SEQ ID NO: 14.

[0009] In some embodiments, the composition comprises a complementary peptide or polypeptide component of the bioluminescent complex, wherein the target analyte binding agent and the complementary peptide or polypeptide component of the bioluminescent complex form a bioluminescent analyte detection complex in the presence of a target analyte.

[0010] In some embodiments, the composition that comprises the luminogenic substrate and the target analyte binding agent are combined in a dried formulation, and the complementary peptide or polypeptide component of the bioluminescent complex comprises a liquid formulation, wherein the liquid formulation is added to the dried formulation and forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0011] In some embodiments, the composition comprising the luminogenic substrate, the target analyte binding agent, and the complementary peptide or polypeptide component of the bioluminescent complex are combined in a dried formulation, wherein the dried formulation forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0012] In some embodiments, the complementary peptide or polypeptide component comprises a second target analyte binding element that forms the bioluminescent analyte detection complex in the presence of the target analyte.

[0013] In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 6, and wherein the complementary peptide or polypeptide component of the bioluminescent complex comprises at least 60% sequence identity with SEQ ID NO: 10.

[0014] In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 6, and wherein the complementary peptide or polypeptide component of the bioluminescent complex comprises at least 60% sequence identity with SEQ ID NO: 14.

[0015] Embodiments of the present disclosure also include a composition comprising a dried formulation comprising (a) a first target analyte binding agent comprising a first target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 9, and (b) a second target analyte binding agent comprising a second target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 10.

[0016] In some embodiments, the dried formulation further comprises a luminogenic substrate.

[0017] In some embodiments, the composition further comprises a liquid formulation comprising the target analyte.

[0018] Embodiments of the present disclosure also include a composition comprising a dried formulation comprising (a) a first target analyte binding agent comprising a first target analyte binding element and a polypeptide component

having at least 60% sequence identity with SEQ ID NO: 12, and (b) a second target analyte binding agent comprising a second target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 14.

[0019] In some embodiments, the dried formulation further comprises a luminogenic substrate.

[0020] In some embodiments, the composition further comprises a liquid formulation comprising the target analyte.

[0021] Embodiments of the present disclosure also include a composition comprising a dried formulation comprising (a) a first target analyte binding agent comprising a first target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 13, (b) a second target analyte binding agent comprising a second target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 15, and (c) a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 12.

[0022] In some embodiments, the dried formulation further comprises a luminogenic substrate.

[0023] In some embodiments, the composition further comprises a liquid formulation comprising the target analyte.

[0024] Embodiments of the present disclosure also include a composition comprising (a) a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 9, and (b) a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 10 or SEQ ID NO: 11.

[0025] Embodiments of the present disclosure also include a composition comprising (a) a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 10 or SEQ ID NO: 11, and (b) a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 9.

[0026] Embodiments of the present disclosure also include a composition comprising (a) a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 12, and (b) a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 14.

[0027] In some embodiments, the dried formulation further comprises a luminogenic substrate.

[0028] In some embodiments, the liquid formulation further comprises a luminogenic substrate.

[0029] In some embodiments, the liquid formulation further comprises a sample comprising a target analyte, and wherein a bioluminescent analyte detection complex forms upon combining the dried formulation and the liquid formulation in the presence of the target analyte.

[0030] In some embodiments, the composition further comprises a second complementary peptide or polypeptide component of the bioluminescent complex, wherein the target analyte binding agent, the first complementary peptide or polypeptide component of the bioluminescent complex, and the second complementary peptide or polypeptide component of the bioluminescent complex form a bioluminescent analyte detection complex in the presence of a target analyte.

[0031] In some embodiments, the composition comprising the target analyte binding agent comprises a dried formulation, and wherein the first complementary peptide or polypeptide component and the second complementary peptide or polypeptide of the bioluminescent complex comprise a liquid formulation; wherein the liquid formulation is added to the dried formulation and forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0032] In some embodiments, the composition comprising the target analyte binding agent, and either the first or the second complementary peptide or polypeptide component are combined in a dried formulation, and wherein the first or the second complementary peptide or polypeptide component that is not present in the dried formulation comprises a liquid formulation; wherein the liquid formulation is added to the dried formulation and forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0033] In some embodiments, the target analyte binding agent, the first complementary peptide or polypeptide component, and the second complementary peptide or polypeptide component are combined in a dried formulation that forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0034] In some embodiments, the dried formulation further comprises a luminogenic substrate.

[0035] In some embodiments, the liquid formulation further comprises a luminogenic substrate.

[0036] In some embodiments, the liquid formulation further comprises a sample comprising a target analyte, and wherein a bioluminescent analyte detection complex forms upon combining the dried formulation and the liquid formulation in the presence of the target analyte.

[0037] In some embodiments, either the first or the second complementary peptide or polypeptide component comprises a second target analyte binding element that forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0038] In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 6, and wherein either the first or the second complementary peptide or polypeptide component of the bioluminescent complex comprises at least 60% sequence identity with either SEQ ID NO: 13 or SEQ ID NO: 15.

[0039] Embodiments of the present disclosure also include a composition comprising (a) a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 6, and (b) a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO:

15, and a second complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15.

[0040] Embodiments of the present disclosure also include (a) a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 6, and a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15, and (b) a liquid formulation comprising a second complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15.

[0041] Embodiments of the present disclosure also include (a) a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 6, and complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15, and (b) a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15.

[0042] Embodiments of the present disclosure also include (a) a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 13, and a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 15, and (b) a liquid formulation comprising a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 6.

[0043] Embodiments of the present disclosure also include (a) a dried formulation comprising a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 6, and (b) a liquid formulation comprising a first target analyte binding agent comprising a target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 13, and a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 15.

[0044] Embodiments of the present disclosure also include a composition comprising a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 13, a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 15, and a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 6.

[0045] In some embodiments, the dried formulation further comprises a luminogenic substrate.

[0046] In some embodiments, the liquid formulation further comprises a luminogenic substrate.

[0047] In some embodiments, the liquid formulation further comprises a sample comprising a target analyte, and wherein a bioluminescent analyte detection complex forms

upon combining the dried formulation and the liquid formulation in the presence of the target analyte.

[0048] In some embodiments, a bioluminescent signal produced in the presence of the luminogenic substrate is substantially increased when the target analyte binding agent contacts one or more of the complementary peptide or polypeptide components of the bioluminescent complex, as compared to a bioluminescent signal produced by the target analyte binding agent and the luminogenic substrate alone.

[0049] In some embodiments, the target analyte is a target antibody.

[0050] In some embodiments, the target analyte binding agent comprises an element that binds non-specifically to antibodies.

[0051] In some embodiments, the target analyte binding agent comprises an element that binds specifically to an antibody.

[0052] In some embodiments, the target antibody is an antibody against a pathogen, toxin, or therapeutic biologic.

[0053] In some embodiments, a target analyte binding element is selected from the group consisting of an antibody, a polyclonal antibody, a monoclonal antibody, a recombinant antibody, an antibody fragment, protein A, an Ig binding domain of protein A, protein G, an Ig binding domain of protein G, protein A/G, an Ig binding domain of protein A/G, protein L, a Ig binding domain of protein L, protein M, an Ig binding domain of protein M, an oligonucleotide probe, a peptide nucleic acid, a DARPin, an aptamer, an affimer, a protein domain, and a purified protein.

[0054] In some embodiments, the luminogenic substrate is selected from coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW, 1667, JRW-1743, JRW-1744, and other coelenterazine analogs or derivatives.

[0055] In some embodiments, the composition further comprises a polymer.

[0056] In some embodiments, the polymer is a naturally-occurring biopolymer. In some embodiments, the naturally-occurring biopolymer is selected from pullulan, trehalose, maltose, cellulose, dextran, and a combination of any thereof. In some embodiments, the naturally-occurring biopolymer is pullulan.

[0057] In some embodiments, the polymer is a cyclic saccharide polymer or a derivative thereof. In some embodiments, the polymer is hydroxypropyl P-cyclodextrin.

[0058] In some embodiments, the polymer is a synthetic polymer. In some embodiments, the synthetic polymer is selected from polystyrene, poly(meth)acrylate, and a combination of any thereof. In some embodiments, the synthetic polymer is a block copolymer comprising at least one poly(propylene oxide) block and at least one poly(ethylene oxide) block. In some embodiments, the synthetic polymer is poloxamer 188.

[0059] In some embodiments, the composition further comprises a substance to reduce autoluminescence.

[0060] In some embodiments, the substance to reduce autoluminescence is ATT (6-Aza-2-thiothymine), a derivative or analog of ATT, a thionucleoside, thiourea, and the like.

[0061] In some embodiments, the composition further comprises a buffer, a surfactant, a reducing agent, a salt, a radical scavenger, a chelating agent, a protein, or any

combination thereof. In some embodiments, the surfactant is selected from polysorbate 20, polysorbate 40, and polysorbate 80.

[0062] In some embodiments, the composition is used in conjunction with an analyte detection platform to detect an analyte in a sample.

[0063] In some embodiments, sample is selected from blood, serum, plasma, urine, stool, cerebral spinal fluid, interstitial fluid, saliva, a tissue sample, a water sample, a soil sample, a plant sample, a food sample, a beverage sample, an oil, and an industrial fluid sample.

[0064] Embodiments of the present disclosure also include a method of detecting an analyte in a sample comprising combining any of the compositions described above with a sample comprising a target analyte.

[0065] In some embodiments, detecting the target analyte in the sample comprises detecting a bioluminescent signal generated from an analyte detection complex.

[0066] In some embodiments, the method further comprises quantifying a bioluminescent signal generated from the analyte detection complex.

[0067] In some embodiments, the bioluminescent signal generated from the analyte detection complex is proportional to the concentration of the analyte.

[0068] In some embodiments, one or more of the components of the composition exhibits enhanced stability within the composition compared to the component in solution alone.

[0069] Embodiments of the present disclosure also include systems and methods for the detection of an analyte or analytes in a sample. In particular, the present disclosure provides compositions, assays, and methods for detecting and/or quantifying a target analyte using a bioluminescent complex comprising substrates, peptides, and/or polypeptides capable of generating a bioluminescent signal that correlates to the presence, absence, or amount of the target analyte.

[0070] Embodiments of the present disclosure include a lateral flow detection system. In accordance with these embodiments, the system includes an analytical membrane that includes a detection region and a control region. In some embodiments, the detection region includes a first target analyte binding agent immobilized to the detection region, a conjugate pad comprising a second target analyte binding agent, and a sample pad. In some embodiments, the first target analyte binding agent and the second target analyte binding agent form a bioluminescent analyte detection complex in the at least one detection region when a target analyte is detected in a sample.

[0071] In some embodiments, the first target analyte binding agent includes a target analyte binding element and is non-luminescent. In some embodiments, the second target analyte binding agent includes a target analyte binding element and a bioluminescent polypeptide. In some embodiments, the bioluminescent polypeptide has at least 60% sequence identity with SEQ ID NO: 5.

[0072] In some embodiments, the first target analyte binding agent includes a target analyte binding element and a polypeptide component of a bioluminescent complex, and the second target analyte binding agent includes a target analyte binding element and a peptide component of a bioluminescent complex. In some embodiments, a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target

analyte binding agent contacts the second target analyte binding agent, as compared to a bioluminescent signal produced by the first target analyte binding agent and the luminogenic substrate alone.

[0073] In some embodiments, the first target analyte binding agent includes a target analyte binding element and a peptide component of a bioluminescent complex, and the second target analyte binding agent includes a target analyte binding element and a polypeptide component of a bioluminescent complex. In some embodiments, a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent, as compared to a bioluminescent signal produced by the first target analyte binding agent and the luminogenic substrate alone.

[0074] In some embodiments, the polypeptide component of a bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 6. In some embodiments, the polypeptide component of a bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 10. In some embodiments, the polypeptide component of a bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 12. In some embodiments, the polypeptide component of a bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 14.

[0075] In some embodiments, the first target analyte binding agent includes a target analyte binding element and a first peptide component of a tripartite bioluminescent complex, and the second target analyte binding agent includes a target analyte binding element and a second peptide component of the tripartite bioluminescent complex. In some embodiments, a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent and a polypeptide component of the tripartite bioluminescent complex as compared to a bioluminescent signal produced by (i) the first target analyte binding agent, the second target analyte binding agent, and/or the polypeptide component and (ii) the luminogenic substrate alone.

[0076] In some embodiments, the first peptide component of a tripartite bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 11. In some embodiments, the second first peptide component of a tripartite bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 13. In some embodiments, the polypeptide component of a tripartite bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 12.

[0077] In some embodiments, the target analyte is a target antibody. In some embodiments, the first target analyte binding element includes an agent that binds non-specifically to antibodies. In some embodiments, the second target analyte binding element comprises an agent that binds specifically to the target antibody. In some embodiments, the target antibody is an antibody against a pathogen, toxin, or therapeutic biologic.

[0078] In some embodiments, a target analyte binding element is selected from the group consisting of an antibody, a polyclonal antibody, a monoclonal antibody, a recombinant antibody, an antibody fragment, protein A, an Ig binding domain of protein A, protein G, an Ig binding domain of protein G, protein A/G, an Ig binding domain of protein A/G, protein L, a Ig binding domain of protein L,

protein M, an Ig binding domain of protein M, an oligonucleotide probe, a peptide nucleic acid, a DARPin, an aptamer, an affimer, a protein domain, and a purified protein. [0079] In some embodiments, the system further includes a luminogenic substrate. In some embodiments, the luminogenic substrate is selected from coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, and other coelenterazine analogs or derivatives. In some embodiments, the luminogenic substrate is applied to the system as part of a composition that includes the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any thereof. In some embodiments, the luminogenic substrate is applied to the system as part of a composition that includes the luminogenic substrate and a substance to reduce autoluminescence such as ATT (6-Aza-2-thiothymine), a derivative or analog of ATT, a thionucleoside, thiourea, and the like.

[0080] In some embodiments, the composition is applied to at least one of the sample pad, the conjugation pad, the detection region, and the control region.

[0081] In some embodiments, the analytical membrane includes a plurality of detection regions with each detection region comprising a distinct target analyte binding agent having distinct target analyte binding elements.

[0082] In some embodiments, the system further includes a device for detecting or quantifying bioluminescent signals from the analyte detection complex.

[0083] Embodiments of the present disclosure also include a conjugate pad comprising at least one target analyte binding agent. In accordance with these embodiments, the at least one target analyte binding agent includes a target analyte binding element and one of: a bioluminescent polypeptide comprising at least 60% sequence identity with SEQ ID NO: 5; a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 9; a peptide comprising at least 60% sequence identity with SEQ ID NO: 10; a peptide comprising at least 60% sequence identity with SEQ ID NO: 11; a peptide comprising at least 60% sequence identity with SEQ ID NO: 13; a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 12; a peptide comprising at least 60% sequence identity with SEQ ID NO: 14; or a fluorophore capable of being activated by energy transfer from an Ophophorus luciferase.

[0084] In some embodiments, the target analyte binding agent includes a target analyte binding element and one of: a bioluminescent polypeptide of SEQ ID NO: 5; a polypeptide of SEQ ID NO: 9; a peptide of SEQ ID NO: 10; a peptide of SEQ ID NO: 11; a peptide of SEQ ID NO: 13; a polypeptide of SEQ ID NO: 12; a peptide of SEQ ID NO: 14; or a fluorophore capable of being activated by energy transfer from an Ophophorus luciferase.

[0085] In some embodiments, the conjugate pad further includes a luminogenic substrate. In some embodiments, the luminogenic substrate is selected from coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, and other coelenterazine analogs or derivatives. In some embodiments, the luminogenic substrate contained on or within the conjugate pad as part of a composition that includes the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any

thereof. In some embodiments, the luminogenic substrate is applied to the system as part of a composition that includes the luminogenic substrate and a substance to reduce autoluminescence such as ATT (6-Aza-2-thiothymine), a derivative or analog of ATT, a thionucleoside, thiourea, and the like.

[0086] Embodiments of the present disclosure also include an analytical membrane that includes a detection region and a control region. In accordance with these embodiments, the detection region includes at least one target analyte binding agent immobilized to the detection region.

[0087] In some embodiments, the at least one target analyte binding agent includes a target analyte binding element and one of: a bioluminescent polypeptide comprising at least 60% sequence identity with SEQ ID NO: 5; a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 9; a peptide comprising at least 60% sequence identity with SEQ ID NO: 10; a peptide comprising at least 60% sequence identity with SEQ ID NO: 11; a peptide comprising at least 60% sequence identity with SEQ ID NO: 13; a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 12; a peptide comprising at least 60% sequence identity with SEQ ID NO: 14; or a fluorophore capable of being activated by energy transfer from an Ophophorus luciferase.

[0088] In some embodiments, the target analyte binding agent includes a target analyte binding element and one of: a bioluminescent polypeptide of SEQ ID NO: 5; a polypeptide of SEQ ID NO: 9; a peptide of SEQ ID NO: 10; a peptide of SEQ ID NO: 11; a peptide of SEQ ID NO: 13; a polypeptide of SEQ ID NO: 12; a peptide of SEQ ID NO: 14; or a fluorophore capable of being activated by energy transfer from an Ophophorus luciferase.

[0089] In some embodiments, the analytical membrane further includes a plurality of detection regions with each detection region comprising a distinct target analyte binding agent having distinct target analyte binding elements. In some embodiments, the analytical membrane further includes a luminogenic substrate. In some embodiments, the luminogenic substrate is selected from coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, and other coelenterazine analogs or derivatives.

[0090] In some embodiments, the luminogenic substrate is reversibly conjugated to the conjugate pad as part of a composition including the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any thereof. In some embodiments, the luminogenic substrate is part of a composition that includes the luminogenic substrate and a substance that reduces autoluminescence such as ATT (6-Aza-2-thiothymine), a derivative or analog of ATT, a thionucleoside, thiourea, and the like.

[0091] Embodiments of the present disclosure also include a solid phase detection platform comprising a detection region. In accordance with these embodiments, the detection region includes at least one target analyte binding agent conjugated to the detection region. In some embodiments, the at least one target analyte binding agent includes a target analyte binding element and one of: a bioluminescent polypeptide comprising at least 60% sequence identity with SEQ ID NO: 5; a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 9; a peptide comprising at least 60% sequence identity with SEQ ID NO: 10; a peptide comprising at least 60% sequence identity with SEQ ID NO:

11; a peptide comprising at least 60% sequence identity with SEQ ID NO: 13; a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 12; a peptide comprising at least 60% sequence identity with SEQ ID NO: 14; or a fluorophore capable of being activated by energy transfer from an *Oplophorus* luciferase.

[0092] In some embodiments, the target analyte binding agent includes a target analyte binding element and one of: a bioluminescent polypeptide of SEQ ID NO: 5; a polypeptide of SEQ ID NO: 9; a peptide of SEQ ID NO: 10; a peptide of SEQ ID NO: 11; a peptide of SEQ ID NO: 13; a polypeptide of SEQ ID NO: 12; a peptide of SEQ ID NO: 14; or a fluorophore capable of being activated by energy transfer from an *Oplophorus* luciferase.

[0093] In some embodiments, the detection platform includes: a first target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 6 conjugated to the detection region; and a second target analyte binding agent comprising a target analyte binding element and a peptide comprising at least 60% sequence identity with SEQ ID NO: 10 applied to the detection region.

[0094] In some embodiments, the detection platform includes: a first target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 10 conjugated to the detection region; and a second target analyte binding agent comprising a target analyte binding element and a peptide comprising at least 60% sequence identity with SEQ ID NO: 6 applied to the detection region.

[0095] In some embodiments, the detection platform includes: a first target analyte binding agent comprising a target analyte binding element and a peptide comprising at least 60% sequence identity with SEQ ID NO: 11 conjugated to the detection region; a second target analyte binding agent comprising a target analyte binding element and a peptide comprising at least 60% sequence identity with SEQ ID NO: 13 applied to the detection region; and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 12 applied to the detection region.

[0096] In some embodiments, the detection platform includes: a first target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 6 conjugated to the detection region; and a second target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 14 applied to the detection region.

[0097] In some embodiments, the detection platform includes: a first target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 14 conjugated to the detection region; and a second target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 6 applied to the detection region.

[0098] In some embodiments, the detection platform includes: a first target analyte binding agent comprising a target analyte binding element and a bioluminescent polypeptide at least 60% sequence identity with SEQ ID NO: 5 conjugated to the detection region; and a second target analyte binding agent comprising a target analyte binding

element and a fluorophore capable of being activated by energy transfer from the bioluminescent polypeptide applied to the detection region.

[0099] In some embodiments, the detection platform includes: a first target analyte binding agent comprising a target analyte binding element and a bioluminescent polypeptide at least 60% sequence identity with SEQ ID NO: 5 applied to the detection region; and a second target analyte binding agent comprising a target analyte binding element and a fluorophore capable of being activated by energy transfer from the bioluminescent polypeptide conjugated to the detection region.

[0100] In some embodiments, the detection platform further includes a plurality of detection regions with each detection region comprising a distinct target analyte binding agent having distinct target analyte binding elements. In some embodiments, the detection platform further includes a control region. In some embodiments, the detection platform further includes a luminogenic substrate. In some embodiments, the luminogenic substrate is selected from coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, and other coelenterazine analogs or derivatives. In some embodiments, the luminogenic substrate is reversibly conjugated to the conjugate pad as part of a composition comprising the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any thereof. In some embodiments, the luminogenic substrate is part of a composition comprising the luminogenic substrate and a substance that reduces autoluminescence such as ATT (6-Aza-2-thiothymine), a derivative or analog of ATT, a thionucleoside, thiourea, and the like.

[0101] Embodiments of the present disclosure also include a solution phase detection platform that includes at least one detection receptacle and a lyophilized tablet (lyocake). In accordance with these embodiments, the lyocake comprises a target analyte binding agent comprising a target analyte binding element and one of: a bioluminescent polypeptide comprising at least 60% sequence identity with SEQ ID NO: 5; a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 9; a peptide comprising at least 60% sequence identity with SEQ ID NO: 10; a peptide comprising at least 60% sequence identity with SEQ ID NO: 11; a peptide comprising at least 60% sequence identity with SEQ ID NO: 13; a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 12; a peptide comprising at least 60% sequence identity with SEQ ID NO: 14; or a fluorophore capable of being activated by energy transfer from an *Oplophorus* luciferase.

[0102] In some embodiments, the target analyte binding agent comprises a target analyte binding element and one of: a bioluminescent polypeptide of SEQ ID NO: 5; a polypeptide of SEQ ID NO: 9; a peptide of SEQ ID NO: 10; a peptide of SEQ ID NO: 11; a peptide of SEQ ID NO: 13; a polypeptide of SEQ ID NO: 12; a peptide of SEQ ID NO: 14; or a fluorophore capable of being activated by energy transfer from an *Oplophorus* luciferase.

[0103] In some embodiments, the lyocake comprises: a first target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 6; and a second target analyte binding agent comprising a target analyte binding

element and a peptide comprising at least 60% sequence identity with SEQ ID NO: 10.

[0104] In some embodiments, the lyocake comprises: a first target analyte binding agent comprising a target analyte binding element and a peptide comprising at least 60% sequence identity with SEQ ID NO: 11; a second target analyte binding agent comprising a target analyte binding element and a peptide comprising at least 60% sequence identity with SEQ ID NO: 13; and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 12.

[0105] In some embodiments, the lyocake comprises: a first target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with SEQ ID NO: 6; and a second target analyte binding agent comprising a target analyte binding element and a polypeptide comprising at least 60% sequence identity with ID NO: 14.

[0106] In some embodiments, the lyocake comprises: a first target analyte binding agent comprising a target analyte binding element and a bioluminescent polypeptide at least 60% sequence identity with SEQ ID NO: 5; and a second target analyte binding agent comprising a target analyte binding element and a fluorophore capable of being activated by energy transfer from the bioluminescent polypeptide.

[0107] In some embodiments, the detection platform comprises a 96-well microtiter plate comprising a plurality of detection receptacles, and at least two distinct target analyte binding agents comprising distinct target analyte binding elements.

[0108] In some embodiments, the lyocake comprises a luminogenic substrate. In some embodiments, the luminogenic substrate is selected from coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, and other coelenterazine analogs or derivatives.

[0109] In some embodiments, the lyocake comprises a luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any thereof.

[0110] In some embodiments, the lyocake comprises a luminogenic substrate and a substance to reduce autoluminescence such as ATT (6-Aza-2-thiothymine), a derivative or analog of ATT, a thionucleoside, thiourea, and the like.

[0111] In some embodiments, the detection platform further comprises at least one sample. In some embodiments, the sample is selected from blood, serum, plasma, urine, stool, cerebral spinal fluid, interstitial fluid, saliva, a tissue sample, a water sample, a soil sample, a plant sample, a food sample, a beverage sample, an oil, and an industrial fluid sample.

[0112] Embodiments of the present disclosure also include a method of detecting an analyte in a sample using the lateral flow assay systems described above. In accordance with these embodiments, the method includes applying a sample to the sample pad, facilitating flow of the sample from the sample pad to the conjugate pad, and then from the conjugate pad to the detection region and the control region on the analytical membrane. In some embodiments, the first target analyte binding agent, the second target analyte binding agent, and the target analyte form the analyte detection complex in the at least one detection region when the target analyte is detected in the sample.

[0113] In some embodiments, the sample is a sample from a subject selected from blood, serum, plasma, urine, stool, cerebral spinal fluid, interstitial fluid, tissue, and saliva. In some embodiments, the sample is selected from a water sample, a soil sample, a plant sample, a food sample, a beverage sample, an oil, and an industrial fluid sample. In some embodiments, detecting the target analyte in the sample comprises detecting a bioluminescent signal generated from the analyte detection complex.

[0114] In some embodiments, the method further comprises quantifying a bioluminescent signal generated from the analyte detection complex. In some embodiments, the method further comprises diagnosing a subject from which the sample was obtained as having or not having a disease based on the detection of the analyte.

[0115] Embodiments of the present disclosure also include a method of detecting an analyte in a sample using the solid phase detection platform described above. In accordance with these embodiments, the method includes exposing a sample to the detection region and control region. In some embodiments, the at least one target analyte binding agent and the at least one target analyte form an analyte detection complex in the at least one detection region when the target analyte is detected in the sample.

[0116] In some embodiments, the sample is a sample from a subject selected from blood, serum, plasma, urine, stool, cerebral spinal fluid, interstitial fluid, tissue, and saliva. In some embodiments, the sample is selected from a water sample, a soil sample, a plant sample, a food sample, a beverage sample, an oil, and an industrial fluid sample. In some embodiments, detecting the target analyte in the sample comprises detecting a bioluminescent signal generated from the analyte detection complex.

[0117] In some embodiments, the method further comprises quantifying a bioluminescent signal generated from the analyte detection complex. In some embodiments, the method further comprises diagnosing a subject from which the sample was obtained as having or not having a disease based on the detection of the analyte.

[0118] Embodiments of the present disclosure also include a method of producing a substrate for use in a bioluminescent assay. In accordance with these embodiments, the method includes applying a solution onto a substrate. In some embodiments, the solution contains at least one target analyte binding agent comprising a target analyte binding element and one of a polypeptide component of a bioluminescent complex or a peptide component of a bioluminescent complex. In some embodiments, the method includes drying the substrate containing the solution.

[0119] In some embodiments, the solution further includes a complementary peptide or polypeptide component of the bioluminescent complex. In some embodiments, the target analyte binding agent and the complementary peptide or polypeptide component of the bioluminescent complex form a bioluminescent analyte detection complex in the presence of a target analyte.

[0120] In some embodiments, the solution comprises a protein buffer and at least one excipient. In some embodiments, the solution comprises a luminogenic substrate.

[0121] In some embodiments, the substrate comprising the dried solution is W-903 paper, FTA paper, FTA Elute paper, FTA DMPK paper, Ahlstrom A-226 paper, M-TFN paper, FTA paper, FP705 paper, Bode DNA collection paper, nitrocellulose paper, nylon paper, cellulose paper, Dacron

paper, cotton paper, and polyester papers, or combinations thereof. In some embodiments, the substrate is a mesh comprising plastic, nylon, metal, or combinations thereof.

[0122] In some embodiments, drying the substrate containing the solution comprises drying at a temperature from about 30° C. to 40° C. for a period of time between about 30 mins and 2 hours. In some embodiments, drying the substrate containing the solution comprises lyophilizing and/or freezing the substrate.

[0123] In some embodiments, the method further comprises drying the at least one target analyte binding agent and/or the complementary peptide or polypeptide component of the bioluminescent complex onto a first substrate, and drying the luminogenic substrate onto a second substrate.

[0124] In accordance with these embodiments, a bioluminescent signal is generated upon exposure of the substrate containing the solution to the target analyte, and in some embodiments, the bioluminescent signal is proportional to the concentration of the target analyte.

[0125] In some embodiments, the at least one target analyte binding agent and/or the complementary peptide or polypeptide component of the bioluminescent complex exhibit(s) enhanced stability when dried on the substrate.

[0126] Embodiments of the present disclosure include a composition comprising a luminogenic substrate, a target analyte binding agent comprising a target analyte binding element and a polypeptide component of a bioluminescent complex, and a complementary polypeptide component of the bioluminescent complex. In accordance with these embodiments, the target analyte binding agent and the complementary polypeptide component of the bioluminescent complex are capable of forming a bioluminescent analyte detection complex in the presence of a target analyte.

[0127] In some embodiments, the composition further comprises a second target analyte binding agent comprising a second target analyte binding element and a second polypeptide component of a bioluminescent complex.

[0128] In some embodiments, the first and second target analyte binding agents bind separate portions of the same target analyte.

[0129] In some embodiments, the first and second polypeptide components of the bioluminescent complex bind the complementary polypeptide component of the bioluminescent complex to form a bioluminescent analyte detection complex in the presence of the target analyte.

[0130] In some embodiments, the first and the second polypeptide components are linked to a modified dehalogenase capable of forming a covalent bond with a haloalkane substrate.

[0131] In some embodiments, the first and the second target analyte binding elements comprise a haloalkane substrate.

[0132] In some embodiments, the first or second polypeptide components of the first and second target analyte binding agents comprise: at least 60% sequence identity with SEQ ID NO: 10; at least 60% sequence identity with SEQ ID NO: 11; at least 60% sequence identity with SEQ ID NO: 13; or at least 60% sequence identity with SEQ ID NO: 15.

[0133] In some embodiments, the complementary polypeptide component comprises: at least 60% sequence iden-

tity with SEQ ID NO: 6; at least 60% sequence identity with SEQ ID NO: 9; or at least 60% sequence identity with SEQ ID NO: 12.

[0134] In some embodiments, the target analyte binding element is selected from the group consisting of an antibody, a polyclonal antibody, a monoclonal antibody, a recombinant antibody, an antibody fragment, protein A, an Ig binding domain of protein A, protein G, an Ig binding domain of protein G, protein A/G, an Ig binding domain of protein A/G, protein L, a Ig binding domain of protein L, protein M, an Ig binding domain of protein M, an oligonucleotide probe, a peptide nucleic acid, a DARPin, an aptamer, an affimer, a protein domain, and a purified protein.

[0135] In some embodiments, the target analyte is an antibody, and wherein the target analyte binding element of the first target analyte binding agent comprises antigen recognized by the antibody, and wherein the target analyte binding element of the second target analyte binding agent comprises an Fc binding region.

[0136] In some embodiments, the first and/or second target analyte binding agents further comprise a fluorophore coupled to the first and/or second polypeptide components of the bioluminescent complex.

[0137] In some embodiments, one or more components of the composition is in the form of a lyophilized tablet (lyocake) capable of forming a bioluminescent complex when reconstituted in a solution to detect and/or quantify the target analyte.

[0138] In some embodiments, the composition comprises a solution-phase detection platform capable of detecting and/or quantifying the target analyte.

[0139] In some embodiments, the polypeptide components and the luminogenic substrate are in the form of a lyophilized tablet (lyocake) capable of forming a bioluminescent complex when reconstituted in a solution to detect and/or quantify the target analyte.

[0140] Embodiments of the present disclosure also includes a method of detecting an analyte in a sample comprising combining any of the compositions described above with a sample comprising a target analyte.

[0141] In some embodiments, detecting the target analyte in the sample comprises detecting a bioluminescent signal generated from an analyte detection complex.

[0142] In some embodiments, the method further comprises quantifying a bioluminescent signal generated from the analyte detection complex.

[0143] In some embodiments, the bioluminescent signal generated from the analyte detection complex is proportional to the concentration of the analyte.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[0144] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawings will be provided by the Office upon request and payment of the necessary fee.

[0145] FIG. 1 shows a representative schematic diagram of a lateral flow assay for detecting and/or quantifying a target analyte(s) in a sample based on bioluminescent complex formation, according to one embodiment of the present disclosure.

[0146] FIG. 2 shows a representative schematic diagram of a solid phase detection platform for detecting and/or

quantifying target analytes in a sample based on bioluminescent complex formation, according to one embodiment of the present disclosure.

[0147] FIG. 3 shows representative images demonstrating that components of the bioluminescent complexes produce detectable bioluminescence after being applied to a solid support substrate (e.g., membrane), dried, and stored at room temperature.

[0148] FIG. 4 shows representative images demonstrating that components of the bioluminescent complexes produce detectable bioluminescence after being applied to membrane and paper-based solid support substrates.

[0149] FIG. 5 shows a representative assay schematic (left) and a representative graph (right) demonstrating the ability of components of the bioluminescent complexes to be used as reporters on target analyte binding agents for target analyte detection.

[0150] FIG. 6 shows a representative depiction of an assay platform using components of the bioluminescent complexes as reporters on target analyte binding agents for target analyte detection.

[0151] FIGS. 7A-7E show representative stability tests of an assay platform using components of the bioluminescent complexes as reporters on target analyte binding agents for target analyte detection, according to one embodiment of the present disclosure (FIG. 7A at 4° C.;

[0152] FIG. 7B at 25° C.; FIG. 7C at 37° C.; FIG. 7D at 37° C. with NanoLuc added; and FIG. 7E at 4° C. and 37° C. with HiBiT added).

[0153] FIGS. 8A-8B show representative tests of storage conditions of an assay platform using components of the bioluminescent complexes as reporters on target analyte binding agents for target analyte detection, according to one embodiment of the present disclosure (FIG. 8A at 4° C. and 25° C.; FIG. 8B at 4° C. and 25° C. with a sucrose-based protein buffer).

[0154] FIGS. 9A-9C show representative images from a solid phase assay platform (FIG. 9A) in which a bioluminescence signal was produced in complex sampling environments (whole blood in FIG. 9B and serum in FIG. 9C) indicating target analyte detection.

[0155] FIG. 10A-10B shows that RLU signal derived from Whatman 903 paper spots after rehydration with an assay buffer can be measured either quantitatively (FIG. 10A) or qualitatively (FIG. 10B).

[0156] FIGS. 11A-11B show representative graphs demonstrating the ability of a high affinity dipeptide, Pep263, to form bioluminescent complexes (Pep263 is a peptide comprising the 39 and 010 stands of the NanoTrip complex; see, e.g., U.S. patent application Ser. No. 16/439,565 (PCT/US2019/036844), which is herein incorporated by reference in its entirety).

[0157] FIG. 12 shows representative results of a solid phase assay demonstrating qualitative assessment of bioluminescence from paper punches placed into a standard microtiter plate using a standard camera from an iPhone (e.g., iPhone 6S) or from an imager (e.g., LAS4000).

[0158] FIGS. 13A-13B include quantitative analysis of the same solid phase assay depicted in FIG. 12, but luminescence was detected using a luminometer on day 3 of storage at 25° C. (raw RLU values are provided in FIG. 13A; RLU values over background are provided in FIG. 13B).

[0159] FIGS. 14A-14C include a quantitative time course of the same solid phase assay as depicted in FIGS. 12-13,

demonstrating stability of all the proteins in the experimental conditions at all temps tested over the time frame. Maximum RLU values are provided at 4° C. (FIG. 14A), 25° C. (FIG. 14B), and 37° C. (FIG. 14C).

[0160] FIGS. 15A-15D include representative RLU signal kinetic results collected on day 0 of an accelerated stability study performed under two buffer conditions at 25° C. and 60° C. (raw RLU values are provided in FIGS. 15A and 15B; RLU values over background are provided in FIGS. 15C and 15D).

[0161] FIGS. 16A-16B include time-course results for an accelerated stability study of the proteins placed using the conjugation buffer conditions defined in FIG. 15. Maximum RLU values are provided at 25° C. (FIG. 16A) and 60° C. (FIG. 16B).

[0162] FIG. 17 shows a comparison of the impact of buffer conditions on luminescence from NanoLuc dried onto a nitrocellulose membrane.

[0163] FIG. 18 shows the effects of membrane blocking and sucrose pre-treatment on lateral flow assays performed in a running buffer of 20×SSC, 1% BSA, pH 7.0, and 10 μM N205 (Live Cell Substrate; LCS).

[0164] FIG. 19 shows the effects of membrane blocking and sucrose pre-treatment on lateral flow assays performed in a running buffer of 0.01 μM PBS, 1% BSA, pH 7.0, and 10 μM Permeable Cell Substrate (PCS).

[0165] FIG. 20 shows the effects of membrane blocking and sucrose pre-treatment on lateral flow assays performed in a running buffer of 5× LCS dilution buffer+5× LCS—diluted to 1× in PBS.

[0166] FIG. 21 shows effects of membrane properties on bioluminescent reagent absorption and capillary action in a lateral flow assay.

[0167] FIGS. 22A-22B show bioluminescent signal from NanoBiT/HiBiT complementation on nitrocellulose (left) and Whatman grade 541 (right) papers (FIG. 22A), and a compilation image from a corresponding movie taken across total exposure time (FIG. 22B).

[0168] FIG. 23 shows bioluminescent signal from Nano-BiT/HiBiT complementation on Whatman 903 paper, with a spike of additional substrate and liquid at 20 minutes.

[0169] FIG. 24 shows bioluminescent signal from Nano-BiT/HiBiT complementation on Whatman 903 paper.

[0170] FIGS. 25A-25C show bioluminescent signal resulting from reconstitution with a dipeptide of LgTrip and substrate in Whatman 903 paper, which was prepared with BSA (FIG. 25B) or without BSA (FIG. 25A); FIG. 25C shows maximum RLU signals obtained for each concentration tested in FIG. 25B.

[0171] FIGS. 26A-26B show bioluminescent signal resulting from reconstitution with a dipeptide of LgTrip and substrate from a lyocake (FIG. 26A), along with a titration of the dipeptide; FIG. 26B shows maximum RLU signals obtained for each concentration tested in FIG. 26A.

[0172] FIG. 27 shows bioluminescent signal in three different solid phase materials (Whatman 903, Ahlstrom 237, and Ahlstrom 6613H) resulting from reconstitution with a dipeptide added to dried LgTrip and substrate, or NanoLuc added to dried LgTrip and substrate.

[0173] FIG. 28 shows bioluminescent signal generated from Whatman 903 spots containing Lg/Trip/substrate and stored under ambient conditions over 25 days; spots were exposed to 1 nM dipeptide in PBS.

[0174] FIGS. 29A-29C show bioluminescent signal (RLU) for NanoLuc (FIG. 29A), LgBiT (FIG. 29B), and LgTrip (FIG. 29C) that were dried in Whatman 903 papers with various protein buffer formulations and reconstituted with furimazine.

[0175] FIGS. 30A-30C show bioluminescent signal ( $B_{max}$ ) for NanoLuc (FIG. 30A), LgBiT (FIG. 30B), and LgTrip (FIG. 30C) that were dried in Whatman 903 papers with various protein buffer formulations and reconstituted with furimazine, as shown in FIG. 29.

[0176] FIGS. 31A-31B show bioluminescent background levels for LgBiT (FIG. 31A) and LgTrip (FIG. 31B) that were dried in Whatman 903 papers with various protein buffer formulations and reconstituted with furimazine, as shown in FIG. 29.

[0177] FIGS. 32A-32F show bioluminescent signal (RLU signal kinetics) after reconstitution with furimazine in FIGS. 32A-32C;  $B_{max}$  in FIGS. 32D-32F) for NanoLuc (FIGS. 32A and 32D), LgBiT (FIGS. 32B and 32E), and LgTrip (FIGS. 32C and 32F) that were dried in Whatman 903 papers with various protein buffer formulations and reconstituted with furimazine after 6 days of storage at 60° C.

[0178] FIG. 33 includes representative embodiments of all-in-one lyophilized cakes ("lyocakes") or tablets containing all necessary reagents to perform an analyte detection test supporting several types of assay formats including cuvettes, test tubes, large volumes in bottles, snap test type assays, etc.

[0179] FIG. 34 shows bioluminescent signal from substrate movement across a lateral flow strip containing Nano-Luc from a compilation image corresponding to a movie taken across total exposure time.

[0180] FIG. 35 shows bioluminescent signal from Nano-Luc movement across a lateral flow strip from a compilation image corresponding to a movie taken across total exposure time.

[0181] FIG. 36 shows various tracers generated by tethering fumonisin B1 to a peptide tag (e.g., comprising SEQ ID NO: 10) via a biotin/streptavidin linkage, via a HaloTag linkage, or directly (e.g., via sulfo-SE labeling described in, for example, U.S. patent application Ser. No. 16/698,143 (PCT/US2019/063652), herein incorporated by reference), which can be used in competitive binding assays in accordance with the materials and methods described herein.

[0182] FIG. 37 shows an exemplary competitive binding assay in which varying concentrations of unlabeled fumonisin B1 disrupts the bioluminescent complex and results in decreased luminescence and the ability to detect/quantify the amount of fumonisin B1 in a sample.

[0183] FIGS. 38A-38B show bioluminescent signal resulting from a lyophilized cake containing LgBiT and substrate when reconstituted with a dipeptide in PBS (FIG. 38A); FIG. 38B shows maximum RLU signals obtained for each concentration tested in FIG. 38A.

[0184] FIG. 39 shows the bioluminescent signal resulting from reconstitution of LgBiT or LgTrip 3546 that was lyophilized directly into a standard 96-well plate with or without substrate; reconstitution was performed with dipeptide in PBS with or without substrate.

[0185] FIGS. 40A-40C show the bioluminescent signal resulting from the complementation of LgBiT-protein G, SmBiT-TNF $\alpha$ , and substrate in Whatman 903 paper spots

(FIGS. 40A-40B) and in a lyocake format (FIG. 40C) after reconstitution with varying concentrations of the target analyte Remicade in PBS.

[0186] FIGS. 41A-41C show the bioluminescent signal resulting from the complementation of LgTrip, SmTrip9-protein G, HiBiT-TNF $\alpha$ , and substrate in Whatman 903 paper spots (FIG. 41A) and in a lyocake format (FIG. 41B-41C) after reconstitution with varying concentrations of the target analyte Remicade in PBS.

[0187] FIGS. 42A-42E show the bioluminescent signal resulting from the complementation of bioluminescent complexes dried down in a form that does not include a substrate (FIGS. 42B-42C: mesh-based lyocakes; FIGS. 42D-42E: mesh-based film); the substrate is added separately to generate the bioluminescent signal in the presence of the analyte.

[0188] FIG. 43 shows lyophilized cake formations and colorimetric pHs of four different furimazine substrate formulations.

[0189] FIG. 44 shows the kinetic activity performance of various furimazine (Fz) substrate formulations in the presence of purified NanoLuc (Nluc) enzyme.

[0190] FIG. 45 shows the activity performance of a furimazine substrate formulation that had been stored at 60° C. for the indicated time in days.

[0191] FIGS. 46A-46B show thermal stability over time in days of various furimazine substrate formulations maintained at ambient temperature (FIG. 46A) or 60° C. (FIG. 46B) as analyzed by HPLC for absolute furimazine concentration remaining after reconstitution in PBS, pH 7.0 containing 0.01% BSA.

[0192] FIG. 47 shows the amount of furimazine remaining for various furimazine substrate formulations after 12 days of reconstitution in water as analyzed by HPLC indicating liquid stability.

[0193] FIG. 48 shows a schematic representation of the homogenous tripartite immunoassay for the analyte interleukin-6 (IL-6).

[0194] FIG. 49 shows an example of an SDS-PAGE gel of antibody labeling with tripartite-HaloTag fusion proteins. Variants of SmTrip9 or SmTrip10 were fused to HaloTag and expressed, purified, and used to label mouse anti-human IL-6 antibodies.

[0195] FIGS. 50A-50B show the signal kinetics of a solution-based homogeneous tripartite IL-6 immunoassay with and without IL-6 (raw RLUs in FIG. 50A, and fold response in FIG. 50B).

[0196] FIGS. 51A-51B show the dose response curve of recombinant human IL-6 for the solution-based homogeneous IL-6 tripartite immunoassay (log graph in FIG. 51A; linear graph in FIG. 51B).

[0197] FIGS. 52A-52C show the lyophilized cake product (FIG. 52A; #1 and #2) and IL-6 immunoassay performance and shelf-stability of various formulated, single reagent lyophilized cakes without furimazine (Fz; FIG. 52B) and with furimazine (Fz; FIG. 52C) after reconstitution following storage at ambient temperature for the indicating time in days.

[0198] FIGS. 53A-53B show cake appearance (FIG. 53A) and performance (FIG. 53B) and shelf-stability of a formulated, lyophilized single-reagent IL-6 tripartite immunoassays stored for 90 days at ambient storage.

[0199] FIG. 54 shows the signal kinetics of a single reagent, lyophilized tripartite IL-6 immunoassay post-reconstitution.

[0200] FIG. 55 shows the compatibility of a lyophilized single reagent IL-6 immunoassay with complex human matrices.

[0201] FIGS. 56A-56B show a lyophilized single-reagent, IL-6 tripartite immunoassay in a pre-filled 96-well microtiter plate (FIG. 56A) and a rhIL-6 dose response curve using the lyophilized, single reagent, IL-6 tripartite immunoassay assay plate following reconstitution (FIG. 56B).

[0202] FIGS. 57A-57B show the assay performance of the solution-based IL-6 tripartite immunoassay in single formulation excipients (FIG. 57A) and in various formulated solutions (FIG. 57B).

[0203] FIG. 58 shows a schematic representation of the homogenous tripartite immunoassay for the model analyte cardiac troponin I.

[0204] FIGS. 59A-59B show dose response curves for the solution-based, homogeneous cardiac troponin I tripartite immunoassay using recombinant human cardiac troponin I in raw RLU (FIG. 59A) and signal over background (FIG. 59B).

[0205] FIG. 60 shows the assay performance in raw RLUs of the single-reagent, formulated lyophilized troponin cardiac I tripartite immunoassay after reconstitution with 0.01% BSA in PBS or 10% normal pooled human serum diluted in general serum diluent.

[0206] FIGS. 61A-61B show raw RLU results of the solution-based, homogeneous IL-6 tripartite immunoassay background signals in the presence of human sera when using assay buffers 0.01% BSA in PBS (FIG. 61A) and in general serum diluent (FIG. 61B).

[0207] FIGS. 62A-62B show the raw Bmax RLU results of the solution-based, homogeneous IL-6 tripartite immunoassay in the presence of 50 ng/ml of rhIL-6 in the presence of human sera when using assay buffers 0.01% BSA in PBS (FIG. 62A) and in general serum diluent (FIG. 62B).

[0208] FIGS. 63A-63D show the signal to background results of the solution-based, homogeneous IL-6 tripartite immunoassay in the presence or absence of 50 ng/ml rhIL-6 with increasing amounts of normal pooled human serum (FIGS. 63A and 63C) or normal pooled human plasma (FIGS. 63B and 63D) when run in either 0.01% BSA in PBS or General Serum Diluent as assay buffer and NanoGlo (Promega Cat #N113) (FIGS. 63C and 63D) or Live Cell (Promega Cat #N205) substrates (FIGS. 63A and 63B).

[0209] FIG. 64 shows the signal-to-background results of the solution-based, homogeneous IL-6 tripartite immunoassay in the presence or absence of 50 ng/ml rhIL-6 with increasing amounts of normal, pooled human sera and pooled human sera that has been depleted of endogenous IgG when using general serum diluent as assay buffer.

[0210] FIGS. 65A-65C show the results of background RLU (FIG. 65A), Bmax RLU (FIG. 65B), and resulting signal over background (FIG. 65C) for the solution-based, homogeneous IL-6 tripartite immunoassay in the presence or absence of 50 ng/ml rhIL-6 with increasing amounts of human blood chemistry panel components provided in the VeriChem matrix plus chemistry reference kit.

[0211] FIGS. 66A-66C show the results of background RLU (FIG. 66A), Bmax RLU (FIG. 66B), and resulting signal over background (FIG. 66C) for the solution-based, homogeneous IL-6 tripartite immunoassay in the presence or

absence of 50 ng/ml rhIL-6 with increasing amounts of pooled normal human urine and NanoGlo (Promega Cat #N113) or Live Cell (Promega Cat #N205) substrates.

[0212] FIGS. 67A-67C show the raw RLU activity assay response of reconstituted lyophilized formulated furimazine tested with purified NanoLuc enzyme (Nluc) (FIG. 67A), formulated LgTrip polypeptide (SEQ ID NO: 12) tested with purified di-peptide (SEQ ID NO: 14) (FIG. 67B), and formulated furimazine and LgTrip polypeptide (SEQ ID NO: 12) tested with purified di-peptide (SEQ ID NO: 14) combined analyzing the thermal stability of the lyophilized vials (FIG. 67C).

[0213] FIG. 68 shows a schematic representation of a homogenous tripartite immunoassay for three anti-TNF $\alpha$  biologics: Remicade, Enbrel, and Humira.

[0214] FIGS. 69A-69C show the assay performance in raw RLUs of the solution-based, homogenous tripartite (LgTrip 3546+SmTrip9 pep521+SmTrip10) immunoassays quantitating the anti-TNF $\alpha$  biologics Remicade, Humira, and Enbrel.

[0215] FIGS. 70A-70B show the kinetic assay performance displayed as raw RLUs of reconstituted formulated, lyophilized single-reagent immunoassays for detection of Remicade using NanoTrip (tripartite-NanoLuc; FIG. 70A) and NanoBiT (FIG. 70B).

[0216] FIG. 71 shows the thermal stability at ambient temperatures of the single-reagent, lyophilized NanoBiT ("Bits") and NanoTrip ("Trips;" tripartite NanoLuc) immunoassay systems for the detection of Remicade. Lyocakes were reconstituted at the time points indicated in the absence or presence of 100 nM Remicade, and the resulting raw RLU were analyzed.

[0217] FIGS. 72A-72D show representative results using the NanoBiT system to detect Remicade in which the formulated components are separated into two separate cakes prior to use in the assay: (FIG. 72A) an image of two separate, lyophilized components with one containing LgBiT-TNF $\alpha$  fusion protein and furimazine (yellow), and the other containing the SmBiT-protein G fusion protein (white); (FIG. 72B) an image after manually combining the two lyophilized components in FIG. 72A; (FIG. 72C) an image of the reconstituted lyophilized components; and (D) kinetic bioluminescence RLU signals resulting in the presence of increasing amounts of Remicade.

[0218] FIG. 73 shows the resulting kinetic bioluminescence RLU signal resulting in the presence of increasing amounts of Remicade using the dual-lyophilized NanoTrip immunoassay system, whereby the TNF $\alpha$ +furimazine and protein G fusion proteins were formulated, lyophilized separately, and then combined prior to reconstitution.

[0219] FIG. 74 shows a schematic representation of the homogenous, NanoTrip (tripartite NanoLuc), cell-based immunoassay system for detection of anti-EGFR biologics (e.g., panitumumab).

[0220] FIG. 75 shows a panitumumab dose response curve using the homogenous, cell-based NanoTrip immunoassay system for anti-EGFR biologics.

[0221] FIG. 76 shows a panitumumab dose response curve using the homogenous, cell-based NanoTrip immunoassay system for anti-EGFR biologics testing different variants of SmTrip9 (SEQ ID NO: 13) fused to protein G.

[0222] FIGS. 77A-77B show a Remicade dose response curve using the homogenous, solution-based NanoTrip immunoassay system for anti-TNF $\alpha$  biologics testing dif-

ferent variants of SmTrip9 (SEQ ID NO: 13) fused to protein G (FIG. 77A), and a Remicade dose response curve using the lyophilized NanoTrip immunoassay system for anti-TNF $\alpha$  biologics (FIG. 77B).

[0223] FIG. 78 shows a schematic representation of the tripartite IL-6 immunoassay system using antibodies directly labeled with reactive peptides (e.g., SEQ ID NO: 18).

[0224] FIGS. 79A-79C show denaturing SDS-PAGE gel analysis of directly-labeled antibody conjugates.

[0225] FIG. 80 shows the raw RLU output from IL-6 titration in the presence of anti-IL-6 antibody pairs directly labeled with reactive peptides HW-0984 (SEQ ID NO: 20), HW-1010 (SEQ ID NO: 24), and HW-0977 (SEQ ID NO: 18).

[0226] FIG. 81 shows the raw RLU output from IL-6 titration in the presence of anti-IL-6 antibody pairs directly labeled with reactive peptides HW-0984 (SEQ ID NO: 20) and HW-1053 (SEQ ID NO: 19).

[0227] FIG. 82 shows the raw RLU output from IL-6 titration in the presence of anti-IL-6 antibody pairs labeled with reactive peptides HW-1042 (SEQ ID NO: 20), HW-1050 (SEQ ID NO: 27), HW-1052 (SEQ ID NO: 25), HW-1043 (SEQ ID NO: 24) and HW-1055 (SEQ ID NO: 25).

[0228] FIG. 83 shows the raw RLU output from IL-6 titration in the presence of individual anti-IL-6 antibodies directly labeled with reactive peptides HW-0977 (SEQ ID NO: 18), HW-0984 (SEQ ID NO: 20), HW-1010 (SEQ ID NO: 24), HW-1042 (SEQ ID NO: 20), HW-1050 (SEQ ID NO: 27), HW-1052 (SEQ ID NO: 25), HW-1053 (SEQ ID NO: 19), HW-1043 (SEQ ID NO: 24), and HW-1055 (SEQ ID NO: 25).

[0229] FIG. 84 shows the raw RLU output from IL-6 titration in the presence of LgTrip 5146 (SEQ ID NO: 451) and anti-IL-6 antibody pairs labeled with reactive peptides HW-1050 (SEQ ID NO: 27), HW-1043 (SEQ ID NO: 24), and HW-0977 (SEQ ID NO: 18).

[0230] FIG. 85 shows a schematic representation of the tripartite IL-6 immunoassay model using antibodies directly labeled with reactive peptides containing fluorophores, enabling BRET between the luciferase and labeled antibodies.

[0231] FIG. 86 shows IL-6 induced BRET between the complemented tripartite luciferase and fluorophores on the labeled anti-IL-6 antibodies.

[0232] FIGS. 87A-87C show the luminescence derived from luminogenic substrates N113 Fz (FIG. 87A), JRW-1404 (FIG. 87B), and JRW-1482 (FIG. 87C) in complex matrices.

#### DETAILED DESCRIPTION

[0233] Embodiments of the present disclosure provide systems and methods for the detection of an analyte or analytes in a sample. In particular, the present disclosure provides compositions, assays, and methods for detecting and/or quantifying a target analyte using a bioluminescent complex comprising substrates, peptides, and/or polypeptides capable of generating a bioluminescent signal that correlates to the presence, absence, or amount of the target analyte.

[0234] Most rapid diagnostic bioassays are based on immunological principles. Some embodiments of the present disclosure combine immunoassay-based concepts with

the advantages of bioluminescence, which include a large linear range and extremely low background, among other advantages. However, despite these advantages, point-of-care bioluminescence-based immunoassays are not yet commercially available. Some reasons for this may be that many currently available luciferases have low signal, which inherently limits their usefulness in immunoassays. Additionally, when a bioluminescent signal output is configured to be conditional (e.g., through complementation or bioluminescence resonance energy transfer (BRET)), the signal can be reduced even further. Many currently available luciferases also have a low tolerance or sensitivity to certain assay conditions, such as high temperatures, non-optimal buffer compositions, and complex sample matrices, thus requiring specialized chemistries to be compatible with point-of-care devices.

[0235] Embodiments of the present disclosure also address the need for “all-in-one” assay formats for analyte detection, which until the present application, have not been developed or described in the prior art. For example, Tenda, K. et al. (Angew. Chem. Int. Ed. 57, 15369-15373 (2018)) discloses paper devices where the substrate and bioluminescent components are dried onto separate sections of the paper, rather than being included together in a single-format system. Additionally, Yu, Q. et al. (Science 361, 1122-1126 (2018)) discloses that, although the bioluminescent components can be dried together, the substrate is separately mixed with the analyte-of-interest and subsequently added to the paper rather than drying the substrate and the bioluminescent components in a single format system. As described further herein, embodiments of the present disclosure provide methods, compositions, and systems that include all the necessary components of a bioluminescent detection complex (excluding the analyte-of-interest) in a single-format (e.g., “all-in-one”) system. This contrasts with currently available systems, which include at least one of the necessary bioluminescent components in a separate format/solution. Thus, embodiments of the present disclosure provide surprising and unexpected advantages over currently available bioluminescent analyte detection systems.

[0236] To address the need for bioluminescent-based point-of-care immunoassay platforms that are not necessarily limited to the use of typical immunoassay reagents, embodiments of the present disclosure include the use of the NanoLuc® bioluminescent platform, including compositions and methods for the assembly of a bioluminescent complex from two or more peptide and/or polypeptide components. In some embodiments, the peptide and/or polypeptide components are not fragments of a preexisting protein (e.g., are not complementary subsequences of a known polypeptide sequence), but confer bioluminescent activity via structural complementation (See, e.g., WO/2014/151736 (Intl. App. No. PCT/US2014/026354) and U.S. patent application Ser. No. 16/439,565 (PCT/US2019/036844), herein incorporated by reference in their entireties), as described further herein. In some embodiments, peptide and/or polypeptide components are non-luminescent in the absence of complementation and/or complementation enhances bioluminescence of a peptide or polypeptide component. In some embodiments, target analyte binding agents are labeled with the various components of the bioluminescent complexes described herein without comprising the ability of the binding agents to bind their target analytes. Components of the bioluminescent com-

plexes of the present disclosure are configured to be compatible with currently available point-of-care devices and systems such as lateral flow devices, paper-based spot tests, dip stick tests, lab-on-a-chip, microfluidic devices, pre-filled 96-well microtiter plates, and the like.

[0237] For example, embodiments of the present disclosure incorporate NanoLuc®-based technologies (e.g., Nano-BiT, NanoTrip, Nano-Glo (e.g., NANOGLO Live Cell Substrate or NANOGLO LCS (Promega Cat. Nos. N205 and N113)), NanoBRET, etc.) into target analyte detection assays that can be embedded in a solid phase assay or device, including plastics, matrices, and membranes of various composition, and/or used in other assay formats such as lyophilized cakes or tablets for solution phase assays, all of which function reliably even in complex sampling environments (e.g., blood components, food matrix, soil samples, stool, urine, water, and other human and animal biological samples). In some embodiments, NanoLuc®-based reporter systems are incorporated into lateral flow assay (LFA) technology, paper spot tests, and similar devices. LFAs are a commonly used point-of-care technology used to measure a variety of target analytes including, but not limited to, antibodies, bacterial and viral antigens, metabolites, proteins, and the like. As demonstrated in FIG. 1, LFAs can be combined with NanoLuc®-based reporter technology to provide a multiplexed viral infection detection assay to detect anti-viral antibodies at the point of care. The only currently available, approved emergency use immunoassay to detect Zika exposure is a traditional plate based, multi-step sandwich ELISA to detect the presence of anti-Zika IgM in blood samples. In contrast to this system, the multiplexed capability of a NanoLuc®-based bioluminescent reporter platform allows for the rapid detection of multiple antibodies in a sample, whether the antibodies recognize multiple different epitopes of the same virus, or whether they recognize multiple different epitopes on more than one virus. The ability to detect and identify viral infections quickly and sensitively with bioluminescence will aid treatment decisions. In addition to antibodies and antigens, the small size of the component peptides of the bioluminescent complexes described herein allow for the detection of many other target analytes using alternative binding agents and materials, such as, but not limited to, DARPins, aptamers, oligonucleotide probes, peptide nucleic acids (PNAs), and locked nucleic assays (LNAs).

[0238] Section headings as used in this section and the entire disclosure herein are merely for organizational purposes and are not intended to be limiting.

### 1. Definitions

[0239] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art. In case of conflict, the present document, including definitions, will control. Preferred methods and materials are described below, although methods and materials similar or equivalent to those described herein can be used in practice or testing of the present disclosure. All publications, patent applications, patents and other references mentioned herein are incorporated by reference in their entirety. The materials, methods, and examples disclosed herein are illustrative only and not intended to be limiting.

[0240] The terms “comprise(s),” “include(s),” “having,” “has,” “can,” “contain(s),” and variants thereof, as used

herein, are intended to be open-ended transitional phrases, terms, or words that do not preclude the possibility of additional acts or structures. The singular forms “a,” “and” and “the” include plural references unless the context clearly dictates otherwise. Many embodiments herein are described using open “comprising” language. Such embodiments encompass multiple closed “consisting of” and/or “consisting essentially of” embodiments, which may alternatively be claimed or described using such language. The present disclosure also contemplates other embodiments “comprising,” “consisting of” and “consisting essentially of,” the embodiments or elements presented herein, whether explicitly set forth or not.

[0241] For the recitation of numeric ranges herein, each intervening number there between with the same degree of precision is explicitly contemplated. For example, for the range of 6-9, the numbers 7 and 8 are contemplated in addition to 6 and 9, and for the range 6.0-7.0, the number 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, and 7.0 are explicitly contemplated.

[0242] “Bioluminescence” refers to production and emission of light by a chemical reaction catalyzed by, or enabled by, an enzyme, protein, protein complex, or other biomolecule (e.g., bioluminescent complex). In typical embodiments, a substrate for a bioluminescent entity (e.g., bioluminescent protein or bioluminescent complex) is converted into an unstable form by the bioluminescent entity; the substrate subsequently emits light.

[0243] “Complementary” refers to the characteristic of two or more structural elements (e.g., peptide, polypeptide, nucleic acid, small molecule, etc.) of being able to hybridize, dimerize, or otherwise form a complex with each other. For example, a “complementary peptide and polypeptide” are capable of coming together to form a complex. Complementary elements may require assistance to form a complex (e.g., from interaction elements), for example, to place the elements in the proper conformation for complementarity, to co-localize complementary elements, to lower interaction energy for complementation, etc.

[0244] “Complex” refers to an assemblage or aggregate of molecules (e.g., peptides, polypeptides, etc.) in direct and/or indirect contact with one another. In one aspect, “contact,” or more particularly, “direct contact” means two or more molecules are close enough so that attractive noncovalent interactions, such as Van der Waal forces, hydrogen bonding, ionic and hydrophobic interactions, and the like, dominate the interaction of the molecules. In such an aspect, a complex of molecules (e.g., a peptide and polypeptide) is formed under assay conditions such that the complex is thermodynamically favored (e.g., compared to a non-aggregated, or non-complexed, state of its component molecules). As used herein the term “complex,” unless described as otherwise, refers to the assemblage of two or more molecules (e.g., peptides, polypeptides or a combination thereof).

[0245] “Derivative” of an antibody as used herein may refer to an antibody having one or more modifications to its amino acid sequence when compared to a genuine or parent antibody and exhibit a modified domain structure. The derivative may still be able to adopt the typical domain configuration found in native antibodies, as well as an amino acid sequence, which is able to bind to targets (antigens) with specificity. Typical examples of antibody derivatives are antibodies coupled to other polypeptides, rearranged

antibody domains, or fragments of antibodies. The derivative may also comprise at least one further compound, such as a protein domain linked by covalent or non-covalent bonds. The linkage can be based on genetic fusion according to the methods known in the art. The additional domain present in the fusion protein comprising the antibody may preferably be linked by a flexible linker, advantageously a peptide linker, wherein said peptide linker comprises plural, hydrophilic, peptide-bonded amino acids of a length sufficient to span the distance between the C-terminal end of the further protein domain and the N-terminal end of the antibody or vice versa. The antibody may be linked to an effector molecule having a conformation suitable for biological activity or selective binding to a solid support, a biologically active substance (e.g., a cytokine or growth hormone), a chemical agent, a peptide, a protein, or a drug, for example.

**[0246]** “Fragment” refers to a peptide or polypeptide that results from dissection or “fragmentation” of a larger whole entity (e.g., protein, polypeptide, enzyme, etc.), or a peptide or polypeptide prepared to have the same sequence as such. Therefore, a fragment is a subsequence of the whole entity (e.g., protein, polypeptide, enzyme, etc.) from which it is made and/or designed. A peptide or polypeptide that is not a subsequence of a preexisting whole protein is not a fragment (e.g., not a fragment of a preexisting protein). A peptide or polypeptide that is “not a fragment of a preexisting bioluminescent protein” is an amino acid chain that is not a subsequence of a protein (e.g., natural or synthetic) that: (1) was in physical existence prior to design and/or synthesis of the peptide or polypeptide, and (2) exhibits substantial bioluminescent activity.

**[0247]** As used herein, the term “antibody fragment” refers to a portion of a full-length antibody, including at least a portion of the antigen binding region or a variable region. Antibody fragments include, but are not limited to, Fab, Fab', F(ab')<sub>2</sub>, Fv, scFv, Fd, variable light chain, variable heavy chain, diabodies, and other antibody fragments that retain at least a portion of the variable region of an intact antibody. See, e.g., Hudson et al. (2003) Nat. Med. 9:129-134; herein incorporated by reference in its entirety. In certain embodiments, antibody fragments are produced by enzymatic or chemical cleavage of intact antibodies (e.g., papain digestion and pepsin digestion of antibody) produced by recombinant DNA techniques, or chemical polypeptide synthesis. For example, a “Fab” fragment comprises one light chain and the C<sub>H1</sub> and variable region of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule. A “Fab” fragment comprises one light chain and one heavy chain that comprises additional constant region, extending between the C<sub>H1</sub> and C<sub>H2</sub> domains. An interchain disulfide bond can be formed between two heavy chains of a Fab' fragment to form a “F(ab')<sub>2</sub>” molecule. An “Fv” fragment comprises the variable regions from both the heavy and light chains, but lacks the constant regions. A single-chain Fv (scFv) fragment comprises heavy and light chain variable regions connected by a flexible linker to form a single polypeptide chain with an antigen-binding region. Exemplary single chain antibodies are discussed in detail in WO 88/01649 and U.S. Pat. Nos. 4,946,778 and 5,260,203; herein incorporated by reference in their entireties. In certain instances, a single variable region (e.g., a heavy chain variable region or a light

chain variable region) may have the ability to recognize and bind antigen. Other antibody fragments will be understood by skilled artisans.

**[0248]** “Isolated polynucleotide” as used herein may mean a polynucleotide (e.g., of genomic, cDNA, or synthetic origin, or a combination thereof) that, by virtue of its origin, the isolated polynucleotide is not associated with all or a portion of a polynucleotide with which the “isolated polynucleotide” is found in nature; is operably linked to a polynucleotide that it is not linked to in nature; or does not occur in nature as part of a larger sequence.

**[0249]** “Non-luminescent” refers to an entity (e.g., peptide, polypeptide, complex, protein, etc.) that exhibits the characteristic of not emitting a detectable amount of light in the visible spectrum (e.g., in the presence of a substrate). For example, an entity may be referred to as non-luminescent if it does not exhibit detectable luminescence in a given assay. As used herein, the term “non-luminescent” is synonymous with the term “substantially non-luminescent”. For example, a non-luminescent polypeptide is substantially non-luminescent, exhibiting, for example, a 10-fold or more (e.g., 100-fold, 200-fold, 500-fold, 1×10<sup>3</sup>-fold, 1×10<sup>4</sup>-fold, 1×10<sup>5</sup>-fold, 1×10<sup>6</sup>-fold, 1×10<sup>7</sup>-fold, etc.) reduction in luminescence compared to a complex of the polypeptide with its non-luminescent complement peptide. In some embodiments, an entity is “non-luminescent” if any light emission is sufficiently minimal so as not to create interfering background for a particular assay.

**[0250]** “Non-luminescent peptide” and “non-luminescent polypeptide” refer to peptides and polypeptides that exhibit substantially no luminescence (e.g., in the presence of a substrate), or an amount that is beneath the noise, or a 10-fold or more (e.g., 100-fold, 200-fold, 500-fold, 1×10<sup>3</sup>-fold, 1×10<sup>4</sup>-fold, 1×10<sup>5</sup>-fold, 1×10<sup>6</sup>-fold, 1×10<sup>7</sup>-fold, etc.) when compared to a significant signal (e.g., luminescent complex) under standard conditions (e.g., physiological conditions, assay conditions, etc.) and with typical instrumentation (e.g., luminometer, etc.). In some embodiments, such non-luminescent peptides and polypeptides assemble, according to the criteria described herein, to form a bioluminescent complex. As used herein, a “non-luminescent element” is a non-luminescent peptide or non-luminescent polypeptide. The term “bioluminescent complex” refers to the assembled complex of two or more non-luminescent peptides and/or non-luminescent polypeptides. The bioluminescent complex catalyzes or enables the conversion of a substrate for the bioluminescent complex into an unstable form; the substrate subsequently emits light. When uncomplexed, two non-luminescent elements that form a bioluminescent complex may be referred to as a “non-luminescent pair.” If a bioluminescent complex is formed by three or more non-luminescent peptides and/or non-luminescent polypeptides, the uncomplexed constituents of the bioluminescent complex may be referred to as a “non-luminescent group.”

**[0251]** “Peptide” and “polypeptide” as used herein, and unless otherwise specified, refer to polymer compounds of two or more amino acids joined through the main chain by peptide amide bonds (—C(O)NH—). The term “peptide” typically refers to short amino acid polymers (e.g., chains having fewer than 25 amino acids), whereas the term “polypeptide” typically refers to longer amino acid polymers (e.g., chains having more than 25 amino acids).

[0252] "Preexisting protein" refers to an amino acid sequence that was in physical existence prior to a certain event or date. A "peptide that is not a fragment of a preexisting protein" is a short amino acid chain that is not a fragment or sub-sequence of a protein (e.g., synthetic or naturally-occurring) that was in physical existence prior to the design and/or synthesis of the peptide.

[0253] "Sample," "test sample," "specimen," "sample from a subject," and "patient sample" as used herein may be used interchangeable and may be a sample of blood, such as whole blood, tissue, urine, serum, plasma, amniotic fluid, cerebrospinal fluid, placental cells or tissue, endothelial cells, leukocytes, or monocytes. The sample can be used directly as obtained from a patient or can be pre-treated, such as by filtration, distillation, extraction, concentration, centrifugation, inactivation of interfering components, addition of reagents, and the like, to modify the character of the sample in some manner as discussed herein or otherwise as is known in the art.

[0254] "Sequence identity" refers to the degree two polymer sequences (e.g., peptide, polypeptide, nucleic acid, etc.) have the same sequential composition of monomer subunits. The term "sequence similarity" refers to the degree with which two polymer sequences (e.g., peptide, polypeptide, nucleic acid, etc.) have similar polymer sequences. For example, similar amino acids are those that share the same biophysical characteristics and can be grouped into the families, e.g., acidic (e.g., aspartate, glutamate), basic (e.g., lysine, arginine, histidine), non-polar (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan) and uncharged polar (e.g., glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine). The "percent sequence identity" (or "percent sequence similarity") is calculated by: (1) comparing two optimally aligned sequences over a window of comparison (e.g., the length of the longer sequence, the length of the shorter sequence, a specified window), (2) determining the number of positions containing identical (or similar) monomers (e.g., same amino acids occurs in both sequences, similar amino acid occurs in both sequences) to yield the number of matched positions, (3) dividing the number of matched positions by the total number of positions in the comparison window (e.g., the length of the longer sequence, the length of the shorter sequence, a specified window), and (4) multiplying the result by 100 to yield the percent sequence identity or percent sequence similarity. For example, if peptides A and B are both 20 amino acids in length and have identical amino acids at all but 1 position, then peptide A and peptide B have 95% sequence identity. If the amino acids at the non-identical position shared the same biophysical characteristics (e.g., both were acidic), then peptide A and peptide B would have 100% sequence similarity. As another example, if peptide C is 20 amino acids in length and peptide D is 15 amino acids in length, and 14 out of 15 amino acids in peptide D are identical to those of a portion of peptide C, then peptides C and D have 70% sequence identity, but peptide D has 93.3% sequence identity to an optimal comparison window of peptide C. For the purpose of calculating "percent sequence identity" (or "percent sequence similarity") herein, any gaps in aligned sequences are treated as mismatches at that position.

[0255] "Subject" and "patient" as used herein interchangeably refers to any vertebrate, including, but not limited to, a mammal and a human. In some embodiments, the subject

may be a human or a non-human. The subject or patient may be undergoing forms of treatment. "Mammal" as used herein refers to any member of the class Mammalia, including, without limitation, humans and nonhuman primates such as chimpanzees and other apes and monkey species; farm animals such as cattle, sheep, pigs, goats, llamas, camels, and horses; domestic mammals such as dogs and cats; laboratory animals including rodents such as mice, rats, rabbits, guinea pigs, and the like. The term does not denote a particular age or sex. Thus, adult and newborn subjects, as well as fetuses, whether male or female, are intended to be included within the scope of this term.

[0256] "Subsequence" refers to peptide or polypeptide that has 100% sequence identify with another, larger peptide or polypeptide. The subsequence is a perfect sequence match for a portion of the larger amino acid chain.

[0257] "Substantially" as used herein means that the recited characteristic, parameter, and/or value need not be achieved exactly, but that deviations or variations, including for example, tolerances, measurement error, measurement accuracy limitations and other factors known to skill in the art, may occur in amounts that do not preclude the effect the characteristic was intended to provide. A characteristic or feature that is substantially absent (e.g., substantially non-luminescent) may be one that is within the noise, beneath background, below the detection capabilities of the assay being used, or a small fraction (e.g., <1%, <0.1%, <0.01%, <0.001%, <0.00001%, <0.000001%, <0.0000001%) of the significant characteristic (e.g., luminescent intensity of a bioluminescent protein or bioluminescent complex).

[0258] "Variant" is used herein to describe a peptide or polypeptide that differs in amino acid sequence by the insertion, deletion, or conservative substitution of amino acids, but retain at least one biological activity. "SNP" refers to a variant that is a single nucleotide polymorphism. Representative examples of "biological activity" include the ability to be bound by a specific antibody or to promote an immune response. Variant is also used herein to describe a protein with an amino acid sequence that is substantially identical to a referenced protein with an amino acid sequence that retains at least one biological activity. A conservative substitution of an amino acid (e.g., replacing an amino acid with a different amino acid of similar properties, such as hydrophilicity, degree, and distribution of charged regions) is recognized in the art as typically involving a minor change. These minor changes can be identified, in part, by considering the hydropathic index of amino acids, as understood in the art. The hydropathic index of an amino acid is based on a consideration of its hydrophobicity and charge. It is known in the art that amino acids of similar hydropathic indexes can be substituted and still retain protein function. In one aspect, amino acids having hydropathic indexes of  $\pm 2$  are substituted. The hydrophilicity of amino acids can also be used to reveal substitutions that would result in proteins retaining biological function. A consideration of the hydrophilicity of amino acids in the context of a peptide permits calculation of the greatest local average hydrophilicity of that peptide, a useful measure that has been reported to correlate well with antigenicity and immunogenicity. Substitution of amino acids having similar hydrophilicity values can result in peptides retaining biological activity, for example immunogenicity, as is understood in the art. Substitutions may be performed with amino acids having hydrophilicity values within  $\pm 2$  of each other. Both

the hydrophobicity index and the hydrophilicity value of amino acids are influenced by the particular side chain of that amino acid. Consistent with that observation, amino acid substitutions that are compatible with biological function are understood to depend on the relative similarity of the amino acids, and particularly the side chains of those amino acids, as revealed by the hydrophobicity, hydrophilicity, charge, size, and other properties.

**[0259]** “Target analyte” or “analyte” as used herein refers to a substance in a sample that can be detected, quantified, measured, tested, and/or monitored, often as part of a method of evaluating a process or condition (e.g., diagnostic or prognostic assay). Target analytes can include, but are not limited to, a protein, a peptide, a polypeptide, an enzyme, a cofactor, a nucleotide, a polynucleotide, DNA, RNA, a small molecule compound, an antibody, and any variation, combination, and derivative thereof.

**[0260]** “Target analyte binding agent” as used herein refers to an agent capable of binding to a target analyte. In some embodiments, target analyte binding agents include agents that can bind multiple substances, such as a target

some embodiments, target analyte binding agents can include target analyte binding elements capable of binding a group or class of analytes (e.g., protein L binding to antibodies); and in other embodiments, target analyte binding agents can include target analyte binding elements capable of binding a specific analyte (e.g., an antigen binding a monoclonal antibody). A target analyte binding agent may be an antibody, antibody fragment, a receptor domain that binds a target ligand, proteins or protein domains that bind to immunoglobulins (e.g., protein A, protein G, protein A/G, protein L, protein M), a binding domain of a proteins that bind to immunoglobulins (e.g., protein A, protein G, protein A/G, protein L, protein M), oligonucleotide probe, peptide nucleic acid, DARPin, aptamer, affimer, a purified protein, or a protein domain (either the analyte itself or a protein that binds to the analyte), and analyte binding domain(s) of proteins etc. Table A provides a lists of exemplary binding moieties that could be used singly or in various combinations in methods, systems, and assays (e.g., immunoassays) herein.

TABLE 1

Exemplary target analyte binding agents.	
Binding Moiety A	Binding Moiety B
Protein A	Protein A
Ig Binding domain of protein A	Ig binding domain of protein A
Protein G	Protein G
Ig Binding domain of protein G	Ig binding domain of protein G
Protein L	Protein L
Ig Binding domain of protein L	Ig binding domain of protein L
Protein M	Protein M
Ig Binding domain of protein M	Ig binding domain of protein M
polyclonal antibody against analyte X	polyclonal antibody: same antibody or second polyclonal antibody recognizing same target analyte X
monoclonal antibody	monoclonal antibody recognizing different epitope on same target analyte X
recombinant antibody	recombinant antibody recognizing different epitope on same target analyte X
scFv	scFv recognizing different epitope on same target analyte X
variable light chain ( $V_L$ ) of antibody (monoclonal, recombinant, polyclonal) recognizing target analyte X protein (e.g. receptor) binding domain 1 that binds to analyte X	variable heavy chain ( $V_H$ ) of same antibody (monoclonal, recombinant, polyclonal) recognizing target analyte X protein (e.g. receptor) binding domain 2 that binds to analyte X
(Fab) fragment	(Fab) fragment from different antibody recognizing different epitope to same target analyte X
Fab' fragment	Fab' from different antibody recognizing different epitope to same target analyte X
Fv fragment	Fv from different antibody recognizing different epitope to same target analyte X
F(ab')2 fragment	F(ab')2 from different antibody recognizing different epitope to same target analyte X
oligonucleotide probe	oligonucleotide probe to same DNA or RNA target but recognizing non-overlapping sequence
DARPin	DARPin recognizing non-overlapping domain of same target
peptide nucleic acid	peptide nucleic acid recognizing same DNA or RNA target but non-overlapping sequence
aptamer	aptamer binding to same target analyte X but recognizing non-overlapping sequence or epitope
affimer	aptamer binding to same target analyte X but recognizing different epitope

analyte and a solid phase support. In some embodiments, target analyte binding agents include agents that bind both a target analyte (e.g., via a target analyte binding element) and a distinct peptide/polypeptide to form a target analyte detection complex (e.g., to generate a bioluminescent signal). In

**[0261]** Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. For example, any nomenclatures used in connection with, and techniques of,

cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those that are well known and commonly used in the art. The meaning and scope of the terms should be clear; in the event, however of any latent ambiguity, definitions provided herein take precedent over any dictionary or extrinsic definition. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

## 2. Bioluminescence

[0262] The present disclosure includes materials and methods related to bioluminescent polypeptides, bioluminescent complexes and components thereof, and bioluminescence resonance energy transfer (BRET).

[0263] In some embodiments, provided herein are solid phase and/or lateral flow assays, devices, and systems incorporating bioluminescent polypeptides and/or bioluminescent complexes (of non-luminescent peptide(s) and/or non-luminescent polypeptide components) based on (e.g., structurally, functionally, etc.) the luciferase of *Ophophorus gracilirostris*, the NanoLuc® luciferase (Promega Corporation; U.S. Pat. Nos. 8,557,970; 8,669,103; herein incorporated by reference in their entireties), the NanoBiT (U.S. Pat. No. 9,797,889; herein incorporated by reference in its entirety), or NanoTrip (U.S. patent application Ser. No. 16/439,565; and U.S. Prov. Appln. Ser. No. 62/941,255; both of which are herein incorporated by reference in their entireties). As described below, in some embodiments, the compositions, assays, devices, methods, and systems herein incorporate commercially available NanoLuc®-based technologies (e.g., NanoLuc® luciferase, NanoBRET, NanoBiT, NanoTrip, NanoGlo, etc.), but in other embodiments, various combinations, variations, or derivations from the commercially available NanoLuc®-based technologies are employed.

### a. NanoLuc

[0264] PCT Appln. No. PCT/US2010/033449, U.S. Pat. No. 8,557,970, PCT Appln. No. PCT/2011/059018, and U.S. Pat. No. 8,669,103 (each of which is herein incorporated by reference in their entirety and for all purposes) describe compositions and methods comprising bioluminescent polypeptides. Such polypeptides find use in embodiments herein and can be used in conjunction with the compositions, assays, devices, systems, and methods described herein.

[0265] In some embodiments, compositions, assays, devices, systems, and methods provided herein comprise a bioluminescent polypeptide of SEQ ID NO: 5, or having at least 60% (e.g., 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100%, or ranges therebetween) sequence identity with SEQ ID NO: 5.

[0266] In some embodiments, any of the aforementioned bioluminescent polypeptides are linked (e.g., fused, chemically linked, etc.) to a binding element or other component of the assays and systems described herein.

[0267] In some embodiments, any of the aforementioned bioluminescent polypeptides, or fusions or conjugates thereof (e.g., with a binding element, etc.), are immobilized to a portion of a device described herein (e.g., a detection or control region of a lateral flow assay, a solid phase detection element, etc.).

### b. NanoBiT

[0268] PCT Appln. No. PCT/US14/26354 and U.S. Pat. No. 9,797,889 (each of which is herein incorporated by reference in their entirety and for all purposes) describe compositions and methods for the assembly of bioluminescent complexes; such complexes, and the peptide and polypeptide components thereof, find use in embodiments herein and can be used in conjunction with the assays and methods described herein.

[0269] In some embodiments, provided herein are non-luminescent (NL) polypeptides having at least 60% (e.g., 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100%, or ranges therebetween) sequence identity with SEQ ID NO: 9, but less than 100% (e.g., <99%, <98%, <97%, <96%, <95%, <94%, <93%, <92%, <91%, <90%) sequence identity with SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 6.

[0270] In some embodiments, provided herein are non-luminescent (NL) peptides having at least 60% (e.g., 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100%, or ranges therebetween) sequence identity with SEQ ID NO: 10, but less than 100% (e.g., <99%, <98%, <97%, <96%, <95%, <94%, <93%, <92%, <91%, <90%) sequence identity with SEQ ID NO: 1, SEQ ID NO: 4, and SEQ ID NO: 8.

[0271] In some embodiments, provided herein are NL peptides having at least 60% (e.g., 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100%, or ranges therebetween) sequence identity with SEQ ID NO: 11, but less than 100% (e.g., <99%, <98%, <97%, <96%, <95%, <94%, <93%, <92%, <91%, <90%) sequence identity with SEQ ID NO: 1, SEQ ID NO: 4, and SEQ ID NO: 8.

[0272] In some embodiments, any of the aforementioned NL peptides or NL polypeptides are linked (e.g., fused, chemically linked, etc.) to a binding element or other component of the composition, assays, devices, methods, and systems described herein.

[0273] In some embodiments, any of the aforementioned NL peptides or NL polypeptides, or fusions or conjugates thereof (e.g., with a binding element, etc.), are immobilized to a portion of a device described herein (e.g., a detection or control region of a lateral flow assay, a solid phase detection element, etc.).

[0274] In some embodiments, provided herein is a lateral flow detection system comprising: an analytical membrane comprising a detection region and a control region, wherein the detection region comprises a first target analyte binding agent immobilized to the detection region; a conjugate pad comprising a second target analyte binding agent; and a sample pad; wherein the first target analyte binding agent comprises a first target analyte binding element and a first NanoBiT-based NL peptide or NL polypeptide component (as described above), and wherein the second target analyte binding agent comprises a second target analyte binding element and a complementary NanoBiT-based NL peptide or NL polypeptide component (as described above). In some embodiments, the first target analyte binding agent and the second target analyte binding agent form an analyte detection complex in the at least one detection region when a target analyte is detected in a sample. In some embodiments, a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent, as compared to a bioluminescent

signal produced by the second target analyte binding agent or the first target analyte binding agent and the luminogenic substrate alone.

[0275] In some embodiments, provided herein is solid-phase detection system comprising: an solid phase substrate comprising a first target analyte binding agent and a second target analyte binding agent; wherein the first target analyte binding agent comprises a first target analyte binding element and a first NanoBiT-based NL peptide or NL polypeptide component (as described above), and wherein the second target analyte binding agent comprises a second target analyte binding element and a complementary NanoBiT-based NL peptide or NL polypeptide component (as described above). In some embodiments, the first target analyte binding agent and the second target analyte binding agent form an analyte detection complex in the solid-phase substrate when a target analyte is detected in a sample. In some embodiments, a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent, as compared to a bioluminescent signal produced by the second target analyte binding agent or the first target analyte binding agent and the luminogenic substrate alone.

c. NanoTrip

[0276] U.S. patent application Ser. No. 16/439,565 (PCT/US2019/036844) and U.S. Prov. Appln. Ser. No. 62/941,255 (both of which are herein incorporated by reference in their entireties and for all purposes) describes compositions, systems, and methods for the assembly of bioluminescent complexes. Such complexes, and the peptides and polypeptide components thereof, find use in embodiments herein and can be used in conjunction with the assays and methods described herein.

[0277] In some embodiments, provided herein are non-luminescent (NL) polypeptides having at least 60% (e.g., 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100%, or ranges therebetween) sequence identity with SEQ ID NO: 12, but less than 100% (e.g., <99%, <98%, <97%, <96%, <95%, <94%, <93%, <92%, <91%, <90%) sequence identity with SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 6, and SEQ ID NO: 9.

[0278] In some embodiments, provided herein are non-luminescent (NL) peptides having at least 60% (e.g., 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100%, or ranges therebetween) sequence identity with SEQ ID NO: 11, but less than 100% (e.g., <99%, <98%, <97%, <96%, <95%, <94%, <93%, <92%, <91%, <90%) sequence identity with SEQ ID NO: 1, SEQ ID NO: 4, and SEQ ID NO: 8.

[0279] In some embodiments, provided herein are NL peptides having at least 60% (e.g., 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100%, or ranges therebetween) sequence identity with SEQ ID NO: 13, but less than 100% (e.g., <99%, <98%, <97%, <96%, <95%, <94%, <93%, <92%, <91%, <90%) sequence identity with SEQ ID NO: 1, SEQ ID NO: 3, and SEQ ID NO: 7.

[0280] In some embodiments, provided herein are NL peptides having at least 60% (e.g., 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100%, or ranges therebetween) sequence identity with SEQ ID NO: 14, but less than 100% (e.g., <99%, <98%, <97%, <96%, <95%, <94%, <93%, <92%, <91%, <90%) sequence iden-

tity with SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 7, and SEQ ID NO: 8.

[0281] In some embodiments, any of the aforementioned NanoTrip-based NL peptide or NL polypeptides are linked (e.g., fused, chemically linked, etc.) to a binding element or other component of the compositions, methods, devices, assays, and systems described herein.

[0282] In some embodiments, any of the aforementioned NanoTrip-based NL peptide or NL polypeptides, or fusions or conjugates thereof (e.g., with a binding element, etc.), are immobilized to a portion of a device described herein (e.g., a detection or control region of a lateral flow assay, a solid phase detection element, etc.).

[0283] In some embodiments, provided herein is a lateral flow detection system comprising: an analytical membrane comprising a detection region and a control region, wherein the detection region comprises a first target analyte binding agent immobilized to the detection region; a conjugate pad comprising a second target analyte binding agent; and a sample pad; wherein the first target analyte binding agent comprises a first target analyte binding element and a first NanoTrip-based NL peptide (as described above), and wherein the second target analyte binding agent comprises a second target analyte binding element and a complementary NanoTrip-based NL peptide (as described above). In some embodiments, the first target analyte binding agent and the second target analyte binding agent form an analyte detection complex in the at least one detection region in the presence of a NanoTrip-based NL polypeptide component (as described above) when a target analyte is detected in a sample. In some embodiments, a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent in the presence of a NanoTrip-based NL polypeptide component, as compared to a bioluminescent signal produced by the second target analyte binding agent or the first target analyte binding agent and the luminogenic substrate alone.

[0284] In some embodiments, provided herein is a solid-phase detection system comprising: a solid phase (e.g., paper substrate, etc.) comprising a first target analyte binding agent and a second target analyte binding agent, wherein the first target analyte binding agent comprises a first target analyte binding element and a first NanoTrip-based NL peptide (as described above), and wherein the second target analyte binding agent comprises a second target analyte binding element and a complementary, second NL Nano-Trip-based peptide (as described above). In some embodiments, the first target analyte binding agent and the second target analyte binding agent form an analyte detection complex in the presence of a NanoTrip-based NL polypeptide (as described above) when a target analyte is detected in a sample. In some embodiments, a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent and a NanoTrip-based NL polypeptide, as compared to a bioluminescent signal produced by the second target analyte binding agent or the first target analyte binding agent and the luminogenic substrate alone.

d. NanoBRET

[0285] As disclosed in PCT Appln. No. PCT/US13/74765 and U.S. patent application Ser. No. 15/263,416 (herein incorporated by reference in their entireties and for all

purposes) describe bioluminescence resonance energy transfer (BRET) compositions, systems, and methods (e.g., incorporating NanoLuc®-based technologies); such compositions, systems and methods, and the bioluminescent polypeptide and fluorophore-conjugated components thereof, find use in embodiments herein and can be used in conjunction with the compositions, systems, devices, assays, and methods described herein.

**[0286]** In some embodiments, any of the NanoLuc®-based, NanoBiT-based, and/or NanoTrip-based (described in sections a-c, above) peptides, polypeptide, complexes, fusions, and conjugates may find use in BRET-based applications with the compositions, assays, methods, devices, and systems described herein. For example, in certain embodiments, a first target analyte binding agent comprises a first target analyte binding element and a NanoLuc®-based, NanoBiT-based, and/or NanoTrip-based polypeptide, peptide, or complex, and a second target analyte binding agent comprises a second target analyte binding element and a fluorophore (e.g., fluorescent protein, small molecule fluorophore, etc.), wherein the emission spectrum of the NanoLuc®-based, NanoBiT-based, and/or NanoTrip-based polypeptide, peptide, or complex overlaps the excitation spectrum of the fluorophore. In some embodiments, the NanoLuc®-based, NanoBiT-based, and/or NanoTrip-based polypeptide, peptide, or complex can be prepared in lyophilized form, which can include, or not include, the lumogenic substrate (e.g., furimazine).

**[0287]** In some embodiments, a target analyte binding agent comprises a target analyte binding element and a fluorophore capable of being activated by energy transfer from a bioluminescent polypeptide.

**[0288]** As used herein, the term “energy acceptor” refers to any small molecule (e.g., chromophore), macromolecule (e.g., autofluorescent protein, phycobiliproteins, nanoparticle, surface, etc.), or molecular complex that produces a readily detectable signal in response to energy absorption (e.g., resonance energy transfer). In certain embodiments, an energy acceptor is a fluorophore or other detectable chromophore. Suitable fluorophores include, but are not limited to: xanthene derivatives (e.g., fluorescein, rhodamine, Oregon green, eosin, Texas red, etc.), cyanine derivatives (e.g., cyanine, indocarbocyanine, oxacarbocyanine, thiacyanine, merocyanine, etc.), naphthalene derivatives (e.g., dansyl and prodan derivatives), oxadiazole derivatives (e.g., pyridyloxazole, nitrobenzoxadiazole, benzoxadiazole, etc.), pyrene derivatives (e.g., cascade blue), oxazine derivatives (e.g., Nile red, Nile blue, cresyl violet, oxazine 170, etc.), acridine derivatives (e.g., proflavin, acridine orange, acridine yellow, etc.), arylmethine derivatives (e.g., auramine, crystal violet, malachite green, etc.), tetrapyrrole derivatives (e.g., porphyrin, phtalocyanine, bilirubin, etc.), CF dye (Biotium), BODIPY (Invitrogen), ALEXA FLuoR (Invitrogen), DYLIGHT FLUOR (Thermo Scientific, Pierce), ATTO and TRACY (Sigma Aldrich), FluoProbes (Interchim), DY and MEGASTOKES (Dyomics), SULFO CY dyes (CYANDYE, LLC), SETAU AND SQUARE DYES (SETA BioMedicals), QUASAR and CAL FLUOR dyes (Biosearch Technologies), SURELIGHT DYES (APC, RPE, PerCP, Phycobilisomes)(Columbia Biosciences), APC, APCXL, RPE, BPE (Phyco-Biotech), autofluorescent proteins (e.g., YFP, RFP, mCherry, mKate), quantum dot nanocrystals, etc. In some embodiments, a fluorophore is a rhodamine analog (e.g., carboxy rhodamine analog), such as

those described in U.S. patent application Ser. No. 13/682, 589, herein incorporated by reference in its entirety.

#### e. HALOTAG

**[0289]** Some embodiments herein comprise a capture protein capable of forming a covalent bond with a capture ligand. The capture protein may be linked to a first element (e.g., a peptide component of a bioluminescent complex) and the capture ligand to a second element (e.g., a target analyte binding element (e.g., an antibody or antigen binding protein)) and the formation of a covalent bond links the first and second elements to each other. In some embodiments, linking the first and second elements creates a target analyte binding agent. In some embodiments, two or more target analyte binding agents so formed can bind to a complementary polypeptide component (e.g., LgTrip) and form a bioluminescent complex in the presence of an analyte (e.g., a target antigen recognized by the target analyte binding element) (See e.g., FIGS. 48 and 58). In some embodiments, the capture ligand is a haloalkane (aka “alkyl halide”). In some embodiments, the capture ligand is a chloroalkane. In some embodiments, the capture ligand is —A—X. In some embodiments, X is Cl. In some embodiments, —A—X is —(CH<sub>2</sub>)<sub>6</sub>Cl. When the capture ligand is a haloalkane, the capture protein is typically a dehalogenase enzyme modified to form covalent bonds with its substrate (See, e.g., U.S. Pat. Nos. 7,425,436; 7,429,472; 7,867,726; 7,888,086; 7,935,803; U.S. Pat. No. RE42,931; U.S. Pat. Nos. 8,168,405; 8,202,700; 8,257,939; herein incorporated by reference in their entireties).

**[0290]** One such modified dehalogenase is the commercially-available HALOTAG protein (SEQ ID NO: 720). In some embodiments, a capture protein comprises a polypeptide with at least 70% sequence identity (e.g., 75% identity, 80% identity, 85% identity, 90% identity, 95% identity, 98% identity, 99% identity) with SEQ ID NO.: 720. Some embodiment comprise a fusion protein of the capture protein (e.g., HALOTAG) and another peptide/polypeptide element (e.g., a binding moiety, a peptide/polypeptide component of a bioluminescent complex, etc.). In some embodiments, a capture ligand is a haloalkane comprising a halogen (e.g., Cl, Br, F, I, etc.) covalently attached to the end of an alkyl chain (e.g., (CH<sub>2</sub>)<sub>4-24</sub>). In some embodiments, the other end of the alkyl chain is attached to a linker or to another element (e.g., a peptide, analyte, etc.). A linker may comprise an alkyl chain or substituted alkyl chain (e.g., C=O, NH, S, O, carbamate, ethylene etc.) such as those disclosed in U.S. patent application Ser. No. 14/207,959, herein incorporated by reference.

### 3. Compositions and Formulations

**[0291]** Embodiments of the present disclosure include compositions and formulations comprising one or more of the peptide and/or polypeptide components of the bioluminescent complexes provided herein. In accordance with these embodiments, compositions and formulations of the present disclosure can include a lumogenic substrate and/or various other components. The compositions and methods provided herein can be used to formulate shelf-stable liquid formulations (e.g., used in a solution phase assay format) and shelf-stable dried formulations (e.g., used in a solid phase assay format) capable of producing a luminescent signal in the presence of an analyte-of-interest, even after storage for prolonged time periods. As described further below, the compositions and formulations of the present

disclosure can include one or more components of NanoLuc, NanoBiT, NanoTrip, and NanoBRET as well as the various luminogenic substrates described herein (e.g., furimazine).

[0292] In contrast to many currently available fluorescent and colorimetric assays, the compositions and formulations of the present disclosure provide means for conducting bioassays in which one or more of the peptide and/or polypeptide components of the bioluminescent complexes exist in a stable, dried formulation that is capable of being reconstituted in a solution containing, for example, a complementary peptide/polypeptide and/or a luminogenic substrate, such that the bioluminescent complex is formed in the presence of the analyte-of-interest. In some embodiments, the compositions and formulations of the present disclosure provide the means for conducting robust solid phase bioassays in which the bioluminescent signal produced is quantitative and proportional to the concentration of the analyte-of-interest.

[0293] In some embodiments, the compositions and formulations of the present disclosure include a luminogenic substrate and a target analyte binding agent that includes a target analyte binding element and a polypeptide component of a bioluminescent complex or a peptide component of a bioluminescent complex. In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 6, at least 60% sequence identity with SEQ ID NO: 9, or at least 60% sequence identity with SEQ ID NO: 12. In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 70% sequence identity with SEQ ID NO: 6, at least 70% sequence identity with SEQ ID NO: 9, or at least 70% sequence identity with SEQ ID NO: 12. In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 80% sequence identity with SEQ ID NO: 6, at least 80% sequence identity with SEQ ID NO: 9, or at least 80% sequence identity with SEQ ID NO: 12. In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 85% sequence identity with SEQ ID NO: 6, at least 85% sequence identity with SEQ ID NO: 9, or at least 85% sequence identity with SEQ ID NO: 12. In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 90% sequence identity with SEQ ID NO: 6, at least 90% sequence identity with SEQ ID NO: 9, or at least 90% sequence identity with SEQ ID NO: 12. In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 95% sequence identity with SEQ ID NO: 6, at least 95% sequence identity with SEQ ID NO: 9, or at least 95% sequence identity with SEQ ID NO: 12.

[0294] In other embodiments, the peptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 10, at least 60% sequence identity with SEQ ID NO: 11, at least 60% sequence identity with SEQ ID NO: 13, or at least 60% sequence identity with SEQ ID NO: 14. In some embodiments, the peptide component of the target analyte binding agent comprises at least 70% sequence identity with SEQ ID NO: 10, at least 70% sequence identity with SEQ ID NO: 11, at least 70% sequence identity with SEQ ID NO: 13, or at least 70% sequence identity with SEQ ID NO: 14. In some embodiments, the peptide component of the target analyte binding agent comprises at least 80% sequence identity with SEQ ID NO: 10, at least 80% sequence identity with SEQ

ID NO: 11, at least 80% sequence identity with SEQ ID NO: 13, or at least 80% sequence identity with SEQ ID NO: 14. In some embodiments, the peptide component of the target analyte binding agent comprises at least 85% sequence identity with SEQ ID NO: 10, at least 85% sequence identity with SEQ ID NO: 11, at least 85% sequence identity with SEQ ID NO: 13, or at least 85% sequence identity with SEQ ID NO: 14. In some embodiments, the peptide component of the target analyte binding agent comprises at least 90% sequence identity with SEQ ID NO: 10, at least 90% sequence identity with SEQ ID NO: 11, at least 90% sequence identity with SEQ ID NO: 13, or at least 90% sequence identity with SEQ ID NO: 14. In some embodiments, the peptide component of the target analyte binding agent comprises at least 95% sequence identity with SEQ ID NO: 10, at least 95% sequence identity with SEQ ID NO: 11, at least 95% sequence identity with SEQ ID NO: 13, or at least 95% sequence identity with SEQ ID NO: 14.

[0295] In some embodiments, the composition or formulation comprises a complementary peptide or polypeptide component of the bioluminescent complex. In accordance with these embodiments, the target analyte binding agent and the complementary peptide or polypeptide component of the bioluminescent complex can form a bioluminescent analyte detection complex in the presence of a target analyte. In some embodiments, the composition that comprises the luminogenic substrate and the target analyte binding agent can be combined in a dried formulation, and the complementary peptide or polypeptide component of the bioluminescent complex can be formulated as a liquid formulation. In some embodiments, the liquid formulation is added to the dried formulation and forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration. In other embodiments, the composition or formulation comprising the luminogenic substrate, the target analyte binding agent, and the complementary peptide or polypeptide component of the bioluminescent complex are combined in a dried formulation, wherein the dried formulation forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0296] In some embodiments, the complementary peptide or polypeptide component comprises a second target analyte binding element that forms the bioluminescent analyte detection complex in the presence of the target analyte. In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 6, and wherein the complementary peptide or polypeptide component of the bioluminescent complex comprises at least 60% sequence identity with SEQ ID NO: 10. In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 6, and wherein the complementary peptide or polypeptide component of the bioluminescent complex comprises at least 60% sequence identity with SEQ ID NO: 14.

[0297] Embodiments of the present disclosure also include a composition or formulation comprising a dried formulation that includes a first target analyte binding agent comprising a first target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 9, and a second target analyte binding agent comprising a second target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 10. In some embodi-

ments, the dried formulation further comprises a luminogenic substrate. In some embodiments, the composition further comprises a liquid formulation comprising the target analyte.

[0298] Embodiments of the present disclosure also include a composition comprising a dried formulation that includes a first target analyte binding agent comprising a first target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 12, and a second target analyte binding agent comprising a second target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 14. In some embodiments, the dried formulation further comprises a luminogenic substrate. In some embodiments, the composition further comprises a liquid formulation comprising the target analyte.

[0299] Embodiments of the present disclosure also include a composition comprising a dried formulation that includes a first target analyte binding agent comprising a first target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 13, a second target analyte binding agent comprising a second target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 15, and a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 12. In some embodiments, the dried formulation further comprises a luminogenic substrate. In some embodiments, the composition further comprises a liquid formulation comprising the target analyte.

[0300] Embodiments of the present disclosure also include a composition that includes a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 9, and a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 10 or SEQ ID NO: 11.

[0301] Embodiments of the present disclosure also include a composition that includes a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 10 or SEQ ID NO: 11, and a liquid formulation that contains a second target analyte binding agent comprising a target analyte binding element and a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 9.

[0302] Embodiments of the present disclosure also include a composition that includes a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 12, and a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 14. In some embodiments, the dried formulation further comprises a luminogenic substrate. In some embodiments, the liquid formulation further comprises a luminogenic substrate. In some embodiments, the liquid formulation further includes a sample comprising a target analyte. In accordance with

these embodiments, a bioluminescent analyte detection complex forms upon combining the dried formulation and the liquid formulation in the presence of the target analyte. [0303] In some embodiments, the composition further comprises a second complementary peptide or polypeptide component of the bioluminescent complex. In accordance with these embodiments, the target analyte binding agent, the first complementary peptide or polypeptide component of the bioluminescent complex, and the second complementary peptide or polypeptide component of the bioluminescent complex form a bioluminescent analyte detection complex in the presence of a target analyte.

[0304] In some embodiments, the composition comprising the target analyte binding agent are produced as a dried formulation. In some embodiments, the first complementary peptide or polypeptide component and the second complementary peptide or polypeptide of the bioluminescent complex are produced as a liquid formulation. In accordance with these embodiments, the liquid formulation can be added to the dried formulation, which facilitates the formation of the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0305] In some embodiments, the composition comprising the target analyte binding agent, and either the first or the second complementary peptide or polypeptide component are combined in a dried formulation, and the first or the second complementary peptide or polypeptide component that is not present in the dried formulation are produced as a liquid formulation. The liquid formulation can be added to the dried formulation, which facilitates the formation of the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0306] In some embodiments, the target analyte binding agent, the first complementary peptide or polypeptide component, and the second complementary peptide or polypeptide component are combined in a dried formulation that forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration. In some embodiments, the dried formulation further comprises a luminogenic substrate. In some embodiments, the liquid formulation further comprises a sample comprising a target analyte, wherein a bioluminescent analyte detection complex forms upon combining the dried formulation and the liquid formulation in the presence of the target analyte.

[0307] In some embodiments, either the first or the second complementary peptide or polypeptide component comprises a second target analyte binding element that forms the bioluminescent analyte detection complex in the presence of the target analyte upon rehydration.

[0308] In some embodiments, the polypeptide component of the target analyte binding agent comprises at least 60% sequence identity with SEQ ID NO: 12, and wherein either the first or the second complementary peptide or polypeptide component of the bioluminescent complex comprises at least 60% sequence identity with either SEQ ID NO: 13 or SEQ ID NO: 15.

[0309] Embodiments of the present disclosure also include a composition that includes a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 12, and a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least

60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15, and further including a second complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15.

[0310] Embodiments of the present disclosure also include a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 12, and a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15, and further including a liquid formulation comprising a second complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15.

[0311] Embodiments of the present disclosure also include a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a polypeptide component having at least 60% sequence identity with SEQ ID NO: 12, and complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15, and a liquid formulation comprising a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 13 or SEQ ID NO: 15.

[0312] Embodiments of the present disclosure also include a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 13, and a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 15, and further including a liquid formulation comprising a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 12.

[0313] Embodiments of the present disclosure also include a dried formulation comprising a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 12, and a liquid formulation comprising a first target analyte binding agent comprising a target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 13, and a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 15.

[0314] Embodiments of the present disclosure also include a composition comprising a dried formulation comprising a first target analyte binding agent comprising a target analyte binding element and a peptide component having at least 60% sequence identity with SEQ ID NO: 13, a second target analyte binding agent comprising a target analyte binding element and a complementary peptide component having at least 60% sequence identity with SEQ ID NO: 15, and a complementary polypeptide component having at least 60% sequence identity with SEQ ID NO: 12. In some embodiments, the dried formulation further comprises a luminogenic substrate. In some embodiments, the liquid formulation further comprises a luminogenic substrate. In some embodiments, the liquid formulation further comprises a luminogenic substrate. In some embodiments, the liquid formulation further comprises a sample comprising a target analyte, and wherein a bioluminescent analyte detection complex forms upon combining

the dried formulation and the liquid formulation in the presence of the target analyte.

[0315] In some embodiments, a bioluminescent signal produced in the presence of the luminogenic substrate is substantially increased when the target analyte binding agent contacts one or more of the complementary peptide or polypeptide components of the bioluminescent complex, as compared to a bioluminescent signal produced by the target analyte binding agent and the luminogenic substrate alone.

[0316] In some embodiments, the target analyte is a target antibody. In some embodiments, the target analyte binding agent comprises an element that binds non-specifically to antibodies. In some embodiments, the target analyte binding agent comprises an element that binds specifically to an antibody. In some embodiments, the target antibody is an antibody against a pathogen, toxin, or therapeutic biologic.

[0317] In some embodiments, a target analyte binding element is selected from the group consisting of an antibody, a polyclonal antibody, a monoclonal antibody, a recombinant antibody, an antibody fragment, protein A, an Ig binding domain of protein A, protein G, an Ig binding domain of protein G, protein A/G, an Ig binding domain of protein A/G, protein L, a Ig binding domain of protein L, protein M, an Ig binding domain of protein M, an oligonucleotide probe, a peptide nucleic acid, a DARPin, an aptamer, an affimer, a protein domain, and a purified protein.

[0318] In some embodiments, the luminogenic substrate is selected from coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, and other coelenterazine analogs or derivatives. In some embodiments, the coelenterazine analogs or derivatives are pro-luminogenic substrates such as those disclosed in U.S. Pat. No. 9,487,520, herein incorporated by reference. In some embodiments, the coelenterazine analogs or derivatives are Enduazine (Promega Corporation) and Vivazine (Promega Corporation).

[0319] In some embodiments, the composition further comprises a polymer. In some embodiments, the polymer is a naturally-occurring biopolymer. In some embodiments, the naturally-occurring biopolymer is selected from pullulan, trehalose, maltose, cellulose, dextran, and a combination of any thereof. In some embodiments, the naturally-occurring biopolymer is pullulan. In some embodiments, the polymer is a cyclic saccharide polymer or a derivative thereof. In some embodiments, the polymer is hydroxypropyl  $\beta$ -cyclodextrin.

[0320] In some embodiments, the polymer is a synthetic polymer. In some embodiments, the synthetic polymer is selected from polystyrene, poly(meth)acrylate, and a combination of any thereof. In some embodiments, the synthetic polymer is a block copolymer comprising at least one poly(propylene oxide) block and at least one poly(ethylene oxide) block. In some embodiments, the synthetic polymer is poloxamer 188.

[0321] In some embodiments, the composition further comprises a buffer, a surfactant, a reducing agent, a salt, a radical scavenger, a chelating agent, a protein, or any combination thereof. In some embodiments, the is surfactant selected from polysorbate 20, polysorbate 40, and polysorbate 80.

[0322] In some embodiments, the composition further comprises a substance that reduces autoluminescence. In some embodiments, the substance is ATT (6—Aza-2-thiothymine), a derivative or analog of ATT, a thionucleoside,

thiourea, and the like. In some embodiments, the substance is a thionucleoside disclosed in U.S. Pat. No. 9,676,997, herein incorporated by reference. In some embodiments, the substance is thiourea, which use for reducing autoluminescence is disclosed in U.S. Pat. Nos. 7,118,878; 7,078,181; and 7,108,996, herein incorporated by reference.

[0323] In some embodiments, the composition is used in conjunction with an analyte detection platform to detect an analyte in a sample. In some embodiments, sample is selected from blood, serum, plasma, urine, stool, cerebral spinal fluid, interstitial fluid, saliva, a tissue sample, a water sample, a soil sample, a plant sample, a food sample, a beverage sample, an oil, and an industrial fluid sample.

[0324] Embodiments of the present disclosure also include a method of detecting an analyte in a sample comprising combining any of the compositions described above with a sample comprising a target analyte. In some embodiments, detecting the target analyte in the sample comprises detecting a bioluminescent signal generated from an analyte detection complex. In some embodiments, the method further comprises quantifying a bioluminescent signal generated from the analyte detection complex. In some embodiments, the bioluminescent signal generated from the analyte detection complex is proportional to the concentration of the analyte. In some embodiments, one or more of the components of the composition exhibits enhanced stability within the composition compared to the component in solution alone.

[0325] The various embodiments of the compositions and formulations described above demonstrate enhanced stability, as demonstrated in the Examples and FIGS. For example, when produced as a dried formulation such as a lyocake, when dried onto a substrate or matrix (e.g., Whatman 903, Ahlstrom 237, and Ahlstrom 6613H; wells of a 96-well plate, nylon mesh), or when dried in various protein buffer formulations, with or without the luminogenic substrate, the compositions and formulations of the present disclosure exhibit enhanced stability when stored for a prolonged period of time. As provided herein, the compositions and formulations of the present disclosure are able to generate a luminescent signal in the presence of a target analyte after storage for extended periods of time. In some embodiments, the compositions and formulations of the present disclosure exhibit enhanced stability as compared to compositions and formulations that contain the same or similar components of a bioluminescent complex (e.g., complementary peptides/polypeptides, luminogenic substrates), but which are formulated without one or more of the other components of the formulation, and/or are not formulated according to the methods described herein.

[0326] In some embodiments, the compositions and formulations of the present disclosure exhibit enhanced stability for at least about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 2 weeks, 3 weeks, 4 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 12 months, and up to 1 year. In some embodiments, the compositions and formulations of the present disclosure exhibit enhanced stability at temperatures ranging from about 0° C. to 65° C., from about 4° C. to 65° C., from about 10° C. to 65° C., from about 15° C. to 65° C., from about 15° C. to 65° C., from about 20° C. to 65° C., from about 25° C. to 65° C., from about 30° C. to 65° C., from about 35° C. to 65° C., from about 37° C. to 65° C., from about 40° C. to 65° C., from about 45° C. to 65° C.,

from about 50° C. to 65° C., from about 55° C. to 65° C., from about 60° C. to 65° C., from about 4° C. to 55° C., from about 10° C. to 50° C., from about 15° C. to 45° C., and from about 20° C. to 40° C.

#### 4. Detection Assays and Systems

[0327] Embodiments of the present disclosure include compositions, systems, assays, and methods for detecting one or more analytes in a sample. In accordance with these embodiments, described below are exemplary assays and devices for use with various embodiments herein. The following devices and assays should not be viewed as limiting the full scope of the systems, assays, and methods described herein.

##### a. Lateral Flow Assays

[0328] In certain embodiments, the present disclosure provides compositions and materials for conducting a lateral flow assay (e.g., a lateral flow immunoassay). Lateral flow assays are based on the principles of immunochromatography and can be used to detect, quantify, test, measure, and monitor a wide array of analytes, such as, but not limited to, analytes pertaining to monitoring ovulation, detecting/diagnosing infectious diseases/organisms, analyzing drugs of abuse, detecting/quantifying analytes important to human physiology, security screening, veterinary testing, agriculture applications, environmental testing, product quality evaluation, etc.

[0329] As shown in FIG. 1, embodiments of the present disclosure include lateral flow detection systems (100) for detecting and/or quantifying a target analyte based on bioluminescent complex formation. In some embodiments, lateral flow assay systems of the present disclosure include an analytical membrane (105) that is divided into one or more detection regions (110) and one or more control regions (115). The detection region or regions can include a target analyte binding agent immobilized to a portion of the detection region such that it is not displaced when facilitating lateral flow across the analytical membrane. Lateral flow assay systems of the present disclosure can also include a conjugate pad (120) within which a target analyte binding agent is contained. In some embodiments, a target analyte binding agent is contained within the conjugate pad but flows from the conjugate pad and across the analytical membrane towards the detection and control regions when lateral flow occurs. Lateral flow assay systems of the present disclosure can also include a sample pad (125) that is positioned at one distal end of the lateral flow assay system (e.g., opposite an absorbent pad). A sample that contains (or may contain) a target analyte is applied to the sample pad. In some embodiments, a lateral flow assay system also comprises a wicking pad (130) at an end of the device distal to the sample pad. The wicking pad generates capillary flow of the sample from the sample pad through the conjugate pad, analytical membrane, detection region, and control region.

[0330] In accordance with these embodiments, upon addition of a sample to the sample pad, the facilitation of lateral flow causes a target analyte within the sample to contact a first target analyte binding agent within the conjugate pad; subsequently, lateral flow causes the target analyte and the first target analyte binding agent to contact a second target analyte binding agent immobilized to a detection region of the analytical membrane. The presence and/or quantity of the target analyte is then determined based on detection of

the analyte in the detection region (e.g., in the presence of a luminogenic substrate for the bioluminescent complex) and/or in comparison to the control.

[0331] In some embodiments, the above lateral flow systems make use of one or more NanoLuc®-based technologies (e.g., NanoBiT, NanoTrip, NanoBRET, etc.) for detection of the bound target analyte.

[0332] In an exemplary embodiment, as shown in FIG. 1, a target analyte is an antibody generated in a subject in response to being exposed to an infectious disease/organism. The first target analyte binding agent includes a both a target analyte binding element that binds the antibody (e.g., a non-specific antibody binding agent (e.g., protein L)) and a first peptide or polypeptide capable of interacting with a distinct peptide or polypeptide to generate a bioluminescent signal (e.g., a NanoBiT non-luminescent peptide or polypeptide or variant thereof (e.g., one of SEQ ID NOs: 9-11 or 12/14)). The second target analyte binding agent can include a target analyte binding element that binds the antibody, such as an epitope of an antigen recognized by the antibody, and a second peptide or polypeptide capable of interacting with a the first peptide or polypeptide to generate a bioluminescent signal (e.g., a NanoBiT non-luminescent peptide or polypeptide or variant thereof (e.g., one of SEQ ID NOs: 9-11 or 12/14)). Once the bioluminescent complex firms at the detection region, the bioluminescent signal can be detected and/or quantified (e.g., in the presence of a luminogenic substrate for the bioluminescent complex), thus indicating the presence/quantity of the antibody in the sample.

[0333] As shown in FIG. 1, lateral flow assays of the present disclosure can be configured to test for multiple different analytes such as antibodies generated to distinct diseases/microorganisms, in a single sample from a subject (e.g., multiplexing). In accordance with these embodiments, the analytical membrane can include a plurality of detection regions with each detection region comprising a distinct target analyte binding agent having distinct target analyte binding elements (e.g., distinct disease antigens).

[0334] In an alternative lateral flow embodiment to the one depicted in FIG. 1, a target analyte is an antibody generated in a subject in response to being exposed to an infectious disease/organism. The first target analyte binding agent that includes a both a target analyte binding element that binds the antibody (e.g., an epitope of an antigen recognized by the antibody) and a bioluminescent polypeptide (e.g., NanoLuc or a variant thereof (e.g., SEQ ID NO: 5, SEQ ID NO: 6)). The second target analyte binding agent can include a target analyte binding element that binds the antibody, such as a non-specific antibody binding agent (e.g., protein L). Detection of bioluminescence in the detection region (e.g., in the presence of a luminogenic substrate for the bioluminescent complex) then indicates that both target analyte binding agents bound to the target analyte, and therefore the target analyte was present in the sample.

[0335] In another exemplary alternative embodiment, a target analyte is an antibody generated in a subject in response to being exposed to an infectious disease/organism. The first target analyte binding agent includes a both a target analyte binding element that binds the antibody (e.g., a non-specific antibody binding agent (e.g., protein L), a target-specific (e.g., antibody) binding agent) and a first non-luminescent (NL) peptide tag (e.g., SEQ ID NO: 13 or 11 or variants thereof) capable of interacting with a second

non-luminescent (NL) peptide (e.g., SEQ ID NO: 11 or 13 or variants thereof) and a non-luminescent (NL) polypeptide (e.g., SEQ ID NO: 12 or variants thereof) to generate a bioluminescent signal. The second target analyte binding agent includes a target analyte binding element that binds the antibody (e.g., a target-specific (e.g., antibody) binding agent, a non-specific antibody binding agent (e.g., protein L)) and a second NL peptide tag (e.g., SEQ ID NO: 11 or 13 or variants thereof). Formation of the bioluminescent complex in the presence of the NL polypeptide component (e.g., SEQ ID NO: 12 or variants thereof) and a luminogenic substrate in the detection region indicates the presence of the target analyte in the sample. The bioluminescent signal is detected and/or quantified to detect/quantity the antibody in the sample.

[0336] Additional alternatives to the exemplary embodiments set forth above are contemplated. For example, alternative binding agents, target analytes, detectable elements, order of the various components (e.g., non-specific binding agent/target-specific binding agent, target-specific binding agent/non-specific binding agent, target-specific binding agent/target-specific binding agent, etc.) are described herein and embodiments incorporating various combinations of the components are within the scope herein.

[0337] In some embodiments, a target analyte is not an antibody, but is instead a small molecule, peptide, protein, carbohydrate, lipid, etc. In some embodiments, the lateral flow assays and systems described above are configured (e.g., using one or more NanoLuc®-based technologies (e.g., NanoBiT, NanoTrip, NanoBRET, etc.)) for the detection of any such target analytes.

b. Solid Phase Assays

[0338] Embodiments of the present disclosure include compositions, assays, systems, devices, and methods for detecting one or more analytes in a sample. In accordance with these embodiments, the present disclosure provides compositions and materials for conducting a solid phase assay (e.g., a solid phase platform for conducting an immunoassay). Solid phase detection platforms are generally the simplest form of an immunoassay and can be used to detect, quantify, test, measure, and monitor a wide array of analytes such as, but not limited to, analytes pertaining to monitoring ovulation, detecting/diagnosing infectious diseases/organisms, analyzing drugs of abuse, detecting/quantifying analytes important to human physiology, veterinary testing, security screening, agriculture applications, environmental testing, and product quality evaluation. In contrast to lateral flow assays, solid phase detection platforms do not involve facilitating the flow of assay reagents across a membrane, but instead typically include a solid support to which components of the assay are attached or contained within (e.g., dipstick test or spot test).

[0339] As shown in FIG. 2, embodiments of the present disclosure include solid phase detection platforms (200) for detecting and/or quantifying a target analyte based on bioluminescent complex formation. In some embodiments, solid phase detection platforms of the present disclosure include one or more detection regions (205) and one or more control regions (210) to which a sample is applied. In some embodiments, the detection region or regions includes a target analyte binding agent within and/or conjugated to a portion of the detection region. Solid phase detection platforms of the present disclosure can also include a solid support (215) to which the detection regions and the control

regions are attached and demarcated from each other, and which allow for a sample to be applied to the detection and control regions (e.g., dipstick test).

[0340] In accordance with these embodiments, a sample or a portion of a sample is applied to the detection and control regions of the solid phase assay platform such that a target analyte contacts a target analyte binding agent (220) conjugated to and/or within the detection region under conditions such that the binding event and/or the immobilization of the target analyte on the solid phase is detectable (e.g., a bioluminescent entity is immobilized, a bioluminescent complex is formed), thereby indicating the presence of the analyte in the sample.

[0341] In some embodiments, the solid phase assay platform includes a first target analyte binding agent (e.g., a target-specific binding agent (e.g., target-specific antibody, antigen for the target antibody, etc.)) immobilized on the solid phase. A second target analyte binding agent (e.g., a target-specific binding agent (e.g., target-specific antibody, antigen for the target antibody, etc.), a non-specific binding agent (e.g., protein L)) linked to a bioluminescent polypeptide (e.g., SEQ ID NO: 5 or variants thereof) is added to the solid phase with the sample (e.g., concurrently, sequentially, etc.). If both target analyte binding agent bind to the target analyte, the bioluminescent polypeptide becomes immobilized on the solid phase. Detection/quantification of bioluminescence on the solid phase (e.g., after a wash step) indicates the presence/amount of target analyte in the sample. In some cases, the first target analyte binding agent is conjugated to the detection region, and the second target analyte binding agent (attached to the bioluminescent polypeptide) is applied to the detection region with or without the sample. In some cases, the second target analyte binding agent is conjugated to the detection region, and the first target analyte binding agent (attached to the bioluminescent polypeptide) is applied to the detection region with or without the sample. In accordance with these embodiments, immobilization of bioluminescence at the detection region can be detected and/or quantified when in the presence of a luminogenic substrate (as described further below), thus indicating the presence (or absence) of the antibody in the sample.

[0342] In alternative embodiments, a solid phase assay platform utilizes a binary complementation approach, in which a bioluminescent complex is formed upon binding of two non-luminescent (NL) peptide/polypeptide components (e.g., NanoBiT system), to detect a target analyte. Multiple configurations of solid phase assays and systems utilizing a binary complementation approach are within the scope herein. For example, an exemplary system can include (i) a first target analyte binding agent linked to a first NL peptide or NL polypeptide (e.g., SEQ ID NOs: 9 or 10 or variants thereof) capable of interacting with high affinity with a second distinct NL polypeptide or NL peptide (e.g., SEQ ID NOs: 10 or 9 or variants thereof) to generate a bioluminescent signal, and (ii) a second target analyte binding agent linked to the complementary NL polypeptide or NL peptide, wherein the second target analyte binding agent is immobilized to the solid phase. Upon binding of the target analyte binding agents to the target analyte, a bioluminescent complex is formed on the solid phase and the bioluminescent signal is detectable/quantifiable, when in the presence of a luminogenic substrate (as described further below).

[0343] In other embodiments, a solid phase assay platform utilizes a tripartite complementation approach, in which a bioluminescent complex is formed upon binding of two non-luminescent (NL) peptide components and a non-luminescent (NL) polypeptide component (e.g., NanoTrip system), to detect a target analyte. In some embodiments, the solid phase assay platform includes: (i) a first target analyte binding agent comprising both a target analyte binding element (e.g., general or specific) and a NL peptide (e.g., SEQ ID NOs: 11 or 13) capable of forming a tripartite bioluminescent complex (e.g., NanoTrip complex), (ii) a second target analyte binding agent comprising both a target analyte binding element (e.g., specific) and a NL peptide (e.g., SEQ ID NOs: 11 or 13) capable of forming a tripartite bioluminescent complex (e.g., NanoTrip complex), (iii) a NL polypeptide component of the tripartite bioluminescent complex (e.g., NanoTrip complex), and (iv) a luminogenic substrate. In some cases, the first target analyte binding agent is conjugated to the detection region, and the second target analyte binding agent is applied to the detection region with or without the sample. In some cases, the second target analyte binding agent is conjugated to the detection region, and the first target analyte binding agent is applied to the detection region with or without the sample. Once the bioluminescent complex forms at the detection region, the bioluminescent signal is detected and/or quantified, thus indicating the presence (or absence) of the antibody in the sample.

[0344] In other embodiments, the solid phase assay platform includes (i) a first target analyte binding agent comprising a target analyte binding element and a NanoLuc®-based peptide or polypeptide, (ii) target analyte binding agent comprising a target analyte binding element and a fluorophore, and (iii) optionally the additional peptide/polypeptide components to form a bioluminescent complex (e.g., in embodiments in which the NanoLuc®-based peptide or polypeptide is not a bioluminescent polypeptide, e.g. non-luminescent), wherein upon binding of the first and second target analyte binding agents to a target analyte in a sample, in the presence of any additional components necessary for bioluminescence (e.g., luminogenic substrate, complementary components, etc.), emission from the NanoLuc®-based components (e.g., NanoLuc® protein or bioluminescent complex) excites the fluorophore (e.g., via BRET). In some cases, the first target analyte binding agent is conjugated to the detection region, and the second target analyte binding agent is applied to the detection region with or without the sample. In some cases, the second target analyte binding agent is conjugated to the detection region, and the first target analyte binding agent is applied to the detection region with or without the sample.

[0345] As shown in FIG. 2, solid phase platforms of the present disclosure can be configured to test for multiple different analytes, such as antibodies generated to distinct diseases/microorganisms, in a single sample from a subject (e.g., multiplexing). In accordance with these embodiments, the solid phase platforms can include a plurality of detection regions with each detection region comprising a distinct target analyte binding agent having distinct target analyte binding elements (e.g., distinct disease antigens).

[0346] In some embodiments, the solid phase platforms of the present disclosure can include a plurality of detection regions such as one or more wells of a microtiter plate, for example. In such embodiments, one or more distinct target

analyte binding agents can be conjugated (e.g., coated) to wells of the microtiter plate along one or more of the other detection reagents required to carry out a particular bioluminescent assay (e.g., a second target analyte binding agent, a luminogenic substrate, assay buffer, etc.). In some embodiments, one or more of the other detection reagents (reagents not conjugated to the microtiter plate) required to carry out the assay can be added to the wells of the microtiter plate in the form of a lyophilized cake (lyocake) or tablet and reconstituted as part of the bioluminescent assay.

#### c. Solution Phase Assays

[0347] Embodiments of the present disclosure include compositions, assays, systems, devices, and methods for detecting one or more analytes in a sample. In accordance with these embodiments, the present disclosure provides compositions and materials for conducting a solution phase assay (e.g., a liquid-based format for conducting an immunoassay within a solution). Solution phase detection platforms can be used to detect, quantify, test, measure, and monitor a wide array of analytes such as, but not limited to, analytes pertaining to monitoring ovulation, detecting/diagnosing infectious diseases/organisms, analyzing drugs of abuse, detecting/quantifying analytes important to human physiology, veterinary testing, security screening, agriculture applications, environmental testing, and product quality evaluation. In contrast to lateral flow assays and solid phase detection platforms, solution phase detection platforms typically include a receptacle for the solution/liquid in which reactions involving the detection reagents take place, instead of conjugating one or more of the detection reagents to a solid support or membrane to facilitate detection.

[0348] For example, as shown in FIG. 33, embodiments of solution phase platforms of the present disclosure can include one or more components of the bioluminescent complexes in a tablet or lyophilized cake that can be reconstituted in a solution (e.g., buffered solution) to facilitate analyte detection. In some embodiments, the tablet or lyocake can include all the reagents necessary to carry out a reaction to detect an analyte. Such lyocakes or tablets are compatible with many different assay formats, including but not limited to, cuvettes, wells of microtiter plates (e.g., 96-well microtiter plate), test tubes, large volume bottles, SNAP assays, and the like.

[0349] In some embodiments, the solution phase assay platform includes a lyocake or tablet comprising one or more of a first target analyte binding agent (e.g., a target-specific binding agent (e.g., target-specific antibody, antigen for the target antibody, etc.)), a second target analyte binding agent (e.g., a target-specific binding agent (e.g., target-specific antibody, antigen for the target antibody, etc.), and a non-specific binding agent (e.g., protein L)) linked to a bioluminescent polypeptide (e.g., SEQ ID NO: 5 and variants thereof). Detection/quantification of bioluminescence in the solution indicates the presence/amount of target analyte in the sample.

[0350] In some embodiments, a solution phase assay platform utilizes a binary complementation approach, in which a bioluminescent complex is formed upon binding of two non-luminescent (NL) peptide/polypeptide components (e.g., NanoBiT system), to detect a target analyte. Multiple configurations of solution phase assays and systems utilizing a binary complementation approach are within the scope herein. For example, an exemplary system can include (i) a first target analyte binding agent linked to a first NL peptide

or NL polypeptide (e.g., SEQ ID NOs: 9 or 10 or variants thereof) capable of interacting with high affinity with a second distinct NL polypeptide or NL peptide (e.g., SEQ ID NOs: 10 or 9 or variants thereof) to generate a bioluminescent signal, and (ii) a second target analyte binding agent linked to the complementary NL polypeptide or NL peptide. Upon binding of the target analyte binding agents to the target analyte, a bioluminescent complex is formed in the solution and the bioluminescent signal is detectable/quantifiable, when in the presence of a luminogenic substrate (as described further below).

[0351] In other embodiments, a solution phase assay platform utilizes a tripartite complementation approach, in which a bioluminescent complex is formed upon binding of two non-luminescent (NL) peptide components and a non-luminescent (NL) polypeptide component (e.g., NanoTrip system), to detect a target analyte. In some embodiments, the solution phase assay platform includes: (i) a first target analyte binding agent comprising both a target analyte binding element (e.g., general or specific) and a NL peptide (e.g., SEQ ID NOs: 11 or 13) capable of forming a tripartite bioluminescent complex (e.g., NanoTrip complex), (ii) a second target analyte binding agent comprising both a target analyte binding element (e.g., specific) and a NL peptide (e.g., SEQ ID NOs: 11 or 13) capable of forming a tripartite bioluminescent complex (e.g., NanoTrip complex), (iii) a NL polypeptide component of the tripartite bioluminescent complex (e.g., NanoTrip complex), and (iv) a luminogenic substrate. Once the bioluminescent complex forms in the solution, the bioluminescent signal is detected and/or quantified, thus indicating the presence (or absence) of the antibody in the sample.

[0352] In other embodiments, the solution phase assay platform includes (i) a first target analyte binding agent comprising a target analyte binding element and a NanoLuc®-based peptide or polypeptide, (ii) target analyte binding agent comprising a target analyte binding element and a fluorophore, and (iii) optionally the additional peptide/polypeptide components to form a bioluminescent complex (e.g., in embodiments in which the NanoLuc®-based peptide or polypeptide is not a bioluminescent polypeptide, e.g., non-luminescent), wherein upon binding of the first and second target analyte binding agents to a target analyte in a sample, in the presence of any additional components necessary for bioluminescence (e.g., luminogenic substrate, complementary components, etc.), emission from the NanoLuc®-based components (e.g., NanoLuc® protein or bioluminescent complex) excites the fluorophore (e.g., via BRET).

[0353] Solution phase platforms of the present disclosure can be configured to test for multiple different analytes (e.g., multiplexing), such as antibodies generated to distinct diseases/microorganisms in a single sample from a subject. In some embodiments, one or more of the detection reagents required to carry out a bioluminescent reaction to detect/quantify an analyte are present in one or more receptacles of a particular assay platform being used (e.g., individual wells of a 96-well plate), for example, as a lyocake or tablet that is to be reconstituted in a buffered solution. In other embodiments, one or more types of a sample solution are already present in the receptacles, and one or more lyocakes or tables are added to the receptacles and rehydrated to facilitate a bioluminescent reaction. In accordance with these embodiments, the solution phase platforms can include a plurality of receptacles comprising a distinct target analyte

binding agent having distinct target analyte binding elements (e.g., distinct disease antigens).

#### d. Other Assays

**[0354]** Embodiments of the present disclosure include compositions, assays, systems, devices, and methods for detecting one or more analytes in a sample using other assay platforms known in the art. For example, target analytes can be detected and/or measured using the bioluminescent polypeptides and/or complexes described herein in the context of a microfluidic and/or chip-based assay. Because microfluidic systems integrate a wide variety of operations for manipulating fluids, such as chemical or biological samples, these systems are applicable to many different areas, such as biological and medical diagnostics. One type of microfluidic device is a microfluidic chip. Microfluidic chips may include micro-scale features (or micro-features), such as channels, valves, pumps, and/or reservoirs for storing fluids, for routing fluids to and from various locations on the chip, and/or for reacting fluidic reagents.

**[0355]** Microfluidic chips, or labs-on-a-chip (LOC), configured with bioluminescent polypeptides and/or complexes that include peptides and polypeptides capable of generating a bioluminescent signal in the presence of the target analyte offer increased flexibility for automation, integration, miniaturization, and multiplexing. For example, pathogen detection based on microfluidic chips use reaction chambers that are usually on the micro- or nano-scale, which allows devices to be miniaturized and portable; this is particularly advantageous for point-of-care testing. LOC technology allows for the integration of sample preparation, amplification, and signal detection, which reduces the time need to generate results. The high throughput and low consumption of sample and reagents make the technology flexible and relatively cost effective. Nucleic acid-based microfluidic pathogen detection for the detection of bacteria, viruses, and fungi that eliminates the need for PCR or real-time PCR for amplification is a distinct advantage of the bioluminescent complexes of the present disclosure.

### 5. Assay Compositions, Components, and Methods of Manufacturing

**[0356]** Embodiments of the present disclosure also include methods of manufacturing an assay platform for use with bioluminescent peptides and polypeptides for target analyte detection. Although assay platforms may vary depending on various factors, such as the analyte being detected, the complexity of the sampling environment, and the diagnostic parameters, the compositions, materials and methods of the present disclosure can be applied to most currently available assay platforms, such as solid phase assays, lateral flow assays, and microfluidic-based assays.

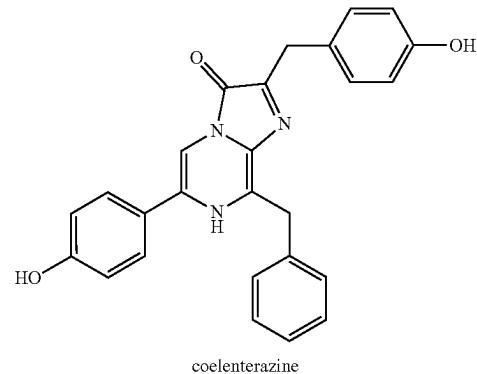
#### a. Luminogenic Substrates

**[0357]** In some embodiments, methods of manufacturing assay platforms of the present disclosure include application of a luminogenic substrate. Luminogenic substrates, such as coelenterazine, and analogs and derivatives thereof, can decompose during storage thereby resulting in loss of the substrate before addition to or use in a biological assay. Such decomposition can be the result of instability of the luminogenic substrate in solution over time in a temperature-dependent manner. This decomposition results in waste of the luminogenic substrate and reduced sensitivity and repro-

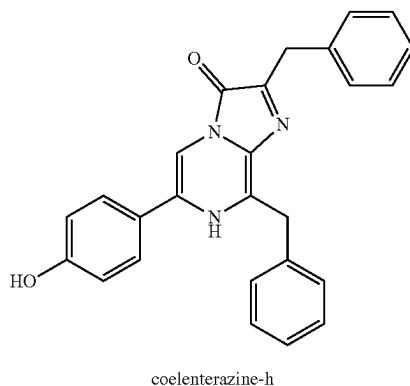
ducibility of luminescent measurements derived from biological assays that employed the decomposed luminogenic substrate.

**[0358]** Provided herein are compositions that include a luminogenic substrate, such as coelenterazine or an analog or derivative thereof. Exemplary coelenterazine analogs include coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, and JRW-1744.

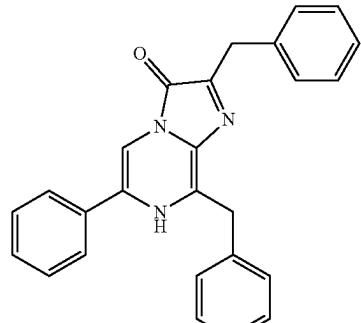
**[0359]** In some embodiments, the substrate is coelenterazine, which has the following structure:



**[0360]** Exemplary coelenterazine analogs include coelenterazine-h (2-deoxycoelenterazine or 2,8-dibenzyl-6-(4-hydroxyphenyl)imidazo[1,2-a]pyrazin-3(7H)-one), coelenterazine-h-h (dideoxycoelenterazine or 2,8-dibenzyl-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one), furimazine (8-benzyl-2-(furan-2-ylmethyl)-6-phenylimidazo[1,2-a]pyrazin-3(7H)-one), JRW-0238 (8-benzyl-2-(furan-2-ylmethyl)-6-(3-hydroxyphenyl)imidazo[1,2-a]pyrazin-3(7H)-one), JRW-1404 (8-benzyl-6-(2-fluoro-3-hydroxyphenyl)-2-(furan-2-ylmethyl)imidazo[1,2-a]pyrazin-3(7H)-one), JRW-1482 (6-(3-amino-2-fluorophenyl)-8-benzyl-2-(furan-2-ylmethyl)imidazo[1,2-a]pyrazin-3(7H)-one), JRW-1667 (6-(3-amino-2-fluorophenyl)-8-(2-fluorobenzyl)-2-(furan-2-ylmethyl)imidazo[1,2-a]pyrazin-3(7H)-one), JRW-1744 (6-(3-amino-2-fluorophenyl)-8-benzyl-2-(furan-2-ylmethyl)imidazo[1,2-a]pyrazin-3(7H)-one), and JRW-1743 (6-(3-amino-2-fluorophenyl)-8-(2-fluorobenzyl)-2-(furan-2-ylmethyl)imidazo[1,2-a]pyrazin-3(7H)-one), which have the following structures:

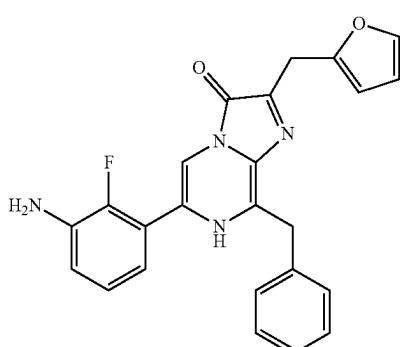


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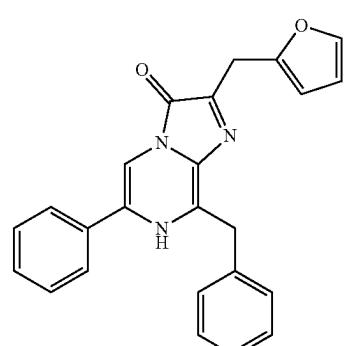


coelenterazine-hh

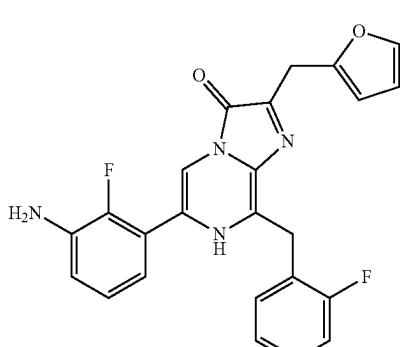
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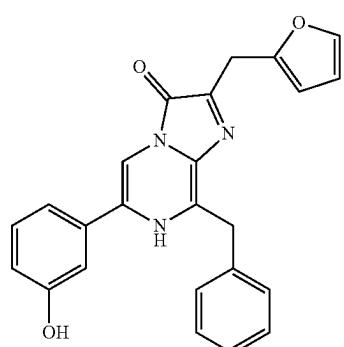
JRW-1482



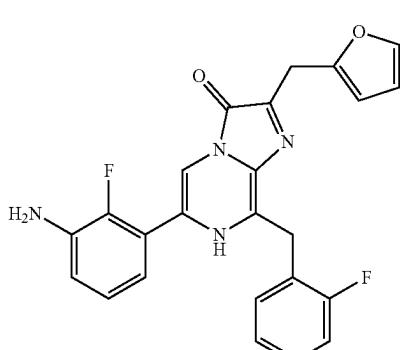
furimazine



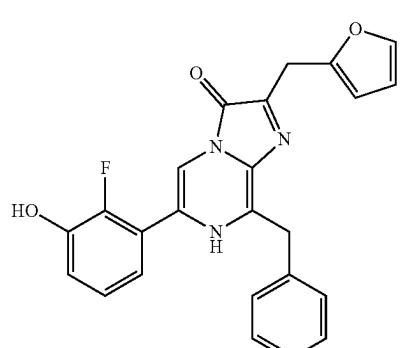
JRW-1667



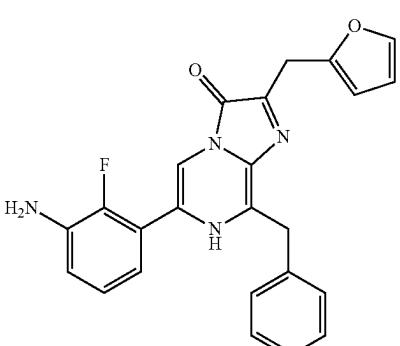
JRW-0238



JRW-1743



JRW-1404



JRW-1744

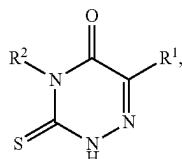
[0361] Additional exemplary coelenterazine analogs include coelenterazine-n, coelenterazine-f, coelenterazine-hcp, coelenterazine-cp, coelenterazine-c, coelenterazine-e, coelenterazine-fcp, coelenterazine-i, coelenterazine-icp, coelenterazine-v, 2-methyl coelenterazine, and the like. In some embodiments, the compound may be a coelenterazine analog described in WO 2003/040100; U.S. Pat. Pub. 2008/

0248511 (e.g., paragraph [0086]); U.S. Pat. No. 8,669,103; WO 2012/061529; U.S. Pat. Pub. 2017/0233789; U.S. Pat. No. 9,924,073; U.S. Pat. Pub. 2018/0030059; U.S. Pat. No. 10,000,500; U.S. Pat. Pub. 2018/0155350; U.S. patent application Ser. No. 16/399,410 (PCT/US2019/029975); U.S. patent application Ser. No. 16/548,214 (PCT/US2019/047688); U.S. Pat. Pub. 2014/0227759; U.S. Pat. Nos. 9,840,730; 7,268,229; 7,537,912; 8,809,529; 9,139,836; 10,077,244; 9,487,520; 9,924,073; 9,938,564; 9,951,373; 10,280,447; 10,308,975; 10,428,075; the disclosures of which are incorporated by reference herein in their entireties. In some embodiments, coelenterazine analogs include pro-substrates such as, for example, those described in U.S. Pat. Pub. 2008/0248511; U.S. Pat. Pub. 2012/0707849; U.S. Pat. Pub. 2014/0099654; U.S. Pat. Nos. 9,487,520; 9,927,430; 10,316,070; herein incorporated by reference in their entireties. In some embodiments, the compound is furimazine. In some embodiments, the compound is JRW-0238. In some embodiments, the compound is JRW-1743. In some embodiments, the compound is JRW-1744.

[0362] Provided herein are compositions that include a luminogenic substrate, such as coelenterazine or an analog or derivative thereof, and a polymer or a paper/fibrous substrate for the manufacture of bioluminescent target analyte detection platforms. Compositions that stabilize and/or enhance the reconstitution efficiency of luminogenic substrates such as coelenterazine or an analog or derivative thereof, are described in U.S. patent application Ser. No. 16/592,310 (PCT/US2019/054501); herein incorporated by reference in its entirety. In some embodiments, the composition stabilizes the compound against decomposition. In some embodiments, the composition stabilizes the compound against decomposition as compared to a composition that does not contain the polymer or paper/fibrous substrate. In some embodiments, the polymer or the paper/fibrous substrate reduces or suppresses the formation of one or more decomposition products from the compound. In some embodiments, the compositions enhance the reconstitution efficiency or reconstitution rate of the substrate.

[0363] Additionally, embodiments of the present disclosure include means for stabilizing (e.g., enhancing storage stability) the compositions described further herein. In some embodiments, enhancing the storage stability of the compositions provided herein includes methods and compositions for stabilizing a luminogenic substrate. The luminogenic substrate may be, but is not limited to, coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, a derivative thereof, an analog thereof, or any combination thereof. The compositions may include the luminogenic substrate, a thionucleoside, and an organic solvent. The composition may not include or contain a luminogenic enzyme. As provided in U.S. Pat. No. 9,676,997, which is herein incorporated by reference, a thionucleoside may be a compound of formula (I) or a tautomer thereof,

(I)



wherein

[0364] R<sup>1</sup> is hydrogen, alkyl, substituted alkyl, alkyl-aryl, alkyl-heteroaryl, cycloalkyl, aryl, heteroaryl, carboxylic acid, ester, NR<sup>a</sup>R<sup>b</sup>, imine, hydroxyl, or oxo;

[0365] R<sup>2</sup> is hydrogen, NR<sup>a</sup>R<sup>b</sup>, imine, alkyl, or aryl; and

[0366] R<sup>a</sup> and R<sup>b</sup> are each independently hydrogen, alkyl, or aryl.

[0367] In some embodiments, the compound of formula (I) may be ATT (6-methyl-3-thioxo-3,4-dihydro-1,2,4-triazin-5(2H)-one); 3-(4-Amino-5-oxo-3-thioxo-2,3,4,5-tetrahydro-1,2,4-triazin-6-yl)propanoic acid; tetrahydro-2-methyl-3-thioxo-1,2,4-triazine-5,6-dione; 4-((2-furylmethylene)amino)-3-mercaptop-6-methyl-1,2,4-triazin-5(4H)-one; 6-benzyl-3-sulfanyl-1,2,4-triazin-5-ol; 4-amino-3-mercaptop-6-methyl-1,2,4-triazin-5(4H)-one; 3-(5-oxo-3-thioxo-2,3,4,5-tetrahydro-1,2,4-triazin-6-yl)propanoic acid; (E)-6-methyl-4-((thiophen-2-ylmethylene)amino)-3-thioxo-3,4-dihydro-1,2,4-triazin-5(2H)-one; (E)-6-methyl-4-((3-nitrobenzylidene)amino)-3-thioxo-3,4-dihydro-1,2,4-triazin-5(2H)-one; (E)-4-((4-(diethylamino)benzylidene)amino)-6-methyl-3-thioxo-3,4-dihydro-1,2,4-triazin-5(2H)-one; ATCA ethyl ester; TAK-0021, TAK-0020, TAK-0018, TAK-0009, TAK-0014, TAK-0007, TAK-0008, TAK-0003, and TAK-0004, as provided in U.S. Pat. No. 9,676,997 (incorporated herein by reference); 3-thioxo-6-(trifluoromethyl)-3,4-dihydro-1,2,4-triazin-5(2H)-one; 6-cyclopropyl-3-thioxo-3,4-dihydro-1,2,4-triazin-5(2H)-one; 6-(hydroxymethyl)-3-thioxo-3,4-dihydro-1,2,4-triazin-5(2H)-one; or any combinations thereof.

[0368] In some embodiments, a thionucleoside may stabilize the luminogenic substrate against decomposition over time, in the presence of light, in the absence of light, and/or at different temperatures. The thionucleoside may stabilize the luminogenic substrate against decomposition into one or more decomposition products over time, in the presence of light, in the absence of light, and/or at different temperatures. As such, inclusion of the thionucleoside in the compositions described further herein may stabilize the luminogenic substrate against decomposition by suppressing or reducing the formation of the one or more decomposition products as compared to a composition that does not include the thionucleoside. This, in turn, provides the capability of storing or incubating the luminogenic substrate for a period of time at a particular temperature, in the presence of light, and/or in the absence of light without significant decomposition of the luminogenic substrate before use of the luminogenic substrate in an assay. In accordance with these embodiments, the inclusion of a thionucleoside in the compositions described herein can enhance storage stability of the compositions. These embodiments also relate to methods for stabilizing the luminogenic substrate. Such a method may stabilize the luminogenic substrate against decomposition and/or suppress or reduce the formation of the one or more decomposition products. The method may include contacting the luminogenic substrate with an effective amount of the thionucleoside (e.g., 225 mM) in the presence of the organic solvent. This contacting step may include forming the composition described above.

[0369] In some embodiments, one or more of the non-luminous (NL) peptide/polypeptide components that form the bioluminescent complexes described above can be included with or without a luminogenic substrate as part of a composition, such as a lyophilized powder. These compositions can be applied directly, with or without other

components, to a portion of a detection platform, or they can be reconstituted as part of a separate solution that is applied to the detection platform.

[0370] Coelenterazine and analogs and derivatives thereof may suffer from challenges associated with their reconstitution into buffer systems used in many assays such as the bioluminogenic methods described herein. For example, coelenterazines, or analogs or derivatives thereof, such as furimazine, may dissolve slowly and/or inconsistently in buffer solutions (e.g., due to the heterogeneous microcrystalline nature of the solid material). While dissolution in organic solvent prior to dilution with buffer may provide faster and more consistent results, coelenterazine compounds may suffer from instability in organic solutions on storage, including both thermal instability and photo-instability. In some embodiments, the composition further comprises a polymer. As further described herein, the presence of the polymer may stabilize the compound against decomposition, and the presence of the polymer may improve the solubility of the compound in water or in aqueous solutions.

[0371] The polymer may be a naturally-occurring biopolymer or a synthetic polymer. In some embodiments, the polymer is a naturally-occurring biopolymer. Suitable naturally-occurring biopolymers are carbohydrates, including disaccharides (e.g., trehalose and maltose), and polysaccharides (e.g., pullulan, dextran, and cellulose). Mixtures of naturally-occurring biopolymers may also be used. In some embodiments, the polymer is pullulan, which is a polysaccharide that includes maltotriose repeating units. Maltotriose is a trisaccharide that includes three glucose units that are linked via a-1,4 glycosidic bonds. The maltotriose units within the pullulan polymer are linked to each other via a-1,6 glycosidic bonds.

[0372] In some embodiments, the polymer is a synthetic polymer. A synthetic polymer may be a homopolymer, copolymer, or block copolymer (e.g., diblock copolymer, triblock copolymer, etc.). Non-limiting examples of suitable polymers include, but are not limited to polyamines, polyethers, polyamides, polyesters, polycarbamates, polyureas, polycarbonates, polystyrenes, polyimides, polysulfones, polyurethanes, polyacetylenes, polyethylenes, polyethyleneimines, polyisocyanates, polyacrylates, polymethacrylates, polyacrylonitriles, and polyarylates. Non-limiting examples of specific polymers include poly(caprolactone) (PCL), ethylene vinyl acetate polymer (EVA), poly(lactic acid) (PLA), poly(L-lactic acid) (PLLA), poly(glycolic acid) (PGA), poly(lactic acid-co-glycolic acid) (PLGA), poly(L-lactic acid-co-glycolic acid) (PLLG), poly(D,L-lactide) (PDLA), poly(L-lactide) (PLLA), poly(D,L-lactide-co-caprolactone), poly(D,L-lactide-co-caprolactone-co-glycolide), poly(D,L-lactide-co-PEO-co-D,L-lactide), poly(D,L-lactide-co-PPO-co-D,L-lactide), polyalkyl cyanoacrylate, polyurethane, poly-L-lysine (PLL), hydroxypropyl methacrylate (HPMA), poly(ethylene glycol), poly-L-glutamic acid, poly(hydroxy acids), polyanhydrides, polyorthoesters, poly(ester amides), polyamides, poly(ester ethers), polycarbonates, polyalkylenes (e.g., polyethylene and polypropylene), polyalkylene glycols (e.g., poly(ethylene glycol) (PEG)), polyalkylene terephthalates (e.g., poly(ethylene terephthalate), etc.), polyvinyl alcohols (PVA), polyvinyl ethers, polyvinyl esters (e.g., poly(vinyl acetate), etc.), polyvinyl halides (e.g., poly(vinyl chloride) (PVC), etc.), polyvinylpyrrolidone, polysiloxanes, polystyrene (PS), polyurethanes, derivatized

celluloses (e.g., alkyl celluloses, hydroxylcelluloses, cellulose ethers, cellulose esters, nitro celluloses, hydroxypropylcellulose, carboxymethylcellulose, etc.), polymers of acrylic acids ("polyacrylic acids") (e.g., poly(methyl(meth)acrylate) (PMMA), poly(ethyl(meth)acrylate), poly(butyl(meth)acrylate), poly(isobutyl(meth)acrylate), poly(hexyl(meth)acrylate), poly(isodecyl(meth)acrylate), poly(lauryl(meth)acrylate), poly(phenyl(meth)acrylate), poly(methyl acrylate), poly(isopropyl acrylate), poly(isobutyl acrylate), poly(octadecyl acrylate), polydioxanone and its copolymers (e.g., polyhydroxalkanoates, polypropylene fumarate), polyoxymethylene, poloxamers, poly(ortho)esters, poly(butyric acid), poly(valeric acid), poly(lactide-co-caprolactone), trimethylene carbonate, and mixtures and copolymers thereof.

[0373] In some embodiments, the composition further comprises a paper substrate. As further described herein, the presence of the paper substrate may stabilize the compound against decomposition, and the presence of the paper substrate may improve the solubility of the compound in aqueous solutions. Exemplary paper substrates include, but are not limited to, Whatman brand papers, (e.g., W-903 paper, FTA paper, FTA Elute paper, FTA DMPK paper, etc.), Ahlstrom papers (e.g., A-226 paper, etc.), M-TFN paper, FTA paper, FP705 paper, Bode DNA collection paper, nitrocellulose paper, nylon paper, cellulose paper, Dacron paper, cotton paper, and polyester papers, and combinations thereof.

[0374] In addition to the compound and the polymer and/or the paper substrate, the composition may include additional components such as buffers, surfactants, salts, proteins, or any combination thereof. For example, the composition may include a buffer such as a phosphate buffer, a borate buffer, an acetate buffer, or a citrate buffer, or other common buffers such as bicine, tricine, tris(hydroxymethyl)aminomethane (tris), N-[tris(hydroxymethyl)methyl]-3-amino-1-propanesulfonic acid (TAPS), 3-[N-tris(hydroxymethyl)methylamino]-2-hydroxypropanesulfonic acid (TAPSO), 2-[4-(2-hydroxyethyl)piperazin-1-yl]ethanesulfonic acid (HEPES), N-[tris(hydroxymethyl)methyl]-2-aminoethanesulfonic acid (TES), piperazine-N,N'-bis(2-ethanesulfonic acid) (PIPES), 2-(N-morpholino)ethanesulfonic acid (MES), or the like.

[0375] In some embodiments, the composition may include a surfactant. Exemplary surfactants include non-ionic surfactants, anionic surfactants, cationic surfactants, and zwitterionic surfactants. For example, the surfactant may be a non-ionic surfactant such as sorbitan 20.

[0376] In some embodiments, the composition may include a salt, such as sodium chloride, potassium chloride, magnesium chloride, or the like.

[0377] In some embodiments, the composition may include a protein. For example, the composition can include a carrier protein to prevent surface adsorption of lumino-genic enzymes that may be added in downstream assays. In some embodiments, the protein may be bovine serum albumin (BSA).

[0378] In some embodiments, the composition may include a substance that reduces autoluminescence. In some embodiments, the substance is ATT (6-Aza-2-thiothymine), a derivative or analog of ATT, a thionucleoside, thiourea, and the like. In some embodiments, the substance is a thionucleoside disclosed in U.S. Pat. No. 9,676,997, herein incorporated by reference. In some embodiments, the sub-

stance is thiourea, which use for reducing autoluminescence is disclosed in U.S. Pat. Nos. 7,118,878; 7,078,181; and 7,108,996, herein incorporated by reference.

[0379] The composition may be in the form of a lyophilized powder. Such a composition can be prepared by drying a mixture of the components of the composition. For example, the composition can be prepared by dissolving the compound in a solvent (e.g., an organic solvent) to form a first solution, adding the polymer to the first solution to form a second solution, and then drying the second solution to provide the composition. In some embodiments, the drying step may comprise lyophilization. This may provide the composition in the form of a powder. In some embodiments, the drying step may comprise air-drying. This may provide the composition in the form of a malleable disk.

[0380] In some embodiments (e.g., those in which the composition includes a polymer rather than a paper substrate), the composition is in the form of a solution. When the composition is a solution, the composition may have a pH of about 5.5 to about 8.0, e.g., about 6.5 to about 7.5. In some embodiments, the composition has a pH of about 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0.

#### b. Lateral Flow Components

[0381] In some embodiments, the present disclosure provides methods of manufacturing a lateral flow assay platform that includes a conjugate pad, an analytical membrane, a sample pad, and other components necessary for facilitating lateral flow across a membrane (e.g., an absorbent pad). For example, a conjugate pad can include at least one target analyte binding agent reversibly conjugated to the conjugate pad, such that the target analyte binding agent is able to be transferred from the conjugate pad to the analytical membrane when lateral flow is applied, whereupon the target analyte binding agent can bind a target analyte and form a bioluminescent complex. In some embodiments, the target analyte binding agent includes a target analyte binding element to facilitate binding to the target analyte, as well as a bioluminescent polypeptide or component of a bioluminescent complex, such as a bioluminescent polypeptide of SEQ ID NO: 5 (NanoLuc and variants thereof), a non-luminescent (NL) polypeptide of SEQ ID NO: 9 (LgBiT), an NL peptide of SEQ ID NO: 10 (SmBiT), an NL peptide of SEQ ID NO: 11 (HiBiT), an NL polypeptide of SEQ ID NO: 12 (LgTrip-3546), an NL peptide of SEQ ID NO: 13 (SmTrip), an NL peptide of SEQ ID NO: 14 ( $\beta$ 9/ $\beta$ 10 dipeptide), or variants thereof. In some embodiments, target analyte binding agent comprises a fluorophore capable of being activated by energy transfer (e.g., from a bioluminescent polypeptide or component of a bioluminescent complex).

[0382] In some embodiments, the conjugate pad comprises a first target analyte binding agent. In some embodiments, the first target analyte binding agent comprises a first target analyte binding element and a first bioluminescent polypeptide or a first component of a bioluminescent complex (e.g., NL peptide or NL polypeptide). In some embodiments, the target analyte binding agent is stored on or within the conjugate pad such that it remains with the conjugate pad until being displaced by lateral flow through the device.

[0383] In some embodiments, the conjugate pad comprises a luminogenic substrate, such as coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744,

other coelenterazine analogs or derivatives, a pro-substrate, and/or other substrates (e.g., coelenterazine analog or derivative) described herein. In some embodiments, the luminogenic substrate is reversibly conjugated to the conjugate pad. In some embodiments, the luminogenic substrate is dried on or within the conjugate pad. In some embodiments, the luminogenic substrate is part of a composition comprising the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any thereof (e.g., described in greater detail above and/or in U.S. Prov. Appln. Ser. No. 62/740,622. In some embodiment, the luminogenic substrate is applied as part of a composition or solution, such as a protein buffer. In some embodiment, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 5% w/v BSA; 0.25% v/v Tween 20; 10% w/v sucrose. In some embodiments, luminogenic substrate is added to the protein buffer and dried for 1 hour at 37° C. onto a substrate or matrix (e.g., filter paper or membrane). In other embodiments, the luminogenic substrate is applied as a separate reagent as part of an assay method or system.

[0384] In some embodiments, the assay platform includes an analytical membrane comprising a detection region and a control region to facilitate the detection of the bioluminescent complex indicating target analyte detection. The detection region can include at least one target analyte binding agent immobilized to the detection region such that it will not be displaced by the application of lateral flow across the membrane. In some embodiments, the analytical membrane includes at least one target analyte binding agent. In some embodiments, the target analyte binding agent comprises a target analyte binding element and a bioluminescent polypeptide or a first component of a bioluminescent complex (e.g., NL peptide or NL polypeptide).

[0385] In some embodiments, the analytical membrane includes a plurality of detection regions with each detection region comprising a distinct target analyte binding agent comprising distinct target analyte binding elements (e.g., multiplexing capability).

[0386] In some embodiments, the analytical membrane comprises a luminogenic substrate, such as coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, other coelenterazine analogs or derivatives, a pro-substrate, or other substrates (e.g., coelenterazine analog or derivative) described herein. In some embodiments, the luminogenic substrate is reversibly conjugated to and/or contained on/within the analytical membrane, for example, as part of a composition comprising the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any thereof. In some embodiment, the luminogenic substrate is applied as part of a composition or solution, such as a protein buffer. In some embodiment, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 5% w/v BSA; 0.25% v/v Tween 20; 10% w/v sucrose. In some embodiments, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 5% w/v BSA; 0.25% v/v Tween 20; 5% w/v pullulan. In some embodiments, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 1-5% w/v BSA; 0.25% v/v Tween 20. In some embodiments, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 1-5% w/v Prionex; 0.25% v/v Tween 20. In some embodiments, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 1-5% w/v BSA, 5 mM ATT. In some embodiments, the protein buffer

includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 1-5% v/v Prionex, 5 mM ATT. In some embodiments, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 1-5% w/v BSA, 5 mM ATT, 5 mM ascorbate. In some embodiments, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 1-5% w/v Prionex, 5 mM ATT, 5 mM ascorbate. In some embodiments, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 1-5% w/v BSA, 5 mM ATT, 5 mM ascorbate. In some embodiments, the protein buffer includes; 1-5% w/v BSA, 5 mM ATT, 5 mM ascorbate. In some embodiments, luminogenic substrate is added to the protein buffer and dried for 1 hour at 37° C. onto a substrate or matrix (e.g., filter paper or membrane). In other embodiments, the luminogenic substrate is applied as a separate reagent as part of an assay method or system.

#### c. Solid Phase Components

[0387] In some embodiments, the present disclosure provides methods of manufacturing a solid phase detection platform (e.g., dipstick assay or spot test) that includes a detection region and a control region. In some embodiments, the detection region comprises at least one target analyte binding agent conjugated to the detection region. In some embodiments, the detection region comprises at least one target analyte binding agent that is not conjugated to the detection region. Such a non-conjugated binding agent may be added to the detection region (e.g., with the sample or as part of a detection reagent) or may reside on or within the detection region, without conjugation. In some embodiments, the non-conjugated binding agent comprises a target analyte binding element and bioluminescent polypeptide or component of a bioluminescent complex, such as a bioluminescent polypeptide of SEQ ID NO: 5 (NanoLuc and variants thereof), a non-luminescent (NL) polypeptide of SEQ ID NO: 9 (LgBiT), an NL peptide of SEQ ID NO: 10 (SmBiT), an NL peptide of SEQ ID NO: 11 (HiBiT), an NL polypeptide of SEQ ID NO: 12 (LgTrip-3546), an NL peptide of SEQ ID NO: 13 (SmTrip), an NL peptide of SEQ ID NO: 14 ( $\beta$ 9/ $\beta$ 10 dipeptide), or variants thereof.

[0388] In some embodiments, the solid phase detection platform includes a plurality of detection regions with each detection region comprising a distinct target analyte binding agent comprising distinct target analyte binding elements (e.g., multiplexing capability). In some embodiments, one or more distinct target analyte binding agents can be conjugated (e.g., coated) to wells of a microtiter plate, along one or more of the other detection reagents required to carry out a particular assay (e.g., a second target analyte binding agent, a luminogenic substrate, assay buffer, etc.). In other embodiments, the detection reagents can be applied as a separate reagent as part of an assay method or system (e.g., as part of a lyocake or tablet and reconstituted as part of the assay).

[0389] The detection platform can also include a luminogenic substrate, such as coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, other coelenterazine analogs or derivatives, a pro-substrate, or other substrates (e.g., coelenterazine analog or derivative) described herein. In some embodiments, the luminogenic substrate is reversibly conjugated to the detection region. In some embodiments, the luminogenic substrate is stably stored on or within the detection region. In some embodiments, the luminogenic substrate is part of a composition comprising the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dex-

tran, polystyrene, poly(meth)acrylate, and a combination of any thereof. In some embodiments, the luminogenic substrate is applied as part of a composition or solution, such as a protein buffer, detection reagent, or with the sample. In some embodiments, the protein buffer includes 20 mM Na<sub>3</sub>PO<sub>4</sub>; 5% w/v BSA; 0.25% v/v Tween 20; 10% w/v sucrose. In some embodiments, luminogenic substrate is added to the protein buffer and dried for 1 hour at 37° C. onto a substrate or matrix (e.g., filter paper, membrane, individual wells of a microtiter plate). In other embodiments, the luminogenic substrate is applied as a separate reagent as part of an assay method or system (e.g., as part of a lyocake or tablet and reconstituted as part of the assay).

[0390] Embodiments of the present disclosure also include methods for producing a substrate or matrix for use in a bioluminescent assay. In accordance with these embodiments, the method includes generating a solution or liquid formulation containing at least one target analyte binding agent comprising a target analyte binding element and one of a polypeptide component of a bioluminescent complex or a peptide component of a bioluminescent complex. In some embodiments, the solution includes a protein buffer and at least one excipient, including but not limited to, a surfactant, a reducing agent, a salt, a radical scavenger, a chelating agent, a protein, or any combination thereof. In some embodiment, the solution includes a complementary peptide or polypeptide component of the bioluminescent complex, such that the target analyte binding agent and the complementary peptide or polypeptide component of the bioluminescent complex form a bioluminescent analyte detection complex in the presence of a target analyte. In some embodiments, the solution comprises a luminogenic substrate.

[0391] After generating the solution or liquid formulation, the method includes applying the solution to the surface of a substrate or matrix. In some embodiments, the substrate or matrix is W-903 paper, FTA paper, FTA Elute paper, FTA DMPK paper, Ahlstrom A-226 paper, M-TFN paper, FTA paper, FP705 paper, Bode DNA collection paper, nitrocellulose paper, nylon paper, cellulose paper, Dacron paper, cotton paper, and polyester papers, or combinations thereof. In other embodiments, the substrate or matrix is a mesh comprising plastic, nylon, metal, or combinations thereof.

[0392] Embodiments of the method also include drying the substrate or matrix after the solution has been applied to the substrate or matrix. In some embodiments, drying the substrate or matrix containing the solution comprises drying the substrate or matrix at a temperature from about 30° C. to 65° C., from about 30° C. to 60° C., from about 30° C. to 55° C., from about 30° C. to 50° C., from about 30° C. to 45° C., or from about 30° C. to 40° C. In some embodiments, the matrix or substrate is dried from about 15 mins to 8 hours, from about 30 mins to 7 hours, from about 45 mins to 6 hours, from about 1 hour to 5 hours, from about 2 hours to 4 hours, from about 30 mins to 2 hours, or from about 30 mins to 1 hour. In some embodiments, drying the substrate containing the solution comprises lyophilizing and/or freezing the substrate.

[0393] In some embodiments, the method includes drying the at least one target analyte binding agent and/or the complementary peptide or polypeptide component of the bioluminescent complex onto a first substrate, and drying the luminogenic substrate onto a second substrate. In some embodiments, the at least one target analyte binding agent and/or the complementary peptide or polypeptide compo-

ment of the bioluminescent complex are dried onto a paper based substrate, and the luminogenic substrate is dried onto a mesh (see, e.g., FIGS. 42A-42E).

[0394] In accordance with these embodiments, the substrate or matrix can be used in a bioluminescent assay to detect a target analyte. For example, a bioluminescent signal can be generated upon exposure of the substrate or matrix containing the solution to the target analyte. In some embodiments, the bioluminescent signal is proportional to the concentration of the target analyte. In some embodiments, the at least one target analyte binding agent and/or the complementary peptide or polypeptide component of the bioluminescent complex exhibit(s) enhanced stability when dried on the substrate, as described further herein.

#### d. Solution Phase Components

[0395] In some embodiments, the present disclosure provides methods of manufacturing a solution phase detection platform (as described herein) that includes one or more detection regions and control regions (e.g., wells of a 96-well microtiter plate). For example, as shown in FIG. 33, embodiments of solution phase platforms of the present disclosure can include one or more components of the bioluminescent complexes described herein in a tablet or lyophilized cake that can be reconstituted in a solution (e.g., buffered solution) to facilitate analyte detection. In some embodiments, the tablet or lyocake can include all the reagents necessary to carry out a reaction to detect an analyte and are included as part of a solution phase detection platform (e.g., present in one or more wells of a 96-well microtiter plate). Such lyocakes or tablets are compatible with many different assay formats, including but not limited to, cuvettes, wells of microtiter plates (e.g., 96-well microtiter plate), test tubes, large volume bottles, SNAP assays, and the like.

[0396] In some embodiments, one or more components of the bioluminescent complexes described herein can be added to a detection region and/or may already be present within a detection region, in the presence or absence of a sample. The detection reagents can then be reconstituted (e.g., rehydrated) as part of carrying out the detection of an analyte in the sample. In some embodiments, the detection reagent comprises a target analyte binding element and bioluminescent polypeptide or component of a bioluminescent complex, such as a bioluminescent polypeptide of SEQ ID NO: 5 (NanoLuc and variants thereof), a non-luminescent (NL) polypeptide of SEQ ID NO: 9 (LgBiT), an NL peptide of SEQ ID NO: 10 (SmBiT), an NL peptide of SEQ ID NO: 11 (HiBiT), an NL polypeptide of SEQ ID NO: 12 (LgTrip-3546), an NL peptide of SEQ ID NO: 13 (SmTrip), an NL peptide of SEQ ID NO: 14 ( $\beta$ 9/ $\beta$ 10 dipeptide), or variants thereof.

[0397] The solution phase detection platform can also include a luminogenic substrate, such as coelenterazine, coelenterazine-h, coelenterazine-h-, furimazine, JRW-0238, JRW-1404, JRW-1482, JRW-1667, JRW-1743, JRW-1744, other coelenterazine analogs or derivatives, a pro-substrate, or other substrates (e.g., coelenterazine analog or derivative) described herein. In some embodiments, the luminogenic substrate is part of a composition comprising the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any thereof. In some embodiments, the luminogenic substrate is applied as part of a composition or solution, such as a protein buffer,

detection reagent, or with the sample. In some embodiments, the luminogenic substrate is applied as a separate reagent as part of an assay method or system, and in other embodiments, it is part of a lyocake or tablet that includes one or more detection reagents.

#### 6. Target Analytes

[0398] Embodiments of the present disclosure find use in the detection/quantification of target analytes and include target analyte binding agents capable of binding to or interacting with a target analyte via a target analyte binding element. In some embodiments, target analyte binding agents include target analyte binding elements capable of binding a group or class of analytes (e.g., protein L binding generally to antibodies), such binding elements may be referred to herein as “non-specific” or the like; in other embodiments, target analyte binding agents include target analyte binding elements capable of binding a specific analyte (e.g., an antigen binding a monoclonal antibody), such binding elements may be referred to herein as “target specific” or the like.

[0399] In some embodiments, target analyte binding agents and corresponding target analyte binding elements are generated to detect one or more analytes associated with a disease state or environmental condition. Target analyte binding elements can be independently selected from the group consisting of an antibody (e.g., polyclonal, monoclonal, and/or recombinant), antibody fragment (e.g., Fab, Fab', F(ab')<sub>2</sub>, Fv, scFv, Fd, variable light chain, variable heavy chain, diabodies, scFv, etc.), protein A, an Ig binding domain of protein A, protein G, an Ig binding domain of protein G, protein A/G, an Ig binding domain of protein A/G, protein L, a Ig binding domain of protein L, protein M, an Ig binding domain of protein M, an oligonucleotide probe, a peptide nucleic acid, a DARPin, an aptamer, an affimer, a purified protein (e.g., either the analyte itself or a protein that binds to the analyte), and analyte binding domain(s) of proteins.

[0400] In some embodiments, target analyte binding elements comprise an antigen or epitope recognized by an antibody (the target analyte) such as an antibody generated by a subject in response to an immunogenic reaction to a pathogen, which can indicate that the subject is infected with the pathogen. In some embodiments, the target analyte is an antibody against Zika virus, Dengue virus, West Nile virus, Yellow Fever virus, and/or Chikungunya virus, and the target analyte binding element is an immunogenic epitope specifically recognized by the antibody. In some embodiments, the target analyte is an antibody against Hep A, B, C, D or E. In some embodiments, the target analyte is an antibody against Mumps, measles, Rubella, RSV, EBV, Herpes, Influenza, Varicella-Zoster, prenatal Zika, or parainfluenza type 1, 2, or 3. In some embodiments, the target analyte is an antibody against Arbovirus, HIV, prenatal Hepatitis, CMV, Hantavirus, polio virus, or parvovirus. In some embodiments, the target analyte is an antibody against Tick borne disease (e.g., Lyme disease). In some embodiments, the target analyte is an antibody against *Bordetella pertussis*, pneumococcus, *chlamydia*, *streptococcus*, *M. pneumoniae*, *S. pneumoniae*, *shigella* producing bacteria, *E. coli*, *Enterobacter*, syphilis, gonorrhea. In some embodiments, the target analyte is an autoantibody against ANA, Cardiolipin, celiac disease, insulin, GAD65, IA-2, Reticulin, Thyroglobulin, RNP, cytoplasmic neutrophil, thyrotrypin receptor, thyroperoxidase, platelet antibody, PLAR2, myo-

cardial, GBM, tissue transglutaminase, or thyroid stimulating. In some embodiments, the target analyte is a toxin or an antibody against a toxin (e.g., diphtheria, tetanus). In some embodiments, the target analyte is from a parasite or an antibody against a parasite (e.g., *trichinella*, trichinosis, *Trypanosoma cruzi*, *Toxoplasma gondii*). In some embodiments, the target analyte is a therapeutic biologic or an antibody against the therapeutic biologic (Vedolizumab, Adalimumab, infliximab, certolizumab, entanercept, Opdivo, Keytruda, ipilimumab, Ustekinumab, secukinumab, guselkumab, Tocilizumab, rituximab, panitumumab, trastuzumab, cetuximab, ofatumumab, epratuzumab, abatacept, tofacitinib).

[0401] Other target analytes include known biomarkers associated with a pathogenic organism, such as a virus, bacterium, protozoa, prion, fungus, parasitic nematode, or other microorganism. Disease biomarkers can include markers of the pathogenic organism itself and/or markers of a subject's reaction to an infection by the pathogenic organism. Diseases that can be detected using the assays and methods of the present disclosure include any of the following: *Acinetobacter* infections (*Acinetobacter baumannii*), Actinomycosis (*Actinomyces sraelii*, *Actinomyces gerencseriae* and *Propionibacterium propionicus*), African sleeping sickness or African trypanosomiasis (*Trypanosoma brucei*), AIDS (HIV), Amebiasis (*Entamoeba histolytica*), Anaplasmosis (*Anaplasma* species), Angiostrongylasis (*Angiostrongylus*), Anisakiasis (*Anisakis*), Anthrax (*Bacillus anthracis*), Arcanobacterium *haemolyticum* infection (*Arcanobacterium haemolyticum*), Argentine Teagan fever (Junin virus), Ascariasis (*Ascaris lumbricoides*), Aspergillosis (*Aspergillus* species), Astrovirus infection (Astromviridae family), Babesiosis (*Babesia* species), *Bacillus cereus* infection (*Bacillus cereus*), Bacterial pneumonia (multiple bacteria), *Bacteroides* infection (*Bacteroides* species), Balantidiasis (*Balantidium coli*), Bartonellosis (*Bartonella*), *Baylisascaris* infection (*Baylisascaris* species), BK virus infection (BK virus), Black Piedra (Piedra hortae), Blastocystosis (*Blastocystis* species), Blastomycosis (*Blastomyces dermatitidis*), Bolivian hemorrhagic fever (Machupo virus), Brazilian hemorrhagic fever (Sabii virus), Brucellosis (*Brucella* species), Bubonic plague (*Yersinia Pestis*), Burkholderia infection (usually *Burkholderia cepacia* and other *Burkholderia* species), Buruli ulcer (*Mycobacterium ulcerans*), Calicivirus infection (Caliciviridae family), Campylobacteriosis (*Campylobacter* species), Candidiasis (usually *Candida albicans* and other *Candida* species), Carrion's disease (*Bartonella bacilliformis*), Cat-scratch disease (*Bartonella henselae*), Cellulitis (usually Group A *Streptococcus* and *Staphylococcus*), Chagas Disease (*Trypanosoma cruzi*), Chancroid (*Haemophilus ducreyi*), Chickpox (Varicella zoster virus or VZV), Chikungunya (Alphavirus), *Chlamydia* (*Chlamydia trachomatis*), Cholera (*Vibrio cholerae*), Chromoblastomycosis (usually *Fonsecaea pedrosoi*), Chytridiomycosis (Batrachochytrium dendrobatidis), Clonorchiasis (*Clonorchis sinensis*), *Clostridium difficile* colitis (*Clostridium difficile*), Coccidioidomycosis (*Coccidioides immitis* and *Coccidioides posadasii*), Colorado tick fever (Colorado tick fever virus or CTFV), Common cold (usually rhinoviruses and coronaviruses), Creutzfeldt-Jakob disease (PRNP), Crimean-Congo hemorrhagic fever (Crimean-Congo hemorrhagic fever virus), Cryptococcosis (*Cryptococcus neoformans*), Cryptosporidiosis (*Cryptosporidium* species), Cutaneous larva

migrans (usually *Ancylostoma braziliense*; multiple other parasites), Cyclosporiasis (*Cyclospora cayetanensis*), Cysticercosis (*Taenia solium*), Cytomegalovirus infection (Cytomegalovirus), Dengue fever (Dengue viruses: DEN-1, DEN-2, DEN-3 and DEN-4), Desmodesmus infection (Green algae Desmodesmus armatus), Dientamoebiasis (*Dientamoeba fragilis*), Diphtheria (*Corynebacterium diphtheriae*), Diphyllobothriasis (*Diphyllobothrium*), Dracunculiasis (*Dracunculus medinensis*), Ebola hemorrhagic fever (Ebolavirus or EBOV), Echinococcosis (*Echinococcus* species), Ehrlichiosis (*Ehrlichia* species), Enterobiasis (*Enterobius vermicularis*), *Enterococcus* infection (*Enterococcus* species), Enterovirus infection (Enterovirus species), Epidemic typhus (*Rickettsia prowazekii*), Erythema infectiosum (Parvovirus B19), Exanthem subitum (Human herpesvirus 6 or HHV-6; Human herpesvirus 7 or HHV-7), Fascioliasis (*Fasciola hepatica* and *Fasciola gigantica*), Fasciolopsisiasis (*Fasciolopsis buski*), Fatal familial insomnia (PRNP), Filariasis (Filarioidea superfamily), *Fusobacterium* infection (*Fusobacterium* species), Gas gangrene (usually *Clostridium perfringens*; other *Clostridium* species), Geotrichosis (*Geotrichum candidum*), Gerstmann-Straussler-Scheinker syndrome (PRNP), Giardiasis (*Giardia lamblia*), Glanders (*Burkholderia mallei*), Gnathostomiasis (*Gnathostoma spinigerum* and *Gnathostoma hispidum*), Gonorrhea (*Neisseria gonorrhoeae*), Granuloma inguinale (*Klebsiella granulomatis*), Group A streptococcal infection (*Streptococcus pyogenes*), Group B streptococcal infection (*Streptococcus agalactiae*), *Haemophilus influenzae* infection (*Haemophilus influenzae*), Hand, foot and mouth disease (Enteroviruses, mainly Coxsackie A virus and Enterovirus 71 or EV71), Hantavirus Pulmonary Syndrome (Sin Nombre virus), Heartland virus disease (Heartland virus), *Helicobacter pylori* infection (*Helicobacter pylori*), Hemolytic-uremic syndrome (*Escherichia coli* O157:H7, 0111 and 0104:H4), Hemorrhagic fever with renal syndrome (Bunyaviridae family), Hepatitis A (Hepatitis A virus), Hepatitis B (Hepatitis B virus), Hepatitis C (Hepatitis C virus), Hepatitis D (Hepatitis D Virus), Hepatitis E (Hepatitis E virus), Herpes simplex (Herpes simplex virus 1 and 2 (HSV-1 and HSV-2)), Histoplasmosis (*Histoplasma capsulatum*), Hookworm infection (*Ancylostoma duodenale* and *Necator americanus*), Human bocavirus infection (Human bocavirus or HBOV), Human ewingii ehrlichiosis (*Ehrlichia ewingii*), Human granulocytic anaplasmosis (*Anaplasma phagocytophylum*), Human metapneumovirus infection (Human metapneumovirus or hMPV), Human monocytic ehrlichiosis (*Ehrlichia chaffeensis*), Human papillomavirus (HPV) infection (Human papillomavirus or HPV), Human parainfluenza virus infection (Human parainfluenza viruses or HPIV), Hymenolepiasis (*Hymenolepis nana* and *Hymenolepis diminuta*), Epstein-Barr virus infectious mononucleosis (Epstein-Barr virus or EBV), Influenza (Orthomyxoviridae family), Isosporiasis (*Isospora belli*), Kingella kingae infection (Kingella kingae), Kuru (PRNP), Lassa fever (Lassa virus), Legionellosis (*Legionella pneumophila*), Legionellosis (*Legionella pneumophila*), Leishmaniasis (*Leishmania* species), Leprosy (*Mycobacterium leprae* and *Mycobacterium lepromatosis*), Leptospirosis (Leptospira species), Listeriosis (*Listeria monocytogenes*), Lyme disease (*Borrelia burgdorferi*, *Borrelia garinii*, and *Borrelia afzelii*), Lymphatic filariasis (*Wuchereria bancrofti* and *Brugia malayi*), Lymphocytic choriomeningitis (Lymphocytic choriomeningitis virus or LCMV), Malaria (*Plasmodium* species), Mar-

burg hemorrhagic fever (Marburg virus), Measles (Measles virus), Middle East respiratory syndrome (Middle East respiratory syndrome coronavirus), Melioidosis (*Burkholderia pseudomallei*), Meningococcal disease (*Neisseria meningitidis*), Metagonimiasis (usually *Metagonimus yokagawai*), Microsporidiosis (Microsporidia phylum), Molluscum contagiosum (Molluscum contagiosum virus or MCV), Monkeypox (Monkeypox virus), Mumps (Mumps virus), Murine typhus (*Rickettsia typhi*), *Mycoplasma pneumonia* (*Mycoplasma pneumoniae*), Mycetoma (numerous species of bacteria (Actinomycetoma) and fungi (Eumycetoma)), Myiasis (parasitic dipterous fly larvae), Neonatal conjunctivitis (most commonly *Chlamydia trachomatis* and *Neisseria gonorrhoeae*), Norovirus (Norovirus), Nocardiosis (usually *Nocardia asteroides* and other *Nocardia* species), Onchocerciasis (*Onchocerca volvulus*), Opisthorchiasis (*Opisthorchis viverrini* and *Opisthorchis felineus*), Paracoccidioidomycosis (*Paracoccidioides brasiliensis*), Paragonimiasis (usually *Paragonimus westermani* and other *Paragonimus* species), Pasteurellosis (*Pasteurella* species), Pediculosis capitis (*Pediculus humanus capitis*), Pediculosis corporis (*Pediculus humanus corporis*), Pediculosis pubis (Phthirus pubis), Pertussis (*Bordetella pertussis*), Plague (*Yersinia pestis*), Pneumococcal infection (*Streptococcus pneumoniae*), *Pneumocystis pneumonia* (*Pneumocystis jirovecii*), Pneumonia (multiple causes), Poliomyelitis (Poliiovirus), *Prevotella* infection (*Prevotella* species), Primary amoebic meningoencephalitis (usually *Naegleria fowleri*), Progressive multifocal leukoencephalopathy (JC virus), Psittacosis (*Chlamydophila psittaci*), Q fever (*Coxiella burnetii*), Rabies (Rabies virus), Relapsing fever (*Borrelia hermsii*, *Borrelia recurrentis*, and other *Borrelia* species), Respiratory syncytial virus infection (Respiratory syncytial virus (RSV)), Rhinosporidiosis (*Rhinosporidium seeberi*), Rhinovirus infection (Rhinovirus), Rickettsial infection (*Rickettsia* species), Rickettsialpox (*Rickettsia akari*), Rift Valley fever (Rift Valley fever virus), Rocky Mountain spotted fever (*Rickettsia rickettsiae*), Rotavirus infection (Rotavirus), Rubella (Rubella virus), *Salmonellosis* (*Salmonella* species), Severe Acute Respiratory Syndrome (SARS coronavirus), Scabies (*Sarcoptes scabiei*), Scarlet fever (Group A *Streptococcus* species), Schistosomiasis (*Schistosoma* species), Sepsis (multiple causes), Shigellosis (*Shigella* species), Shingles (Varicella zoster virus or VZV), Smallpox (Variola major or Variola minor), Sporotrichosis (*Sporothrix schenckii*), Staphylococcal food poisoning (*Staphylococcus* species), Staphylococcal infection (*Staphylococcus* species), Strongyloidiasis (*Strongyloides stercoralis*), Subacute sclerosing panencephalitis (Measles virus), Syphilis (*Treponema pallidum*), Taeniasis (*Taenia* species), Tetanus (*Clostridium tetani*), Tinea barbae (usually *Trichophyton* species), Tinea capitidis (usually *Trichophyton tonsurans*), Tinea corporis (usually *Trichophyton* species), Tinea cruris (usually *Epidermophyton floccosum*, *Trichophyton rubrum*, and *Trichophyton mentagrophytes*), Tinea manuum (*Trichophyton rubrum*), Tinea nigra (usually *Hortaea werneckii*), Tinea pedis (usually *Trichophyton* species), Tinea unguium (usually *Trichophyton* species), Tinea versicolor (*Malassezia* species), Toxocariasis (*Toxocara canis* or *Toxocara cati*), Toxocariasis (*Toxocara canis* or *Toxocara cati*), Toxoplasmosis (*Toxoplasma gondii*), Trachoma (*Chlamydia trachomatis*), Trichinosis (*Trichinella spiralis*), Trichomoniasis (*Trichomonas vaginalis*), Trichuriasis (*Trichuris trichiura*), Tuberculosis (usually *Mycobacterium tuberculosis*), Tulare-

mia (*Francisella tularensis*), Typhoid fever (*Salmonella enterica* subsp. *enterica*, serovar *typhi*), Typhus fever (*Rickettsia*), *Ureaplasma urealyticum* infection (*Ureaplasma urealyticum*), Valley fever (*Coccidioides immitis* or *Coccidioides posadasii*), Venezuelan equine encephalitis (Venezuelan equine encephalitis virus), Venezuelan hemorrhagic fever (Guanarito virus), *Vibrio vulnificus* infection (*Vibrio vulnificus*), *Vibrio parahaemolyticus* enteritis (*Vibrio parahaemolyticus*), Viral pneumonia (multiple viruses), West Nile Fever (West Nile virus), White piedra (*Trichosporon beigelii*), *Yersinia pseudotuberculosis* infection (*Yersinia pseudotuberculosis*), Yersiniosis (*Yersinia enterocolitica*), Yellow fever (Yellow fever virus), Zygomycosis (Mucorales order (Mucormycosis) and Entomophthorales order (Entomophthoramycosis)), and Zika fever (Zika virus).

## 7. Methods of Detecting, Quantifying, and Diagnosing

**[0402]** Embodiments of the present disclosure include methods of detecting and/or quantifying a target analyte in a sample with an assay platform (e.g., solid phase detection platform or lateral flow assay) that uses bioluminescent polypeptides or bioluminescent complexes (and components thereof; e.g., non-luminescent peptide or polypeptides) for target analyte detection. Embodiments also include methods of diagnosing a disease state or evaluating an environmental condition based on detecting and/or quantifying a target analyte in a sample.

**[0403]** In some embodiments, a method of detecting an analyte in a sample includes using a lateral flow assay system or a solid phase detection platform as described herein. In accordance with these embodiments, the method includes applying a sample to a sample pad; facilitating flow of the sample from the sample pad to a conjugate pad, and then from the conjugate pad to a detection region and a control region on an analytical membrane. The method can include a first target analyte binding agent, a second target analyte binding agent, and a target analyte that form an analyte detection complex in the at least one detection region when the target analyte is detected in the sample. In some embodiments, methods comprise one or more steps of: sample addition, reagent (e.g., detection reagent) addition, washing, waiting, etc.

**[0404]** In some embodiments, the sample is a biological sample from a subject, such as blood, serum, plasma, urine, stool, cerebral spinal fluid, interstitial fluid, and saliva. In other embodiments, the sample is a sample from a natural or industrial environment, such as a water sample, a soil sample, a plant sample, a food sample, a beverage sample, an oil, and an industrial fluid sample. The method includes detecting the target analyte in the sample by detecting a bioluminescent signal generated from the analyte detection complex. In some embodiments, the target analyte in the sample is quantified based on the bioluminescent signal generated from the analyte detection complex. In some embodiments, the method includes diagnosing a subject from which the sample was obtained as having or not having a disease based on the detection of the analyte.

## 8. Competition

**[0405]** Some embodiments herein utilize competition between a labeled analyte and a target analyte in a sample to detect/quantify the target analyte in a sample. Exemplary embodiments comprise the use of (i) an analyte (e.g.,

identical or similar to the target analyte) labeled with detectable element described herein (e.g., NanoLuc®-based technology (e.g., NanoLuc, NanoBiT, NanoTrip, NanoBRET, or components (e.g., peptides, polypeptides, etc.) of variants thereof)), and (ii) a binding moiety for the target analyte (e.g., fused or linked to a second detectable element described herein (e.g., NanoLuc®-based technology (e.g., NanoLuc, NanoBiT, NanoTrip, NanoBRET, or components (e.g., peptides, polypeptides, etc.) of variants thereof)). In the absence of the target analyte from a sample, the detectable elements produce a detectable signal (e.g., via complementation between the detectable elements, via BRET, etc.) is produced by the system. When the system is exposed to a sample (e.g., biological sample, environmental sample, etc.), the bioluminescent signal is reduced if the target analyte is present in the sample (the labeled analyte will be competed out of the complex).

**[0406]** Various embodiments herein utilize such competition immunoassays for small molecule detection. In some embodiments, the target small molecule is a toxin (e.g., mycotoxin, etc.), metabolite (e.g., amino acid, glucose molecule, fatty acid, nucleotide, cholesterol, steroid, etc.), vitamin (e.g., vitamin A, vitamin B1, vitamin B2, Vitamin B3, vitamin B5, vitamin B7, vitamin B9, vitamin B12, vitamin C, vitamin D, vitamin E, vitamin H or vitamin K, etc.), coenzyme or cofactor (e.g., coenzyme A, coenzyme B, coenzyme M, coenzyme Q, cytidine triphosphate, acetyl coenzyme A, reduced nicotinamide adenine dinucleotide (NADH), nicotinamide adenine (NAD+), nucleotide adenosine monophosphate, nucleotide adenosine triphosphate, glutathione, heme, lipoamide, molybdopterin, 3'-phosphoadenosine-5'-phosphosulfate, pyrroloquinoline quinone, tetrahydrobiopterin, etc.), biomarker or antigen (e.g., erythropoietin (EPO), ferritin, folic acid, hemoglobin, alkaline phosphatase, transferrin, apolipoprotein E, CK, CKMB, parathyroid hormone, insulin, cholesterlyl ester transfer protein (CETP), cytokines, cytochrome c, apolipoprotein Al, apolipoprotein All, apolipoprotein BI, apolipoprotein B-100, apolipoprotein B48, apolipoprotein CII, apolipoprotein CIII, apolipoprotein E, triglycerides, HD cholesterol, LDL cholesterol, lecithin cholesterol acyltransferase, paraxonase, alanine aminotransferase (ALT), aspartate transferase (AST), CEA, HER-2, bladder tumor antigen, thyroglobulin, alpha-fetoprotein, PSA, CA 125, CA 19.9, CA 15.3, leptin, prolactin, osteoponitin, CD 98, fascin, troponin I, CD20, HER2, CD33, EGFR, VEGFA, etc.), drug (cannabinoid (e.g., tetrahydrocannabinol (THC), cannabidiol (CBD) and cannabinol (CBN), etc.), opioid (e.g., heroin, opium, fentanyl, etc.), stimulant (e.g., cocaine, amphetamine, methamphetamine, etc.), club drug (e.g., MDMA, flunitrazepam, gamma-hydroxybutyrate, etc.), dissociative drug (e.g., ketamine, phencyclidine, *salvia*, dextromethorphan, etc.), hallucinogens (e.g., LSD, mescaline, psilocybin, etc.), explosive (e.g., 2,4,6-trinitrotoluene (TNT) and hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX), pentaerythritol tetranitrate (PETN), etc.), toxic chemical (e.g., tabun (GA), sarin (GB), soman (GD), cyclosarin (GF), 2-(dimethylamino)ethyl N, N-dimethylphosphoramido-fluoride (GV), VE, VG, VM, VP, VR, VS, or VX nerve agent), etc.

**[0407]** In some embodiments, small molecule detection immunoassays, such as the one exemplified in Example 5 and the like, are performed in the solid phase, lateral flow, and other assays and devices described herein.

## 9. EXAMPLES

**[0408]** It will be readily apparent to those skilled in the art that other suitable modifications and adaptations of the methods of the present disclosure described herein are readily applicable and appreciable and may be made using suitable equivalents without departing from the scope of the present disclosure or the aspects and embodiments disclosed herein. Having now described the present disclosure in detail, the same will be more clearly understood by reference to the following examples, which are merely intended only to illustrate some aspects and embodiments of the disclosure and should not be viewed as limiting to the scope of the disclosure. The disclosures of all journal references, U.S. patents, and publications referred to herein are hereby incorporated by reference in their entireties.

**[0409]** The present disclosure has multiple aspects, illustrated by the following non-limiting examples.

### Example 1

#### Solid Phase Materials

**[0410]** As shown in FIG. 3, components of the bioluminescent complexes of the present disclosure produce detectable bioluminescence after being applied to a solid support substrate (e.g., membrane). Antibodies labeled with NanoLuc® components (e.g., target analyte binding agents) were applied to a membrane that was either blocked (Buffer 1; upper two membranes on left and right panels) or unblocked (Buffer 2; lower two membranes on left and right panels) and then dried at room temperature with nitrogen or at 37° C. without nitrogen. Using an Imagequant LAS4000 imaging platform (1 second exposure), detectable bioluminescence was produced under these conditions. These results demonstrate that components of the bioluminescent complexes of the present disclosure can be successfully used in solid phase and lateral flow assay platforms, which may involve drying reagents and application to solid phase materials, and exposure to various temperatures and processing conditions.

**[0411]** As shown in FIG. 4, components of the bioluminescent complexes produce detectable bioluminescence after being applied to membrane and paper-based solid support matrices. Compositions that included buffer, substrate (e.g., furimazine), and two complementary components of a bioluminescent complex (e.g., HiBiT and LgBiT) were applied to a nitrocellulose membrane (left three panels), or filter paper (Whatman 541 shown in the middle three panels; Whatman 903 shown in right three panels). These components were then dried, shipped at 4° C. and then tested 24 hours later using an LAS4000 imaging platform (30 second and 5 min exposures). Detectable bioluminescence was produced under these conditions, with filter paper matrices allowing for brighter bioluminescent signal than nitrocellulose membranes. Matrices made with glass and synthetic fibers (e.g., Ahlstrom grade 8950) also yielded detectable bioluminescent signal (data not shown) demonstrating that components of the bioluminescent complexes of the present disclosure can be successfully used with various matrix materials.

### Example 2

Detecting Target Analytes with Bioluminescent Complexes [0412] As shown in FIG. 5, components of the bioluminescent complexes (e.g., non-luminescent peptides and polypeptides) of the present disclosure can be used as target analyte binding agents for target analyte recognition. For example, as shown in FIG. 5 (left panel), polyclonal goat anti-mouse IgG3 antibodies (e.g., target analyte binding elements) were conjugated to components of the bioluminescent complexes (e.g., LgBiT and SmBiT). In the presence of the target analyte (e.g., mouse IgG3), a bioluminescent complex was formed, and a bioluminescent signal was produced from the complementary interaction of the components of the bioluminescent complex (FIG. 5, right panel) with increased signal being produced as the concentration of the target analyte increased. These results demonstrate the feasibility of detecting target analytes using the components of the bioluminescent complexes of the present disclosure.

[0413] As shown in FIG. 6, embodiments of the present disclosure include a solid phase assay platform using components of the bioluminescent complexes as target analyte binding agents for target analyte recognition. Four test spots were prepared on Whatman 903 filter paper as shown, and target analyte was added thereafter (FIG. 6, top panel). In one embodiment, 20 ng of goat-anti-mouse-conjugated to a component of the bioluminescent complex (e.g., SmBiT), and 20 ng of goat-anti-mouse-conjugated to a complementary component of the bioluminescent complex (e.g., LgBiT) were each prepared in 5  $\mu$ l of protein buffer (20 mM Na<sub>3</sub>PO<sub>4</sub>; 5% w/v BSA; 0.25% v/v Tween 20; 10% w/v sucrose) and dried for 1 hour at 37° C. onto the paper in the locations indicated. Additionally, 5  $\mu$ l of a 5 mM solution of furimazine in ethanol was applied to the spots as indicated under high vacuum for 15 mins (FIG. 6, top panel). The prepared spots were then stored for one week at 4° C. As demonstrated, in the presence of the target analyte (e.g., mouse IgG3; spot #2), a bioluminescent complex was formed, and a bioluminescent signal was produced from the complementary interaction of the components of the bioluminescent complex (FIG. 6, bottom panel). Although background bioluminescent signal was produced with no target analyte present (spot #4), the signal produced in the presence of the target analyte and the luminogenic substrate (e.g., furimazine) is substantially increased as compared to the signal produced with the luminogenic substrate alone (compare spots #2 and #4).

[0414] Additional tests of substrate and protein stability were performed and are depicted in FIGS. 7A-7E. These tests were performed as described above with the additional step of adding a fully functional bioluminescent complex (e.g., NanoLuc) after the addition of the target analyte to test luminogenic substrate stability. As demonstrated in FIGS. 7A-7C, components of the bioluminescent complex lose activity when stored at higher temperatures (e.g., 37° C.) for two weeks. The loss of bioluminescent signal does not appear to be due to instability or breakdown of the luminogenic substrate, as the addition of a fully functional bioluminescent complex (e.g., NanoLuc) still produced a signal (FIG. 7D). Additionally, to test whether breakdown of one or more components of the bioluminescent complex was responsible for the reduced bioluminescent signal, a non-antibody conjugated component (e.g., HiBiT) was added that was not subject to storage conditions. As demonstrated in FIG. 7E, addition of the non-antibody conjugated com-

ponent led to the production of a bioluminescent signal at 4° C. but not 37° C., thus indicating that the degradation of the complementary component of the bioluminescent complex (e.g., LgBiT) was likely leading to the loss of signal.

[0415] Additional tests of storage conditions were performed and are depicted in FIGS. 8A-8B. These tests were performed as described above, except that the test spots were stored for a total of 3 months. As shown in FIG. 8A, detectable bioluminescent signal was produced in the presence of the target analyte at both 4° C. and 25° C. even after 3 months of storage, albeit with somewhat reduced activity. The addition of a fully functional bioluminescent complex (e.g., NanoLuc) produced a signal (FIG. 8B), but the signal appeared to be dependent upon the use of protein buffer (compare spots #1 and #2) suggesting that the luminogenic substrate is stabilized by the protein buffer.

### Example 3

#### Detecting Target Analytes in Complex Sampling Environments

[0416] FIGS. 9A-9C include representative images from a solid phase assay platform (e.g., spot test) testing whether bioluminescent complex formation and analyte detection could occur in complex sampling environments. As shown in FIG. 9A, a luminogenic substrate and two complementary components of a bioluminescent complex (HiBiT and LgBiT) were applied to Whatman 903 filter paper, with each component also having a target analyte-binding element (polyclonal anti-mouse IgM), as described above, and stored at 4° C. for 6 weeks. An EDTA-collected whole blood sample (FIG. 9B) and a 100% serum sample (FIG. 9C) were each spiked with 10 pg mouse IgG3 (target analyte) and applied to the spots indicated in FIG. 9A. Corresponding control samples were not spiked with mouse IgG3. These results demonstrate the feasibility of detecting target analytes in complex sampling environments using the components of the bioluminescent complexes of the present disclosure.

### Example 4

#### Qualitative and Quantitative Assessment

[0417] FIGS. 10A-10B include representative results of a solid phase assay demonstrating that bioluminescent signal can be both quantitatively (FIG. 10A) and qualitatively (FIG. 10B) assessed. As shown in FIG. 10A, 10  $\mu$ M of luminogenic substrate (e.g., furimazine) was applied to filter paper and placed in a microtiter plate. PBS assay buffer containing NanoLuc® enzyme was then added, and bioluminescent signal was quantitatively (FIG. 10A, right panel) and qualitatively assessed (FIG. 10B). Additionally, bioluminescent signal was effectively assessed using a luminometer (FIG. 10B, left panel) as well as a smart phone (FIG. 10B, right panel).

[0418] These results demonstrate that the assays and methods of the present disclosure can include comparing levels of bioluminescence corresponding to target analyte detection with various control samples to facilitate rapid quantitative and qualitative assessment. For example, assay formats can include a plurality of control samples with varying concentrations of target analyte that can act as standards against which test samples can be assessed.

[0419] In accordance with these methods, a bioluminescent signal can be assessed both quantitatively and qualitatively using a high affinity dipeptide capable of forming a

bioluminescent complex with LgBiT or LgTrip. The results shown in FIGS. 11A-11B include representative graphs (RLUs in FIG. 11A; S/B in FIG. 11B) demonstrating the ability of a high affinity dipeptide, pep263, to form bioluminescent complexes with LgBiT and LgTrip. The high affinity dipeptide pep263 comprises the j9 and o10 stands of the NanoTrip complex. (See, e.g., U.S. patent application Ser. No. 16/439,565 (PCT/US2019/036844), and U.S. Prov. Appln. Ser. No. 62/941,255, both of which are herein incorporated by reference in their entirety.)

[0420] Additionally, FIG. 12 shows representative results of a solid phase assay demonstrating qualitative assessment of bioluminescence from paper punches placed into a standard microtiter plate using a standard camera from an iPhone or from an imager (e.g., LAS4000). This spot test assay assessed the functional stability of different LgBiT components dried onto Whatman 903 paper. Whatman 903 protein saver spot cards (1/8" punches) were used along with the following protein buffer: 20 mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 10% w/v sucrose. A 1000× NanoLuc® stock solution was diluted 1:1000 in protein buffer. About 5 µL of this reaction solution was applied to Spot 1. For HT-LgBiT complexes, about 5 µL of 106.8 nM protein per spot was used. About 20 µM stock protein was diluted 1:100 in protein buffer. About 534 µL stock was diluted in 466 µL in protein buffer. About 5 µL of this conjugation solution was added to Spot 2. For LgTrip (2098) complexes, about 5 µL of 106.8 nM protein per spot was used. About 9.6 µM protein stock was obtained by diluting about 11.6 µL of stock in 988 µL of protein buffer to make 1 mL of 106.8 nM solution. About 5 µL of this conjugation solution was added to Spot 3. For LgTrip (3546) complexes, about 5 µL of 106.8 nM protein per spot. About 94 µM protein stock was obtained by diluting about 1.13 µL of LgTrip stock into 998.87 µL protein buffer. About 5 µL of this conjugation solution was added to Spot 4. After all the protein was added, the samples were dried at 30° C. for 1 hour at 4° C., 25° C., and 37° C.

[0421] Methods for assessing RLU activity for these experiments included imaging at day 6 for all at 25° C. and 37° C. (following the 4° C. time frame of 1 or 2 days); day 8 at 4° C. for LgTrip 3546; and day 9 for NanoLuc, LgBiT, and LgTrip 2098. Furimazine was tested at 50µM and about 1.2 µM dipeptide was used for NanoBiT and NanoTrip experiments. All spots were placed into a plate with substrate reagents, images were captured with an iPhone and with an LAS4000 imaging system, then inserted into the plate reader. NanoGlo Live Cell Substrate cat #N205B (lot 189096) was used, along with assay buffer 1× PBS, pH 7.0).

[0422] FIGS. 13A-13B show quantitative analysis of the same solid phase assay depicted in FIG. 12, but luminescence was detected using a luminometer on day 3 at 25° C. (RLUs in FIG. 13A; S/B in FIG. 13B). These quantitative data support the qualitative data from FIG. 12. Materials and methods used for FIG. 12 are the same used for FIGS. 13A-13B (e.g., add 1µM dipeptide+50 µM live cell substrate in PBS, pH 7.0 and read on a luminometer). In some cases, the elevated background of LgBiT can decrease the S/B ratio.

[0423] FIGS. 14A-14C show a quantitative time course of the same solid phase assay as depicted in FIGS. 12-13 demonstrating stability of all the proteins in the experimental conditions at all temps tested over the time frame. B<sub>max</sub> RLU values at 50µM furimazine over time (0 to 60 days) are shown for 4° C. (FIG. 14A), 25° C. (FIG. 14B), and 37° C.

(FIG. 14C). These quantitative data are consistent with FIGS. 12 and 13, demonstrating stability in all the complexes tested and at all temps tested over the time frame. Materials and methods used for FIG. 12 are the same used for FIGS. 14A-14C.

#### Example 5

##### Buffer Compositions

[0424] Experiments were also conducted to test short-term, or accelerated, stability of the complexes in different buffer compositions from 0 to 90 minutes. Methods included using about a 1.068 nM concentration of each protein absorbed and dried on Whatman 903 paper spots (1/8"). Protein samples were prepared and dried on paper spots with either protein buffer or PBS buffer (see each figure for specific buffer composition used). Stock concentrations included NanoLuc at 1000× (0.4 mg/mL), LgBiT-1672-11s-His at 20 µM, and LgTrip (3546) at 94 µM. Protein buffer was comprised of 20 mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 10% w/v sucrose. Luminescence activity was tested using the dipeptide added with furimazine in 100 µL assay buffer PBS, pH 7.0 (final [dipeptide]=1 nM; final [furimazine]=50µM). Samples were read at time point 0 (fresh out of 4° C.), then placed into 60° C. and 25° C. for continued testing. A 1000× stock solution of NanoLuc was diluted 1:1000 in protein buffer (1 mL), or 10 µL of stock was diluted into 990 µL of protein buffer for a 1.068 nM stock (see each figure for specific buffer composition used). About 5 µL of each concentration was added to a paper spot for testing. For each protein tested (LgBiT and LgTrip), appropriate dilutions were made in each buffer to ensure that about 5 µL of 1.068 nM protein was used per spot. After all protein was added, the samples were dried at 35° C. for 1 hour, and 40 spots per condition and temperature were prepared.

[0425] FIGS. 15A-15D show representative results collected on day 0 of an accelerated stability study performed under two buffer conditions at 25° C. and 60° C. (FIGS. 15A and 15C use protein buffer, whereas FIGS. 15B and 15D use PBS). These data demonstrate that the complexes tested did not tolerate PBS as the buffer condition for input into the Whatman 903 paper, as compared to the protein buffer. Buffer conditions appear to affect stability even at early time points. In some cases, LgTrip 3546 exhibited better activity, suggesting somewhat better chemical stability than NanoLuc and LgBiT under these conditions.

[0426] FIGS. 16A-16B show results for the accelerated stability study depicted in FIG. 15, but over a 0 to 50-day time course. FIG. 16A includes results of samples tested in protein buffer at 25° C., and FIG. 16B includes results of samples tested in protein buffer at 60° C. The same materials and methods were used as in FIG. 15. These results demonstrate that the complexes remain stable under these conditions (at 25° C. and 60° C.) up until at least 50 days.

[0427] FIG. 17 shows a comparison of the impact of buffer conditions on luminescence from NanoLuc dried onto a nitrocellulose membrane to assess NanoLuc® stability in the context of a lateral flow assay. Four different conditions were tested: Condition 1: Mouse-anti Hum+IgG-Nluc in PBS, pH 7.4; Condition 2: IgG-Nluc in PBS, pH 7.4; Condition 3: Mouse-anti Hum+IgG-Nluc in loading buffer (20 mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 10% w/v sucrose); Condition 4: IgG Nluc in loading buffer (20

mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 10% w/v sucrose). Each condition was applied to the membranes and either dried at RT or at 37° C.

[0428] For these experiments, the following solutions were prepared: (1) 5 µl mouse/antihuman into 995 1 Addition buffer (0.1 M PBS, pH 7.4); (2) 5 1 anti-mouse-NanoLuc in 995 1 Addition buffer (0.1 M PBS, pH 7.4); (3) 5 1 mouse/antihuman in protein buffer (20 mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 10% w/v sucrose); and (4) 5 1 anti-mouse-NanoLuc in 995 1 protein buffer (20 mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 10% w/v sucrose). About 0.5 ml of solution (1) was loaded into an airbrush and applied to the left side of a nitrocellulose strip (Strip 1 and 2). The strips were allowed to dry either at RT or at 37° C. for 1 hour. About 0.5 ml of solution (2) was applied to the entire surface of strip 1 and strip 2 and allowed to dry at RT or at 37° C.; forming condition 1 and 2, respectively. About 0.5 ml of solution (3) was loaded into an airbrush and applied to the left side of a nitrocellulose strip (Strip 3 and 4). The strip was allowed to dry either at RT or at 37° C. for 1 hour. About 0.5 ml of solution (4) was applied to the entire surface of strip 3 and strip 4 and allowed to dry at RT or 37° C.; forming condition 3 and 4, respectively. For imaging, a 1× solution of substrate was prepared (4mls PBS+1 ml Nano-Glo LCS Dilution Buffer+50ul Nano-Glo Live Cell Substrate) and overlaid on each strip with 1 ml of substrate solution; imaging began immediately thereafter.

[0429] These data demonstrate that buffer formulations are important for activity in lateral flow membranes. In conditions 1-4, where protein was just applied to the membrane in PBS, very little to no light was observed when the membranes were exposed to freshly prepared Nano-Glo Live Cell substrate. In contrast, protein that was prepared with a loading buffer that contained additional components such as Na<sub>3</sub>PO<sub>4</sub>, BSA, Tween 20, and sucrose showed considerable light output. This suggests that the particular loading buffer used to add the protein to the surface of the membrane is important for stability and function (FIG. 17).

#### Example 6

##### Lateral Flow Assay Components

[0430] Experiments were conducted to test different membrane blocking agents and assay running buffers to facilitate proper movement of proteins and targets during a lateral flow assay. Four strips were used, and the design of each (with or without sucrose and blocking agent) is shown in the schematic below the far left image of FIG. 18. Briefly, strip 1 included a blocked membrane with sucrose pre-treatment on a conjugation pad; strip 2 included a blocked membrane with no sucrose pre-treatment on a conjugation pad; strip 3 included an unblocked membrane with sucrose pre-treatment on a conjugation pad; and strip 4 included an unblocked membrane with no sucrose pre-treatment on a conjugation pad.

[0431] The blocking buffer was comprised of 1% w/v polyvinyl alcohol in 20 mM tris, pH 7.4. Conjugation pre-treatment included 30% sucrose w/v in DI water. The conjugation pad was Ahlstrom grade 8950 (chopped glass with binder, 50 g/m<sup>2</sup>), and the membrane was nitrocellulose. For blocking, the membrane was soaked in blocking buffer for 30 min at RT, and subsequently removed from buffer, washed with DI water, and dried for 30 min at 35° C. For

secondary pre-treatment, sucrose solution was applied to the membrane pad near where conjugation reagent (substrate) will be applied. The membrane was dried for 1 hr at 35° C. To prepare the proteins, about 5 µL anti-mouse-NanoLuc was added to 995 1 protein buffer. About 1 mL of protein solution was placed into an airbrush and a light coating was applied to the conjugation pad. This was allowed to dry for 1 hr at 35° C. Strips were then assembled on backing card. Additionally, for FIGS. 18-20, the following buffers compositions were tested: Buffer 1 was comprised of 20×SSC, 1% BSA, pH 7.0+10 µM LCS (FIG. 18). Buffer 2 was comprised of 0.01 µM PBS, 1% BSA, pH 7.0+10 µM PCS (FIG. 19). And Buffer 3 was comprised of 5× LCS dilution buffer+5× LCS—diluted to 1× in PBS (FIG. 20).

[0432] FIG. 18 shows the effects of membrane blocking and sucrose pre-treatment on lateral flow assays performed in a running buffer of 20×SSC, 1% BSA, pH 7.0+10 µM LCS. FIG. 19 shows the effects of membrane blocking and sucrose pre-treatment on lateral flow assays performed in a running buffer of 0.01 µM PBS, 1% BSA, pH 7.0+10 µM Permeable Cell Substrate (PCS). FIG. 20 shows the effects of membrane blocking and sucrose pre-treatment on lateral flow assays performed in a running buffer of 5× LCS dilution buffer+5× LCS—diluted to 1× in PBS. These data demonstrate that membrane treatment and protein buffers do affect assay fluid flow within the conjugation pad and across the lateral flow membrane.

[0433] Experiments were also conducted to assess different membranes and membrane properties within the context of a lateral flow assay such as the effects of membrane properties on absorption and capillary action. FIG. 21 shows the effects of membrane properties on bioluminescent reagent absorption and capillary action in a lateral flow assay. Membranes containing different pore sizes were tested for flow efficiency. Each membrane was unblocked and contain a 30% w/v sucrose pretreatment on approximately the bottom 1/3 of the strip. Other materials included a Conjugation pad (Ahlstrom grade 8950, chopped glass with binder, 50 g/m<sup>2</sup>); a Sample Pad (Cellulose glass fiber CFSP203000 (Millipore)); and an Absorption pad (Cotton linters, grade 238 (Ahlstrom)). The following membrane conditions were tested:

- [0434] 1. nitrocellulose FF170HP (Ahlstrom)
- [0435] 2. nitrocellulose Hi-Flow Plus HFC18002 (Millipore)-180 sec/4 cm
- [0436] 3. nitrocellulose Hi-Flow Plus HFC13502 (Millipore)-135 sec/4 cm
- [0437] 4. nitrocellulose Hi-Flow Plus HFC09002 (Millipore)-90 sec/4 cm
- [0438] 5. nitrocellulose Hi-Flow Plus HFC12002 (Millipore)-120 sec/4 cm
- [0439] 6. nitrocellulose Hi-Flow Plus HFC07502 (Millipore)-75 sec/4 cm
- [0440] 7. nitrocellulose FF170HP (Ahlstrom)—NEGATIVE CONTROL.

[0441] Running buffer was comprised of 5× LCS dilution buffer+5× LCS—diluted to 1× in PBS. Membranes were pre-treated by applying 30% sucrose solution to the membrane, covering ~1.5 cm of the bottom of the strip, the allowed to dry at 35° C. for 1 hour. Proteins were prepared by adding about 5 µL anti-mouse-NanoLuc in 995 µL protein buffer. About 1 mL of protein solution was added to an airbrush, which was used to lightly coat conjugation pad. This was allowed to dry at 35° C. for 1 hour. The negative

control for these experiments contained protein buffer without protein, which was applied with an airbrush in the same manner as the test conditions. Strips were assembled on backing card. The conjugation pad, sample pad, and wicking pad were cut to be 2 cm×1 cm. The sample pad and conjugation pad were overlapped by ~1.8 cm. The total dimensions of the strip were about 6 cm×1 cm.

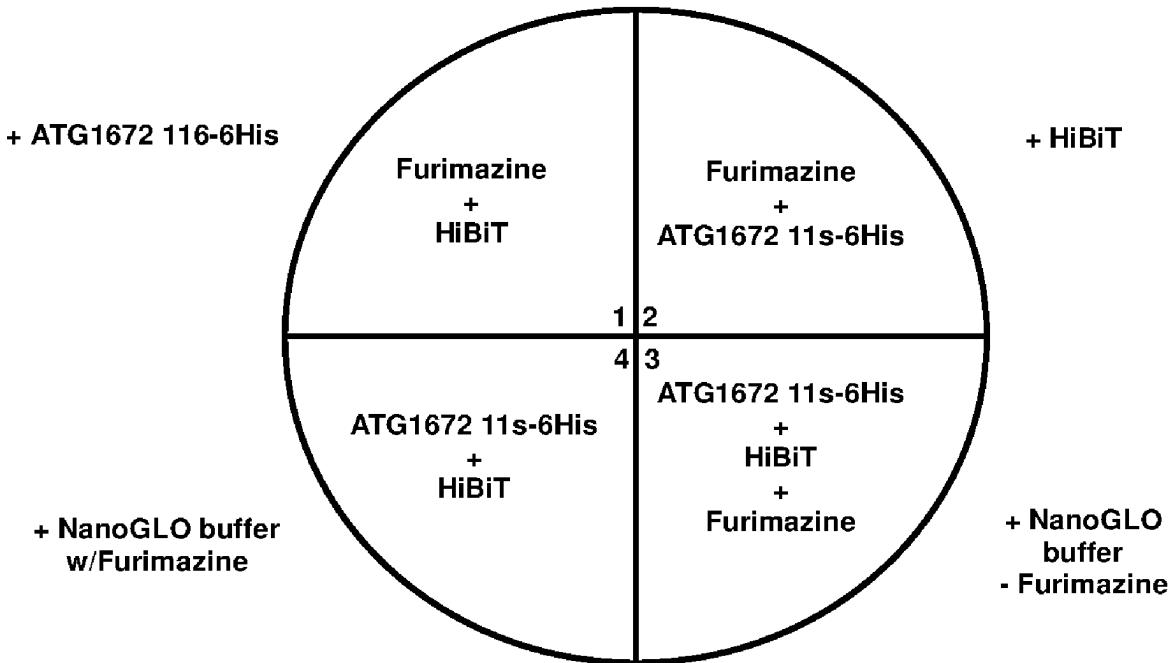
[0442] An imaging program was created to capture 5 sec exposure images every 30 seconds for a total of about 10 minutes. Imaging was repeated if it appeared that there was still NanoLuc flowing across the membrane. Images were stacked into movies using ImageJ, and the final images included in FIG. 21 are the accumulative signal of all images taken over time.

[0443] These results suggest that strips 4 and 6 (boxed in FIG. 21) had the most complete NanoLuc traveling out of conjugation pad and into sample reservoir, based on the conditions used in these experiments.

#### Example 7

##### Bioluminescent Complex Formation

[0444] Experiments were conducted to evaluate bioluminescent complex formation in the presence of various reagents on membrane and filter paper. Experiments were designed and conducted according to the schematic below, which shows the four different conditions tested.



**[0445]** For these experiments, 2.5  $\mu\text{L}$  of HaloTag-HiBiT was added to 498  $\mu\text{L}$  protein buffer. About 5  $\mu\text{L}$  of this solution was spotted on both the membrane and filter paper in quadrants 1, 3, and 4 (see above schematic) and allowed to dry at 37° C. for 1 hour. About 2.5  $\mu\text{L}$  of ATG-1672-11S-6His was diluted in 498  $\mu\text{L}$  of protein buffer, and about 5  $\mu\text{L}$  was spotted directly onto nitrocellulose membrane and filter paper in quadrants 2, 3, and 4 (see above schematic). Membranes were allowed to dry at RT for 1 hour. Furimazine was prepared as a 5 mM stock solution in EtOH. About 5  $\mu\text{L}$  of this solution was spotted onto both the membrane, and the filter paper in quadrants 1, 2, and 3 and immediately placed under high vacuum for 15 minutes. About 2.5  $\mu\text{L}$  of stock protein (20  $\mu\text{M}$ ) was diluted in 498  $\mu\text{L}$  of NanoGLO buffer, which does not contain substrate. About 5  $\mu\text{L}$  was added to the quadrant indicated above and subsequently read in a luminometer.

**[0446]** FIGS. 22A-22B show bioluminescent signal from NanoBiT/HiBiT complementation on nitrocellulose (left) and Whatman grade 541 (right) papers (FIG. 22A), and a compilation image from a corresponding movie taken across total exposure time (movies can be made available upon request). Images were captured at increasing exposure times starting with 1 sec and ending with 10 min exposure (1s, 3s, 10s, 30s, 1m, 2, 3, 4, 5, 10m) for a total time (26 min) after the addition of the reagents indicated 26.

**[0447]** These results suggest that filter paper may provide an increased signal as compared to the membrane. Also, the conditions present in quadrant 4 did not produce detectable luminescence, which could indicate that complex formation was impeded by one or more of the other reagents present.

**[0448]** Experiments were conducted to assess the effects of increased substrate concentration on complex formation. FIG. 23 shows bioluminescent signal from NanoBiT/HiBiT complementation on Whatman grade 903 paper, with a spike of additional substrate and liquid at 20 minutes. FIG. 23 is a representative compilation image from a corresponding movie taken across total exposure time (movies can be made available upon request). About 2.5  $\mu\text{l}$  of purified LgBiT or HiBiT was diluted in 498 1  $\times$  LCS Buffer and added directly to the filter paper (consistent with the conditions in quadrant 1) in a 10  $\mu\text{L}$  volume (2:1 LgBiT to HiBiT ratio). The original substrate was NanoBRET NanoGlo (5  $\mu\text{L}$  was added at 5 mM), and the additional submerged substrate was NanoBRET NanoGlo (5 mM stock), diluted 1:5 in 1 $\times$  NanoGlo buffer, which was diluted to 1 $\times$  in PBS. About 500  $\mu\text{L}$  was added to cover the filter paper. Images were captured at repeating 30 sec exposures during the entire time duration.

**[0449]** Spiking in additional substrate (furimazine) in an excess of liquid volume showed that signal returns, suggesting that as components start to move within the additional fluid, more complexes may be forming due to their increased mobility. This experiment also indicates that the enzyme retains activity with substrate concentration being the limiting factor that can be remedied by the addition of excess substrate.

**[0450]** FIG. 24 shows bioluminescent signal from NanoBiT/HiBiT complementation on Whatman 903 paper, instead of Whatman 541 paper, with the experimental conditions consistent with those in the above schematic diagram (quadrants 1-4 in FIG. 22). Buffer was added to rehydrate the membrane near the end of the experiment. FIG. 24 is a representative compilation image from a corresponding movie taken across total exposure time (movies can be made

available upon request). The conditions in quadrant 2 appear to provide the strongest luminescent signal.

#### Example 8

##### Spot Tests with LgTrip and Substrate

**[0451]** Experiments were conducted to assess the feasibility of an “all-in-one” spot by first testing paper matrix containing LgTrip 3546 and furimazine to which an analyte-of-interest can be added (e.g., dipeptide). FIGS. 25A-25C show bioluminescent signal resulting from reconstitution with dipeptide of LgTrip 3546 and substrate in Whatman 903 paper, in the presence (FIG. 25B) and absence (FIG. 25A) of BSA, along with a serial dilution of the dipeptide with BSA (FIG. 25C). Two sets of spots were made, each spot being comprised of the following components: 1) 5 mM ATT, 5 mM ascorbate, 5  $\mu\text{M}$  LgTrip 3546, and 1 mM furimazine; 2) 5% BSA, 5 mM ATT, 5 mM ascorbate, 5  $\mu\text{M}$  LgTrip 3546, and 1 mM furimazine.

**[0452]** To prepare the spots, a vial containing 200  $\mu\text{L}$  of 5  $\mu\text{M}$  LgTrip 3546, 5 mM ATT, and 5 mM ascorbic acid was prepared. About 5  $\mu\text{L}$  of this solution was added to each spot, and the spots were then allowed to dry at 35° C. for 1 hour. After drying, 1 mM stock of furimazine in ethanol was prepared. About 5  $\mu\text{L}$  of this solution was added to each spot and allowed to dry at 35° C. for an additional 30 minutes. For luminescent measurements, at the time of testing, 1.2 mM dipeptide stock in water was serially diluted down to 1 $\text{e}^{-10}$   $\mu\text{M}$  in PBS, pH 7.0. About 100  $\mu\text{L}$  of each dipeptide stock was added to a 96-well plate containing a spot and kinetic measurements were started immediately.

**[0453]** These data demonstrate that a stable, concentration dependent response was observed with the addition of the dipeptide (FIG. 25). This experiment highlights that a paper-format containing LgTrip 3546 and substrate can be made and then reconstituted in buffered aqueous media containing a potential analyte of interest (e.g., dipeptide). Different materials were then tested with substrate and LgTrip 3546 input. Either fresh dipeptide was added at 1 nM to test NanoTrip and substrate activity, or fresh Nluc was added to isolate the substrate. FIG. 27 shows bioluminescent signal in three different solid phase materials (Whatman 903, Ahlstrom 237, and Ahlstrom 6613H) resulting from reconstitution with dipeptide of LgTrip 3546 and substrate, or NanoLuc added to dried LgTrip 3546 and substrate. Ahlstrom 6613H seems to be detrimental to signal output over time as it appears that the luminescent signal is decreased in both conditions. Overall, the stability of the assay components can be affected by the composition of the solid matrix materials in which they are imbedded.

**[0454]** FIG. 28 shows bioluminescent signal from Whatman 903 paper that contains both LgTrip 3546 as well as substrate and stored under ambient conditions for over 25 days. Spots were exposed to 1 nM dipeptide in PBS at the time of testing. Overall, this experiment shows that there is no significant loss of signal from the materials after extended storage times under ambient temperature.

#### Example 9

##### Lyophilized Cake Containing LgTrip and Substrate

**[0455]** FIGS. 26A-26B show bioluminescent signal resulting from reconstitution with dipeptide of LgTrip 3546 and substrate from a lyocake (FIG. 26A) along with the sum-

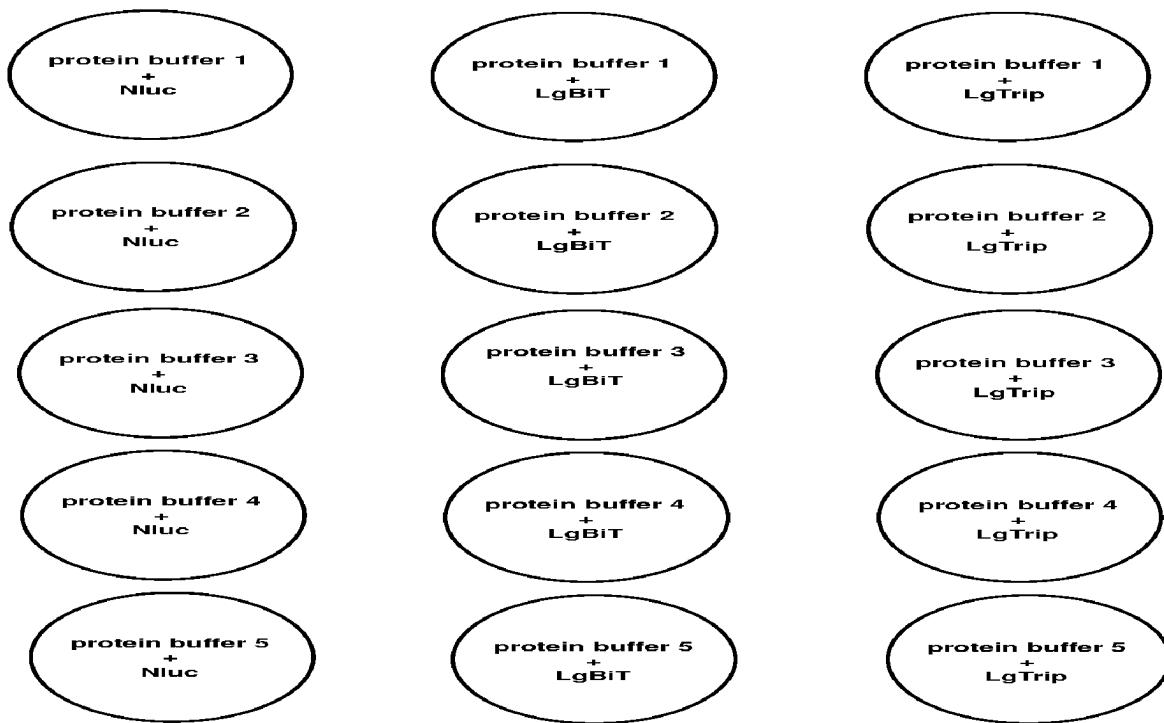
mary data of the titration of the dipeptide (FIG. 26B). To prepare the lyocakes, 5% w/v pullulan was added to water containing 26.3 mM ATT and 11.3 mM ascorbic acid (solution 1). Solution 1 was then aliquoted out into 35  $\mu$ L volumes in snap-cap vials. About 10  $\mu$ L of 95  $\mu$ M LgTrip 3546 protein was then added to each vial and pipetted to mix (solution 2). A 10 mM stock solution of furimazine in ethanol was prepared, and 5  $\mu$ L of this solution was added to each vial and mixed (solution 3). Vials containing solution 3 were placed on dry ice to freeze for 1 hour, and then lyophilized overnight. For luminescent measurements, at the time of testing, 1.2 mM dipeptide stock added to water was serially diluted down to  $10^{-10}$   $\mu$ M in PBS, pH 7.0. About 100  $\mu$ L of each dipeptide stock was added to a lyophilized vial containing LgTrip 3546 and substrate, pipetted briefly to mix, and then placed into a 96-well plate, and kinetic measurements were started immediately.

[0456] These data demonstrate that a stable, concentration dependent bioluminescent response was observed with the addition of the dipeptide (FIG. 26). This experiment highlights that a solid format lyophilized cake or tablet containing LgTrip 3546 and substrate can be made and then reconstituted in aqueous media containing a potential analyte of interest (e.g., dipeptide).

#### Example 10

##### Protein Buffer Formulations

[0457] For FIGS. 29-33, experiments were conducted to test the compatibility of protein components with different protein buffer formulations, according to the experimental design shown in the schematic diagram below.



[0458] For these experiments, Whatman 903 protein saver spot cards were used with the following protein buffer formulations:

[0459] Protein buffer 1: 20 mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 10% w/v sucrose

[0460] Protein buffer 2: 20 mM Na<sub>3</sub>PO<sub>4</sub>, 0.25% v/v tween20, 10% w/v sucrose

[0461] Protein buffer 3: 20 mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20

[0462] Protein buffer 4: 20 mM Na<sub>3</sub>PO<sub>4</sub>, 5% w/v BSA, 0.25% v/v tween20, 2.5% pullulan

[0463] Protein buffer 5: 20 mM Na<sub>3</sub>PO<sub>4</sub>, 0.25% v/v tween20, 2.5% pullulan.

[0464] For NanoLuc, a 1000× stock solution was diluted 1:1000 in protein buffer (1 mL). For a 1.068 nM stock solution, 3  $\mu$ L was diluted into 297  $\mu$ L of protein buffer. About 5  $\mu$ L of each concentration was spotted on the filter paper. For LgBiT-1672-11s-His, 5  $\mu$ L of 1.068 nM protein per spot was used. About 10  $\mu$ L was diluted in 990  $\mu$ L protein buffer for a  $2\text{e}^{-7}$   $\mu$ M stock. About 100  $\mu$ L of a 100 nM protein solution was then prepared, and about 10  $\mu$ L stock was diluted into 990  $\mu$ L protein buffer for 1 nM stock. About 5  $\mu$ L of each concentration was spotted onto filter paper. For LgTrip 3546, about 5  $\mu$ L of 1.068 nM protein was used per spot. About 1.1  $\mu$ L of LgBiT-1672 stock was diluted into 998.94  $\mu$ L protein buffer. About 3  $\mu$ L stock was diluted into 297  $\mu$ L protein buffer. About 5  $\mu$ L of each concentration was spotted onto filter paper. After all protein was added, the samples were dried at 30° C. for about 1 hour. About 40 spots were made for each condition (see above schematic diagram). Spots were tested on day 0 for a baseline and then placed at 60° C. and tested 6 days later. RLU activity was tested by addition of 1 nM of high affinity dipeptide+50  $\mu$ M live cell substrate in PBS, pH 7.0.

[0465] FIGS. 29A-29C show bioluminescent signal, measured by RLUs, in the various protein buffer formulations described above for NanoLuc (FIG. 29A), LgBiT-1672 (FIG. 29B), and LgTrip 3546 (FIG. 29C), and FIGS. 30A-30C show bioluminescent signal, measured by B<sub>max</sub>, in various protein buffer formulations for NanoLuc (FIG.

30A), LgBiT-1672 (FIG. 30B), and LgTrip 3546 (FIG. 30C). Together, these data suggest that BSA is an important component in the protein buffer formulations tested, with NanoLuc and LgTrip 3546 exhibiting the largest decreases in RLU (buffers 2 and 5).

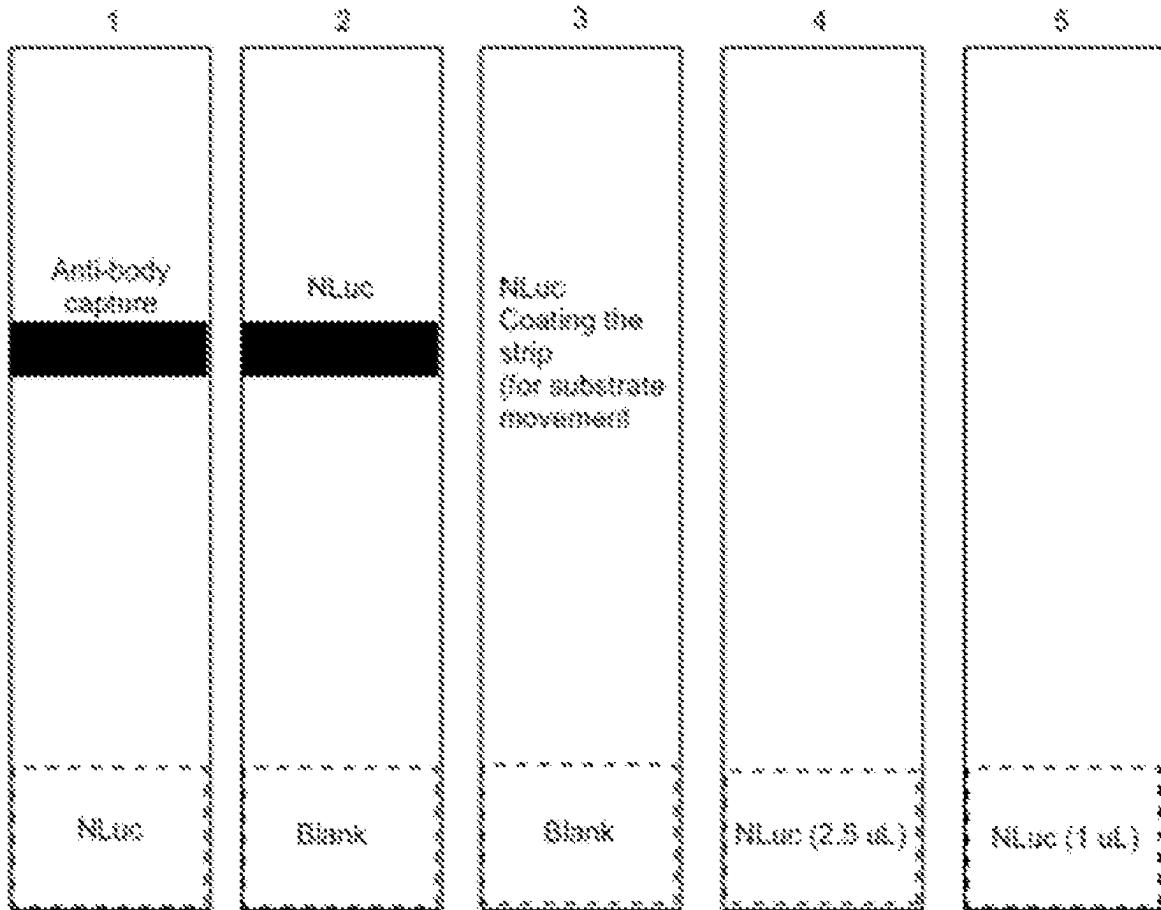
[0466] Experiments were also conducted to assess luminescent background levels in the various protein buffer compositions described above. FIGS. 31A-31B show bioluminescent background levels in various protein buffer compositions for LgBiT-1672 (FIG. 31A) and LgTrip 3546 (FIG. 31B). These data suggest that BSA or pullulan are important components of the protein buffer formulations for LgBiT-1672 for minimizing background luminescence, but there appears to be little to no effect on LgTrip 3546 background levels under these conditions.

[0467] In FIGS. 32A-32F, the kinetics of the above conditions were assessed after addition of dipeptide and substrate in PBS. More specifically, FIGS. 32A-32F show bioluminescent signal (RLUs in FIGS. 32A-32C; B<sub>max</sub> in FIGS. 32D-32F) in various protein buffer formulations for NanoLuc® (FIGS. 32A and 32D), LgBiT-1672 (FIGS. 32B and 32E), and LgTrip 3546 (FIGS. 32C and 32F), after 6 days at 60° C. These data indicate that proteins are stable and maintain activity after 6 days at 60° C. under these conditions, and suggest that BSA is an important component for all proteins buffer formulations. Additionally, FIG. 33 includes representative embodiments of all-in-one lyophilized cakes ("lyocakes") or tablets containing all the necessary reagents to perform an analyte detection test supporting several types of assay formats, including but not limited to, cuvettes, test tubes, large volumes in bottles, snap test type assays, and the like.

#### Example 11

##### Lateral Flow Assays

[0468] For FIGS. 34 and 35, lateral flow assays were performed using the information obtained in the above experiments, and according to the experimental design shown in the schematic diagram below.



[0469] The materials used for these experiments included a Conjugation pad (Ahlstrom grade 8950, chopped glass with binder, 50 g/m<sup>2</sup>), a Sample Pad (Celloose glass fiber CFSP203000 (Millipore)), an Absorption pad (Cotton linters, grade 238 (Ahlstrom)), a Membrane (nitrocellulose Hi-Flow Plus HFC07502 (Millipore), #6 from strip-test 2), and Running buffer (5× LCS dilution buffer+5× LCS diluted to 1× in PBS). Membranes were prepared by applying 30% sucrose solution to the membrane covering about 1.5 cm of the bottom of the strip. The membrane was allowed to dry at 35° C. for 1 hour. Strips were initially cut to be 4.5 cm×1 cm.

[0470] Protein preparations were carried out according to the conditions below:

[0471] Condition 1: 5 μL mouse anti-NanoLuc antibody diluted in 995 μL protein buffer, applied evenly across the conjugation pad with an air brush, and dried in oven at 37° C. Dilute 2.5 μL mouse antibody in 0.5 mL of protein buffer and applied directly to membrane.

[0472] Condition 2: Dilute 2.5 μL of NanoLuc in 0.5 mL of protein buffer and applied directly to membrane. Allowed to dry at 37° C. for 1 hour.

[0473] Condition 3: Treat entire membrane directly with 5 μL of NanoLuc diluted to 1 mL in protein buffer. Applied evenly with airbrush. Allowed to dry at 37° C. for 1 hour.

[0474] Condition 4: 2.5 μL mouse anti-NanoLuc antibody in 997 μL protein buffer. Applied evenly across conjugation pad with airbrush. Allowed to dry at 37° C. for 1 hour.

[0475] Condition 5: 1 μL mouse anti-NanoLuc antibody in 999 μL protein buffer. Applied evenly across conjugation pad with airbrush. Allowed to dry at 37° C. for 1 hour.

[0476] Strips were assembled on backing card with conjugation pad, sample pad, and wicking pad cut to 1 cm×1 cm. Once strips were assembled, they were cut in half lengthwise to a final dimension of 4.5 cm×0.5 cm. For imaging analysis, about 250 1 1× LCS buffer+LCS was diluted in PBS. Images were captured at 5 sec exposures with 5 sec wait time in between images; representative images are compilation images from corresponding movies taken across total exposure time (movies can be made available upon request). Total read time was 2:40 minutes.

[0477] FIG. 34 shows bioluminescent signal from substrate movement across a lateral flow strip from a compilation image corresponding to a movie taken across total exposure time. Substrate was added to the sample window of the lateral flow assay cassette and real time imaging shows substrate movement across the strip, and NanoLuc® activity can be seen throughout the test window (strip #3 in schematic above). By 70 seconds, the substrate flowed across the entire sample window.

[0478] FIG. 35 shows bioluminescent signal from NanoLuc® movement across a lateral flow strip from a compilation image corresponding to a movie taken across total exposure time (strip #s 4 and 5 in the schematic above). Under these conditions, strip #5 appeared to outperform strip #4 with, as demonstrated by the NanoLuc® flowing out of the conjugation pad and into the liquid flow across the membrane to the strip containing the mouse anti-NanoLuc antibody.

### Example 12

#### Fumonisin Detection

[0479] Experiments were conducted during development of embodiments herein to demonstrate the use of NanoLuc®-based technologies in a competition-type immunoassay for the detection of a fumonisin B1, an exemplary small molecule toxin. Such assays can be performed in the devices and systems described herein, and with other small molecule targets and target analytes.

[0480] In an exemplary assay, tracers were generated by tethering fumonisin B1 to a NLpeptide tag (e.g., a peptide tag comprising SEQ ID NO: 10) via a biotin/streptavidin linkage, via a HaloTag linkage, or directly (FIG. 36). In some embodiments, the tracers can be combined with an anti-fumonisin B1 antibody linked to a polypeptide complement of the NLpeptide tag (e.g., a complement comprising SEQ ID NO: 9). A bioluminescent complex can form between the peptide tag and the polypeptide component upon binding of the antibody to the fumonisin B1. Exposure to varying concentrations of unlabeled Fumonisin B1 disrupts the bioluminescent complex and results in decreased luminescence, and the ability to detect/quantify the amount of fumonisin B1 in a sample (FIG. 37).

### Example 13

#### Lyophilized Cake Containing LgBiT and Substrate

[0481] FIGS. 38A-38B show bioluminescent signal resulting from reconstitution with dipeptide of LgBiT and substrate from a lyocake (FIG. 38A) along with a titration of the dipeptide (FIG. 38B). To prepare a lyocake with LgBiT: 5% w/v pullulan in water containing 5 mM ATT and 5 mM ascorbic acid was prepared (solution 1). Solution 1 was then aliquoted out into 45 1 μL volumes in snap-cap vials. About 5 μL of 20 μM LgBiT protein was then added to each vial and pipetted to mix (solution 2). A 10 mM stock solution of furimazine in ethanol was prepared, and 5 μL of this solution was added to each vial and mixed (solution 3). Vials containing solution 3 were placed on dry ice to freeze for 1 hour, and then lyophilized overnight.

[0482] For luminescent measurements, at time of testing, 1.2 mM dipeptide stock in water was serially diluted down to 1e<sup>-10</sup> μM in PBS, pH 7.0. 100 μL of each dipeptide stock was added to a lyophilized vial containing LgBiT and substrate, pipetted briefly to mix, and then placed into a 96-well plate and kinetic measurements were started immediately.

[0483] These data demonstrate that a stable, concentration dependent bioluminescent response was observed with the addition of the dipeptide. This experiment highlights that a solid format containing LgBiT and substrate can be made and then reconstituted in aqueous media containing a potential analyte of interest (e.g., dipeptide).

### Example 14

#### Substrate and LgTrip 3546 or LgBiT Lyophilization

[0484] FIG. 39 shows bioluminescent signal resulting from reconstitution with dipeptide of LgBiT, or LgTrip 3546, and substrate from a lyocake prepared directly into a standard 96-well tissue culture treated plate (Costar 3917). To prepare a lyocake in plates: 2.5% w/v pullulan in water containing 5 mM ATT and 5 mM ascorbic acid was prepared

(solution 1, pH 6.5). Solution 1 was then aliquoted out into 45  $\mu$ l volumes into each well of the plate. 2.6  $\mu$ l of 95  $\mu$ M LgTrip 3546 protein was then added to each vial and pipetted to mix forming condition 1 (LgTrip 3546 alone). Additionally, 5  $\mu$ l of 20  $\mu$ M LgBiT protein was added to each vial and pipetted to mix, forming condition 2 (LgBiT alone). 5  $\mu$ l of ethanol was then added to each well of condition 1 and 2 as a vehicle control.

[0485] Conditions 3 (LgTrip 3546/substrate) and 4 (LgBiT/substrate) were prepared as described above: 2.5% w/v pullulan in water containing 5 mM ATT and 5 mM ascorbic acid was prepared (solution 1, pH 6.5). Solution 1 was then aliquoted out into 45  $\mu$ l volumes into each well of the plate. About 2.6  $\mu$ l of 95  $\mu$ M LgTrip 3546 protein or 5  $\mu$ l of 20  $\mu$ M LgBiT protein was added to each vial and pipetted to mix. Approximately 5  $\mu$ l of 10 mM furimazine in ethanol was then added to each well forming condition 3 and 4 respectively. The plate was then placed in a cooler with dry ice to freeze for 1 hour, followed by lyophilization overnight.

[0486] For luminescent measurements, at time of testing, 1.2 mM dipeptide stock in water was serially diluted down to 1e<sup>-9</sup>  $\mu$ M in PBS, pH 7.0 (FIG. 39). Fresh NanoGlo® substrate was then added to this stock for a final concentration of 10  $\mu$ M substrate. 100  $\mu$ l of this solution was added to wells that contained condition 1 (LgTrip 3546) and 2 (LgBiT). Conditions 3 (LgTrip 3546/substrate) and 4 (LgBiT/substrate) only received 100  $\mu$ l of 1e<sup>-9</sup>  $\mu$ M dipeptide in PBS. After testing, the plates were wrapped in tin foil and left on the bench at ambient temperature.

[0487] This data demonstrates that a lyocake containing either LgBiT or LgTrip 3546 and substrate can be prepared directly within a 96-well plate and reconstituted in the presence of an analyte of interest (dipeptide) leading to stable and robust signal.

#### Example 15

##### Paper Based All-In-One Analyte Detection Systems

[0488] Experiments were conducted to test the efficacy of paper-based detection platforms containing NanoBiT (FIGS. 40A-40B) and NanoTrip (FIG. 41A) complementation systems. Paper spots were created from punching  $\frac{1}{8}$ " diameter circles from Whatman903 spot paper. The spots were treated with 5  $\mu$ l of a master mix solution containing: 5% w/v BSA, 5 mM ATT, 5 mM ascorbate, 40 nM LgBiT-protein G fusion, and 20 nM SmBiT-TNF $\alpha$  in water, pH 6.5. The spots were allowed to dry at 35 °C for 1 hour. A 200  $\mu$ M solution of furimazine in ethanol was prepared, and 5 1  $\mu$ l of this solution was added to each spot. The spots were allowed to dry for an additional 30-60 minutes at 35 °C. At the time of testing, spots were plated into individual wells of a 96-well NBS plate (Costar 3917), and reconstituted with Opti-MEM assay buffer that contained either 0 nM (blank), 1 nM, or 100 nM Remicade.

[0489] FIGS. 40A-40B include assay results using NanoBiT components. In the condition where the spots were exposed to assay buffer containing 1 nM Remicade, there was an increase in overall light output compared to the blank condition/control, which contained no Remicade. An increase in signal is observed as the concentration of Remicade was increased to 100 nM. As shown in FIG. 40B, Remicade was prepared in opti-MEM assay buffer at 100 nM, 10 nM, 1 nM, and 0.1 nM concentrations. At time of

testing, 100 1  $\mu$ l of each solution containing Remicade was added to a well of a 96-well plate containing a spot, and RLU output was measured.

[0490] Similar experiments were performed, as shown in FIG. 41A using NanoTrip components. Spots were created from punching  $\frac{1}{8}$ " diameter circles from Whatman903 spot paper. Each the spot was treated with 5  $\mu$ l of a master mix solution containing: 5% w/v BSA, 5 mM ATT, 5 mM ascorbate, 20  $\mu$ M LgTrip 3546, 100 nM TNF $\alpha$ -15gs-VSHiBiT, SmTrip9 Pep521-15gs-protein G in water, pH 6.5. The spots were allowed to dry at 35 °C for 1 hour. A 200  $\mu$ M solution of furimazine in ethanol was prepared and 5  $\mu$ l of this solution was added to each spot. The spots were allowed to dry for an additional 30 minutes at 35 °C. At the time of testing, spots were plated into individual wells of a 96-well NBSplate (Costar 3917), and reconstituted with opti-MEM assay buffer that contained either 0 nM (blank), 1 nM, or 100 nM Remicade. The results are shown in FIG. 41A.

[0491] These experiments show that it is possible to build and all-in-one, paper-based bioluminescent assay platforms for the detection of an analyte-of-interest using both NanoBiT and NanoTrip complementation systems. In addition, these experiments demonstrate that it is possible to quantify the amount of analyte present in the sample matrix based on a change in overall light output. Increasing the concentration of the analyte-of-interest (i.e. Remicade) led to a proportional increase in the bioluminescent signal (the bioluminescent signal generated from the analyte detection complex is proportional to the concentration of the analyte).

#### Example 16

##### Lyocake Based All-In-One Analyte Detection Systems

[0492] Experiments were also conducted to test the efficacy of lyocake-based detection platforms containing NanoBiT (FIG. 40C) and NanoTrip (FIGS. 41B-41C) complementation systems.

[0493] As shown in FIG. 40C, stability conditions were tested when drying down the components of the bioluminescent complexes. About 45  $\mu$ l of a master mix solution was added to 1.5 mL plastic snap-cap vials. The master mix included: 5% w/v pullulan, 5 mM ATT, 5 mM ascorbate, 40 nM LgBiT-protein G fusion, and 20 nM SmBiT-TNF $\alpha$ , at pH 6.5. About 5-10  $\mu$ l of the substrate furimazine in ethanol was added to each vial, mixed, and placed in dry ice for about 1 hour. The frozen samples were then lyophilized overnight to form a lyocake. At the time of testing, solutions of 100 nM and 10 nM Remicade were prepared in Opti-MEM assay buffer. About 100  $\mu$ l of these solutions were added to the vials containing the NanoBiT Cake, pipetted to mix, and then transferred to a Costar 3600 96-well plate. A blank control was prepared that lacked the analyte Remicade. The results in FIG. 40C demonstrate a proportional increase in signal as the analyte concentration increased, even when all the components of the bioluminescent complex, including the substrate, are frozen and stored in the form of a lyocake, and subsequently exposed to the analyte-of-interest.

[0494] In FIGS. 41B-41C, stability conditions were tested when drying down the components of the bioluminescent complexes. About 45  $\mu$ l of a master mix solution was added to 1.5 mL plastic snap-cap vials. The master mix included: 5% w/v pullulan, 5 mM ATT, 5 mM ascorbate, 9  $\mu$ M LgTrip 3546, 225 nM SmTrip9-Protein G, and 45 nM SmBiT-

TNF $\alpha$ , at pH 6.5. About 5-10  $\mu$ l of the substrate furimazine in ethanol was added to each vial, mixed, and placed in dry ice for about 1 hour. The frozen samples were then lyophilized overnight to form a lyocake. At the time of testing, solutions of 100 nM, 10 nM and 1 nM Remicade were prepared in Opti-MEM assay buffer. About 100  $\mu$ l of these solutions were added to the vials containing the NanoTrip Cake, pipetted to mix, and then transferred to a Costar 3600 96-well plate. A blank control was prepared that lacked the analyte Remicade. The results in FIG. 41B-41C demonstrate a proportional increase in signal as the analyte concentration increased, even when all the components of the bioluminescent complex, including the substrate, are frozen and stored in the form of a lyocake, and subsequently exposed to the analyte-of-interest.

[0495] In the condition where the spots were exposed to assay buffer containing 1 nM Remicade, there was an increase in overall light output compared to the blank condition, which contained no Remicade. An increase in signal was observed as the concentration of Remicade increased to 100 nM. These experiments show that it is possible to build and all-in-one lyocake-based, bioluminescent-based assay platforms for the detection of an analyte-of-interest using both NanoBiT and NanoTrip complementation systems. In addition, these experiments demonstrate that it is possible to quantify the amount of analyte present in the sample matrix based on a change in overall light output. Increasing the concentration of the analyte-of-interest (i.e. Remicade) led to a proportional increase in the bioluminescent signal (the bioluminescent signal generated from the analyte detection complex is proportional to the concentration of the analyte).

#### Example 17

##### Mesh-Based Systems to Separate Substrate from Bioluminescent Complexes for Analyte Detection

[0496] Experiments were conducted to investigate the conditions required to generate a bioluminescent signal when peptide and polypeptide components of the bioluminescent complexes provided herein were produced in a format that does not include the substrate. For example, in one embodiment, an amount of a solution (e.g., containing an analyte-of-interest) is added to a mesh or matrix that has the luminogenic substrate adhered ("caked") to it. Addition of the solution acts to reconstitute the substrate on the mesh, and this solution subsequently interacts with the surface of paper containing the dried down peptides and polypeptides of the bioluminescent complexes of the present disclosure, thus generating a bioluminescent signal (FIG. 42A). The mesh format does not hinder the ability to detect the bioluminescent signal; any bioluminescence detected comes from the surface of the paper, and not from any solution phase that is formed during the experiment.

[0497] As shown in FIG. 42A, bioluminescence is detectable using this format. Whatman 903 paper spots were made to have about 0.25 inch diameters, similar to the nylon mesh. The master mix, which was used to generate the paper spots containing the bioluminescent peptide/polypeptide components, included: 5% w/v BSA, 5 mM ATT, 5 mM ascorbate, 10  $\mu$ M NanoLuc, at pH 6.5. About 10-20 1  $\mu$ l of the master mix was added to the spots and then dried at about 35° C. for about 1 hour. To generate the mesh containing the substrate, a solution of about 0.75% pullulan in water was prepared. About 450  $\mu$ l of this solution was added to a plastic

snap-cap vial. About 50  $\mu$ l of 10 mM furimazine in EtOH was added to the vial and pipetted to mix. About 25  $\mu$ l of this solution was added to the top of the mesh-spots. The mesh spots were then frozen on dry-ice, and lyophilized overnight. At time of testing, the mesh containing the lyocake substrate was placed on top of the spots containing the NanoLuc® protein. The complete system was then added to the well of a 96-well costar 3600 plate. About 10  $\mu$ l of PBS was then added to the top of the mesh to reconstitute the material and the plate was read for RLU light output.

[0498] Experiments were also conducted using LgTrip 3546 bioluminescent components with the mesh-based format. The master mix, which was used to generate the paper spots containing the bioluminescent peptide/polypeptide components, included: 5% w/v BSA, 5 mM ATT, 5 mM ascorbate, 100 nM LgTrip 3546, at pH 6.5. About 10-20  $\mu$ l of the master mix was added to the spots and then dried at about 35° C. for about 1 hour. To generate the mesh containing the substrate, a solution of about 0.75% pullulan in water was prepared. About 450  $\mu$ l of this solution was added to a plastic snap-cap vial. About 50  $\mu$ l of 10 mM furimazine in EtOH was added to the vial and pipetted to mix. About 25  $\mu$ l of this solution was added to the top of the mesh-spots. The mesh spots were then frozen on dry-ice, and lyophilized overnight. At the time of testing, dipeptide ranging from 100 nM to 0.1 nM was prepared in PBS. The spots were placed in wells, and the screen containing the substrate was placed on the surface of the spots. About 10  $\mu$ l of the solutions containing each concentration of peptide was added to the surface of the screen and RLU's were recorded (FIGS. 42B-42C). The blank control did not contain any dipeptide.

[0499] Experiments were also conducted using LgTrip 3546 bioluminescent components with the mesh-based format and by forming a pullulan film. The master mix, which was used to generate the paper spots containing the bioluminescent peptide/polypeptide components, included: 5% w/v BSA, 5 mM ATT, 5 mM ascorbate, 100 nM LgTrip 3546, at pH 6.5. About 10-20 1  $\mu$ l of the master mix was added to the spots and then dried at about 35° C. for about 1 hour. To generate the mesh containing the substrate, a solution of about 2.0% pullulan in water was prepared. About 450  $\mu$ l of this solution was added to a plastic snap-cap vial. About 50  $\mu$ l of 10 mM furimazine in EtOH was added to the vial and pipetted to mix. About 25  $\mu$ l of this solution was added to the top of the mesh-spots. The spots were then allowed to dry under ambient conditions, in the dark, overnight. This method resulted in the formation of a pullulan film that filled the holes of the mesh. At the time of testing, dipeptide ranging from 100 nM to 0.1 nM was prepared in PBS. The spots were placed in wells, and the screen containing the substrate was placed on the surface of the spots. About 10  $\mu$ l of the solutions containing each concentration of peptide was added to the surface of the screen and RLU's were recorded (FIGS. 42D-42E). The blank control did not contain any dipeptide.

[0500] These experiments show that it is feasible to detect bioluminescent signal in a mesh-based format in which the peptide/polypeptide components are separate from the substrate. In addition, in the context of this format, these experiments demonstrate that increasing the concentration of the analyte-of-interest (i.e. dipeptide) leads to a proportional increase in the bioluminescent signal (the biolumi-

nescent signal generated from the analyte detection complex is proportional to the concentration of the analyte).

#### Example 18

Testing Different Formulated, Lyophilized Substrates for Cake Appearance, Reconstituted Kinetic Activity Performance, and Accelerated Thermal Stability

**[0501]** To evaluate the potential application of lyophilization for preservation of the furimazine substrate, formulations containing furimazine were prepared. The 20× stock formulations were as follows:

**[0502]** Condition 1: 100 µM furimazine in ethanol, 5 mM azothiothymine, 5 mM ascorbic acid, 2.5% pullulan w/v, ddH<sub>2</sub>O (Millipore);

**[0503]** Condition 3: 100 µM furimazine in ethanol, 5 mM azothiothymine, 5 mM ascorbic acid, 2.5% pullulan w/v, 20 mM HEPES buffer (pH 8.0), 90 mM glycine, 20 mM histidine, 25 mg/ml sucrose, 0.01% polysorbate 80;

**[0504]** Condition 5: 40 µM furimazine in 85% ethanol+ 15% glycol, 200 mM MES buffer (pH 6.0), 200 mM hydroxypropyl beta cyclodextrin (m.w. 1396 Da), 600 mM sodium ascorbate, 2.5% pullulan w/v; and

**[0505]** Condition 7: 20 µM furimazine in ethanol, 200 mM MES buffer (pH 6.0), 200 mM hydroxypropyl beta cyclodextrin (m.w. 1396 Da), 600 mM sodium ascorbate, 2.5% pullulan w/v.

**[0506]** One mL aliquots of 20× stock solution was dispensed into 10 mL amber glass vials, and a rubber stopper was partially inserted into the vial. Vials were loaded into a lyophilizer (Virtis Genesis 12EL lyophilizer) with shelves pre-chilled to 4.7° C. Product then underwent a freezing step with a shelf temperature of -50° C. for 2 hr after which time the condenser step started. During the run, the condenser temperature ran between -5° C. and -87° C. A vacuum pull down ran next at the pressure set-points of 75 and 200 mTorr. Sublimation lasted ~7.5 hr, and desorption lasted ~16.1 hr. At the end of the lyophilization process, the vials were back-filled with nitrogen and sealed with fully inserted stoppers at -600 Torr of pressure.

**[0507]** Vials were stored at 25° C. or 60° C. and tested at various timepoints post-lyophilization. For activity-based assays, furimazine cakes were reconstituted with 10 mL of PBS containing 0.01% BSA. The vials were shaken manually and allowed to equilibrate at room temperature for 5 minutes. Fifty 1 of the reconstituted substrate was added to 50 µL of 1 ng/mL purified NANOLUC enzyme (Promega) that was reconstituted in the same BSA buffer (final [NanoLuc]=0.5 ng/ml). The controls used were the NANOGLO Live Cell Substrate (Promega Cat. N205) or NANOGLO substrate (Promega Cat. N113) according to manufacturer's protocol, but were diluted into PBS containing 0.01% BSA instead of the dilution buffer provided in the kit (Promega). Assays were performed in solid, white, nonbinding surface (NBS) plates (Costar) and analyzed on a GLOMAX Discover Multimode Microplate Reader (Promega) collecting total luminescence using kinetic or endpoint reads, depending on the experiment. For analysis of absolute [furimazine], reconstituted samples were analyzed on HPLC for absorbance spectra at wavelength 245 nm and the absolute amount remaining from day 0 was plotted.

**[0508]** The appearance of the lyophilized cakes resulting from these formulations are displayed in FIG. 43, which

shows that all 4 conditions tested produced an intact cake, although conditions 5 and 7 did display some cracking. A pH indicator that was supplied for these vials indicated that the resulting cakes had pH values of about 2-3 for Condition 1, pH values of about 7.5 for Condition 3, and pH values of about 6 for Conditions 6 and 7. Signal kinetics of the reconstituted furimazine, when tested with purified NanoLuc, compared to that of furimazine in standard organic storage buffer (N113 and N205) and maintained at -20° C., indicated there was no observable loss in performance due to the formulated buffer and lyophilization process itself, with an improved half-life for conditions 5 and 7 (FIG. 44).

**[0509]** Accelerated thermal stability studies indicated no loss of activity for 3 months for the formulated and lyophilized furimazine for Condition 1, which in stark contrast to the furimazine stored in organic solvent, which lost all activity in about 10 days when stored at this elevated temperature (FIG. 45). HPLC analysis for the absolute [furimazine] remaining after storage at 25° C. and 60° C. supported the activity findings with the formulated and lyophilized substrate containing significantly higher purity of furimazine relative to furimazine in the standard organic storage buffer (FIGS. 46A and 46B). To determine the liquid stability of the formulated, lyophilized furimazine, vials were reconstituted with water and allowed to remain in solution for 12 days prior to analysis by HPLC for total remaining furimazine as compared to day 0. Liquid stability of conditions 5 and 7 were found to be superior (FIG. 47).

#### Example 19

Development of a Solution-Based, Homogeneous Human Interleukin-6 Tripartite Immunoassay Using HaloTag-Peptide Fusions to Chemically Conjugate Monoclonal Antibody Pairs

**[0510]** The basic principle of the homogeneous NanoLuc tripartite (NanoTrip) immunoassay is depicted in FIG. 48. First, a pair of antibodies that target non-overlapping epitopes on IL-6 are chemically conjugated to SmTrip9 (SEQ ID NO: 13) or HiBiT (SEQ ID NO: 11) using the HaloTag® technology. When the labeled antibodies bind an IL-6 analyte, the complementary subunits are brought into proximity thereby reconstituting a bright luciferase in the presence of the LgTrip 3546 protein (SEQ ID NO: 12) and furimazine substrate. This assay is quantitative because the amount of luminescence generated by a standard plate-reading luminometer is directly proportional to the amount of target analyte present.

**[0511]** Genetic fusions containing the SmTrip9 variants (SmTrip9 Pep521; SEQ ID NO: 16) or SmTriplO variants (SmTriplO Pep289 or VSHiBiT; SEQ ID NO: 17 separated by either a 2x or 3x Gly-Ser-Ser-Gly linker to the amino terminus of HaloTag was achieved using the pFN29A HIS6HaloTag T7 Flexi Vector (Promega). Glycerol stocks of *E. coli* expressing HisTag-HaloTag fusion protein was used to inoculate 50 mL starter cultures, which were grown overnight at 37° C. in LB media containing 25 µg/ml kanamycin. Starter cultures were diluted 1:100 into 500 mL fresh LB media containing 25 µg/mL kanamycin, 0.12% glucose, and 0.2% rhamnose. Cultures were grown for 22-24 h at 25° C. Cells were pelleted by centrifugation (10,000 rpm) for 30 min at 4° C. and re-suspended in 50 mL PBS. 1 mL protease inhibitor cocktail (Promega), 0.5 mL RQ1 DNase (Promega), and 0.5 mL of 10 mg/mL lysozyme

(Sigma) were added, and the cell suspension was incubated on ice with mild agitation for 1 h. Cells were lysed by sonication at 15% power at 5 s intervals for 1.5 min (3 min total) and subsequently centrifuged at 10,000 rpm for 30 min at 4° C. Supernatant was collected, and protein purified using HisTag columns (GE) following manufacturer's recommended protocol. Protein was eluted using 500 mM imidazole, dialyzed in PBS, characterized using SDS-PAGE gel and was >95% pure. Proteins were stored in 50% glycerol at -20° C.

[0512] To chemically conjugate the antibodies to the HaloTag-peptide fusion proteins, antibodies were buffered exchanged 2x into 10 mM sodium bicarbonate buffer (pH 8.5) using Zeba spin desalting columns (ThermoFisher). Antibodies were then primed with 200µM amine-reactive HaloTag Succinimidyl Ester (04) Ligand (Promega) for 2 hr shaking at 1000 rpm at 22° C. Unreacted ligand was removed with two passes through Zeba spin columns in PBS buffer. Then, antibodies were covalently labeled with 30 µM of the HaloTag fusion protein overnight at 4° C. while shaking. Excess unreacted HaloTag fusion protein was removed using HaloLink Resin (Promega). Non-denaturing SDS-PAGE gel was used to characterize the conjugated antibodies. Mouse anti-human IL-6 monoclonal antibodies used in the human IL-6 immunoassay were clone 5IL6 (Thermo cat #M620) and clone 505E 9A12 A3 (Thermo cat #AHC0662). SDS-PAGE gels were performed on the labeled antibodies and it was determined that each antibody was labeled with a variable number of peptide-HaloTag fusion proteins, with the primary species containing 3-5 peptide labels (FIG. 49).

[0513] Binding kinetic studies were performed to establish maximum light output and signal duration of the fully complemented system as show in FIG. 50. The signal kinetics were compared between conditions: (1) peptide labeled antibodies and LgTrip 3546 (SEQ ID NO: 12) were pre-equilibrated with rhIL-6 for 90 minutes with addition of furimazine at time 0, (2) peptide labeled antibodies are pre-equilibrated with rhIL-6 for 90 minutes with addition of LgTrip 3546 and furimazine at time 0, and (3) all assay reagents are added to rhIL-6 at time 0. Condition 2 tracks the binding kinetics of LgTrip 3546 (SEQ ID NO: 12) to the peptide labeled antibodies:rhIL-6 complex. Condition 3 tracks the binding kinetics of the antibodies to the analyte and the LgTrip 3546 to the peptides. FIG. 50A displays the raw RLU's and FIG. 50B displays the fold response as calculated by taking the RLU value generated in the presence of 5 ng/ml rhIL-6 divided by the background signal generated in the absence of rhIL-6. The assay buffer used was 0.01% BSA in PBS, pH 7.0, and assay reagent concentrations were 7 ng/ml for each peptide labeled antibody, 1 µM LgTrip 3546 (SEQ ID NO: 12) protein, and furimazine. FIG. 51 displays the dose response curve for the solution-based homogenous IL-6 immunoassay performed in a standard assay buffer consisting of 0.01% BSA in PBS, pH 7.0. This assay was shown to be extremely sensitive with a limit of detection (LOD) of 2.1 pg/ml, which resulted in a broad dynamic range of over 3-4 orders of magnitude, and maintained low variability (CVs <10%) throughout the linear range. For these experiments, 7 ng/ml of each peptide labeled antibody and 1 µM LgTrip 3546 (SEQ ID NO: 12) protein were incubated in the presence of rhIL-6 for 90 minutes. Furimazine was added, and luminescence signal analyzed.

#### Example 20

##### Lyophilized, Single-Reagent Tripartite Immunoassays in Vials

[0514] To evaluate the potential application of lyophilization for preservation of the entire IL-6 tripartite immunoassay in a single vial, formulations containing peptide labeled antibodies (SmTrip9 Pep521 (SEQ ID NO: 16) and SmTrip10 Pep289 (SEQ ID NO: 17)), LgTrip 3546 (SEQ ID NO: 12), and furimazine were prepared. The 20x stock formulations are as follows:

[0515] Formulation A: 20 mM HEPES buffer (pH 8.0), 90 mM glycine, 20 mM histidine, 25 mg/ml sucrose, 0.01% polysorbate 80, 0.6 ug/ml clone 5IL6 antibody labeled with HaloTag-SmTrip9 Pep521 (SEQ ID NO: 16), 1.2 ug/ml 505E A12 A3 antibody labeled with HaloTag-SmTrip10 Pep289 (SEQ ID NO: 17), and 20 µM LgTrip 3546 (SEQ ID NO: 17).

[0516] Formulation B: 20 mM HEPES buffer (pH 8.0), 90 mM glycine, 20 mM histidine, 25 mg/ml sucrose, 0.01% polysorbate 80, 0.6 ug/ml clone 5IL6 antibody labeled with HaloTag-SmTrip9 Pep521 (SEQ ID NO: 16), 1.2 ug/ml 505E A12 A3 antibody labeled with HaloTag-SmTrip10 Pep289 (SEQ ID NO: 17), 20 µM LgTrip 3546 (SEQ ID NO: 12), and 100 µM furimazine in ethanol.

[0517] Formulation C: 5 mM azothiothymine, 5 mM ascorbic acid, 2.5% pullulan w/v, 20 mM HEPES buffer (pH 8.0), 90 mM glycine, 20 mM histidine, 25 mg/ml sucrose, 0.01% polysorbate 80, 0.6 ug/ml clone 5IL6 antibody labeled with HaloTag-SmTrip9 Pep521 (SEQ ID NO: 16) 1.2 ug/ml 505E A12 A3 antibody labeled with HaloTag-SmTrip10 Pep289 (SEQ ID NO: 17), 20 µM LgTrip 3546 (SEQ ID NO: 12), and 100 µM furimazine in ethanol.

[0518] One mL aliquots of 20x stock solution was dispensed into 10 mL amber glass vials, and a rubber stopper was partially inserted into the vial. Vials were loaded into the lyophilizer (Virtis Genesis 12EL lyophilizer) with shelves pre-chilled to 4.7° C. Product then underwent a freezing step with a shelf temperature of -50° C. for 2 hr after which time the condenser step started. During the run, the condenser temperature ran between -5° C. and -87° C. A vacuum pulled down ran next at the pressure set-points of 75 and 200 mTorr. Sublimation lasted ~7.5 hr, and desorption lasted ~16.1 hr. At the end of the lyophilization process, the vials were back-filled with nitrogen and sealed with fully inserted stoppers at -600 Torr of pressure.

[0519] FIG. 52A displays the resulting lyophilized product for single-reagent, IL-6 NanoTrip (tripartite NanoLuc) immunoassays using formulations A and B..

[0520] Vials were stored at 25° C. and tested at various timepoints post-lyophilization. For activity-based assays, single-reagent cakes were reconstituted with 10 mL of PBS containing 0.01% BSA. The vials were shaken manually and allowed to equilibrate at room temperature for 5 minutes. 50 µl of the reconstituted substrate was added to 50 µl of recombinant human IL-6 (source) reconstituted in the same BSA buffer. Formulation A requires the addition of furimazine, in which NANOGLO Live Cell Substrate (Promega N205) was used. Assays were performed in solid, white, nonbinding surface (NBS) plates (Costar) and analyzed on a GLOMAX Discover Multimode Microplate Reader (Promega) collecting total luminescence using kinetic or end-

point reads, depending on the experiment. FIG. 52B displays the signal/background assay performance of formulation A over a two-week time course at ambient temps showing that this formulation is shelf-stable and displays an excellent dose response curve over the time tested. However, when furimazine is added (i.e. Formulation B), reduced shelf-stability is observed (FIG. 52C).

[0521] FIG. 53A displays the resulting lyophilized product for a single-reagent, IL-6 NanoTrip (tripartite NanoLuc) immunoassay using formulation C. This formula results in a very desirable cake that is intact and mobile from the glass sides without any fragmenting. FIG. 53B displays the signal/background assay performance of formulation C over a 3 month time course of storage at ambient temperatures showing that this formulation is shelf-stable and displays an excellent dose response curve that is unchanged over the time tested. FIG. 54 shows the kinetic profile of an IL-6 dose response of lyophilized formulation C post reconstitution in PBS containing 0.01% BSA.

[0522] To determine the lyophilized assay compatibility with complex human matrices, lyophilized cakes produced with formulation C were reconstituted in PBS (pH 7.0) containing 0.01% BSA. 50  $\mu$ l was added to wells of 96-well microtiter plates containing 50  $\mu$ l of rhIL-6 in 20% normal pooled human serum, citrate collected plasma, or urine. In all experiments, plates were incubated at room temperature for 90 minutes. Final concentration of the assay reagents in all experiments were 60 ng/ml SmTrip10-labeled antibody, 30 ng/ml SmTrip9-labeled antibody, 1  $\mu$ M LgTrip 3546, and 5  $\mu$ M furimazine. Luminescence was analyzed. FIG. 55 displays the signal/background results from these experiments indicating complex sample matrix compatibility with the single-reagent IL-6 NanoTrip immunoassay produced with formulation C.

#### Example 21

##### Lyophilized, Single-Reagent Tripartite Immunoassays in Pre-Filled, 96-Well Microtiter Plates

[0523] To evaluate the potential application of lyophilization for preservation of the entire IL-6 NanoTrip (tripartite NanoLuc) immunoassay directly into a 96-well microtiter plates, formulations containing 5 mM azothiothymine, 5 mM ascorbic acid, 2.5% pullulan w/v, 20 mM HEPES buffer (pH 8.0), 90 mM glycine, 20 mM histidine, 25 mg/ml sucrose, 0.01% polysorbate 80, 0.12 ug/ml clone 5IL6 antibody labeled with HaloTag-SmTrip9 Pep521 (SEQ ID NO: 16), 0.24 ug/ml 505E A12 A3 antibody labeled with HaloTag-SmTrip10 Pep289 (SEQ ID NO: 17), 4 pM LgTrip 3546 (SEQ ID NO: 12), and 100  $\mu$ M furimazine in ethanol (same as formulation C in the previous example, but with a 4 $\times$  reagent addition instead of a 20 $\times$  stock reagent as used in the vials) were used.

[0524] Approximately 25  $\mu$ l aliquots of 4 $\times$  stock solution was dispensed into 96-well microtiter plates. Two types of plates were used: non-binding surface (Costar 3600) and non-treated surface (Costar 3912). Plates were loaded into the lyophilizer (Virtis Genesis 12EL lyophilizer) with shelves pre-chilled to 4.7° C. Product then underwent a freezing step with a shelf temperature of -50° C. for 2 hr after when time the condenser step started. During the run, the condenser temperature ran between -5° C. and -87° C. A vacuum pull down ran next at the pressure set-points of 75 and 200 mTorr. Sublimation lasted ~7.5 hr, and desorption

lasted ~16.1 hr. At the end of the lyophilization process, the plates were back-filled with nitrogen and sealed with adhesive plate cover.

[0525] FIG. 56A depicts one of the plates with the lyophilized material in the bottom of the wells. The lyophilized cakes stayed in an intact cake, but were mobile when using the nonbinding surface plates. The lyophilized material stayed "stuck" on the bottom of the wells in the non-treated plates. FIG. 56B shows the resulting bioluminescence when 1 $\times$  rhIL-6 was added directly to the wells and analyzed for luminescence using a GLOMAX luminometer. The resulting dose response curve showed excellent reconstitution and performance in both plates.

#### Example 22

##### Testing the Effects of Individual Excipients in Formulations Using the Solution-Based, Homogeneous IL-6 Tripartite Immunoassay

[0526] To determine the effects of assay performance of individual excipients used in the lyophilized formulations for the single-reagent NanoTrip (tripartite NanoLuc) immunoassays, the IL-6 model system in the solution-based assay was used with the effects of various excipients analyzed. FIG. 57A displays the assay background signals for the solution-based homogenous IL-6 immunoassay performed in a standard assay buffer consisting of 0.01% BSA in PBS, pH 7.0, and with the addition of various individual excipients as indicated on the X-axis. FIG. 57B displays the IL-6 dose response curve when the assay was performed in different buffers consisting of formulation C from Example 20 and modified versions of formulation C. For these experiments, 30 ng/ml 5IL6 antibody labeled with HaloTag-SmTrip9 Pep521 (SEQ ID NO: 16), 60 ng/ml 505E A12 A3 antibody labeled with HaloTag-SmTrip10 Pep289 (SEQ ID NO: 17), and 1  $\mu$ M LgTrip 3546 (SEQ ID NO: 12) were incubated in the presence of rhIL-6 for 90 minutes. Furimazine (Promega Live Cell Substrate N205) was added according to manufacturer's instruction, but using the formulation indicated as buffer. Luminescent signal was analyzed using a GLOMAX luminometer. These experiments demonstrated that iterative experimentation is required to determine appropriate buffer components for NanoTrip immunoassays.

#### Example 23

##### Creating a Solution-Based and Lyophilized, Single-Reagent Tripartite Immunoassays in Vials for the Target Analyte Human Cardiac Troponin I

[0527] The basic principle of the homogeneous NanoTrip (NanoLuc tripartite) cardiac troponin I immunoassay is depicted in FIG. 58. First, a pair of antibodies that target non-overlapping epitopes on human cardiac troponin I were chemically conjugated to SmTrip9 (or variants thereof) or HiBiT (or variants thereof) using the HaloTag® technology. When the labeled antibodies bind a cardiac troponin I analyte, the complementary subunits are brought into proximity thereby reconstituting a bright luciferase in the presence of the LgTrip 3546 protein and furimazine substrate. This assay is quantitative because the amount of luminescence generated by a standard plate-reading luminometer is directly proportional to the amount of target analyte present.

**[0528]** Genetic fusions containing SmTrip9 Pep521 (SEQ ID NO: 16) or SmTriplO Pep289 (SEQ ID NO: 17) separated by either a 2 $\times$  or 3 $\times$  Gly-Ser-Ser-Gly linker to the amino terminus of HaloTag was achieved using the pFN29A HIS6HaloTag T7 Flexi Vector (Promega). Glycerol stocks of *E. coli* expressing HisTag-HaloTag fusion protein were used to inoculate 50 mL starter cultures, which were grown overnight at 37° C. in LB media containing 25  $\mu$ g/ml kanamycin. Starter cultures were diluted 1:100 into 500 mL fresh LB media, containing 25  $\mu$ g/mL kanamycin, 0.12% glucose, and 0.2% rhamnose. Cultures were grown for 22-24 h at 25° C. Cells were pelleted by centrifugation (10,000 rpm) for 30 min at 4° C. and re-suspended in 50 mL PBS. 1 mL protease inhibitor cocktail (Promega), 0.5 mL RQ1 DNase (Promega), and 0.5 mL of 10 mg/mL lysozyme (Sigma) were added, and the cell suspension was incubated on ice with mild agitation for 1 h. Cells were lysed by sonication at 15% power at 5 s intervals for 1.5 min (3 min total) and subsequently centrifuged at 10,000 rpm for 30 min at 4° C. Supernatant was collected, and protein purified using HisTag columns (GE) following the manufacturer's recommended protocol. Protein was eluted using 500 mM imidazole, dialyzed in PBS, characterized using SDS-PAGE gel and was >95% pure. Proteins were stored in 50% glycerol at -20° C.

**[0529]** To chemically conjugate the antibodies to the HaloTag-peptide fusion proteins, antibodies were buffered exchanged 2 $\times$  into 10 mM sodium bicarbonate buffer (pH 8.5) using Zeba spin desalting columns (ThermoFisher). Antibodies were then primed with 200 $\mu$ M amine reactive HaloTag Succinimidyl Ester (04) Ligand (Promega) for 2 hr shaking at 1000 rpm at 22° C. Unreacted ligand was removed with two passes through Zeba spin columns in PBS buffer. Then, antibodies were covalently labeled with 30  $\mu$ M of the HaloTag fusion protein overnight at 4° C. while shaking. Excess unreacted HaloTag fusion protein was removed using HaloLink Resin (Promega). Non-denaturing SDS-PAGE gel was used to characterize the conjugated antibodies. Anti-human cardiac troponin I monoclonal antibodies used in the human cardiac troponin I immunoassay were recombinant rabbit clone 1H11  $\mu$ L19 (Invitrogen) and monoclonal mouse antibody clone 16A11 (Invitrogen).

**[0530]** FIG. 59A (raw RLU) and 59B (signal/background) display the dose response curve for the solution-based homogenous cardiac troponin I immunoassay performed in a standard assay buffer consisting of 0.01% BSA in PBS, pH 7.0. Purified recombinant human cardiac troponin I (Fitzgerald) was used to generate the dose response curve. For these experiments, 2 ng/ml of clone 1H11  $\mu$ L19 labeled with HaloTag-24gly/ser-SmTrip9 Pep521 (SEQ ID NO: 16), 40 ng/ml of clone 16A11 labeled with HaloTag-8gly/ser-SmallTrip10 Pep289 (SEQ ID NO: 17), and 1  $\mu$ M LgTrip 3546 (SEQ ID NO: 12) protein were incubated in the presence of recombinant human cardiac troponin I for 90 minutes. Furimazine (Promega Live Cell Substrate N205) was added according to the manufacturer's instructions, but using 0.01% BSA in PBS as the buffer. Luminescent signal was analyzed on a GLOMAX luminometer.

**[0531]** To evaluate the potential application of lyophilization for preservation of the entire cardiac troponin I tripartite immunoassay in a single vial, formulations containing the peptide labeled antibodies (SmTrip9 Pep521 (SEQ ID NO: 16) and SmTriplO Pep289 (SEQ ID NO: 17)), LgTrip 3546

(SEQ ID NO: 12), and furimazine were prepared. The 20 $\times$  stock formulations are as follows:

**[0532]** Approximately, 5 mM azothiothymine, 5 mM ascorbic acid, 2.5% pullulan w/v, 20 mM HEPES buffer (pH 8.0), 90 mM glycine, 20 mM histidine, 25 mg/ml sucrose, 0.01% polysorbate 80, 0.08 ug/ml clone 1H11  $\mu$ L19 antibody labeled with HaloTag-SmTrip9 Pep521 (SEQ ID NO: 16), 1.6 ug/ml of clone 16A11 antibody labeled with HaloTag-SmTriplO Pep289 (SEQ ID NO: 17), 20  $\mu$ M LgTrip 3546 (SEQ ID NO: 12), and 200  $\mu$ M furimazine (Promega NANOGLO substrate N113).

**[0533]** One mL aliquots of 20 $\times$  stock solution were dispensed into 10 mL amber glass vials, and a runner stopper was partially inserted into the vial. Vials were loaded into the lyophilizer (Virtis Genesis 12EL lyophilizer) with shelves pre-chilled to 4.7° C. Product then underwent a freezing step with a shelf temperature of -50° C. for 2 hr after which time the condenser step started. During the run, the condenser temperature ran between -5° C. and -87° C. A vacuum pull down ran next at the pressure set-points of 75 and 200 mTorr. Sublimation lasted ~7.5 hr, and desorption lasted ~16.1 hr. At the end of the lyophilization process, the vials were back-filled with nitrogen and sealed with fully inserted stoppers at -600 Torr of pressure.

**[0534]** For activity-based assays, single-reagent cakes were reconstituted with 10 mL of PBS containing 0.01% BSA. The vials were shaken manually and allowed to equilibrate at room temperature for 5 minutes. 50 1  $\mu$ l of the reconstituted single-reagent cardiac troponin I NanoTrip (tripartite NanoLuc) immunoassay was added to 50  $\mu$ l of recombinant human cardiac troponin I (Fitzgerald) that was reconstituted in the same BSA buffer or with 20% human serum diluted in General Serum Diluent (Immunochemistry Technologies). Assays were performed in solid, white, non-binding surface (NBS) plates (Costar) and analyzed on a GLOMAX Discover Multimode Microplate Reader (Promega) collecting total luminescence using an endpoint read. FIG. 60 shows the cardiac troponin I dose response curve of the resulting bioluminescence upon reconstitution of the single-reagent troponin NanoTrip immunoassay with the sample in 0.01% BSA in PBS buffer or in the presence of the complex matrix sample of human serum diluted in General Serum Diluent. Troponin was effectively detected even in the presence of serum using this immunoassay.

#### Example 24

##### Investigating and Mitigating the Effects of Complex Sample Matrices on Tripartite Immunoassay Performance

**[0535]** A solution-based, homogeneous IL-6 NanoTrip (tripartite NanoLuc) immunoassay was tested to determine if the assay was compatible with human sample types commonly analyzed for clinical biomarkers, and factors in the samples that might affect the performance of the assay and possible solutions to mitigate these effects were investigated. This is critical because sample matrix interference effects in immunoassays, defined as the effect of a substance present in the sample that alters the correct value of the result, are a common phenomenon especially in homogeneous formats due to the removal of the wash steps.

**[0536]** Reagents used for the following experiments were the HaloTag-peptide labeled antibodies described in Example 19. 30 ng/ml clone 5IL6 antibody labeled with HaloTag-SmTrip9 Pep521 (SEQ ID NO: 16), 60 ng/ml 505E

A12 A3 antibody labeled with HaloTag-SmTriplO Pep289 (SEQ ID NO: 17), 1  $\mu$ M LgTrip 3546 (SEQ ID NO: 12), and NANOGLO Live Cell Substrate (Promega N205) or NANOGLO substrate (Promega N113), which were used according to the manufacturer's instructions, but were diluted in the given buffer for that experiment. Assays were performed +/- 50 ng/ml recombinant human IL-6 (R&D Systems) with assay backgrounds, and Bmax analyzed. Assays were allowed to incubate on the bench for 90 minutes prior to addition of substrate. Assays were performed in solid, white, nonbinding surface (NBS) plates (Costar) and analyzed on a GLOMAX Discover Multimode Microplate Reader (Promega) collecting total luminescence using an endpoint read.

[0537] FIG. 61 shows the solution-based, homogeneous IL-6 NanoTrip (tripartite NanoLuc) assay background in the presence of increasing normal, pooled human serum when the assay was performed in (A) 0.01% BSA in PBS (pH 7.0) assay buffer or (B) in General Serum Diluent (Immunochemistry Technologies) and using NANOGLO Live Cell Substrate (Promega N205). General Serum Diluent mitigated non-specific IgG effects and had a positive effect by decreasing the assay background. FIG. 62 shows the bioluminescent response when in the presence of 50 ng/ml rhIL-6 and increasing human serum when the assay was performed in (A) 0.01% BSA in PBS (pH 7.0) assay buffer or (B) General Serum Diluent and using NANOGLO Live Cell Substrate (Promega N205). General Serum Diluent displayed a slightly lower Bmax overall, but less of a loss in signal with increasing human serum. FIG. 63A-D shows the fold response of results when the rhIL-6 screening assays were performed with 0.01% BSA in PBS (pH 7.0) or General Serum Diluent and using NANOGLO Live Cell Substrate (Promega N205) or NANOGLO substrate (Promega N113) and testing in increasing amounts of normal, pooled human serum or plasma. Overall, using General Serum Diluent paired with the NANOGLO Live Cell Substrate (Promega N205) provided the best assay results in these complex sample matrices.

[0538] Next, the effects of endogenous IgG in human serum samples had on assay performance was determined. Using the solution-based, homogeneous IL-6 NanoTrip assay +/- 50 ng/ml rhIL-6 in General Serum Diluent, the bioluminescent response when running the assay in normal, pooled human serum or in serum that had been depleted of endogenous IgG was analyzed. FIG. 64 shows the fold response of this experiment, which indicates that endogenous IgG is one of the components in serum that negatively effects the performance of the immunoassay.

[0539] Next, the effects of blood biochemistry on the solution-based, homogenous IL-6 tripartite immunoassay was investigated using the VeriChem reference plus chemistry kit, which contains the following:

Analyte	Units	Level A	Level B	Level C	Level D	Level E
Glucose	mg/dL	5	40	75	110	145
Urea	mg/dL	1.0	7.5	14.0	20.5	27.0
Nitrogen						
Creatinine	mg/dL	0.04	1.24	2.44	3.64	4.84
Calcium	mg/dL	1.0	1.5	2.0	2.5	3.0
Phosphorus	mg/dL	0.2	0.7	1.2	1.7	2.2
Magnesium	mg/dL	0.16	0.46	0.76	1.06	1.36
Magnesium	mEq/L	0.132	0.38	0.63	0.87	1.12
Triglyceride	mg/dL	2	49	240	143	190

[0540] The IL-6 NanoTrip assay was run in the presence of Level A-E diluted in general serum diluent and using NANOGLO Live Cell Substrate (Promega N205) to determine the effects of increasing these blood chemistry components on assay performance. FIG. 65A shows the assay background in raw RLUs, FIG. 65B shows the Bmax signal when in the presence of 50 ng/ml rhIL-6, and FIG. 65C shows the signal over background results. The results indicate that increasing these chemistry components had an effect on increasing assay background as well as decreasing the Bmax impacting the overall signal to background of the assay performance.

[0541] To determine the effects of urine on the solution-based, homogeneous IL-6 NanoTrip immunoassay performance, a IL-6 screening assay in the presence of increasing normal, pooled human urine diluted in General Serum Diluent and NANOGLO substrate (Promega Ni13) or NANOGLO Live Cell Substrate (Promega N205) was performed. FIG. 66A shows the assay background in raw RLUs, FIG. 66B shows the Bmax signal when in the presence of 50 ng/ml rhIL-6, and FIG. 66C shows the signal over background results. The results indicate that the IL-6 NanoTrip immunoassay was compatible with human urine when using the General Serum Diluent paired with the NANOGLO Live Cell Substrate (Promega N205).

#### Example 25

##### Creating a Stable, Lyophilized Substrate and LgTrip Cake Reagent in a Single Vial

[0542] To evaluate the potential application of lyophilization for preservation of furimazine, LgTrip and furimazine were paired with LgTrip 3546 used as a general detection reagent for tripartite applications and supplied in a single vial. Formulations containing furimazine, LgTrip 3546 (SEQ ID NO: 12), and furimazine with LgTrip 3546 were prepared. The 20x stock formulations are as follows:

[0543] Furimazine only formulation: 5 mM azothiothymine, 5 mM ascorbic acid, 2.75% pullulan w/v, 200  $\mu$ M furimazine in ethanol, and ddH<sub>2</sub>O millipore

[0544] LgTrip 3546 only formulation: 5 mM azothiothymine, 5 mM ascorbic acid, 2.75% pullulan w/v, 20  $\mu$ M LgTrip 3546 (SEQ ID NO: 12), and ddH<sub>2</sub>O (Millipore)

[0545] Furimazine with LgTrip 3546 formulation: 5 mM azothiothymine, 5 mM ascorbic acid, 2.75% pullulan w/v, 200  $\mu$ M furimazine in ethanol, 20  $\mu$ M LgTrip 3546 (SEQ ID NO: 12) and ddH<sub>2</sub>O (Millipore).

[0546] One mL aliquots of 20x stock solution was dispensed into 10 mL amber glass vials, and a rubber stopper was partially inserted into the vial. Vials were loaded into the lyophilizer (Virtis Genesis 12EL lyophilizer) with shelves pre-chilled to 4.7° C. Product then underwent a freezing step with a shelf temperature of -50° C. for 2 hr after which time the condenser step started. During the run, the condenser temperature ran between -5° C. and -87° C. A vacuum pull down ran next at the pressure set-points of 75 and 200 mTorr. Sublimation lasted ~7.5 hr and desorption lasted ~16.1 hr. At the end of the lyophilization process, the vials were back-filled with nitrogen and sealed with fully inserted stoppers at -600 Torr of pressure.

[0547] Vials were stored at 25° C. or 60° C. and tested at various time points post-lyophilization. For activity-based assays, lyophilized cakes were reconstituted with 10 mL of PBS containing 0.01% BSA. The vials were shaken manu-

ally and allowed to equilibrate at room temperature for 5 minutes. 50  $\mu$ l of the reconstituted substrate was added to 50  $\mu$ l of purified NANOLUC enzyme (Promega) or dipeptide (SEQ ID NO: 14) that was reconstituted in the same BSA buffer. LgTrip 3546 only formulations required the addition of furimazine in which NANOGLO Live Cell Substrate (Promega N205) was used. Assays were performed in solid, white, nonbinding surface (NBS) plates (Costar) and analyzed on a GLOMAX Discover Multimode Microplate Reader (Promega) collecting total luminescence using an endpoint read. FIG. 67 displays the Bmax signal produced for (A) furimazine only formulation when in the presence of NanoLuc, (B) LgTrip 3546 only formulation when in the presence of the dipeptide, and (C) furimazine with LgTrip 3546 formulation when in the presence of dipeptide. All formulations displayed thermal stability at all temperatures tested for the 100 day duration of the storage conditions, as opposed to the N205 substrate which is predissolved in organic solvent.

#### Example 26

**Creating a Solution-Based and Lyophilized, Single-Reagent Tripartite Immunoassays in Vials for the Target Analytes Anti-TNF $\alpha$  Biologics**

**[0548]** The basic principle of the homogeneous anti-TNF $\alpha$  biologics NanoTrip (tripartite NanoLuc) immunoassay is depicted in FIG. 68. In this model, protein G-SmTrip9 (or variants thereof) fusion proteins and TNF $\alpha$ -HiBiT (or variants thereof) fusion proteins were used. Protein G will bind the Fc region of the anti-TNF $\alpha$  biologic antibody analyte, and the analyte itself will bind the TNF $\alpha$  thus bringing the complementary subunits into proximity, thereby reconstituting a bright luciferase in the presence of the LgTrip 3546 protein and furimazine substrate. This assay is quantitative because the amount of luminescence generated by a standard plate-reading luminometer is directly proportional to the amount of target analyte present.

**[0549]** 6xHis-TNF $\alpha$ -15GS-HiBiT (ATG-3998). Genetic fusions containing the SmTrip10 (SEQ ID NO: 15) separated by a 15GS linker (SSSGGGGSGGGSSGG) to the carboxyl-terminus of TNF $\alpha$  was achieved using the pF4Ag CMV Flexi Vector (Promega). Purified plasmid DNA of the TNF $\alpha$ -strand 10 fusion was transformed into Shuffle T7 *E. coli* K12 (New England Biolabs) and plated at a 1:100 dilution on an LB plate containing 100 g/ml ampicillin and incubated overnight at 37° C. A colony from this plate was used to inoculate 50 mL starter cultures, which were grown overnight at 37° C. in LB media containing 100 g/ml ampicillin. Starter cultures were diluted 1:100 into 500 mL fresh LB media containing 100 g/ml ampicillin and were incubated at 37° C. until it reached an OD of 0.6, at which time a final concentration of 1 mM IPTG was added to the sample. After IPTG inoculation, cultures were grown overnight at 25° C. Cells were pelleted by centrifugation (10,000 rpm) for 30 min at 4° C. and re-suspended in 50 mL TBS, 1 mL protease inhibitor cocktail (Promega), 0.5 mL RQ1 DNase (Promega), and 1 mL of 10 mg/mL lysozyme (Sigma), and the cell suspension was incubated on ice with mild agitation for 1 h. Cells were lysed by three freeze-thaw cycles from -80° C. freezer to a 37° C. water bath and subsequently centrifuged at 10,000 rpm for 30 min at 4° C. Supernatant was collected and protein was purified using Ni Sepharose 6 Fast Flow resin (GE), following manufacturer's

recommended protocol. Protein was eluted using a step-wise imidazole elution starting at 100 mM imidazole and reaching up to 500 mM imidazole, dialyzed in TBS, characterized using SDS-PAGE gel and was >95% pure. Proteins were stored in 50% glycerol at -20° C.

**[0550]** SmTrip9(521)-15GS-PtnG-6xHis (ATG4002). Genetic fusions containing the SmTrip9 (SEQ ID NO: 13) separated by a linker (GSSGGGGSGGGSSGG) to the amino terminus of Protein G was achieved using the pF1A T7 Flexi Vector (Promega). Glycerol stocks of *E. coli* expressing SmTrip9(521)-PtnG fusion protein was used to inoculate 50 mL starter cultures, which were grown overnight at 37° C. in LB media containing 100 g/ml ampicillin. Starter cultures were diluted 1:100 into 500 mL fresh LB media, containing 100 g/mL ampicillin, 0.15% glucose, and 0.1% rhamnose. Cultures were grown for 16-24 h at 25° C. Cells were pelleted by centrifugation (10,000 rpm) for 30 min at 4° C. and re-suspended in 50 mL TBS. 1 mL protease inhibitor cocktail (Promega), 0.5 mL RQ1 DNase (Promega), and 1 mL of 10 mg/mL lysozyme (Sigma) were added, and the cell suspension was incubated on ice with mild agitation for 1 h. Cells were lysed by three freeze-thaw cycles from -80° C. freezer to a 37° C. water bath and subsequently centrifuged at 10,000 rpm for 30 min at 4° C. Supernatant was collected and protein purified using HisTag columns (GE), following manufacturer's recommended protocol. Protein was eluted using gradient elution with a 500 mM imidazole final concentration, dialyzed in TBS, characterized using SDS-PAGE gel and was >95% pure. Proteins were stored in 50% glycerol at -20° C.

**[0551]** FIG. 69 displays the dose response curves for the solution-based homogenous anti-TNF $\alpha$  biologics immunoassay performed in a standard assay buffer consisting of 0.01% BSA in PBS, pH 7.0. For these experiments, 10 nM of protein G-15gly/ser-SmTrip9 Pep521 (SEQ ID NO: 16), 10 nM TNF $\alpha$ -15 gly/ser-SmTrip10 Pep289 (SEQ ID NO: 17), and 1  $\mu$ M LgTrip 3546 (SEQ ID NO: 12) protein were incubated in the presence of (A) Remicade, (B) Humira, and (C) Enbrel for 90 minutes. Furimazine (NANOGLO Live Cell Substrate; Promega N205) was added, and total luminescence signal was analyzed using a GLOMAX Discover.

**[0552]** To evaluate the potential application of lyophilization for preservation of the entire anti-TNF $\alpha$ /TNF $\alpha$  biologics, NanoTrip and NanoBiT immunoassays in single vial formulations containing peptide-labeled fusion proteins and LgTrip 3546 (SEQ ID NO: 12; for NanoTrip assays) and furimazine were prepared. The 20x stock formulations are as follows:

**[0553]** NanoTrip anti-TNF $\alpha$  biologics immunoassay: 5 mM azothiothymine, 5 mM ascorbic acid, 2.75% w/v pullulan, ddH2O (Millipore), 200  $\mu$ M furimazine in ethanol, 200  $\mu$ M LgTrip 3546 protein (SEQ ID NO:12), 200 nM protein G-SmTrip9 Pep521 (SEQ ID NO: 16) fusion protein, and 200 nM TNF $\alpha$ -SmTrip10 Pep289 (SEQ ID NO:17) fusion protein.

**[0554]** NanoBiT anti-TNF $\alpha$  biologics immunoassay: 5 mM azothiothymine, 5 mM ascorbic acid, 2.75% w/v pullulan, ddH2O (Millipore), 200  $\mu$ M furimazine in ethanol, 200 nM protein G-SmBiT (SEQ ID NO:10) fusion protein, and 200 nM TNF $\alpha$ -LgBiT (SEQ ID NO: 12) fusion protein.

**[0555]** One mL aliquots of 20x stock solution was dispensed into 10 mL amber glass vials, and a rubber stopper was partially inserted into the vial. Vials were loaded into the lyophilizer (Virtis Genesis 12EL lyophilizer) with shelves

pre-chilled to 4.7° C. Product then underwent a freezing step with a shelf temperature of -50° C. for 2 hr after which time the condenser step started. During the run, the condenser temperature ran between -5° C. and -87° C. A vacuum pull down ran next at the pressure set-points of 75 and 200 mTorr. Sublimation lasted ~7.5 hr and desorption lasted ~16.1 hr. At the end of the lyophilization process, the vials were back-filled with nitrogen and sealed with fully inserted stoppers at -600 Torr of pressure.

[0556] For activity-based assays, single-reagent cakes were reconstituted with 10 mL of PBS containing 0.01% BSA. The vials were shaken manually and allowed to equilibrate at room temperature for 5 minutes. 50 µl of the reconstituted single-reagent anti-TNF $\alpha$  biologics NanoTrip and NanoBiT immunoassays were added to 50 µl of Remicade in a titration that was reconstituted in the same BSA buffer. Assays were performed in solid, white, nonbinding surface (NBS) plates (Costar) and analyzed on a GLOMAX Discover Multimode Microplate Reader (Promega) collecting total luminescence using a kinetic read. FIG. 70 shows the Remicade dose response curves of the resulting bioluminescence upon reconstitution of the single-reagent Remicade (A) NanoTrip immunoassay or (B) NanoBiT immunoassay.

[0557] Testing the thermal stability of these lyophilized, single-reagent anti-TNF $\alpha$  biologics NanoTrip and NanoBiT immunoassays when stored at ambient temperatures indicated that both assays, when reconstituted in 0.01% BSA in PBS (pH 7.0) in the presence or absence of 100 nM Remicade, displayed shelf stability and a significant increase in signal when the analyte Remicade is present. Results are shown in FIG. 71.

#### Example 27

##### Developing Stable, Lyophilized Tripartite and NanoBiT Immunoassay Using a Split-Reagent Approach

[0558] To evaluate the potential application of lyophilization for preservation of separate components of the anti-TNF $\alpha$  biologics, NanoTrip and NanoBiT immunoassays that are then combined in a single vial formulations containing the peptide labeled fusion proteins and LgTrip 3546 (SEQ ID NO: 12; for NanoTrip assays) and furimazine were prepared. The 20x stock formulations are as follows:

[0559] NanoBiT anti-TNF $\alpha$  biologics immunoassay:

[0560] Furimazine with LgBiT-TNF $\alpha$ : 5 mM azothiostymine, 5 mM ascorbic acid, 2.75% w/v pullulan, ddH<sub>2</sub>O (Millipore), 200 µM furimazine in ethanol, and 200 nM TNF $\alpha$ -LgBiT (SEQ ID NO: 12) fusion protein.

[0561] NanoBiT protein G: 5 mM azothiostymine, 5 mM ascorbic acid, 2.75% w/v pullulan, ddH<sub>2</sub>O millipore, 200 nM protein G-SmBiT (SEQ ID NO: 10) fusion protein

[0562] NanoTrip anti-TNF $\alpha$  biologics immunoassay:

[0563] Furimazine with LgTrip 3546: 5 mM azothiostymine, 5 mM ascorbic acid, 2.75% w/v pullulan, ddH<sub>2</sub>O (Millipore), 200 µM furimazine in ethanol, 20 µM LgTrip 3546 protein (SEQ ID NO: 12).

[0564] Protein G with TNF $\alpha$ : 5 mM azothiostymine, 5 mM ascorbic acid, 2.75% w/v pullulan, ddH<sub>2</sub>O (Millipore), 200 nM protein G-SmTrip9 Pep521 (SEQ ID NO: 16) fusion protein, and 200 nM TNF $\alpha$ -SmTrip10 Pep289 (SEQ ID NO: 17) fusion protein.

[0565] Formulations were lyophilized as separate components then manually combined to create the complete immu-

noassay. Cakes were reconstituted with Opti-MEM (Gibco), and 50 µl added to 50 µl of Remicade in a dose titration. Assays were performed in solid, white, nonbinding surface (NBS) plates (Costar) and analyzed on a GLOMAX Discover Multimode Microplate Reader (Promega) collecting total luminescence using a kinetic read. FIG. 72 displays the process and assay results for the NanoBiT anti-TNF $\alpha$  biologics "split-cake" lyophilized immunoassay. FIG. 72A depicts the independent lyophilized products. FIG. 72B depicts the results after manually combining the two separate cakes into one microcentrifuge tube. FIG. 72C depicts the lyophilized products after reconstitution with Opti-MEM buffer. FIG. 72D displays the kinetic bioluminescence results when in the presence of increasing amounts of Remicade. FIG. 73 displays the kinetic bioluminescence results for the anti-TNF $\alpha$  biologics NanoTrip assay using a kinetic read for bioluminescence in the presence of Remicade after following the same process laid out in FIG. 72. The dual cake format also created a successful immunoassay for Remicade.

#### Example 28

##### Developing a Cell-Based, Homogeneous Tripartite Assay for the Quantitation of Anti-EGFR Biologics

[0566] A bulk transfection was performed on HEK293 cells by preparing a 10 g/ml solution of DNA with a 1:10 dilution of IL6-VSHiBiT-15GS-EGFR (GSSGGGGSGGGGSS) (ATG-4288) and pGEM3Z carrier DNA (Promega). FuGENE HD was added to the DNA mixture to form a lipid:DNA complex. This complex was added to HEK293 cells with an adjusted cell density of 2×10<sup>5</sup> cells/ml and incubated at 37° C. and 5% CO<sub>2</sub> overnight.

[0567] Transfected HEK293 cells were added to 96-well NBS plates (a separate plate for each SmTrip-15GS-G being tested) at a final concentration of 2×10<sup>5</sup> cells/well. A reagent mixture of LgTrip 3546 and SmTrip9-G was added to the cells at a final concentration of 1 µM LgTrip 3546 and 10 nM SmTrip9-15GS-G. A 24-point panitumumab titration was added to each well with a final starting concentration of 100 nM and diluted 1:2 with a final ending concentration of 0 nM. All plates were covered and incubated for an hour at 37° C. and 5% CO<sub>2</sub>. NANOLUC Live Cell Substrate was added to all wells at a final concentration of 10 µM, and luminescence of each plate was subsequently read on a luminometer. The following SmTrip9-G constructs were tested: ATG4002 SmTrip9(521)-15GS-G (SEQ ID NO: 724); ATG4496 SmTrip9(743)-15GS-G (SEQ ID NO: 726); ATG4558 SmTrip9(759)-15GS-G (SEQ ID NO: 728); and ATG4551 SmTrip9(760)-15GS-G (SEQ ID NO: 730). Each configuration was successful in quantitatively detecting panitumumab.

#### Example 29

##### Testing Various SmTrip9-Protein G Fusion Proteins in Solution-Based, Homogeneous Anti-TNF $\alpha$ Biologics Tripartite Immunoassays

[0568] FIG. 77 displays the dose response curves for the solution-based homogenous anti-TNF $\alpha$  biologics immunoassay using SmTrip9 variants SmTrip9 pep521 (SEQ ID NO: 16), SmTrip9 pep743 (SEQ ID NO: 21), SmTrip9 pep759 (SEQ ID NO: 22), or SmTrip 9 pep760 (SEQ ID

NO: 23) in a standard assay buffer consisting of 0.01% BSA in PBS, pH 7.0. For these experiments, 10 nM of protein G-15gly/ser-SmTrip9 variant, 10 nM TNF $\alpha$ -15 gly/ser-SmTripO Pep289 (SEQ ID NO: 17), and 1  $\mu$ M LgTrip 3546 (SEQ ID NO: 12) protein were incubated in the presence of Remicade for 90 minutes. Furimazine (NANOGLO Live Cell Substrate; Promega N205) was added, and total luminescence signal was analyzed using a GLOMAX Discover. All of the SmTrip9 variants were successful in the assay detecting Remicade, albeit with different levels of background and Bmax.

[0569] To evaluate the potential application of lyophilization for preservation of the entire anti-TNF $\alpha$  biologics, NanoTrip immunoassays in single vial formulations containing peptide-labeled fusion proteins and LgTrip 3546 (SEQ ID NO: 12) and furimazine were prepared. The 20x stock formulations are as follows:

[0570] NanoTrip anti-TNF $\alpha$  biologics immunoassay: 5 mM azothiothymine, 5 mM ascorbic acid, 2.75% w/v pullulan, ddH<sub>2</sub>O (Millipore), 200  $\mu$ M furimazine in ethanol, 20  $\mu$ M LgTrip 3546 protein (SEQ ID NO: 12), 200 nM protein G-SmTrip9 variant fusion protein, and 200 nM TNF $\alpha$ -SmTripO Pep289 (SEQ ID NO: 17) fusion protein.

[0571] One mL aliquots of 20x stock solution was dispensed into 10 mL amber glass vials, and a rubber stopper was partially inserted into the vial. Vials were loaded into the lyophilizer (Virtis Genesis 12EL lyophilizer) with shelves pre-chilled to 4.7° C. Product then underwent a freezing step with a shelf temperature of -50° C. for 2 hr after which time the condenser step started. During the run, the condenser temperature ran between -5° C. and -87° C. A vacuum pull down ran next at the pressure set-points of 75 and 200 mTorr. Sublimation lasted ~7.5 hr and desorption lasted ~16.1 hr. At the end of the lyophilization process, the vials were back-filled with nitrogen and sealed with fully inserted stoppers at -600 Torr of pressure. FIG. 77B provides the dose response curve for Remicade using the lyophilized anti-TNF $\alpha$  biologics immunoassay.

### Example 30

#### Direct-Labeling of Antibodies Via Reactive Peptides for Development of Solution-Based, Homogenous IL-6 Immunoassays

[0572] The basic principle of homogeneous NanoLuc tripartite immunoassays with directly-labeled antibodies is depicted in FIG. 78. First, a pair of antibodies that target non-overlapping epitopes on IL-6 are chemically conjugated to SmTrip9 or SmTrip10-based reactive peptides. When the labeled antibodies bind IL-6 analyte, the complementary subunits are brought into proximity, thereby reconstituting a bright luciferase that produces a bioluminescent signal in the presence of the LgTrip protein and furimazine substrate. The amount of luminescence generated by this assay configuration is directly proportional to the amount of target analyte.

[0573] SmTrip9 variants such as Pep693 (SEQ ID NO: 20), Pep895 (SEQ ID NO: 24), and Pep929 (SEQ ID NO: 25) or SmTripO variants such as Pep691 (SEQ ID NO: 18) and Pep692 (SEQ ID NO: 19) were individually dissolved in DMF to 5 mM. Antibodies were buffered exchanged 2x into 10 mM sodium bicarbonate buffer (pH 8.5) using Zeba spin desalting columns (ThermoFisher). Subsequently, these antibodies were combined with 20x molar excess of a reactive peptide for 1 hr at 4° C. while shaking in order to

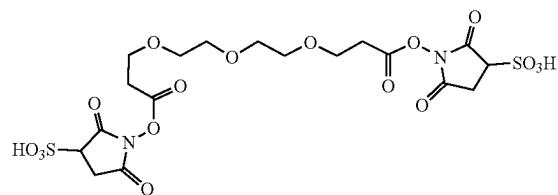
covalently label the proteins. Unreacted label was removed with two passes through Zeba spin columns in PBS buffer. To create the reagents for the exemplary human IL-6 immunoassay, the mouse anti-human IL-6 monoclonal antibodies clone 5IL6 (Thermo cat #M620) and clone 505E 9A12 A3 (Thermo cat #AHC0662) were used. SmTrip9 reactive peptides were used to label antibody 5IL6 while SmTripO reactive peptides were used to label antibody 505E. The denaturing SDS-PAGE gel shown in FIG. 79 was used to characterize the conjugated antibodies. The gel revealed that the degree of antibody labeling was dependent on the peptide sequence and chemical structure of the label.

[0574] FIGS. 80-82 display raw RLU dose response curves for antibody conjugates in the presence of a rhIL-6 titration series. For these experiments, rhIL-6 and antibody conjugates were incubated for 90 minutes with 1  $\mu$ M LgTrip 3546 (SEQ ID NO: 12) in PBS (pH 7.0) with 0.01% BSA. After addition of N205, luminescence signal was measured. Data in FIG. 80 were generated using 15 ng/ml of SmTrip9-labeled variant (HW-0984 or HW-1010) 5IL6 antibody and 60 ng/ml of SmTrip10-labeled variant (HW-0977) 505E antibody. Data in FIG. 81 were generated using 62.5 ng/ml of SmTrip9-labeled (HW-0984) 5IL6 antibody and 60 ng/ml of SmTrip10-labeled (HW-1053) 505E antibody. Data in FIG. 82 were generated using the following concentrations of antibody conjugates: 15 ng/ml HW-1043 (SEQ ID NO: 24)+30 ng/ml HW-1053 (SEQ ID NO: 18), 15 ng/ml HW-1052 (SEQ ID NO: 25)+15 ng/ml HW-1053, (SEQ ID NO: 18) 15 ng/ml HW-1055 (SEQ ID NO: 25)+15 ng/ml HW-1053 (SEQ ID NO: 18), 60 ng/ml HW-1042 (SEQ ID NO: 20)+8 ng/ml HW-1053 (SEQ ID NO: 18), and 60 ng/ml HW-1050 (SEQ ID NO: 27)+8 ng/ml HW-1053 (SEQ ID NO: 18). In this experiment, SmTrip9 variant labels HW-1050 (SEQ ID NO: 27) and HW-1043 (SEQ ID NO: 24) gave the best signal to background displaying close to 10<sup>6</sup> RLUs in the presence of high rhIL-6 concentrations and low light output in the absence of the analyte. In contrast, SmTrip9 variant labels HW-1055 (SEQ ID NO: 25 (SulfoSE-PEG3)) and HW-1052 (SEQ ID NO: 25 (SulfoSE-PEG6)) had high signal even in the absence of rhIL-6 suggesting these labels spontaneously assemble into the reconstituted luciferase. FIG. 83 displays light output from titration of individual antibody conjugates in PBS (pH 7.0) with 0.01% BSA, 1  $\mu$ M LgTrip 3546 (SEQ ID NO: 12), and N205. Most conjugates show RLUs equivalent to furimazine background (~100 RLU), and no increase in RLU with increasing concentration of labeled antibodies. Conjugates HW-0984 (SEQ ID NO: 20) and HW-1053 (SEQ ID NO: 19) were exceptions, generating increasing RLUs with concentration and reaching over 1,000 at concentrations above 100 ng/ml. In FIG. 84, two SmTrip9 conjugates with high S/B (labeled with HW-1050 (SEQ ID NO: 27) and HW-1043 (SEQ ID NO: 24)) were assayed under conditions described for FIG. 82, but with 1  $\mu$ M LgTrip 5146 (SEQ ID NO: 451), producing results similar to LgTrip 3546 (SEQ ID NO: 12), demonstrating the feasibility of using different LgTrp variants to construct these assays.

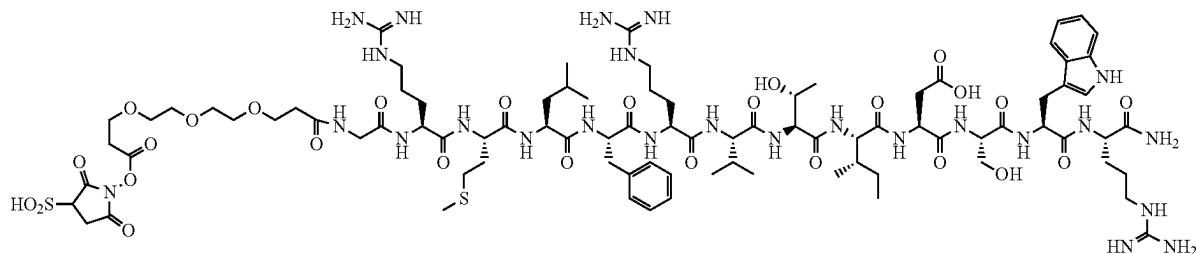
[0575] Components for homogeneous tripartite NanoLuc immunoassays can also be constructed by direct-labeling antibodies with SmTrip9 or SmTrip10 variants that contain a fluorophore such as tetramethylrhodamine (TMR). This is depicted schematically in FIG. 85 including the expected BRET from the luciferase to the fluorophore labels. Kinetic reads for BRET with labels HW-0987 (SmTrip9 variants with TMR) and HW-0992 (SmTripO variants with TMR) in the IL-6 immunoassay are shown in FIG. 86. BRET was observed only in the presence of rhIL-6 analyte demonstrating the complementation and energy transfer are occurring when the analyte brings these components together.

## Example 31

SulfoSE-PEG3-SmTrip9 Pep693 (HW-0984)

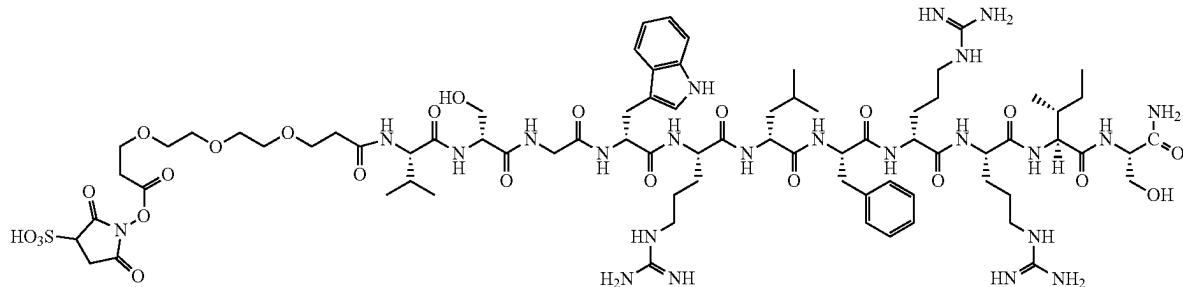


**[0576]** 3,3'-(oxybis(ethane-2,1-diyl))bis(oxy)dipropionic acid (55 mg, 0.22 mmol) was dissolved in anhydrous DMF, and then diisopropylethylamine (120 mg, 0.88 mmol) and HATU (176 mg, 0.45 mmol) added. The mixture was stirred for five minutes. Meanwhile, N-hydroxy-2,5-dioxopyrrolidine-3-sulfonic acid (90 mg, 0.46 mmol) was dissolved in 5 ml DMSO and then added to the previous solution dropwise. The mixture was stirred for another hour until LC-MS shows disappearance of acid. The solution was directly used in the next step. Calculated: m/z=603.05 [M<sup>+</sup>]; measured (ESI): m/z=603.04 [M<sup>+</sup>].



SulfoSE-PEG3-SmTrip9 Pep693 (HW-0984)

**[0577]** SmTrip9 Pep693 (GRMLFRVTINSWR, 27 mg, 0.045 mmol) was dissolved in DMF. The solution was then added to the previous PEG3 bis Sulfo-SE solution. The mixture was then stirred for another hour and directly purified by preparative HPLC. Calculated: m/z=1022.98 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1023.09 [M+2H]<sup>2+</sup>.



SulfoSE-PEG3-SmTrip10 Pep691 (HW-0977)

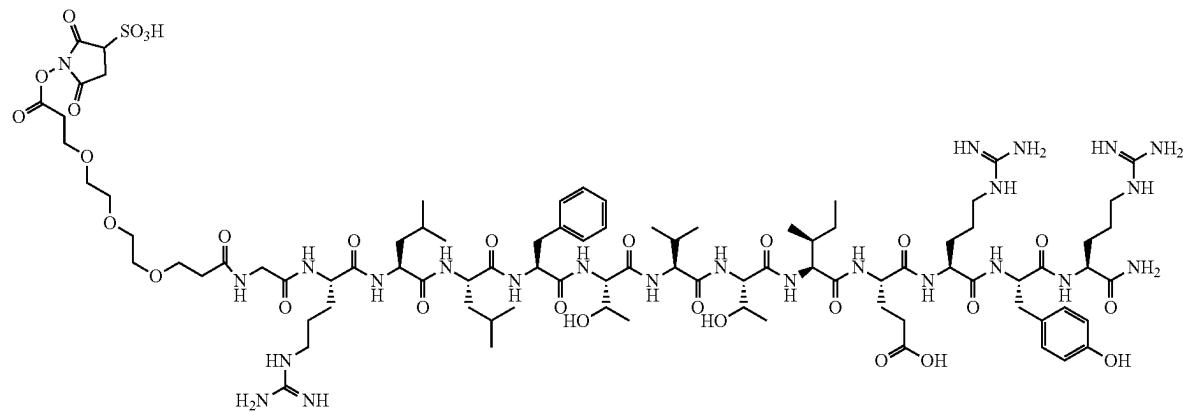
## Example 32

SulfoSE-PEG3-SmTriplO Pep691 (HW-0977)

**[0578]** HW-0977 was synthesized by the same method as HW-0984. Calculated: m/z=892.93 [M+2H]<sup>2+</sup>; measured (ESI): m/z=893.61 [M+2H]<sup>2+</sup>.

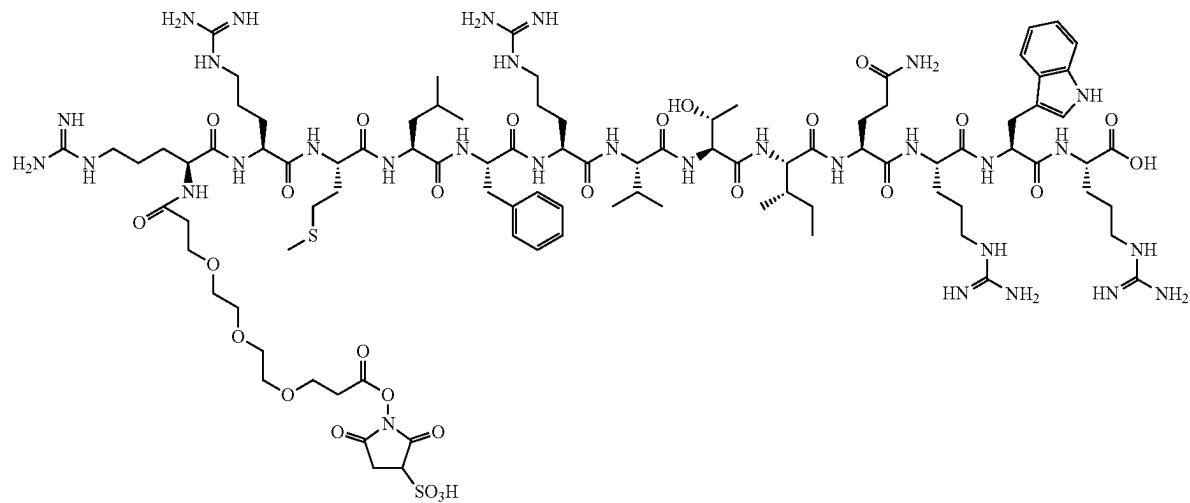
## Example 33

SulfoSE-PEG3-SmTrip9 Pep895 (HW-1010)



**[0579]** HW-1010 was synthesized by the same method as HW-0984. Calculated: m/z=1016.51 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1016.92 [M+2H]<sup>2+</sup>.

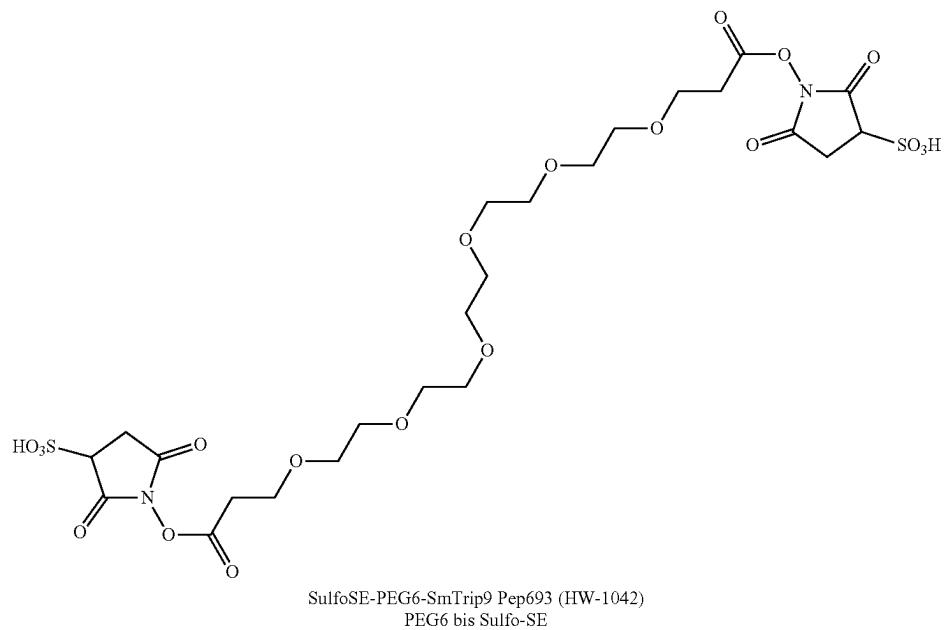
## Example 34



SulfoSE-PEG3-SmTrip9 Pep929 (HW-1055)

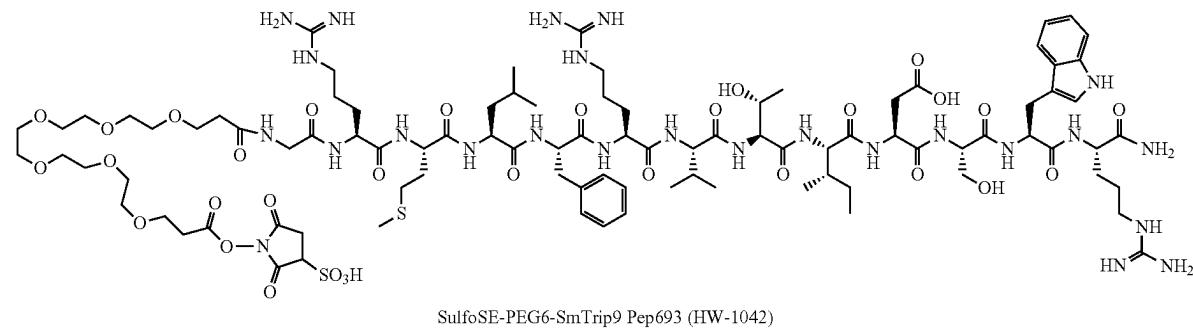
**[0580]** HW-1055 was synthesized by the same method as HW-0984. Calculated: m/z=1114.06 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1113.95 [M+2H]<sup>2+</sup>.

Example 35



**[0581]** Bis PEG6-acid (39 mg, 0.10 mmol) was dissolved in anhydrous DMF and then diisopropylethylamine (53 mg, 0.4 mmol) and HATU (78 mg, 0.20 mmol) added. The mixture was stirred for five minutes. Meanwhile, N-hydroxy-2,5-dioxopyrrolidine-3-sulfonic acid (40 mg, 0.20

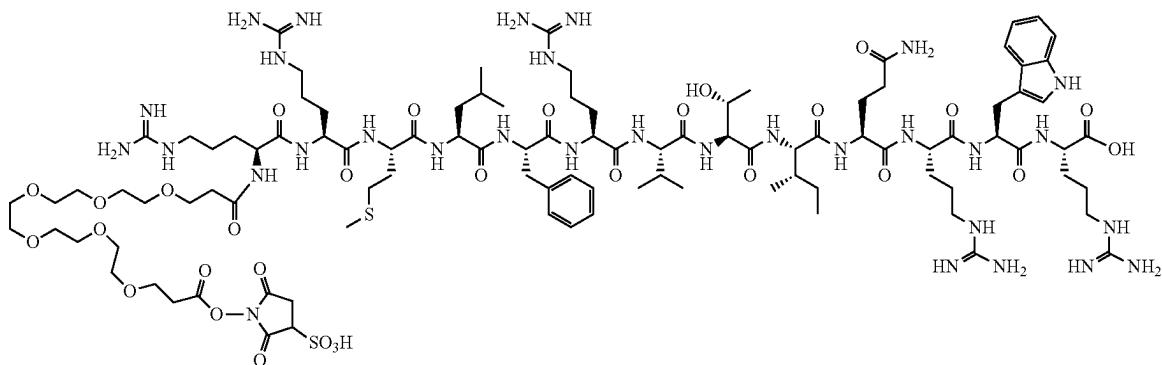
mmol) was dissolved in 5 ml DMSO and then added to the previous solution dropwise. The mixture was stirred for another hour until LC-MS shows disappearance of acid. The solution was directly used in the next step. Calculated: m/z=735.13 [M<sup>-</sup>]; measured (ESI): m/z=735.04 [M].



**[0582]** SmTrip9 Pep693 (GRMLFRVTINSWR, 20 mg, 0.013 mmol) was dissolved in DMF. The solution was then added to the previous PEG6 bis Sulfo-SE solution. The mixture was then stirred for another hour and directly

purified by preparative HPLC. Calculated: m/z=1089.02 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1088.94 [M+2H]<sup>2+</sup>.

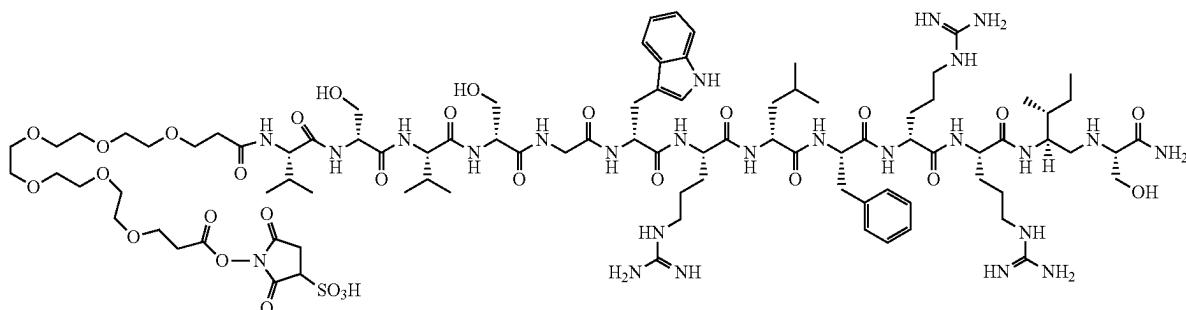
#### Example 36



SulfoSE-PEG6-SmTrip9 Pep929 (HW-1052)

**[0583]** HW-1052 was synthesized by the same method as HW-1042. Calculated: m/z=1180.10 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1179.82 [M+2H]<sup>2+</sup>.

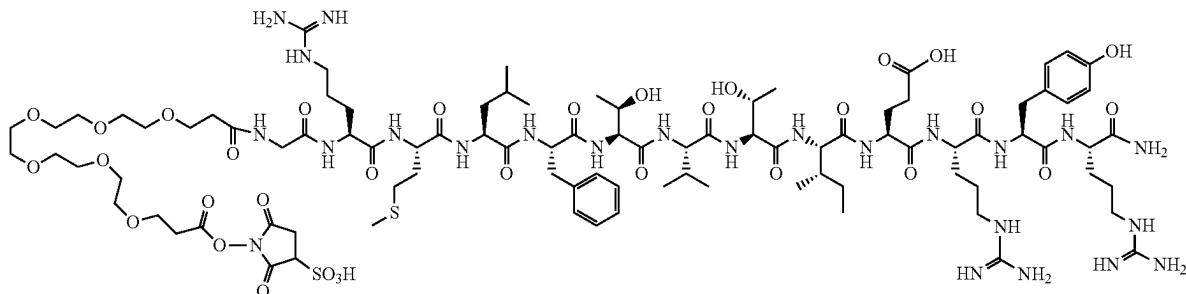
#### Example 37



SulfoSE-PEG6-SmTrip10 Pep692 (HW-1053)

**[0584]** HW-1053 was synthesized by the same method as HW-1042. Calculated: m/z=1052.03 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1051.92 [M+2H]<sup>2+</sup>.

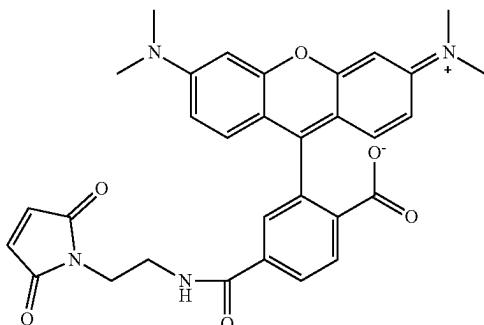
#### Example 38



SulfoSE-PEG6-SmTrip9 Pep895 (HW-1043)

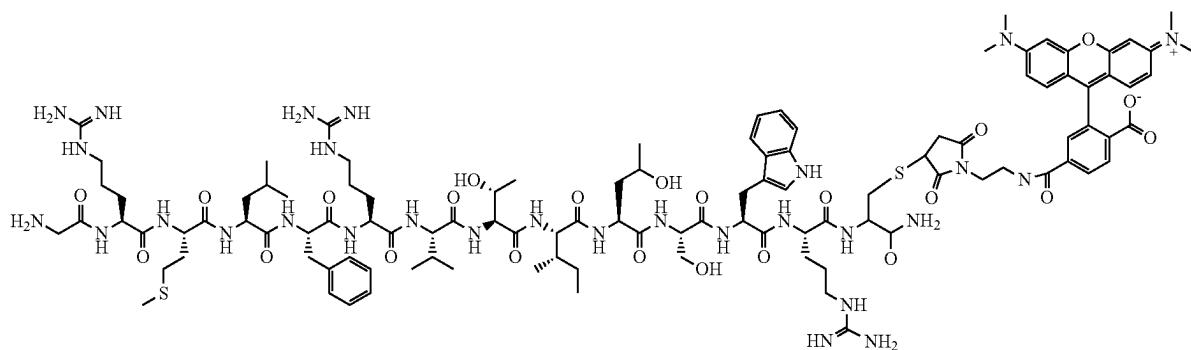
**[0585]** HW-1043 was synthesized by the same method as HW-1042. Calculated: m/z=1082.55 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1082.34 [M+2H]<sup>2+</sup>

Example 39



SulfoSE-PEG3-SmTrip9 Pep938 (HW-0992)  
TAMRA-Maleimide

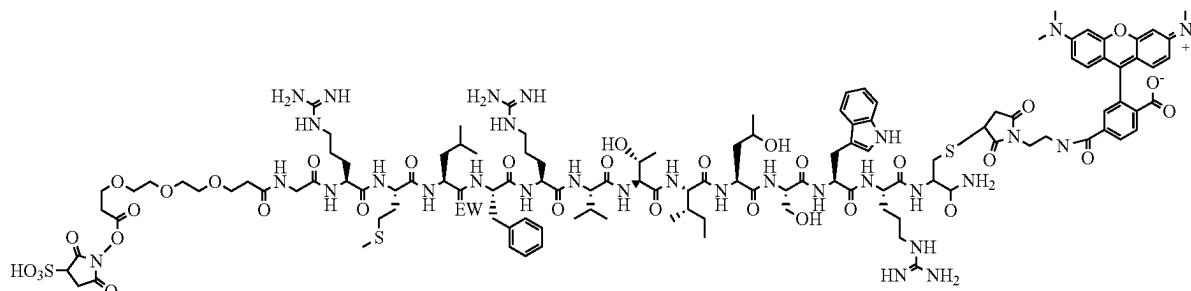
**[0586]** 5-TAMRA (50 mg, 0.116 mmol) was dissolved in DMF. Diisopropylethylamine (45 mg, 0.128 mmol) was added followed by TSTU (38 mg, 0.128 mmol). The mixture was stirred for 20 min, 1-(2-aminoethyl)-1H-pyrrole-2,5-dione (18 mg, 0.128 mmol) added, and the resulting reaction mixture was stirred for another hour and directly purified by preparative HPLC. Calculated: m/z=553.20 [M+H]<sup>+</sup>; measured (ESI): m/z=553.40 [M+H]<sup>+</sup>.



SmTrip9 Pep938-TAMRA

**[0587]** TAMRA-Maleimide (8 mg, 0.014 mmol) was dissolved in DMF. A solution of SmTrip9 (Pep938) (GRML-FRVTINSWRC, 25 mg, 0.014 mmol) in PBS buffer (pH 7.4,

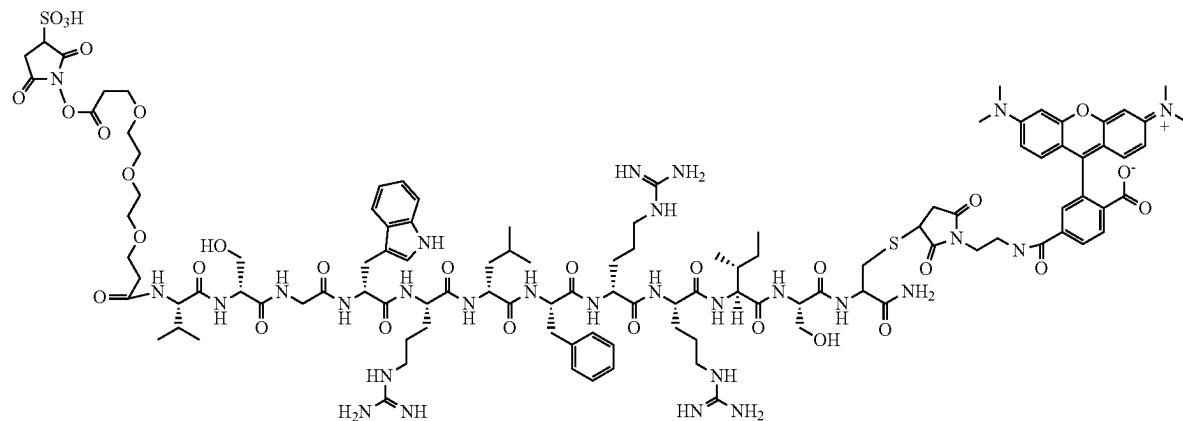
200 mM) was added. The reaction mixture was stirred for two hours and directly purified by preparative HPLC. Calculated: m/z=1146.05 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1146.33 [M+2H]<sup>2+</sup>



SulfoSE-PEG3-SmTrip9 Pep938-TAMRA (HW-0992)

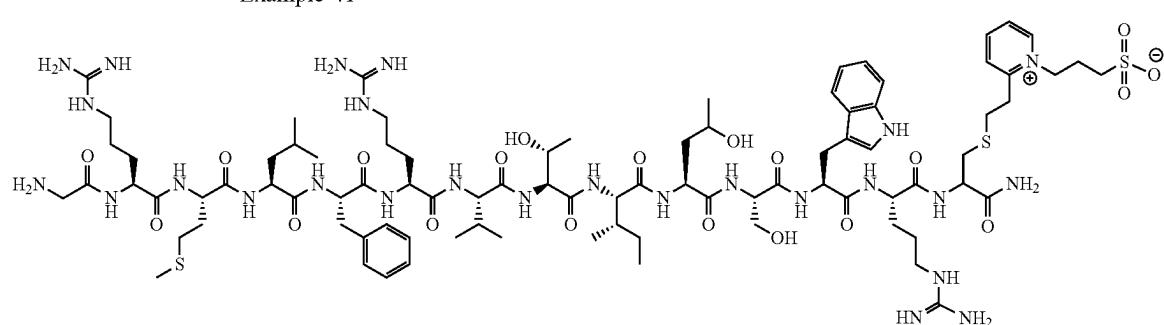
**[0588]** SmTrip9 Pep938-TAMRA (8.5 mg, 0.0038 mmol) was dissolved in DMF. The solution was then added to PEG3 bis Sulfo-SE prepared as shown in synthesis of HW-0984. The reaction mixture was stirred for two hours and directly purified by preparative HPLC. Calculated: m/z=901.05 [M+3H]<sup>3+</sup>; measured (ESI): m/z=901.20 [M+3H]<sup>3+</sup>.

## Example 40



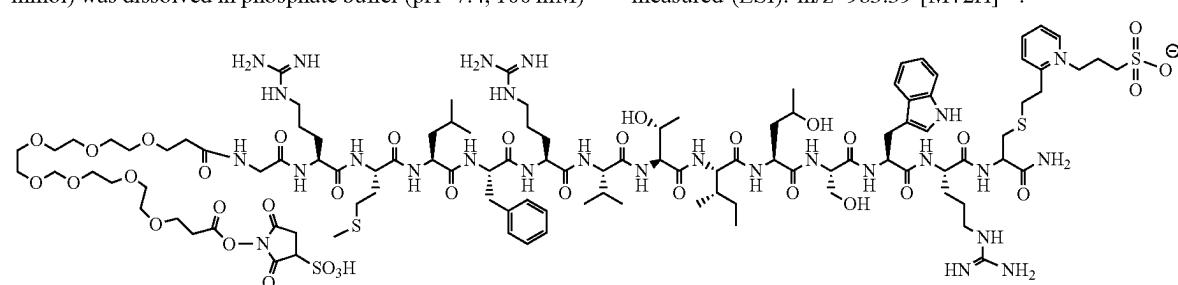
**[0589]** HW-0987 was synthesized by the same method as HW-0992. Calculated: m/z=814.03 [M+3H]<sup>3+</sup>; measured (ESI): m/z=814.40 [M+3H]<sup>3+</sup>.

## Example 41



**[0590]** SmTrip9 Pep938 (GRMLFRVTINSWR, 26 mg, 0.015 mmol) was dissolved in DMSO. 1-(3-Sulfopropyl)-2-vinylpyridinium Hydroxide Inner Salt (3.40 mg 0.015 mmol) was dissolved in phosphate buffer (pH=7.4, 100 mM)

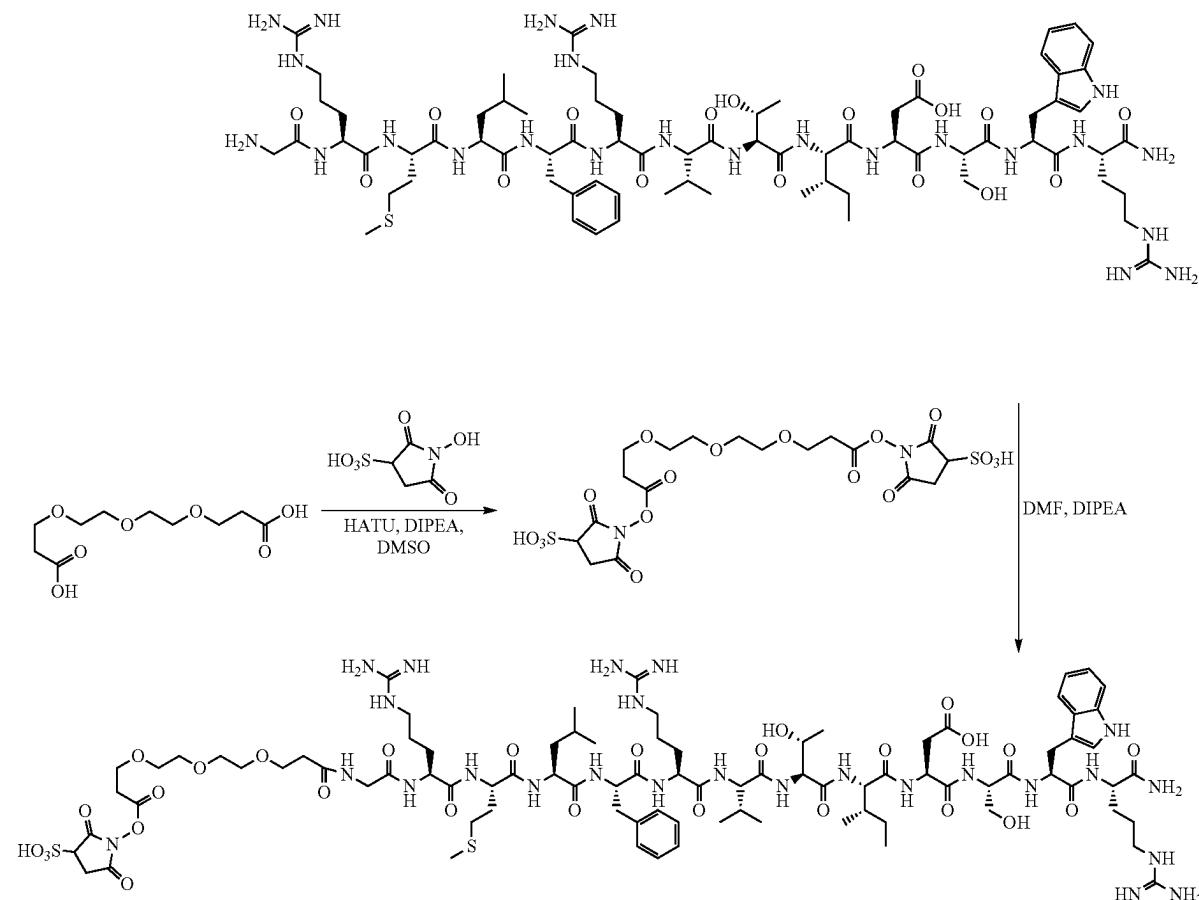
and was added slowly to the peptide solution. The mixture was stirred for another three hours and directly purified by preparative HPLC. Calculated: m/z=983.48 [M+2H]<sup>2+</sup>; measured (ESI): m/z=983.39 [M+2H]<sup>2+</sup>.



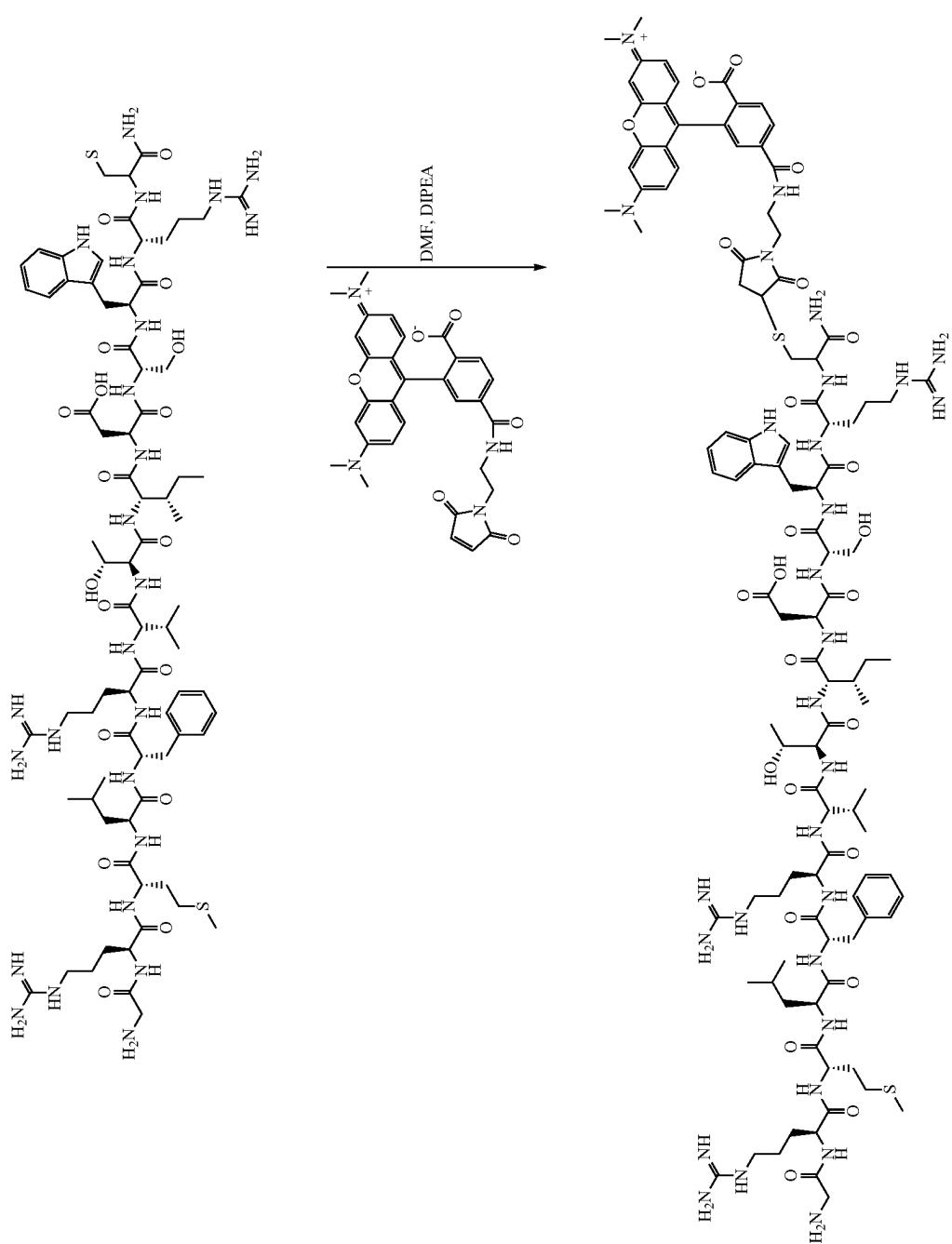
**[0591]** SmTrip9 Pep938-SA (10 mg, 0.005 mmol) was dissolved in DMF. The solution was then added to PEG6 bis Sulfo-SE prepared as shown in HW-0984. The reaction mixture was stirred for two hours and directly purified by

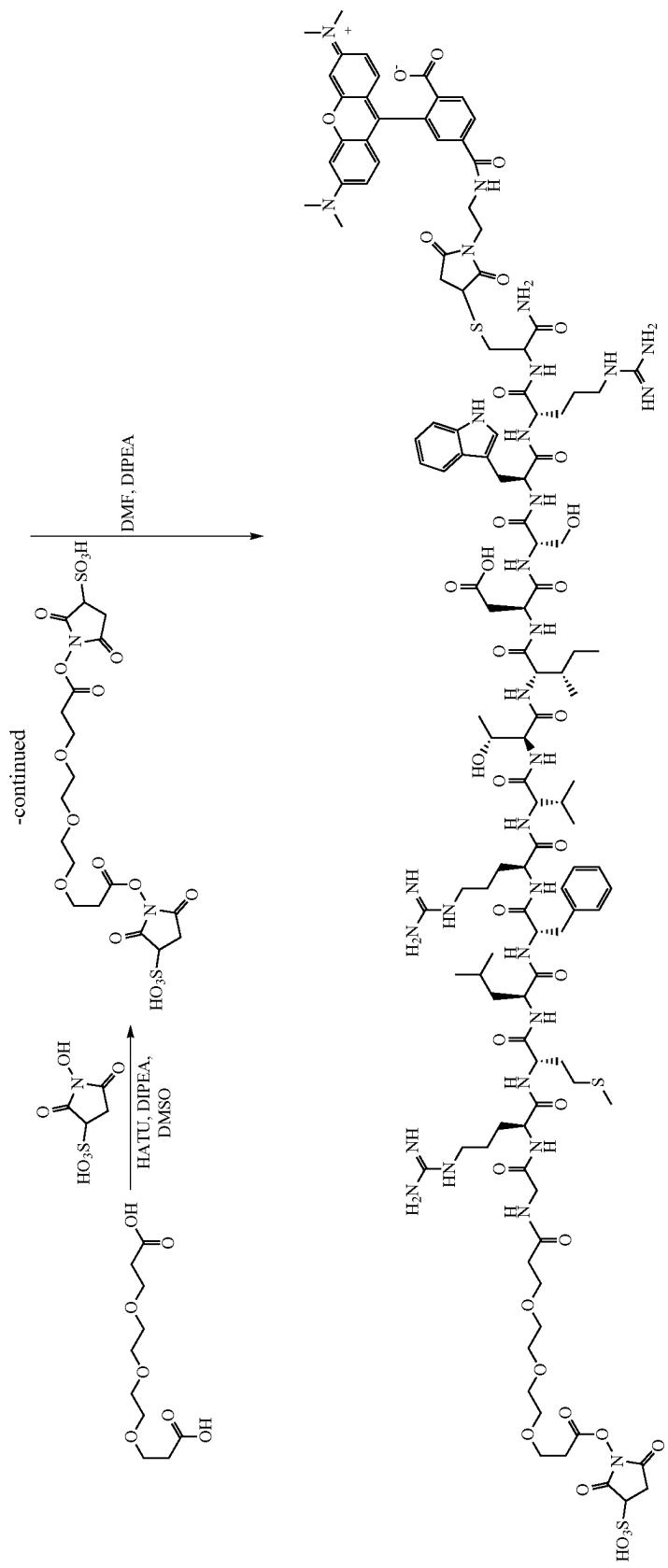
preparative HPLC. Calculated: m/z=1254.05 [M+2H]<sup>2+</sup>; measured (ESI): m/z=1253.98 [M+2H]<sup>2+</sup>.

**[0592]** Shown below is a representative scheme for the synthesis of PEG-linked peptide SulfoSE.



**[0593]** Shown below is a representative scheme for the synthesis of PEG-linked peptide SulfoSE linked to a fluorophore.





## Example 42

Investigating Luminescence in Complex Sample Matrices on Performance of Coelenterazine Derivatives JRW-1404 and JRW-1482

**[0594]** FIG. 87 displays the luminescence derived from coelenterazine derivative substrates JRW-1404 and JRW-1482 in complex sample matrices. 100% samples of plasma (12/28/18), urine (Innovative research 2/25/19), and Human-Sera (2/11/19) were diluted to 10%, 20%, 0%, and 80% in PBS. The sample with “0%” is PBS. In duplicate, 50 1a of each sample was combined with 50 1a NanoLuc diluted to 0.4 ng/ml in PBS. Each substrate was diluted to 20 μM PBS and then 1001 of each diluted substrate was added to the NanoLuc/sample mixtures. Luminescence was measured on a GloMax® Discover plate luminometer.

**[0595]** It is understood that the foregoing detailed description and accompanying examples are merely illustrative and are not to be taken as limitations upon the scope of the disclosure, which is defined solely by the appended claims and their equivalents.

**[0596]** Various changes and modifications to the disclosed embodiments will be apparent to those skilled in the art. Such changes and modifications, including without limitation those relating to the chemical structures, substituents, derivatives, intermediates, syntheses, compositions, formulations, or methods of use of the disclosure, may be made without departing from the spirit and scope thereof.

## Sequences

**[0597]** The following polypeptide sequences each comprise an N-terminal methionine residue or corresponding ATG codon; polypeptide sequences lacking the N-terminal methionine residue or corresponding ATG codon are also within the scope herein and are incorporated herein by reference.

**[0598]** The following peptide sequences each lack an N-terminal methionine residue; peptide sequences comprising an N-terminal methionine residue are also within the scope herein and are incorporated herein by reference.

TABLE 2

		Exemplary peptide, dipeptide, and polypeptide sequences.
SEQ	ID	Sequence
NO	Name	
1	WT OgLuc	MFTLADFVGDWQQTAGYNQDQVLEQGGSSLFQALGVSVTPIQKVVLSGENGLKADIHVIIPYEGLSGFQMGL IEMIFKVVYPVDDHHFKIILHYGTLVIDGVTNPNMIDYFGRPYPGIAVFDGKQITVTGTLWNGNKIYDERLINP DGSLLFRVTINGVTGWRLCENILA
28	WT OgLuc	atggctttacccgtggcagatttcgtggagactggcaacagacaggctgatataaccaaagatcaagtgttag aacaaggaggattgtctagtcgttccaaacctggggatgtcagtccccatccagaatccaggaaagtgtgtgtgc tggggaaatgggttaaaactgtatattcatgtcatccctacggggacttcgtgtttcaatgggt ctgattgaatgtatccaaatgtttaccatgtggatcatcattcaagattatctccattatggta cacttgttattgtggatgtggacacaaacatgttgactactttggacgccttaccctggaaatgtgtgtt tgacggcaagcagatcacatgttactggactctgtggacggcaacaagatctatgtggacgcctgtatcaac ccagatgttactccctccgcgttactatcaatggatgtggacgccttgcgagaacattttgc cc
5	NanoLuc	MVFTLEDVFGDWQQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMG QIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTNPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIYDERLIN PDGSLLFRVTINGVTGWRLCERILA
29	NanoLuc	atgaaacatccccatccccatcgatcgccatggttcacactcgaaagatttcgttggggactggcgac agacagccggatcacacccgtggaccaactggatgtccgtggatggggatgtggatccatgtcatcc gtccgtatgggtctggccggatccatgtggatggggatgtggatccatgtcatccatgtcatcc atcatccatgtggatctgtcatatggccacactgttgcacatgtggatggggatgtggatccatgtcatcc ttcggacggccgtatggatgtggatccatgtggatggggatgtggatccatgtcatccatgtcatcc ggcaacaaaattatcgacggccgtatggatgtggatccatgtggatggggatgtggatccatgtcatcc tgaccggctggccgtgtggacacgcatttgcggatgtggatccatgtcatccatgtcatcc
2	WT OgLuc Lg	MFTLADFVGDWQQTAGYNQDQVLEQGGSSLFQALGVSVTPIQKVVLSGENGLKADIHVIIPYEGLSGFQMGL IEMIFKVVYPVDDHHFKIILHYGTLVIDGVTNPNMIDYFGRPYPGIAVFDGKQITVTGTLWNGNKIYDERLIN D
3	WT OgLuc β9	GSLLFRVTIN
4	WT OgLuc β10	GVTGWRLCENILA
6	WT NanoLuc Lg	MVFTLEDVFGDWQQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMG QIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTNPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKIYDERLIN PD
7	WT NanoLuc β9	GSLLFRVTINV
8	WT NanoLuc β10	GVTGWRLCERILA

TABLE 2-continued

		<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>
SEQ ID NO	Name	Sequence
9	LgBit	MVFTLEDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIT PDGSMLFRVTIN
30	LgBit	atggcttcacactcgaaagatttcgttgggacttggaaacagacagccgcataacctggaccaggcttgc aacaggggagggtgtccaggatgttcgtcagaatctcgccgtgtccgttaactccgatccaaaggattgtccggag cggtaaaatgcctgaagatcgacatccatgtcatatccgtatgaaggctgtgacgcgcgaccaatggcc cagatcgaaagggtgttaagggtgttacccgtgtggatcatcactttaagggtatctgcctatgcca cactggtaatccgacgggttacgcccacatgtgaactatttcggacggccgtatgaaggcatgcgcgttt cgacggcaaaaagatcactgtaaacaggaccctgtggaaacggcaacaaaattatcgacgacgcgcgtatcacc ccggacggccatgtgttccgagtaaccatcaacagccatcatcaccatcaccac
10	SmBit	VTGYRLFEEIL
31	SmBit	gtgaccggctaccggctgttgcaggagattctg
11	HiBit	VSGWRLFKKIS
32	HiBit	gtgagcggctggcgctgttcaagaagatttagc
33	LgTrip 2098	MVFTLEDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIT PD
34	LgTrip 2098	atggcttcacactcgaaagatttcgttgggacttggaaacagacagccgcataacctggaccaggcttgc aacaggggagggtgtccaggatgttcgtcagaatctcgccgtgtccgttaactccgatccaaaggattgtccggag cggtaaaatgcctgaagatcgacatccatgtcatatccgtatgaaggctgtgacgcgcgaccaatggcc cagatcgaaagggtgttaagggtgttacccgtgtggatcatcactttaagggtatctgcctatgcca cactggtaatccgacgggttacgcccacatgtgaactatttcggacggccgtatgaaggcatgcgcgttt cgacggcaaaaagatcactgtaaacaggaccctgtggaaacggcaacaaaattatcgacgacgcgcgtatcacc ccggac
35	LgTrip 3092 His	MKHHHHHHVFLLDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLITPD
36	LgTrip 3092 His	atgaaacatcaccatcaccatcatgtttaacactcgaaagatttcgttgggacttggaaacagacagccgc acacacgtgaccaaaacccgttgcacaggagggtgttcgttcaggatgtcagaatctcgccgtgtccgttaactcc gatccaaaggattgtccggagcggtgaaatgcctgaagatcgacatccatgtcatatccgtatgaagg ctgagccgcaccaatggccacatcgaaagggtgttacccgtgtggatcatcactttaagggtatctgcctatgcca aggtatgcctccatggcactcggttaatcgacgggttacccgtgtggatcatcactttaagggtatctgcctatgcca gtatgtacggcatccgcgtgtccacggcaaaaagatcactgtaaacaggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcaccacccgcac
37	LgTrip 3092	MVFTLEDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIT PD
38	LgTrip 3092	atggcttcacactcgacgatttcgttgggacttggaaacagacagccgcataacctggaccaggcttgc aacaggggagggtgtccaggatgttcgtcagaatctcgccgtgtccgttaactccgatcatcaggattgtccggag cggtaaaatgcctgaagatcgacatccatgtcatatccgtatgaaggctgtgacgcgcgaccaatggcc cagatcgaaagggtgttaagggtgttacccgtgtggatcatcactttaagggtatctgcctatgcca cactggtaatccgacgggttacgcccacatgtgaactatttcggacggccgtatgaaggcatgcgcgttt cgacggcaaaaagatcactgtaaacaggaccctgtggaaacggcaacaaaattatcgacgacgcgcgtatcacc ccggac
13	SmTrip9	GSMLFRVTINS
39	SmTrip9	ggctccatgtgtcccgagtaaccatcaacagc
15	SmTrip10	VSGWRLFKKIS
40	SmTrip10	gtgagcggctggggctgttcaagaagatttagc
41	5P-B9	MVFTLEDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMA QIEKIFKVVYPVDDHHFKVILHYGTLVIDGTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIT PD
42	5P-B9	atggcttcacactcgaaagatttcgttgggacttggaaacagacagccgcataacctggaccaggcttgc aacaggggagggtgtccaggatgttcgtcagaatctcgccgtgtccgttaactccgatccaaaggattgtccgt cggtaaaatgcctgaagatcgacatccatgtcatatccgtatgaaggctgtgacgcgcgaccaatggcc

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
	cagatcgaaaaattttaaagggtgttacccctgtggatcatcatcactttaaagggtatctgcactatggca cactggtaatcgacggggttacgccgaacatgtcaactatttcggacggcgtatgaaggcatcgccgtt cgacggcaaaaagatcaactgttaacagggaccctgtggaaacggcaacaaaattatcgacgagcgcctgtacc ccgac
43 5P(147-157)	GSMLFRVTINV
44 5P(147-157)	ggctccatgctgttccgagtaaccatcaac
45 LgTrip 2098 His	MKHHHHHHVFTLDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGTPNKLNYFGRPYEGIAVFDGKKITVTGTLWNGNKI IDERLITPD
46 LgTrip 2098 His	atggaaacatcaccatcaccatcatgttccacactcgaaagatttcgttgggactggaaacagacagccgc acaacctggaccaagtcttgaacaggagggtgtccagttgtccatcgacatccatccgtatgaagg gtccaaaggattgtccggacggcgtgaaaatggccctgaagatcgacatccatccgtatgaagg ctgagcgcgacccaaatggcccgatcgaaagagggtttaagggtgttacccctgtggatcatcacttta agggtatcctgcctatggcacactcgtaatcgacggggttacgcggcaacatgtgaactatttcggacggcc gtatgaaggcatcgccgttgcacggcaaaaagatcaactgttaacagggaccctgtggaaacggcaacaaaatt atcgacgagcgcctgtacacccccgac
14 SmTrip9/10 Dipeptide (pep263)	GSMLFRVTINSVSGWRLFKKIS
47 SmTrip9/10 Dipeptide (Pep263)	ggctccatgctgttccgagtaaccatcaacacgcgtgagcggctggggctgttcaagaagattgc
48 SmTrip9+ (pep286)	SSWKRGSMFLFRVTINS
49 SmTrip9+ (pep286)	Agcagctggaaagcgcggctccatgtgttccgagtaaccatcaacgc
50 LgTrip 3440	MKHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGTPNKLNYFGRPYDGIAVFDGKKITVTGTLWNGNKI IDERLITPD
51 LgTrip 3440	atggaaacatcaccatcaccatcatgttccacactcgacgatttcgttgggactggaaacagacagccgc acaacctggaccaagtcttgaacaggagggtgtccagttgtccatcgacatccatccgtatgaagg gtatcatgaggattgtccggacggcgtgaaaatggccctgaagatcgacatccatgtcatcattccgtatgaagg ctgagcgcgacccaaatggcccgatcgaaagagggtttaagggtgttacccctgtggatcatcacttta agggtatcctgcctatggcacactcgtaatcgacggggttacgcggcaacagctgaactatttcggacggcc gtatgtatggcatcgccgttgcacggcaaaaagatcaactgttaacagggaccctgtggaaacggcaacaaaatt atcgacgagcgcctgtacacccccgac
52 LgTrip 3121	MKHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGTPSKLNYFGRPYEGIAVFDGKKITVTGTLWNGNKI IDERLITPD
53 LgTrip 3121	atggaaacatcaccatcaccatcatgttccacactcgacgatttcgttgggactggaaacagacagccgc acaacctggaccaagtcttgaacaggagggtgtccagttgtccatcgacatccatccgtatgaagg gtatcatgaggattgtccggacggcgtgaaaatggccctgaagatcgacatccatgtcatcattccgtatgaagg ctgagcgcgacccaaatggcccgatcgaaagagggtttaagggtgttacccctgtggatcatcacttta agggtatcctgcctatggcacactcgtaatcgacggggttacgcggcaacagctgaactatttcggacggcc gtatgtatggcatcgccgttgcacggcaaaaagatcaactgttaacagggaccctgtggaaacggcaacaaaatt atcgacgagcgcctgtacacccccgac
54 LgTrip 3482	MKHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGTPNKLNYFGRPYEGFAVFDGKKITVTGTLWNGNKI IDERLITPD
55 LgTrip 3482	atggaaacatcaccatcaccatcatgttccacactcgacgatttcgttgggactggaaacagacagccgc acaacctggaccaagtcttgaacaggagggtgtccagttgtccatcgacatccatccgtatgaagg gtatcatgaggattgtccggacggcgtgaaaatggccctgaagatcgacatccatgtcatcattccgtatgaagg ctgagcgcgacccaaatggcccgatcgaaagagggtttaagggtgttacccctgtggatcatcacttta agggtatcctgcctatggcacactcgtaatcgacggggttacgcggcaacagctgaactatttcggacggcc gtatgtatggcatcgccgttgcacggcaaaaagatcaactgttaacagggaccctgtggaaacggcaacaaaatt atcgacgagcgcctgtacacccccgac

TABLE 2-continued

		Exemplary peptide, dipeptide, and polypeptide sequences.
SEQ ID NO	Name	Sequence
56	LgTrip 3497	MKHHHHHHHVF TLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPKNLNYFGRPYEGIAVCDGKKITVTGTLWNGNKI IDERLITPD
57	LgTrip 3497	atgaaacatcaccatcaccatcatgttccactcgacgattcggtgggactggaaacagacagccgcct acaacctggaccaagtcttgaacaggagggtgtccagttgtcgagaatctccgtgtccgttaactcc gatcatgaggattgtccggagcggtaaaaatgcctgaagatcgacatccatgtcatcatccgtatgaaggt ctgagcgcgcaccaaattgcggccagatcgaaagggtgtttaaagggtgttacccctgtggatgtatcatcacttta agggtatctgccttatggcacaactgttaatcgacgggttacccgtggatgtatcatcacttta gtatgaaggcatcgcgtgtcgacggcaaaaagatcactgttaacaggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcaccccgac
58	LgTrip 3125	MKHHHHHHHVF TLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPKNLNYFGRPYEGIAVFDGKKISVTGTLWNGNKI IDERLITPD
59	LgTrip 3125	atgaaacatcaccatcaccatcatgttccactcgacgattcggtgggactggaaacagacagccgcct acaacctggaccaagtcttgaacaggagggtgtccagttgtcgagaatctccgtgtccgttaactcc gatcatgaggattgtccggagcggtaaaaatgcctgaagatcgacatccatgtcatcatccgtatgaaggt ctgagcgcgcaccaaattgcggccagatcgaaagggtgtttaaagggtgttacccctgtggatgtatcatcacttta agggtatctgccttatggcacaactgttaatcgacgggttacccgtggatgtatcatcacttta gtatgaaggcatcgcgtgtcgacggcaaaaagatcactgttaacaggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcaccccgac
60	LgTrip 3118	MKHHHHHHHVF TLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPKNLNYFGRPYEGIAVFDGKKITATGTLWNGNKI IDERLITPD
61	LgTrip 3118	atgaaacatcaccatcaccatcatgttccactcgacgattcggtgggactggaaacagacagccgcct acaacctggaccaagtcttgaacaggagggtgtccagttgtcgagaatctccgtgtccgttaactcc gatcatgaggattgtccggagcggtaaaaatgcctgaagatcgacatccatgtcatcatccgtatgaaggt ctgagcgcgcaccaaattgcggccagatcgaaagggtgtttaaagggtgttacccctgtggatgtatcatcacttta agggtatctgccttatggcacaactgttaatcgacgggttacccgtggatgtatcatcacttta gtatgaaggcatcgcgtgtcgacggcaaaaagatcactgttaacaggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcaccccgac
12	LgTrip 3546	MKHHHHHHHVF TLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPKNLNYFGRPYEGIAVFDGKKITTGTLWNGNKI IDERLITPD
62	LgTrip 3546	atgaaacatcaccatcaccatcatgttccactcgacgattcggtgggactggaaacagacagccgcct acaacctggaccaagtcttgaacaggagggtgtccagttgtcgagaatctccgtgtccgttaactcc gatcatgaggattgtccggagcggtaaaaatgcctgaagatcgacatccatgtcatcatccgtatgaaggt ctgagcgcgcaccaaattgcggccagatcgaaagggtgtttaaagggtgttacccctgtggatgtatcatcacttta agggtatctgccttatggcacaactgttaatcgacgggttacccgtggatgtatcatcacttta gtatgaaggcatcgcgtgtcgacggcaaaaagatcactaccacaggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcaccccgac
63	LgTrip 3546 + G (ATG 3572)	MVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPKNLNYFGRPYEGIAVFDGKKITTGTLWNGNKIIDERLIT PDG
64	LgTrip 3546 + G (ATG 3572)	atggcttcacactcgacgattcggtgggactggaaacagacagccgcctacaacctggaccaactgttgc aacaggagggtgtccatgttgcgtcgagaatctccgtgtccgttaactccgtatcatcgaggattgtccggag cggtaaaaatgcctgaagatcgacatccatgtcatcatccgtatgaagggtctgagcgcgcaccaaattggcc cagatcgaaagggtgtttaaagggtgttacccctgtggatgtatcatcactttaagggtatctgccttatggca cactgttaatcgacgggttacccgtggatgtatcatcactttaagggtatctgcacggccgtatgaaggcatcgccgtt cgacggcaaaaagatcactaccacaggaccctgtggaaacggcaacaaaattatcgacgacgcgcgtatcacc cccgacggc
65	LgTrip 3546 - D (ATG 3573)	MVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPKNLNYFGRPYEGIAVFDGKKITTGTLWNGNKIIDERLIT P
66	LgTrip 3546 - D (ATG 3573)	atggcttcacactcgacgattcggtgggactggaaacagacagccgcctacaacctggaccaactgttgc aacaggagggtgtccatgttgcgtcgagaatctccgtgtccgttaactccgtatcatcgaggattgtccggag cggtaaaaatgcctgaagatcgacatccatgtcatcatccgtatgaagggtctgagcgcgcaccaaattggcc cagatcgaaagggtgtttaaagggtgttacccctgtggatgtatcatcactttaagggtatctgccttatggca cactgttaatcgacgggttacccgtggatgtatcatcactttaagggtatctgcacggccgtatgaaggcatcgccgtt cgacggcaaaaagatcactaccacaggaccctgtggaaacggcaacaaaattatcgacgacgcgcgtatcacc ccc

TABLE 2-continued

Exemplary peptide, dipeptide, and polypeptide sequences.		
SEQ ID NO Name	Sequence	
67 LgTrip 3546 - PD (ATG 3574)	MVFTLDDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITTTGTLWNGNKIIDERLIT	
68 LgTrip 3546 - PD (ATG 3574)	atggcttcacactcgacgatttcgtggggacttggaaacagacagccgcataacctggaccaggatccttg aacaggggagggtgtcccgatgttcgtccgtactcccgatcatggaggattgtccggag cggtaaaaatgcctgaagatcgacatccatgtcatatcccgatgaaggctgtggccgacccaaatggcc cagatcgaagagggtttaaagggtgttacccctgtggatgtatcaactttaagggtgatctgcctatggca cactgttaatccacggggtaacggcaacaactgtgaactatttcggacggccgtatgaaggcataccgtt cgacggcaaaaagatcaactaccacaggacccctgtggaaacggcaacaaaattatcgacgacgcgtatcacc	
69 LgTrip 3546 + GS (ATG 3575)	MVFTLDDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITTTGTLWNGNKIIDERLIT PDGS	
70 LgTrip 3546 + GS (ATG 3575)	atggcttcacactcgacgatttcgtggggacttggaaacagacagccgcataacctggaccaggatccttg aacaggggagggtgtcccgatgttcgtccgtactcccgatcatggaggattgtccggag cggtaaaaatgcctgaagatcgacatccatgtcatatcccgatgaaggctgtggccgacccaaatggcc cagatcgaagagggtttaaagggtgttacccctgtggatgtatcaactttaagggtgatctgcctatggca cactgttaatccacggggtaacggcaacaactgtgaactatttcggacggccgtatgaaggcataccgtt cgacggcaaaaagatcaactaccacaggacccctgtggaaacggcaacaaaattatcgacgacgcgtatcacc cccgacggcagc	
71 -V_LgBiT (ATG3618)	MFTLEDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMAQ IIEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLITP DGSMFLFRVTINSHHHHHH	
72 -V_LgBiT (ATG3618)	atgttccacactcgaaaggatttcgtggggacttggaaacagacagccgcataacctggaccaggatccttgaaac aggagggtgtcccgatgttcgtccgtactcccgatcatcccgatgaaggctgtggccgacccaaatggcc tggaaaatgcctgaagatcgacatccatgtcatatcccgatgaaggctgtggccgacccaaatggcc atcgaagagggtttaaagggtgttacccctgtggatgtatcaactttaagggtgatctgcctatggcacac tggtaatcgacggggtaacccatgtgaactatttcggacggccgtatgaaggcataccgttgcgttgc cgacggcaaaaagatcaactgtaaacaggacccctgtggaaacggcaacaaaattatcgacgacgcgtatcacc gacggcgttccatgtcccgatgaaccatcaacagccatcatcaccatcaccactaa	
73 -VF_LgBiT (ATG3619)	MTLEDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMAQI EEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLITPD GSMFLFRVTINSHHHHHH	
74 -VF_LgBiT (ATG3619)	atgacactcgaaaggatttcgtggggacttggaaacagacagccgcataacctggaccaggatccttgaaacagg gagggtgtccgttgcagaatctcccgatgtccgtactcccgatccaaggattgtccggagccgttgc aaatgcctgaagatcgacatccatgtcatatcccgatgaaggctgtggccgacccaaatggcc gaagggtttaaagggtgttacccctgtggatgtatcaactttaagggtgatctgcctatggcacactgg taatcgacggggtaacccatgtgaactatttcggacggccgtatgaaggcataccgttgcgttgc caaaaagatcaactgtaaacaggacccctgtggaaacggcaacaaaattatcgacgacgcgtatcacc ggccatgttcccgatgaaccatcaacagccatcatcaccatcaccactaa	
75 -VFT_LgBiT (ATG3620)	MLEDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMAQIE EEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLITPDG SMLFLFRVTINSHHHHHH	
76 -VFT_LgBiT (ATG3620)	atgctcgaaaggatttcgtggggacttggaaacagacagccgcataacctggaccaggatccttgaaacaggag gtgtccgttgcagaatctcccgatgtccgtactcccgatccaaggattgtccggagccgttgc tgccctgaagatcgacatccatgtcatatcccgatgaaggctgtggccgacccaaatggcc gagggtttaaagggtgttacccctgtggatgtatcaactttaagggtgatctgcctatggcacactgg tcgacggggtaacccatgtgaactatttcggacggccgtatgaaggcataccgttgcgttgc aaaggatcaactgtaaacaggacccctgtggaaacggcaacaaaattatcgacgacgcgtatcacc ggccatgttcccgatgaaccatcaacagccatcatcaccatcaccactaa	
77 -VFTL_LgBiT (ATG3621)	MEDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMAQIEE VFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLITPDGS MLFLFRVTINSHHHHHH	
78 -VFTL_LgBiT (ATG3621)	atggaaggatttcgtggggacttggaaacagacagccgcataacctggaccaggatccttgaaacaggagg tgtcccgatgtccgtcagaatctcccgatgtccgtactcccgatccaaggattgtccggagccgttgc cctgaagatcgacatccatgtcatatcccgatgaaggctgtggccgacccaaatggcc gtgtttaaagggtgttacccctgtggatgtatcaactttaagggtgatctgcctatggcacactgt acggggtaacccatgtgaactatttcggacggccgtatgaaggcataccgttgcgttgc gtactgtaaacaggacccctgtggaaacggcaacaaaattatcgacgacgcgtatcacc ggccatgttcccgatgaaccatcaacagccatcatcaccatcaccactaa	

TABLE 2-continued

		Exemplary peptide, dipeptide, and polypeptide sequences.
SEQ ID NO	Name	Sequence
79	(M) FKKIS-GSSG-LgBiT (ATG3632)	MFKKISGSSGVFTLEDGVGDWEQTAAYNLQDQLVLEQGGVSSLQNLA SVTPIQ RIVRSGENAL KIDI HVI I PYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGR PYEGIAVFDGKKITVTGTLWNGN KI DIDERLITPDGSMLFRVTINSHHHHHH
80	(M) FKKIS-GSSG-LgBiT (ATG3632)	atgttcaagaagattacggctcgagcggtgtttcacactcgaa gatttcgttgggactggaa cagacacagccgc tacaacctggacc aagtccctga acaggaggtgtcccgagccgt gaaaatgc cctga agatc gacatccatgtcatcatcccgat aactcgatccaaaggattgtcccgagccgt gaaaatgc cctga agatc gacatccatgtcatcatcccgat aacagggtgacgcgc accaaatgc cccagatc gacagagggtttaagggtgttaccctgtggatgatc atc tttaaagggtgatccctgc ctatggc acactgtt aatcgc acgggttacccgc aacatgtgtaactatccgg acggccgtatg aggcatcgcgtgttcgacgg caaaaagatc actgtaa cagggaccctgtggaa cggcaacaaaattt aacattatcgc acggcgcctgatc acccgc acggcctccatgttccgagta accatcaacagccatcatcacc accatcaccactaa
81	(M) KKIS-GSSG-LgBiT (ATG3633)	MKKISGSSGVFTLEDGVGDWEQTAAYNLQDQLVLEQGGVSSLQNLA SVTPIQ RIVRSGENAL KIDI HVI I PYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGR PYEGIAVFDGKKITVTGTLWNGN KI DIDERLITPDGSMLFRVTINSHHHHHH
82	(M) KKIS-GSSG-LgBiT (ATG3633)	atagaagaagattacggctcgagcggtgtttcacactcgaa gatttcgttgggactggaa cagacacacccgc cttacaacctggacc aagtccctga acaggaggtgtcccgagccgt gaaaatgc cctga agatc gacatccatgtcatcatcccgat aactccgtccatcccgat aacagggtttaagggtgttaccctgtggatgatc atcact ttaaagggtgatccctgc ctatggc acactgtt aatcgc acgggttacccgc aacatgtgtaactatccggac ccgtatg aggcatcgcgtgttcgacgg caaaaagatc actgtaa cagggaccctgtggaa cggcaacaaaattt attatcgc acggcgcctgatc acccgc acggcctccatgttccgagta accatcaacagccatcatcacc accatcaccactaa
83	(M) KIS-GSSG-LgBiT (ATG3634)	MKISGSSGVFTLEDGVGDWEQTAAYNLQDQLVLEQGGVSSLQNLA SVTPIQ RIVRSGENAL KIDI HVI I PYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGR PYEGIAVFDGKKITVTGTLWNGN KI DIDERLITPDGSMLFRVTINSHHHHHH
84	(M) KIS-GSSG-LgBiT (ATG3634)	atagaagattacggctcgagcggtgtttcacactcgaa gatttcgttgggactggaa cagacacacccgc cttacaacctggacc aagtccctga acaggaggtgtcccgagccgt gaaaatgc cctga agatc gacatccatgtcatcatcccgat aactccgtccatcccgat aacagggtttaagggtgttaccctgtggatgatc atcactt aagggtgatccctgc ctatggc acactgtt aatcgc acgggttacccgc aacatgtgtaactatccggac ccgtatg aggcatcgcgtgttcgacgg caaaaagatc actgtaa cagggaccctgtggaa cggcaacaaaattt atcgc acggcgcctgatc acccgc acggcctccatgttccgagta accatcaacagccatcatcaccatc accactaa
85	(M) IS-GSSG-LgBiT (ATG3635)	MISGSSGVFTLEDGVGDWEQTAAYNLQDQLVLEQGGVSSLQNLA SVTPIQ RIVRSGENAL KIDI HVI I PYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGR PYEGIAVFDGKKITVTGTLWNGN KI DIDERLITPDGSMLFRVTINSHHHHHH
86	(M) IS-GSSG-LgBiT (ATG3635)	atgatttagcggtcgagcggtgtttcacactcgaa gatttcgttgggactggaa cagacacacccgc tacaacctggacc aagtccctga acaggaggtgtcccgatccatcccgat ccaaggatttgccggagccgt gaaaatgc cctga agatc gacatccatgtcatcatcccgat aactccgtccatcccgat aacagggtttaagggtgttaccctgtggatgatc atcactt aagggtgatccctgc ctatggc acactgtt aatcgc acgggttacccgc aacatgtgtaactatccggac ccgtatg tgaaggcatcgcgtgttcgacgg caaaaagatc actgtaa cagggaccctgtggaa cggcaacaaaattt gacgagcgcctgatc acccgc acggcctccatgttccgagta accatcaacagccatcatcaccatc accactaa
87	(M) S-GSSG-LgBiT (ATG3636)	MSGSSGVFTLEDGVGDWEQTAAYNLQDQLVLEQGGVSSLQNLA SVTPIQ RIVRSGENAL KIDI HVI I PYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGR PYEGIAVFDGKKITVTGTLWNGN KI DIDERLITPDGSMLFRVTINSHHHHHH
88	(M) S-GSSG-LgBiT (ATG3636)	atgagcggtcgagcggtgtttcacactcgaa gatttcgttgggactggaa cagacacacccgc tacaaccttggcca aaggatttgccggagccgt gaaaatgc cctga agatc gacatccatgtcatcatcccgat aactccgtccatcccgat aacagggtttaagggtgttaccctgtggatgatc atcactt aagggtgatccctgc ctatggc acactgtt aatcgc acgggttacccgc aacatgtgtaactatccggac ccgtatg tccctgc ctatggc acactgtt aatcgc acgggttacccgc aacatgtgtaactatccggac ccgtatg aggcatcgcgtgttcgacgg caaaaagatc actgtaa cagggaccctgtggaa cggcaacaaaattt gacgagcgcctgatc acccgc acggcctccatgttccgagta accatcaacagccatcatcaccatc accactaa
89	LgTrip + GSM (ATG3722)	MKHHHHHHVFTLDDFVGDW E QTAAYNLQDQLVLEQGGVSSLQNLA SVTPIPMRIVRSGENAL KIDI HVI I PYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGR PYEGIAVFDGKKITVTGTLWNGN KI DIDERLITPDGSML

TABLE 2-continued

		<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>
SEQ ID NO Name	Sequence	
90LgTrip + GSM (ATG3722)	atggaaacatcaccatcaccatcatgtcttccactcgacgatttcgttggggactgggaacagacagccgcct acaacacctggaccaagtccgttaacaggggagggtgtgtccagggttgcagaatctccgtgtccgttaactcc gatcatgaggattgtccggagccgtgaaaatgcctgaaagatcgacatccatgtcatatcccgtatgaaggt ctgagcgccgaccaaataggcccgatcgaaagagggtttaaagggtgttgcacccctgtggatgtatcatcactta agggtatccgtccatggcactgttaatcgacggggtaatcgccgaacaagctgaactatccggacggcc gtatgaaggcatcgccgttgcacggcaaaaagatcactaccacacaggggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcacccccgcacggcagcatgttaa	
91LgTrip + GSML (ATG3723)	MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLQEQQGVSSLQLNQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKKITTGTWLNGNKI IDERLITPDGSML	
92LgTrip + GSML (ATG3723)	atggaaacatcaccatcaccatcatgtcttccactcgacgatttcgttggggactgggaacagacagccgcct acaacacctggaccaagtccgttaacaggggagggtgtgtccagggttgcagaatctccgtgtccgttaactcc gatcatgaggattgtccggagccgtgaaaatgcctgaaagatcgacatccatgtcatatcccgtatgaaggt ctgagcgccgaccaaataggcccgatcgaaagagggtttaaagggtgttgcacccctgtggatgtatcatcactta agggtatccgtccatggcactgttaatcgacggggtaatcgccgaacaagctgaactatccggacggcc gtatgaaggcatcgccgttgcacggcaaaaagatcactaccacacaggggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcacccccgcacggcagcatgttaa	
93LgTrip + GSMLF (ATG3724)	MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLQEQQGVSSLQLNQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKKITTGTWLNGNKI IDERLITPDGSMLF	
94LgTrip + GSMLF (ATG3724)	atggaaacatcaccatcaccatcatgtcttccactcgacgatttcgttggggactgggaacagacagccgcct acaacacctggaccaagtccgttaacaggggagggtgtgtccagggttgcagaatctccgtgtccgttaactcc gatcatgaggattgtccggagccgtgaaaatgcctgaaagatcgacatccatgtcatatcccgtatgaaggt ctgagcgccgaccaaataggcccgatcgaaagagggtttaaagggtgttgcacccctgtggatgtatcatcactta agggtatccgtccatggcactgttaatcgacggggtaatcgccgaacaagctgaactatccggacggcc gtatgaaggcatcgccgttgcacggcaaaaagatcactaccacacaggggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcacccccgcacggcagcatgttaa	
95LgTrip - TPD (ATG3725)	MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLQEQQGVSSLQLNQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKKITTGTWLNGNKI IDERLI	
96LgTrip - TPD (ATG3725)	atggaaacatcaccatcaccatcatgtcttccactcgacgatttcgttggggactgggaacagacagccgcct acaacacctggaccaagtccgttaacaggggagggtgtgtccagggttgcagaatctccgtgtccgttaactcc gatcatgaggattgtccggagccgtgaaaatgcctgaaagatcgacatccatgtcatatcccgtatgaaggt ctgagcgccgaccaaataggcccgatcgaaagagggtttaaagggtgttgcacccctgtggatgtatcatcactta agggtatccgtccatggcactgttaatcgacggggtaatcgccgaacaagctgaactatccggacggcc gtatgaaggcatcgccgttgcacggcaaaaagatcactaccacacaggggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcatcactaa	
97LgTrip - ITPD (ATG3726)	MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLQEQQGVSSLQLNQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKKITTGTWLNGNKI IDERL	
98LgTrip - ITPD (ATG3726)	atggaaacatcaccatcaccatcatgtcttccactcgacgatttcgttggggactgggaacagacagccgcct acaacacctggaccaagtccgttaacaggggagggtgtgtccagggttgcagaatctccgtgtccgttaactcc gatcatgaggattgtccggagccgtgaaaatgcctgaaagatcgacatccatgtcatatcccgtatgaaggt ctgagcgccgaccaaataggcccgatcgaaagagggtttaaagggtgttgcacccctgtggatgtatcatcactta agggtatccgtccatggcactgttaatcgacggggtaatcgccgaacaagctgaactatccggacggcc gtatgaaggcatcgccgttgcacggcaaaaagatcactaccacacaggggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcatcactaa	
99LgTrip - LITPD (ATG3727)	MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLQEQQGVSSLQLNQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKKITTGTWLNGNKI IDER	
100LgTrip - LITPD (ATG3727)	atggaaacatcaccatcaccatcatgtcttccactcgacgatttcgttggggactgggaacagacagccgcct acaacacctggaccaagtccgttaacaggggagggtgtgtccagggttgcagaatctccgtgtccgttaactcc gatcatgaggattgtccggagccgtgaaaatgcctgaaagatcgacatccatgtcatatcccgtatgaaggt ctgagcgccgaccaaataggcccgatcgaaagagggtttaaagggtgttgcacccctgtggatgtatcatcactta agggtatccgtccatggcactgttaatcgacggggtaatcgccgaacaagctgaactatccggacggcc gtatgaaggcatcgccgttgcacggcaaaaagatcactaccacacaggggaccctgtggaaacggcaacaaaatt atcgacgacgcgcgtatcatcactaa	
101FRB-15GS-AI-86 (ATG1634)	MVAILWHEMWHEGLEEASRLYFGERNVKGMEVLEPLHAMMERGPQLKETSFNQAYGRDLMEAQEWCRKYM SGNVKDLTQAWDLYYHFVRRISGGGGGGSSSSGGGAIVSGWRLFKKIS	

TABLE 2-continued

		Exemplary peptide, dipeptide, and polypeptide sequences.
SEQ ID NO	Name	Sequence
102	FRB-15GS-AI-86 (ATG1634)	atggtgtccatctctggcatgagatgtggcatgaaggcctgaaagaggcatctcgtttactttggggaaa gaaacgtgaaaggcatgttgaggtgcggcccttcgtcatgtatgaaacggggccccagactctgaa gaaacatcccttaatcaggccatgtgcgagatataatggggcccaagagtggcaggaaatcatgaaa tcagggaatgtcaaggacccacccaaggctggacccatattatcatgtgttccgacgaatcagtgggtt cagggtgtggcgggagcgggtggctcgagcagcggctggagcgtcgagcggctggcggctgttaagaat tagctaa
103	FRB-15GS-AI-289 (ATG3586)	MVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCWKYM SGNVKDLTQAWDLYYHVFRRISSGGGGGGSSSSGAIVSGWRLFKKIS
104	FRB-15GS-AI-289 (ATG3586)	atggtgtccatctctggcatgagatgtggcatgaaggcctgaaagaggcatctcgtttactttggggaaa gaaacgtgaaaggcatgttgaggtgcggcccttcgtcatgtatgaaacggggccccagactctgaa gaaacatcccttaatcaggccatgtgcgagatataatggggcccaagagtggcaggaaatcatgaaa tcagggaatgtcaaggacccacccaaggctggacccatattatcatgtgttccgacgaatcagtgggtt cagggtgtggcgggagcgggtggctcgagcagcggctggagcgtcgagcggctggcggctgttcaa gaatcagctaa
105	FRB-15GS-AI-86 - His6 (ATG3743)	MVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCWKYM SGNVKDLTQAWDLYYHVFRRISSGGGGGGSSSSGAIVSGWRLFKKISHHHHHH
106	FRB-15GS-AI-86 - His6 (ATG3743)	atggtgtccatctctggcatgagatgtggcatgaaggcctgaaagaggcatctcgtttactttggggaaa gaaacgtgaaaggcatgttgaggtgcggcccttcgtcatgtatgaaacggggccccagactctgaa gaaacatcccttaatcaggccatgtgcgagatataatggggcccaagagtggcaggaaatcatgaaa tcagggaatgtcaaggacccacccaaggctggacccatattatcatgtgttccgacgaatcagtgggtt cagggtgtggcgggagcgggtggctcgagcagcggctggagcgtcgagcggctggcggctgttcaa tagccatcatcaccatcaccactaa
107	PRB-15GS-AI-289-His6 (ATG3744)	MVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCWKYM SGNVKDLTQAWDLYYHVFRRISSGGGGGGSSSSGAIVSGWRLFKKISHHHHHH
108	PRB-15GS-AI-289-His6 (ATG3744)	atggtgtccatctctggcatgagatgtggcatgaaggcctgaaagaggcatctcgtttactttggggaaa gaaacgtgaaaggcatgttgaggtgcggcccttcgtcatgtatgaaacggggccccagactctgaa gaaacatcccttaatcaggccatgtgcgagatataatggggcccaagagtggcaggaaatcatgaaa tcagggaatgtcaaggacccacccaaggctggacccatattatcatgtgttccgacgaatcagtgggtt cagggtgtggcgggagcgggtggctcgagcagcggctggagcgtcgagcggctggcggctgttcaa gaatcagccatcatcaccatcaccactaa
109	His6-FRB-5GS-86 (ATG3760)	MKHHHHHHVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQE WCWKYMKSgnvkdltqawdlYYHVFRRISSGGGGVGWRLFKKIS
110	His6-FRB-5GS-86 (ATG3760)	atgaaacatcaccatcaccatcatgtggccatctctggcatgagatgtggcatgaaggcctgaaagaggcat ctcggttactttggggaaaggaaacgtgaaaggcatgttgaggtgcggcccttcgtcatgtatgaa acggggccccccagactctgaaaggaaacatccttaatcaggccatgtgcgagatataatggggcccaagag tggtgccggaaatcatgaaatcagggaatgtcaaggacccacccaaggctggacccatattatcatgtgt tccgacgaatcagtgggttcaggtgggtcgagcggctggcggctgttcaagaagatagctaa
111	His6-FRB-10GS-86 (ATG3761)	MKHHHHHHVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQE WCWKYMKSgnvkdltqawdlYYHVFRRISSGGGGVGWRLFKKIS
112	His6-FRB-10GS-86 (ATG3761)	atgaaacatcaccatcaccatcatgtggccatctctggcatgagatgtggcatgaaggcctgaaagaggcat ctcggttactttggggaaaggaaacgtgaaaggcatgttgaggtgcggcccttcgtcatgtatgaa acggggccccccagactctgaaaggaaacatccttaatcaggccatgtgcgagatataatggggcccaagag tggtgccggaaatcatgaaatcagggaatgtcaaggacccacccaaggctggacccatattatcatgtgt tccgacgaatcagtgggttcaggtgggtcgagcggctggcggctgttcaagaagatagctaa
113	His6-FRB-15GS-86 (ATG3762)	MKHHHHHHVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQE WCWKYMKSgnvkdltqawdlYYHVFRRISSGGGGVGWRLFKKIS
114	His6-FRB-15GS-86 (ATG3762)	atgaaacatcaccatcaccatcatgtggccatctctggcatgagatgtggcatgaaggcctgaaagaggcat ctcggttactttggggaaaggaaacgtgaaaggcatgttgaggtgcggcccttcgtcatgtatgaa acggggccccccagactctgaaaggaaacatccttaatcaggccatgtgcgagatataatggggcccaagag tggtgccggaaatcatgaaatcagggaatgtcaaggacccacccaaggctggacccatattatcatgtgt tccgacgaatcagtgggttcaggtgggtcgagcggctggcggctgttcaagaagatagctaa
115	His6-FRB-5GS-289 (ATG3763)	MKHHHHHHVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQE WCWKYMKSgnvkdltqawdlYYHVFRRISSGGGGVGWRLFKKIS

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
116His6-FRB-5GS-289 (ATG3763)	atggaaacatcaccatcaccatcatgtggccatcctctggcatgagatgtggcatgaaggccttggaaaggagcatctcggtttgtactttggggaaaggAACGTGAAGGCATGTTGGAGGTGCTGGAGGCCCTTGATGCTATGATGGAACGGGGCCCGGCAACTCTGAAGGAAACATCCTTAATCAGGCCTATGTCAGGAGATTAAATGGAGGGCCCAAGAGTGGTCAGGAGTACATGAATACTGGGAATCAGGAACTACCCAAAGCCTGGGACCTCTATTATCATGTGTTCCGACGAATCACTGTGGTGTAGCGTAGCGCTGGCCTGTTAAGAAGATCAGCTAA
117His6-FRB-10GS-289 (ATG3764)	MKHHHHHHHVAILWHEMWHEGLEEASRLYFGERNVKGMFEVILEPLHAMMERGPQTLKETSFNQAYGRDLMEAQE WCRKYMKSGNVKDLTQAQDWLYYHVFRRISSGGGGGGGSVSGWRLFKKIS
118His6-FRB-10GS-289 (ATG3764)	atggaaacatcaccatcaccatcatgtggccatcctctggcatgagatgtggcatgaaggccttggaaaggagcatctcggtttgtactttggggaaaggAACGTGAAGGCATGTTGGAGGTGCTGGAGGCCCTTGATGCTATGATGGAACGGGGCCCGGCAACTCTGAAGGAAACATCCTTAATCAGGCCTATGTCAGGAGATTAAATGGAGGGCCCAAGAGTGGTCAGGAGTACATGAATACTGGGAATCAGGAACTACCCAAAGCCTGGGACCTCTATTATCATGTGTTCCGACGAATCACTGTGGTGTAGCGTAGCGCTGGCCTGTTAAGAAGATCAGCTAA
119His6-FRB-15GS-289 (ATG3765)	MKHHHHHHHVAILWHEMWHEGLEEASRLYFGERNVKGMFEVILEPLHAMMERGPQTLKETSFNQAYGRDLMEAQE WCRKYMKSGNVKDLTQAQDWLYYHVFRRISSGGGGGGGSVSGWRLFKKIS
120His6-FRB-15GS-289 (ATG3765)	atggaaacatcaccatcaccatcatgtggccatcctctggcatgagatgtggcatgaaggccttggaaaggagcatctcggtttgtactttggggaaaggAACGTGAAGGCATGTTGGAGGTGCTGGAGGCCCTTGATGCTATGATGGAACGGGGCCCGGCAACTCTGAAGGAAACATCCTTAATCAGGCCTATGTCAGGAGATTAAATGGAGGGCCCAAGAGTGGTCAGGAGTACATGAATACTGGGAATCAGGAACTACCCAAAGCCTGGGACCTCTATTATCATGTGTTCCGACGAATCACTGTGGTGTAGCGTAGCGCTGGCCTGAGCAGCGGTGGAGTTAGCGTTAGCGCTGGCCTGTTAAGAAGATCAGCTAA
121SmTrip9-FKBP fusion template (ATG780)	M-GSMLFRVTINS-SSSGGGGGGGSSGGVQVETISPQGDRTFPKRQGQTCVVHYTMLEDGKKFDSSRDRNK PFKFLMGKQEVIRGWEEGVAQMSVGQRAKLTISPQDYAYGATGHPGIIPPHATLVDVELLKLE
122SmTrip9-FKBP fusion template (ATG780)	atggggctccatgtgttcccgagaataccatcaacagctcgagttcaggtggggcgagcggtggaggagca gcgggtggaggagtgcaggtaaccatctccccaggagacggggcacccatccccaaagcgccggccagacctg cgtgggtgcactacacccggatgttggaaatggaaatggatgttgggggggggggggggggggggggggggggg aagttagtgcggcaaggagggtgtatccgg gagccaaaactgactatatctcccgattatgcctatggtgccactgggcacccaggcatcatcccaccatgc cactctcgatgtggagttctaaaactggaaatgggttcaggtgggggggggggggggggggggggggggggggg tggagcgatcggtccatgtgttcccgagaataaccatcaacagc
123FKBP-SmTrip9 fusion template (ATG777)	MGVQVETISPQGDRTFPKRQGQTCVVHYTMLEDGKKFDSSRDRNKPKFKMFLGKQEVIRGWEEGVAQMSVGQRA KLTISPQDYAYGATGHPGIIPPHATLVDVELLKLEGSSGGGGSSGGAI-GSMLFRVTINS
124FKBP-SmTrip9 fusion template (ATG777)	Atggggagtgcagggtggaaaccatctccccaggagacggggcacccatccccaaagcgccggccagacctgcgtgg tgcactacacccggatgttggaaatggaaatggatgttgggggggggggggggggggggggggggggggggggg tatgtctggcaaggagggtgtatccgg aaactgactatatctcccgattatgcctatggtgccactgggcacccaggcatcatcccaccatgcac tcgtctcgatgtggagttctaaaactggaaatgggttcaggtgggggggggggggggggggggggggggggg tggagcgatcggtccatgtgttcccgagaataaccatcaacagc
125LgBiT (ATG2623)	MVFTLEDVFQDWQTAAYNLQVLEQGGVSSLNLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVPVDHHFKVILPYGTLVIDGVTNPMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIT PDGSMMLFRVTINSHHHHHHH
126LgBiT (ATG2623)	atgttcttcacactcgaaaggatttcgtggggactggaaacagacacccgcctacaacctggaccacatgttgc aacaggggagggtgttcccgatgttgcgtcagaatctccgcgtgtccgtactcccgatccaaaggattgtccggag cggtggaaaatgcctcgaaatgcgtccatccatccgtatgttgcgtggatcatcactttaagggtgtatccgc cagatcgaaagggtgtttaagggtgttgcgttgcgtggatcatcactttaagggtgtatccgcctatggca cactgttgcgttgcgtgggggttacggccaaatgttgcgtggatcatcactttaagggtgtatccgc cgacggaaaatgcgttgcgtgggggttacggccaaatgttgcgtggatcatcactttaagggtgtatccgc cccgcggccatgtgttcccgagaataaccatcaacagccatcatcaccatcaccactaa
127pep78	NVSGWRLFKKISN
128pep79	NVTGYRLFKKISN
129pep80	VSGWRLFKKISN
130pep81	SGWRLFKKISN
131pep82	GWRLFKKISN
132pep99	VTGYRLFEKISN

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
133 pep219	SGWRLFKKIS
134 pep225	VSGWRL
135 pep226	VSGWRLF
136 pep227	VSGWRLFK
137 pep228	VSGWRLFKK
138 pep229	VSGWRLFKKI
139 pep243	VSGWRLYKKIS
140 pep272	GSMLFRVTINSVSGWALFKKIS
141 pep274	GSMLFRVTINSVTGYRLFEEIL
142 pep287 (WT SmTrip9) + Cterm solubility tag	GSMLFRVTINSSSWKR
143 pep288	VSGVSGWRLFKKIS
144 pep290	VVSGWRLFKKIS
145 pep291	SSWKRSMLFRVTINS
146 pep292	SSWKRMLFRVTINS
147 pep293	SSWKRDGSMLFRVTINS
148 pep294	SSWKRPDGSMMLFRVTINS
149 pep296	SSWKRSMLFRVTINSV
150 pep297	SSWKRMLFRVTINSV
151 pep298	SSWKRDGSMLFRVTINSV
152 pep299	SSWKRPDGSMMLFRVTINSV
153 pep301	SSWKRSMLFRVTINSVS
154 pep302	SSWKRMLFRVTINSVS
155 pep303	SSWKRDGSMLFRVTINSVS
156 pep304	SSWKRPDGSMMLFRVTINSVS
157 pep305	SSWKRGSMMLFRVTIN
158 pep306	SSWKRGSMMLFRVTI
159 pep307	SSWKRSMLFRVTIN
160 pep308	SSWKRMLPRVTIN
161 pep309	SSWKRDGSMLFRVTIN
162 pep310	SSWKRPDGSMMLFRVTIN
163 pep311	SSWKRSMLFRVTI
164 pep312	SSWKRMLPRVTI
165 pep313	SSWKRDGSMLFRVTI
166 pep314	SSWKRPDGSMMLFRVTI

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
167 pep316	VSGWRLFKKISVFTL
168 pep317	VSGWRLFKKISVFT
169 pep318	VSGWRLFKKISVF
170 pep319	VSGWRLFKKISV
171 pep320	VSGWRLCKKIS
172 pep326	VSGWRLFKKISGSMLFRVTINS
173 pep380	SSWKRLFRVTINS
174 pep383	SSWKRFRVTINS
175 pep386	SSWKRRVTINS
176 pep389	SSWKRTPDGSMLFRVTINS
177 pep392	SSWKRITPDGSMLFRVTINS
178 pep395	SSWKRLITPDGSMLFRVTINS
179 pep396	SSRGSMPLFRVTINSWK
180 pep397	SKRGSMPLFRVTINSWS
181 pep398	SWRGSMPLFRVTINS
182 pep400	SSRGSMPLFRVTIWK
183 pep401	SSWKRGSMMLYRVTINS
184 pep402	SSWKRGSMMLWRVTINS
185 pep403	SSWKRGSMMLHRVTINS
186 pep404	SSWKRGSLLFRVTINS
187 pep405	SSWKRGSKLFRVTINS
188 pep406	SSWKRGSRLLFRVTINS
189 pep407	SSWKRGSFLLFRVTINS
190 pep408	SSWKRGSWLFRVTINS
191 pep409	SSWKRGSMMLFRVSINS
192 pep410	SSWKRGSMMLFRVQINS
193 pep411	SSWKRGSMMLFRVNINS
194 SmTrip9-286 with cysteine	SSWKRGSMMLFRVTINSC
195 HiBit with cysteine	CVSGWRLPKKIS
196 SmTrip9-286 with azide	SSWKRGSMMLFRVTINSK(Aza)
197 HiBit with azide	(aza)KVSGWRLPKKIS
198 WT OgLuc dipeptide	GSLLFRVTINGVTGWRLCENILA
199 WT NanoLuc dipeptide	GSLLFRVTINVGVGTGWRLCERILA



TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
217415	MLFRVTINSGVGWK
218416	MLFRVTINSGVGWR
219418	GSMLFRVTINSGVG
220419	GSMLFRVTINSGVGW
221422	GSMLFRVTINSGVGWR
222423	GSMLFRVTINSGVGWK
223434	GSMLFRVTIWK
224435	GSMLFRVTINSWK
225477	MLFRVTINSWK
226478	MLFRVTINSWS
227479	MLFRVTIWS
228480	MLFRVTIWK
229481	MLFRVKINS
230482	GSMLFRVTINSWS
231483	GSMLFRVKINS
232484	GSMLFRVTIWS
233485	MLFRVNINS
234486	MLFRVWINS
235487	LLFRVKINS
236488	FLFRVTINS
237295	SSWKRGSQLFRVTINSV
238300	SSWKRGSQLFRVTINSVS
239412	SSWKRMLPRVTINSGVG
240413	SSWKRMLPRVTINSGVGW
241414	SSWKRMLPRVTINSGVGWR
242415	SSWKRMLPRVTINSGVGWK
243417	MLFRVTINSGVGWK
244418	SSWKRGSQLFRVTINSGVG
245419	SSWKRGSQLFRVTINSGVGW
246420	SSWKRGSQLFRVTINSGVGWR
247421	SSWKRGSQLFRVTINSGVGWK
248424	SSWKRGSQLFRVTINS
249425	SSWKRGSQLFRVKINS
250426	SSWKRGSQLFRVRINS
251427	SSWKRGSQLFRVWINS

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
252428	SSKRGSMFLFRVTIWSV
253429	SSKRGSMFLFRVTIWSVS
254430	SSWRGSMFLFRVTIKS
255431	KRSSGSMFLFRVTIWS
256432	SSKRMLFRVTIWS
257433	KRSSMLFRVTIWS
258445	GSMKFRVTINSWK
259450	GSMLFRKTINSWK
260455	GSMLFRVTKNSWK
261522	GKMLFRVTIWK
262523	GSMKFRVTINSWK
263524	GSMKFRVTIWK
264525	GRMLFRVTINSWK
265526	GRMLFRVTIWK
266527	GSMRFRVTINSWK
267528	GSMRFRVTIWK
268529	GDMLFRVTINSWK
269530	GDMLFRVTIWK
270531	GSMDFRVTINSWK
271532	GSMDFRVTIWK
272533	GEMLFRTINSWK
273535	GSMEFRVTINSWK
274536	GSMEFRVTIWK
275538	GSMLFRVTIWKVK
276539	GSMLFRVTIWSVK
277540	GSMLFRVTIWSK
278541	GSMLFRVTIWKWK
279542	GSMLFRVTIWKKK
280245	GSMLFRVTINS
281292.x	MLFRVTINS
282297.x	MLFVTINSV
283302.x	MLFRVTINSVS
284305.x	GSMLFRVTIN
285306.x	GSMLFRVTI
286307.x	SMLFRVTIN
287308.x	MLFRVTIN

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
288312.x	MLFRVTI
289399	SSKRGSMMLFRVTIWS
290273	GSMLFRVTINSGVSGWALFKKIS
291264	GSMLFRVTINSGVSGWRLFKKIS
292167	VSGWALFKKIS
293331	GSMLFRVTINSGVSGWRLFKKIS
294LgTrip 3546 (no His6)	MVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLA SVTPI MRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVPVDDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITTTGTLWNGNKIIDERLIT PD
295LgTrip 3546 (no His6)	atggtc ttccacactcgacgatttcgttgggacttggaaacagacagccgcctacaacctggaccaggccttg aacaggggagggtgtccatgttgc cagaatctccgcgtgtccgttaactccgcatacatgaggattgtccggag cggtgaaaatgcgcctgaagatcgacatccatgtcatcatccgtatgaaggctgagcgcgcgaccaaatggcc cagatcgaagagggtttaaagggtgttacccctgtggatcatcatcactttaagggtgatccgccttatggca cactggtaatcgcacggggttacccgcacaaactgtaactatttcggacggccgtatgaaggcatccgcgttt cgacggcaaaaagatcaactaccacagggaccctgtggacggcaacaaaattatcgacgagcgcctgtacc ccgcac
296LgTrip 2098 (no His6)	MVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLA SVTPI MRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVPVDDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIT PD
297LgTrip 2098 (no His6)	atggtc ttccacactcgaaaggatttcgttgggacttggaaacagacagccgcctacaacctggaccaggccttg aacaggggagggtgtccatgttgc cagaatctccgcgtgtccgttaactccgcatacatcggattgtccggag cggtgaaaatgcgcctgaagatcgacatccatgtcatcatccgtatgaaggctgagcgcgcgaccaaatggcc cagatcgaagagggtttaaagggtgttacccctgtggatcatcatcactttaagggtgatccgccttatggca cactggtaatcgcacggggttacccgcacatctgtaactatttoggacggccgtatgaaggcatccgcgttt cgacggcaaaaagatcaactgttaacagggaccctgtggacggcaacaaaattatcgacgagcgcctgtacc ccgcac
298157	SVSGWRLFKKIS
299158	NSVSGWRLFKKIS
300206	GWRLFKKIS
301264	GSMLFRVTINSGVSGWRLFKKIS
302489	GSMLFRVTINSWK (N-term unblocked)
303490	GSMLFRVTINSWK (C-term unblocked)
304491	GSMLFRVTINSWK (Both unblocked)
305492	GSMLFRVTINKWK
306493	GSMLFRVTIKSWK
307494	GSMLFRVTINRWK
308495	GSMLFRVTIRSWK
309496	GSMLFRVTINDWK
310497	GSMLFRVTIDSWK
311498	GSMLFRVTINEWK
312499	GSMLFRVTIESWK
313465	GSMRFRVTINSWK (Both termini unblocked)
314466	GSMDFRVTINSWK (Both termini unblocked)

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
315467	GSMEFRVTINSWK (Both termini unblocked)
316468	GSMLFRRTINSWK (Both termini unblocked)
317469	GSMLFRDTINSWK (Both termini unblocked)
318470	GSMLFRETINSWK (Both termini unblocked)
319472	GSMLFRVTDNSWK (Both termini unblocked)
320473	GSMLFRVTENSWK (Both termini unblocked)
321474	GSMKFRVTINSWK (Both termini unblocked)
322475	GSMLFRKTINSWK (Both termini unblocked)
323476	GSMLFRVTKNSWK (Both termini unblocked)
324436	GSMLFRVTINS (N-term unblocked)
325437	GSMLFRVSINS (N-term unblocked)
326438	GSMLFRVNINS (N-term unblocked)
327439	GSKLFRVTINS (N-term unblocked)
328440	GSRLFRVTINS (N-term unblocked)
329441	GSMWFRVTINS (N-term unblocked)
330442	GSMSFRVTINS (N-term unblocked)
331443	GSMNERVTINS (N-term unblocked)
332444	GSMKFRVTINS (N-term unblocked)
333446	GSMLFRWTINS (N-term unblocked)
334447	GSMLFRSTINS (N-term unblocked)
335448	GSMLFRNTINS (N-term unblocked)
336449	GSMLFRKTINS (N-term unblocked)
337451	GSMLFRVTWN S (N-term unblocked)
338452	GSMLFRVTSNS (N-term unblocked)
339453	GSMLFRVTNN S (N-term unblocked)
340454	GSMLFRVTKN S (N-term unblocked)
341456	GSMLFRVTIKS (N-term unblocked)
342Antares ATG 3802	MKHHHHHHVSKGEELIKENMRSKLYLEGSVINGHQFKCTHEGEKPYEGKQTNRIVKVEGGPLPFAFDILATHF MYGSKVF1KYPADLPDYFKQSPEGFTWERVMFEDGGVLATQDTSLQDGELIYNVKVRGVNFANGPVMQK KTGLWEPSTETMYPADGGLEGRCDKALKLVGGGLHVNFKTTYSKSKPVKMPGVHYVDRRLERIKEADNETYYV EQYEHAVARYSNLGGGFTLEDPGDWRLQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIH VIIPYEGLSGDQMGGQIEKIFKVYVPPVDHHFKVILHYGTLVIDGVTNPMDYFGRPYEGIAVFDGKKITVTGT LWNGNKLIDERLINPDGSLLFRVTINGVTGWRLCERILARHELIKENMRSKLYLEGSVINGHQFKCTHEGEKP YEGKQTNRIVKVEGGPLPFADPLDYFKQSPEGFTWERVMFEDGGVLATQD TSLQDGELIYNVKVRGVNFANGPVMQKKT1LWEPSTETMYPADGGLEGRCDKALKLVGGGLHVNFKTTYSK KKPVKMPGVHYVDRRLERIKEADNETYYEQEYEHAVARYSNLGGGMDELYK
343Antares ATG 3802	atggaaacatcacatcacatcatgtgagcaaggagaagaacttataaaaagaaaacatgcggctaaactgt acccgcgggctccgtcaatggcaccaggtaagtgtaccacgcgggtgagggaaagccctatgaggggaa gcgacacaacccatcaaggctcgcaagggggaccctccgttcgccttgatcttgcactcactt atgtacggaaacatgttataaaagtatccgcgcacccctgtattttaaacagtatcccgg gtttcacatgggaaagggtcatgtgtttgaggatggaggctgcactgcactcaggacacctcactgca ggacggcgagctgtatcacatgtgaaggctccgggtgtaaactccctgccaacggccctgtaatgcagaag aagaccctggatggagccgtccaccgaaacatgtaccctgtatgggtggctggagggccatgtgaca





TABLE 2-continued

Exemplary peptide, dipeptide, and polypeptide sequences.		
SEQ ID NO Name	Sequence	
	agccgacaacgaaacttatgttagagcaatatgagcacgcgcgtggctcgatttccaacttggcgaggaaatg gatgaactgtacaag	
352ATG 3817	MKHHHHHHFTLDDFVGDWEQTAAYNLQDVLLEQGGVSSLQNLAVSVPIMRIVRSGENALKIDIHVIIPYEGL SADQMAQIEEVFKVVPVDHHFKVILPYGTLVIDGTPNKLNYFGRPYEGIAVFDGKKITTGTLWNGNKII DERLITPDGGSSGGSGELIKENMRSKLYLEGSVNGHQFKCTHEGEKPYEGKQTNRKVVEGGPLPFAFDIL THPMYGSKVF1KYPADLPDYFKQSFPSEGFTWERVMVFEDGGVLTATQDTSLODGEIYNVKVRGVNPANGPV MQKKTGLWEPSTETMYPADGGLEGRCDKALKLVGGGLHLVNFKTTYSKSKPKVMPGVHYVDRRLERIK TYVEQYEHAVARYSNLGGGMDELYK	
353ATG 3817	Atgaaacatcaccatcaccatcatttcacactcgacgattcggtggggactggaaacagacagccgcata acctggaccaactgcgttgcacaggagggtgtgtccagttgtcagaatctgcgcgtgtccgtactccgat catgaggattgtccggcgcgtgaaaatgcctgaagatcgcacatccatgtcatatcccgtatgaaggctg agccgcgaccaaattggccagatcgaagagggtttaagggtgttgcacccgtgttgcatttcgttgc tgatccctgcctatggcacactgttgcacgggttacgcgcgaacaacttgcgttgcacttgc tgaaaggcatgcgcgtgttgcacggggaaaaatgcacccatccatgcgttgcacccatccatgc gacgacgcgttgcacccgcgcgttgcagggttgcgttgcacccatccatgcgttgcacccatccatgc gtaaaggatacttaggggttgcgttgcacccatccatgcgttgcacccatccatgcgttgc tgaaggataggactaatcgaataaaatgggttgcagggttgcgttgcacccatccatgc actcactttatgtatgggttgcgttgcacccatccatgcgttgcacccatccatgc tccctgcaggattcatggggcgcgttgcagggttgcgttgcagggttgcgttgc ttccttgcaaggacggggaaactgtatccatgcgttgcagggttgcgttgcagggttgc atgcagaagaaaaccttggggggagccctaacggagacaatgttgcacccatccatgc atgtataggcattgttgcgttgcacccatccatgcgttgcagggttgcgttgc aaaccagtcaagatgcgttgcacttgcgttgcagggttgcagggttgcagggttgc ctttagttagacaatgttgcgttgcagggttgcgttgcagggttgcagggttgc g	
354ATG 3818	MKHHHHHHFTLDDFVGDWEQTAAYNLQDVLLEQGGVSSLQNLAVSVPIMRIVRSGENALKIDIHVIIPYEGL SADQMAQIEEVFKVVPVDHHFKVILPYGTLVIDGTPNKLNYFGRPYEGIAVFDGKKITTGTLWNGNKII DERLITPDGRHELIKENMRSKLYLEGSVNGHQFKCTHEGEKPYEGKQTNRKVVEGGPLPFAFDILATHFMYG SKVFIKYPADLPDYFKQSFPSEGFTWERVMVFEDGGVLTATQDTSLODGEIYNVKVRGVNPANGPV GWEPSTETMYPADGGLEGRCDKALKLVGGGLHLVNFKTTYSKSKPKVMPGVHYVDRRLERIK EADNEYTYVEQY EHAVARYSNLGGGMDELYK	
355ATG 3818	Atgaaacatcaccatcaccatcatttcacactcgacgattcggtggggactggaaacagacagccgcata acctggaccaactgcgttgcacaggagggtgtgtccagttgtcagaatctgcgcgtgtccgtactccgat catgaggattgtccggcgcgtgaaaatgcctgaagatcgcacatccatgtcatatcccgtatgaaggctg agccgcgaccaaattggccagatcgaagagggtttaagggtgttgcacccgtgttgcacccatccatgc tgatccctgcctatggcacactgttgcacgggttacgcgcgaacaacttgcgttgcacccatccatgc tgaaggcatgcgcgtgttgcacggggaaaaatgcacccatccatgcgttgcacccatccatgc gacgacgcgttgcacccgcgcgttgcagggttgcgttgcacccatccatgcgttgcacccatccatgc ggtccgttacacgggttgcacccatccatgcgttgcacccatccatgcgttgcacccatccatgc tgcataaaaatgttgcagggttgcgttgcacccatccatgcgttgcacccatccatgc tctaaagggttgcagggttgcgttgcacccatccatgcgttgcacccatccatgc gggagccgttgcagggttgcgttgcagggttgcgttgcacccatccatgc actgtatccatgcgttgcagggttgcgttgcacccatccatgc ggggggaggccctaacggagacaatgttgcacccatccatgc actcgttgcagggttgcgttgcacccatccatgc ggagtgcactacgttgcagggttgcagggttgcagggttgc agcacgcgttgcgttgcagggttgcgttgcagggttgc g	
356LgTrip 2899 (LgTrip 2098 + Q42L)	MKHHHHHHFTLDDFVGDWEQTAAYNLQDVLLEQGGVSSLQNLAVSVPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVPVDHHFKVILPYGTLVIDGTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKI IDERLITPD	
357LgTrip 2899 (LgTrip 2098 + Q42L)	atgaaacatcaccatcaccatcatgttccacactcgaaagattcggtggggactggaaacagacagccgcct acaacactggaccaactgcgttgcacaggagggtgtgtccagttgtcagaatctgcgcgtgtccgtactcc gatccctaaaggattgtccggcgcgttgcacccatccatgc ctgaggatccatgcgttgcagggttgcacccatccatgc atgtatccatgcgttgcagggttgcacccatccatgc gtatgaaggcatgcgcgttgcacggggaaaaatgcacccatccatgc atgcacgcgttgcgttgcagggttgcgttgcagggttgc g	
358ATG-3930	atgAAACATCACCACCATCACCATGtCTTCACACTCGACGATTCTGTTGGGGACTGGGAACAGACAGCCGCCT ACAACCTGACCAAGTCTTGAACAGGGAGGTGTGTCAGTTGCTGAGATCTCGCCGTGTCCTAATCTC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTCTCATCCCGTATGAAGGT CTGAGGCCGACCAAATGCCAGATCGAAAGAGGTGTTAAGGTGGTGTACCCCTGTGGATGATCATCACTTAA AGGTGATCCTGCCCTATGCCACACTGGTAATCGACGGGTTACGCCAACAGCTGAACACTTCCGGACGCC GTATGAAGGCATGCCGTGTCAGCGAACAAAGTCACTGTAACAGGGACCCCTGTGGAACCGAACAAAATT	

TABLE 2-continued

Exemplary peptide, dipeptide, and polypeptide sequences.		
SEQ ID NO Name	Sequence	
359 ATG-3930	MKHHHHHHHVF1DDFVGDWEQTAAYNLDQVLEQGGVSSLLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGLVIDGVTPNKLNYFGRPYEGIAVEDG	
360 SmTrip9-15GS- ProteinG (ATG 4002)	gggagctccGGTGTGGCGGGAGCGGGAGGTGGAGGctcgACGGTATGACGTATAAGTTAACCTTAATGGTA AAAATTGAAAGCGAGACAATCTGAATTAAACCAACGCCGTGACAATTAACAAACTTGTTATTAAATGTTAAAACAT'TGA TAACGACAACCGGTGTTGACGGTGAATGGACTACGACGATCGCAGAAACCTTACGGTCACCAGAAAAACCA GAAGTGTGATCGCTGTTGAAACACCAGCCGTGACAATTAACAAACTTGTTATTAAATGTTAAAACAT'TGA AAGGCAGAAACAACACTGAGGCTGTGATGCTGACTGCGAGAGGTTGTCAAACAAATATGCAATGACA CGGTGTTGACGGTGAGTGGACTACGACGATCGCAGACTAACAGCTTACAGTTACTGAAAACCCAGAAGGTGATC GATCGCTGAGTTAACACCAACCGGTGACAACCTAACAAACTTGTTATTAAATGTTAAAACATTGAAAGGCGAAA CAACTACTAAAGCAGTAGACCGAGAAACTGCCAGAGGCTTCAAACAAATACGCTAACGACAACCGTGTGA TGGTGTGTTGGACTTATGATGATGCCAACAAACCTTACGGTAACGTGAGCATCATCACCATCACCACTAA	
361 SmTrip9-15GS- ProteinG (ATG 4002)	GSSGGGGSGGGGSGMTYKLILNGKTLKGETTEAVDAATAEKVKQYANDNGVDGEWTYDDATKTFVTEKP EVIDASELTPAVITYKLIVINGKTLKGETTTEAVDAATAEKVKQYANDNGVDGEWTYDDATKTFVTEKEPI DASELTPAVITYKLIVINGKTLKGETTTEAVDAATAEKFKQYANDNGVDGWWTYDDATKTFVTEHHHHHH	
362 ATG-3929	atgAAACATCACCATCACCATCATgtcTTCACACTCGACGATTCTGTTGGGACTGGGAACAGACAGCCGCT ACAAACCTGGCCAAGTCTTGACAGGGAGGTGTGTCAGTTGCTGCGAGATCTGCCGTGTCCTGTAACCTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTTCATCATCCGTATGAAGGT CTGAGCGCCGACCAAATGCCAGATCGAAGAGGTGTTAACAGTGGTGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCTATGCCACACTGGTAATCGACGGGTTACGCCAACAGCTGAACATTTCGGACGGCC GTATGAAGGCATGCCGTGTCACGGCTAA	
363 ATG-3929	Mkhhhhhvhft1ddfvgdweqtaaynlqdqvleqggvssllqnlavsvtpimrivrsgenalkidihviipyeg lsadqmaqieevfkvvypvdhhfkvilpyglvidgvtpnklnyfgrpyegiaivedg	
364 ATG-3930	atgAAACATCACCATCACCATCATgtcTTCACACTCGACGATTCTGTTGGGACTGGGAACAGACAGCCGCT ACAAACCTGGCCAAGTCTTGACAGGGAGGTGTGTCAGTTGCTGCGAGATCTGCCGTGTCCTGTAACCTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTTCATCATCCGTATGAAGGT CTGAGCGCCGACCAAATGCCAGATCGAAGAGGTGTTAACAGTGGTGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCTATGCCACACTGGTAATCGACGGGTTACGCCAACAGCTGAACATTTCGGACGGCC GTATGAAGGCATGCCGTGTCACGGCTAAAGATCACTACACACAGGGACCTGTAA	
365 ATG-3930	Mkhhhhhvhft1ddfvgdweqtaaynlqdqvleqggvssllqnlavsvtpimrivrsgenalkidihviipyeg lsadqmagieevfkvvypvdhhfkvilpyglvidgvtpnklnyfgrpyegiafdgkitttfgd	
366 ATG-3931	atgAAACATCACCATCACCATgtcTTCACACTCGACGATTCTGTTGGGACTGGGAACAGACAGCCGCT ACAAACCTGGCCAAGTCTTGACAGGGAGGTGTGTCAGTTGCTGCGAGATCTGCCGTGTCCTGTAACCTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTTCATCATCCGTATGAAGGT CTGAGCGCCGACCAAATGCCAGATCGAAGAGGTGTTAACAGTGGTGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCTATGCCACACTGGTAATCGACGGGTTACGCCAACAGCTGAACATTTCGGACGGCC GTATGAAGGCATGCCGTGTCACGGCTAAAGATCACTACACACAGGGACCTGTAA	
367 ATG-3931	Mkhhhhhvhft1ddfvgdweqtaaynlqdqvleqggvssllqnlavsvtpimrivrsgenalkidihviipyeg lsadqmagieevfkvvypvdhhfkvilpyglvidgvtpnklnyfgrpyegiafdgkitttfgt1	
368 ATG-3932	atgAAACATCACCATCACCATgtcTTCACACTCGACGATTCTGTTGGGACTGGGAACAGACAGCCGCT ACAAACCTGGCCAAGTCTTGACAGGGAGGTGTGTCAGTTGCTGCGAGATCTGCCGTGTCCTGTAACCTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTTCATCATCCGTATGAAGGT CTGAGCGCCGACCAAATGCCAGATCGAAGAGGTGTTAACAGTGGTGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCTATGCCACACTGGTAATCGACGGGTTACGCCAACAGCTGAACATTTCGGACGGCC GTATGAAGGCATGCCGTGTCACGGCTAAAGATCACTACACACAGGGACCTGTAA	
369 ATG-3932	Mkhhhhhvhft1ddfvgdweqtaaynlqdqvleqggvssllqnlavsvtpimrivrsgenalkidihviipyeg lsadqmagieevfkvvypvdhhfkvilpyglvidgvtpnklnyfgrpyegiafdgkitttfgtlwng	
370 ATG-4808	Atggttccgtgagccgtggggctgttcaagaagattagtcacactcgacgattctgtgggactgg aacagacacgcgcctacaacctcgaccaagtccgtacaggatgtccggagccgtgaaaatgccctgaagatcgacatccatgtcatc ctggccatcgatcgatccatgtccgtacactggtaatcgacggggttacgcggcaacaagctgaa ctatccgtatcgatccatgtccgtacactggtaatcgacggggttacgcggcaacaagctgaa aacggcaacaaaattatcgacgacgcgcgtatcgaccccgactaa	
371 ATG-4808	Mvsвшrlffkksft1ddfvgdweqtaaynlqdqvleqggvssllqnlavsvtpimrivrsgenalkidihvi ipyeglsadqmagieevfkvvypvdhhfkvilpyglvidgvtpnklnyfgrpyegiafdgkitttfgtlw ngnkiiderlitpd	
372 ATG-4809	Atggttccgtgagccgtggggctgttcaagaagattagccgtggccatccactcgacgatttc ttggggactggaaacagacacgcgcctacaacctggaccaagtccgtacaggatgtccggagccgtgaaaatgc cagaatctcgccgtccgtactccgtacatcgatcgatccatgtccgtacactggtaatcgacggggttacgcggcaacaagctgaa	

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
	atccatgtcatcatccccatgaaaggctcgagccgcgaccaatggcccgatcgaaagagggtttaaagggtgg tgtaccctgtggatgatcatacttaagggtatcgatctgcctatggcacactggtaatcgacggggttacgcca gaacaagctgaaactatttcggacggccgtatgaaaggcatacgccgttgcacggcaaaaagatcactaccaca gggaccctgtggacggcaacaaaattatcgacgagcgcctgatcaccccgactaa
373ATG-4809	MVSVSGWRLFKKISGSSGGFTLDDFVGDWQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKID IHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITT GTLWNGNKKIIDERLITPD
374ATG-4810	Atgggttcctgtggccgtggggctgttcaagaagattagcggtcgagccgtggctcgagccgtttcacac tcgacgatttcgttgggactggaaacagacagccgcctacaacacctggaccaagtcccttgcacaggagggt gttcagttgtcgacaaatccggctgtcgtaactccatcgatcatcgaggatgtccggagccgtgaaaatggcc ctgaagatcgacatccatgtcatccatgtatgaaagggtatcgccgcaccaatggcccgatcgaaagg tggtaaagggtgttacccctgtggatgatcatacttaagggtatctgcctatggcacactggtaatcg cggggttacggcaacaggtaactatttcggacggccgtatgaaaggcatacgccgttgcacggcaaaaag atcaactaccacaggacccctgtggacggcaacaaaattatcgacgagcgcctgatcaccccgactaa
375ATG-4810	MVSVSGWRLFKKISGSSGGSSGFTLDDFVGDWQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVRSGENA LKIDIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKK ITTTGTLWNGNKKIIDERLITPD
376ATG-4811	Atgggttcctgtggccgtggggctgttcaagaagattagcggtcgagccgtggctcgagccgtggctga gcgggttcacactcgacgatttcgttgggactggaaacagacagccgcctacaacacctggaccaagtcccttga acaggagggtgtccagttgtcgacaaatccggctgtcgtaactccatcgatcgaggatgtccggagcc ggtaaaggatccgttgcacatccatgtatccctgtatgaaagggtatcgccgcaccaatggcc agatcgaaagggtttaagggtgttacccctgtggatgatcatacttaagggtatctgcctatggcac actggtaatcgacgggttacccctgtggacggcaacaaaattatcgacgagcgcctgatcaccc cgccactaa
377ATG-4811	MVSVSGWRLFKKISGSSGGSSGGSSGFTLDDFVGDWQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVS GENALKIDIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAV FDGKKITTGTLWNGNKKIIDERLITPD
378ATG-4812	Atgggttcctgtggccgtggggctgttcaagaagattagcggtcgagccgtggctcgagccgtggctcg gcgggtgtcgacgggttccacactcgacgatttcgttgggactggaaacagacagccgcctacaacaccttga ccaagtccctgtacacgggggtgtcgatgtccgtcgacatccatcgatcgaggatgtccggagcc attgtccggagggtaaaggatccctgtacatccatgtatccctgtatgaaagggtatcgccgc accaatggcccgatcgaaagggtttaagggtgttacccctgtggatgatcatacttaagggtatcc gcctatggcacactggtaatcgacgggttacccctgtggacacaaggtaactatttcggacggccgtatgaaagg atccctgttgcacggcaaaaagatcactaccacaggacccctgtggacggcaacaaaattatcgacgagc gcctgtatcaccccgactaa
379ATG-4812	MVSVSGWRLFKKISGSSGGSSGGSSGFTLDDFVGDWQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMR IVRSGENALKIDIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEG IAVFDGKKITTGTLWNGNKKIIDERLITPD
380ATG-4813	Atgggttcctgtggccgtggggctgttcaagaagattagcggtcgagccgtggctcgagccgtggctcg gcgggtgtcgacgggttccacactcgacgatttcgttgggactggaaacagacagccgc ctacaacctggaccaagtccctgtacacggggagggtgtccgtcgacatccatcgatcatccctgtatgaa ccgatcatcgaggatgtccggagccgtgaaaatccctgtacatccatgtatcgacatccatgtatgaa gtctgagccgcaccaatggcccgatcgaaagggtttaagggtgttacccctgtggatgatcatact taagggtatctccctgtacatccatgtatcgacgggttacccctgtggacacaaggtaactatttcgg ccgtatggacggatcgccgttgcacggcaaaaagatcactaccacaggacccctgtggacggcaacaaa ttatcgacgagcgcctgtatcaccccgactaa
381ATG-4813	MVSVSGWRLFKKISGSSGGSSGGSSGFTLDDFVGDWQTAAYNLDQVLEQGGVSSLQNLAVSVT PIMRIVRSGENALKIDIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNKLNYFGR PYEGIAVFDGKKITTGTLWNGNKKIIDERLITPD
382ATG-4814	Atggtagccgtggccgttcaagaagattagcggtcgagccgtggctcgagccgt gcgtcgacgggtggctcgacgggttccacactcgacgatttcgttgggactggaaacagacagccgc cctggaccaagtccctgtacacggggagggtgtccgtcgacatccatcgatcatccctgtatgaa ataggatgtccggacgggtaaaatccctgtacatccatgtatcgacatccatgtatgaaagggt cgccgcaccaatggcccgatcgaaagggtttaagggtgttacccctgtggatgatcatacttaagg gtatccctgtatggcacactggtaatcgacgggttacccctgtggacacaaggtaactatttcgg acggcatcgccgttgcacggcaaaaagatcactaccacaggacccctgtggacggcaacaaaattatcg acgagcgcctgtatcaccccgactaa

TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
383ATG-4814	MVSGWRLFKKISGSSGGSSGGSSGGSSGGFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLAWSVTPI MIRIVRSGENALKIDIHVIIPYEGLSADQMAQIEEVFKVVPVDHHFKVILPYGTLVIDGVTPNKLNYFGRPY EGIAVFDGKKITTGTLWNGNKIIDERLITPD
384ATG-4815	Atggcttcacactcgacgatttcgttgggacttggaaacagacagccgcataacctggaccaggatccttg aacaggggagggtgtcccgatgttcgtcagaatctcgccgtccgttaactccgatcatggaggatgtccggag cggtaaaatgcctgaagatcgacatccatgtcatatccgtatgaaggctgagccgcaccaaattggcc cagatcgaaagggtttaaagggtgttacccctgtggatgtatcatactttaagggtgatccgcctatggca cactggtaatcgacgggttacggcaacaactgtgaactattccggacggcgtatgaaggcatcgccgttt cgacggcaaaaatcgactaccacaggacccctgtggaaacggcaacaaattatcgacgacgcgtatcacc cccacgtttccgtgagccgtggccgttcaagaagattagctaa
385ATG-4815	MVFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLAWSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVPVDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITTGTLWNGNKIIDERLIT PDVSVSGWRLFKKIS
386ATG-4816	Atggcttcacactcgacgatttcgttgggacttggaaacagacagccgcataacctggaccaggatccttg aacaggggagggtgtcccgatgttcgtcagaatctcgccgtccgttaactccgatcatggaggatgtccggag cggtaaaatgcctgaagatcgacatccatgtcatatccgtatgaaggctgagccgcaccaaattggcc cagatcgaaagggtttaaagggtgttacccctgtggatgtatcatactttaagggtgatccgcctatggca cactggtaatcgacgggttacggcaacaactgtgaactattccggacggcgtatgaaggcatcgccgttt cgacggcaaaaatcgactaccacaggacccctgtggaaacggcaacaaattatcgacgacgcgtatcacc cccacgtttccgtgagccgtggccgttcaagaagattagctaa
387ATG-4816	MVFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLAWSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVPVDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITTGTLWNGNKIIDERLIT PDGSSGVSGWRLFKKIS
388ATG-4817	Atggcttcacactcgacgatttcgttgggacttggaaacagacagccgcataacctggaccaggatccttg aacaggggagggtgtcccgatgttcgtcagaatctcgccgtccgttaactccgatcatggaggatgtccggag cggtaaaatgcctgaagatcgacatccatgtcatatccgtatgaaggctgagccgcaccaaattggcc cagatcgaaagggtttaaagggtgttacccctgtggatgtatcatactttaagggtgatccgcctatggca cactggtaatcgacgggttacggcaacaactgtgaactattccggacggcgtatgaaggcatcgccgttt cgacggcaaaaatcgactaccacaggacccctgtggaaacggcaacaaattatcgacgacgcgtatcacc cccacgtttccgtgagccgtggccgttcaagaagattagctaa
389ATG-4817	MVFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLAWSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVPVDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITTGTLWNGNKIIDERLIT PDGSSGVSGWRLFKKIS
390ATG-4818	Atggcttcacactcgacgatttcgttgggacttggaaacagacagccgcataacctggaccaggatccttg aacaggggagggtgtcccgatgttcgtcagaatctcgccgtccgttaactccgatcatggaggatgtccggag cggtaaaatgcctgaagatcgacatccatgtcatatccgtatgaaggctgagccgcaccaaattggcc cagatcgaaagggtttaaagggtgttacccctgtggatgtatcatactttaagggtgatccgcctatggca cactggtaatcgacgggttacggcaacaactgtgaactattccggacggcgtatgaaggcatcgccgttt cgacggcaaaaatcgactaccacaggacccctgtggaaacggcaacaaattatcgacgacgcgtatcacc cccacgtttccgtgagccgtggccgttcaagaagattagctaa
391ATG-4818	MVFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLAWSVTPIMRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVPVDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITTGTLWNGNKIIDERLIT PDGSSGVSGWRLFKKIS
392ATG-4819	Atggttccgtgagccgtggccgttcaagaagatttagttcacactcgacgatttcgttgggactgg aacagacacgcgcctacaacctggaccaacttcgttgcacaggagggtgtccatgtcagaatctcg cgttccgttaactccgatcatggaggattgtccggagccgtgaaaatgcctgaagatcgacatccatgtcatc atccctgtatggatgtccgttgcggccgaccaatggcccaatgtggatgtatccgcctatggca atggatcatactttaagggtgttacccctgtggacacttccggacggcgtatggcaacactggcc ctatccggccgtatggacggatgtccgttgcacccatggcaaaaatcgactaccacaggacccctgtgg aacggcaacaaaattatcgacgacgcgtatcaccatccccgaccatcaccatcattaa
393ATG-4819	MVSVSGWRLFKKISFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLAWSVTPIMRIVRSGENALKIDIHVI IPYEGLSADQMAQIEEVFKVVPVDHHFKVILPYGTLVIDGVTPNKLNYFGRPYEGIAVFDGKKITTGTLW NGNKIIDERLITPDHHHHHH
394ATG-4820	Atggttccgtgagccgtggccgttcaagaagatttagggccagtcgggttccactcgacgatttcg ttggggactggaaacagacacgcgcctacaacctggaccaacttcgttgcacaggagggtgtccatgt gcagaatctcgccgtccgttaactccgatcatggaggattgtccggagccgtgaaaatgcctgaagatcg atccatgtcatcatccgtatggacggatgtccgttgcacactggtaatcgacgggggttacgg tgtatccctgtggatgtatccgtttaagggtgttacccctgtggacacttccggacactggtaatcg acggcaacacttccgttgcacggccgtatggacggatgtccgttgcacggcaaaaatcgactacc gggacccctgtggaaacggcaacaaaattatcgacgacgcgtatcaccatccccgaccatcaccatcattaa



TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>	
SEQ ID NO Name	Sequence
	gatcatgaggattgtccggagcggtaaaaatgccctgaagatcgacatccatgtcatatcccgtatgaaggt ctgagcgcgaccataatggcccgatcgaagagggtttaagggtgttgcacccgtggatgtatcatcacttta aggtgtatcctgcctatggcacactgttaatcgacgggttacgcccgaacaagctgaactatccggacggcc gtatgaaggcattccgtgtcgacggcaaaaagatcactaccacaggacccgtggaaacggcaacaaaatt atcgacgacgcctgtatcacccccgcacggctcgacgggttccgtgacggcgtggcggcttcaagaagatgtcaa
407ATG-4826	MKHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPMLNYFGRPYEGIAVFDGKKITTTGTLWNGNKI IDERLITPDVSWSGVRLFKKIS
408ATG-4827	Atgaaacatcaccatcaccatcatgtttcacactcgacgatttcgttgggactggaaacagacagccgcct acaacctggaccaagtccatgtggacagggtgttgcacccgtggatgtatccgcgttccgttaactcc gatcatgaggattgtccggacggcgatcgaagagggtttaagggtgttgcacccgtggatgtatcatcacttta aggtgtatcctgcctatggcacactgttaatcgacgggttacgcccgaacaagctgaactatccggacggcc gtatgaaggcattccgtgtcgacggcaaaaagatcactaccacaggacccgtggaaacggcaacaaaatt atcgacgacgcctgtatcacccccgcacggctcgacgggttccgtgacggcgtggcggcttcaagaaga ttagctaa
409ATG-4827	MKHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPMLNYFGRPYEGIAVFDGKKITTTGTLWNGNKI IDERLITPDGSSGVSGWRLFKKIS
410ATG-4828	Atgaaacatcaccatcaccatcatgtttcacactcgacgatttcgttgggactggaaacagacagccgcct acaacctggaccaagtccatgtggacagggtgttgcacccgtggatgtatccgcgttccgttaactcc gatcatgaggattgtccggacggcgatcgaagagggtttaagggtgttgcacccgtggatgtatcatcacttta aggtgtatcctgcctatggcacactgttaatcgacgggttacgcccgaacaagctgaactatccggacggcc gtatgaaggcattccgtgtcgacggcaaaaagatcactaccacaggacccgtggaaacggcaacaaaatt atcgacgacgcctgtatcacccccgcacggctcgacgggttccgtgacggcgtggcggcttcaagaaga agaagatgtcaa
411ATG-4828	MKHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPMLNYFGRPYEGIAVFDGKKITTTGTLWNGNKI IDERLITPDGSSGGSSGVSGWRLFKKIS
412ATG-4829	Atgaaacatcaccatcaccatcatgtttcacactcgacgatttcgttgggactggaaacagacagccgcct acaacctggaccaagtccatgtggacagggtgttgcacccgtggatgtatccgcgttccgttaactcc gatcatgaggattgtccggacggcgatcgaagagggtttaagggtgttgcacccgtggatgtatcatcacttta aggtgtatcctgcctatggcacactgttaatcgacgggttacgcccgaacaagctgaactatccggacggcc gtatgaaggcattccgtgtcgacggcaaaaagatcactaccacaggacccgtggaaacggcaacaaaatt atcgacgacgcctgtatcacccccgcacggctcgacgggttccgtgacggcgtggcggcttcaagaaga tggtcagaagatgtcaa
413ATG-4829	MKHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPMLNYFGRPYEGIAVFDGKKITTTGTLWNGNKI IDERLITPDGSSGGSSGVSGWRLFKKIS
414ATG-2623	atggcttcacactcgaaaggatttcgttgggactggaaacagacagccgcctacaacctggaccaatccttgc aacaggggagggtgtccatgtggatcgacatccatgtccatccgtatggatgttgcggccacaaaatggcc cggtggaaaatggccatgtggatcgacatccatgtccatccgtatggatgttgcggccacaaaatggcc cagatcgaaagggtttaagggtgttgcacccgtggatgtatcatcactttaagggtgttgcggccatggcc cacttgttacccgtggatgttgcacccgtggatgtatcatcactttaagggtgttgcggccatggccatggcc cgacggcaaaaagatcactgttaacaggacccgtggaaacggcaacaaaattatcgacgacgcctgtatcacc cccacggcttccatgttccgtggatgttgcacccatcatcaccatcaccactaa
415ATG-2623	MVFLEDVGDWEQTAAYNLQVLEQGGVSSLQNLAVSVTPIQRIVRSGENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTNPMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKI IDERLITPDGSMFLFRVTINSHHHHHH
416ATG-3745	atggtgacggcgctggcgctgtcaagaaggattggcaccatcaccatcaccatcacttcacactcgacg atttcgttgggactggaaacagacagccgcctacaacctggaccaatccttgcggccatggatgttgcgg tttgcgtggatgttgcacccgtggatgttgcacccgtggatgtatcatcactttaagggtgttgcggccatgg atcgacatccatgtcatcaccatccgtatggacgggtctggacggccgacccatggccatggacggccatgg agggtgttgcacccgtggatgtatcatcactttaagggtgttgcggccatggacggccatggacggccatgg tacggccgacccatggacggccatggacggccatggacggccatggacggccatggacggccatggacggcc accacacaggacccgtggaaacggcaacaaaattatcgacgacgcctgtatcaccatcaccactaa



TABLE 2-continued

Exemplary peptide, dipeptide, and polypeptide sequences.		
SEQ ID NO Name	Sequence	
429ATG-3901	MVFTLEDVGDWKQTAAYNLQDVLEQGGVSSLQNLA SVTPIQRMVRS GENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIT PDGSMLFRVTINSHHHHHH	
430ATG-3945	atggcttcacactcgaa gatttgcgtgggactt ggaagc agac agccgc taca ac ctgg acca agt cctg aacaggagggtgtccagg tttgcgtccgatctccgcgtgtccgtactcccgatccaaaggatggtccggag cggtaaaaatgcctgaagatcgacatccatgtcatccgtatgaagg tctgagcgcgacc aaatggcc cagatcgaagagggtttaa ggtgttacccctgtggatcatcactttaagg tgatectgcctt atggca cactggtaatcgcacggggttacccgaacatctgtgaactatttgcggacccgtatgaaggatcgcgatc cgacggcaaaagatcactgtaa cagggacccgtt ggaac gacgt caaaattatc gac gac gccc tgc ccgcacggctccatgtcttccaga taacccatcaacaggccatcatcaccatcaccactaa	
431ATG-3945	MVFTLEDVGDWKQTAAYNLQDVLEQGGVSSLQNLA SVTPIQRMVRS GENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNDVKIIDERLIT PDGSMLFRVTINSHHHHHH	
432ATG-3984	atggcttcacactcgaa gatttgcgtgggactt ggaagc agac agccgc taca ac ctgg acca agt cctg aacaggagggtgtccagg tttgcgtccgatctccgcgtgtccgtactcccgatccaaaggatggtccggag cggtaaaaatgcctgaagatcgacatccatgtcatccgtatgaagg tctgagcgcgacc aaatggcc cagatcgaagagggtttaa ggtgttacccctgtggatcatcactttaagg tgatectgcctt atggca cactggtaatcgcacggggttacccgaacatctgtgaactatttgcggacccgtatgaaggatcgc cgacggcaaaagatcactgtaa cagggacccgtt ggaac gacgt caaaattatc gac gac gccc tgc ccgcacggctccatgtcttccaga taacccatcaacaggccatcatcaccatcaccactaa	
433ATG-3984	MVFTLEDVGDWKQTAAYNLQDVLEQGGVSSLQNLA SVTPIQRMVRS GENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNDVKIIDERLIT PDGSMSFRVTINSHHHHHH	
434ATG-4147	atggcttcacactcgaa gatttgcgtgggactt ggaagc agac agccgc taca ac ctgg acca agt cctg aacaggagggtgtccagg tttgcgtccgatctccgcgtgtccgtactcccgatccaaaggatggtccggag cggtaaaaatgcctgaagatcgacatccatgtcatccgtatgaagg tctgagcgcgacc aaatggcc cagatcgaagagggtttaa ggtgttacccctgtggatcatcactttaagg tgatectgcctt atggca cactggtaatcgcacggggttacccgaacatctgtgaactatttgcggacccgtatgaaggatcgc cgacggcaaaagatcactgtaa cagggacccgtt ggaac gacgt caaaattatc gac gac gccc tgc ccgcacggctccatgtcttccaga taacccatcaacaggccatcatcaccatcaccactaa	
435ATG-4147	MVFTLEDVGDWKQTAAYNLQDVLEQGGVSSLQNLA SVTPIQRMVRS GENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLIT PDGSMSFRVTINSHHHHHH	
436ATG-4166	atggcttcacactcgaa gatttgcgtgggactt ggaagc agac agccgc taca ac ctgg acca agt cctg aacaggagggtgtccagg tttgcgtccgatctccgcgtgtccgtactcccgatccaaaggatggtccggag cggtaaaaatgcctgaagatcgacatccatgtcatccgtatgaagg tctgagcgcgacc aaatggcc cagatcgaagagggtttaa ggtgttacccctgtggatcatcactttaagg tgatectgcctt atggca cactggtaatcgcacggggttacccgaacatctgtgaactatttgcggacccgtatgaaggatcgc cgacggcaaaagatcactgtaa cagggacccgtt ggaac gacgt caaaattatc gac gac gccc tgc ccgcacggctccatgtcttccaga taacccatcaacaggccatcatcaccatcaccactaa	
437ATG-4166	MVFTLEDVGDWKQTAAYNLQDVLEQGGVSSLQNLA SVTPIQRMVRS GENALKIDIHVIIPYEGLSADQMA QIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGVKIIDERLIT PDGSMSFRVTINSHHHHHH	
438ATG-5037	ATGAAACATCACCACCATCATGTCTCACACTCGACGATTCTGGGACTGGAACAGACAGCCGCCT ACAACCTGGCCAAGTCCTGAACAGGGAGGTGTGTCAGTTGCTCAGAATCTGCCGTGCGTAACCTC GATCATGAGGATTGTCCGGAGCGGTAAAATGCCCTGAAGATCGACATCATGTCTCATCCCCTATGAAGGT CTGAGCGCCGACCAAATGCCCGAGATCGAAGAGGTGTTAAGGTGGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCTATGGCACACTCGGTAACTGACGGGTTACGCCAACAGCTGAACATTTCGGACACCC GTATGAAGGCATGCCGTTCGACGGCAAAAGACTACTACACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCCTGATCACCCCCGACTAA	
439ATG-5037	MKHHHHHHVFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLA SVTPIRMIVRS GENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPYEGIAVFDGKKITVTGTLWNGNKI IDERLITPD	
440ATG-5038	ATGAAACATCACCACCATCATGTCTCACACTCGACGATTCTGGGACTGGAACAGACAGCCGCCT ACAACCTGGCCAAGTCCTGAACAGGGAGGTGTGTCAGTTGCTCAGAATCTGCCGTGCGTAACCTC GATCATGAGGATTGTCCGGAGCGGTAAAATGCCCTGAAGATCGACATCATGTCTCATCCCCTATGAAGGT CTGAGCGCCGACCAAATGCCCGAGATCGAAGAGGTGTTAAGGTGGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCTATGGCACACTCGGTAACTGACGGGTTACGCCAACAGCTGAACATTTCGGACACCC	

TABLE 2-continued

		<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>
SEQ ID NO	Name	Sequence
		GTATGAAGGCATCGCCGTGTCGACGGCGAGAACAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCCTGATCACCCCCGACTAA
441 ATG-5038		MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVEDGEKITTTGTLWNGNKI IDERLITPD
442 ATG-5039		ATGAAACATCACCACCATCACCATCATGTCCTCACACTCGACGATTCGTTGGGACTGGGAACAGAACGCCGCT ACAACCTGGCCAAGTCCTTGAACAGGGAGGTGTGTCAGTTGCTGAGATCTGCCGTGTCCTAACTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTATCATCCGTATGAAGGT CTGAGCGCGACCAAATGCCAGATCGAAAGAGGTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA AGGTGATCTGCCTATGCCAACACTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA GTATGAAGGCATCGCCGTGTCGACGCCAAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCCTGATCACCCCCGACTAA
443 ATG-5039		MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKKITTGTLWNGNKI IDERLITPD
444 ATG-5040		ATGAAACATCACCACCATCACCATCATGTCCTCACACTCGACGATTCGTTGGGACTGGGAACAGAACGCCGCT ACAACCTGGCCAAGTCCTTGAACAGGGAGGTGTGTCAGTTGCTGAGATCTGCCGTGTCCTAACTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTATCATCCGTATGAAGGT CTGAGCGCGACCAAATGCCAGATCGAAAGAGGTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA AGGTGATCTGCCTATGCCAACACTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA GTATGAAGGCATCGCCGTGTCGACGCCAAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCCTGATCGATCCCGACTAA
445 ATG-5040		MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKKITTGTLWNGNKI IDERLIDPD
446 ATG-5041		ATGAAACATCACCACCATCACCATCATGTCCTCACACTCGACGATTCGTTGGGACTGGGAACAGAACGCCGCT ACAACCTGGCCAAGTCCTTGAACAGGGAGGTGTGTCAGTTGCTGAGATCTGCCGTGTCCTAACTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTATCATCCGTATGAAGGT CTGAGCGCGACCAAATGCCAGATCGAAAGAGGTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA AGGTGATCTGCCTATGCCAACACTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA GTATGAAGGCATCGCCGTGTCGACGCCAAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCCTGATCACCGATGACTAA
447 ATG-5041		MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKKITTGTLWNGNKI IDERLITDD
448 ATG-5135		ATGAAACATCACCACCATCACCATCATGTCCTCACACTCGACGATTCGTTGGGACTGGGAACAGAACGCCGCT ACAACCTGGCCAAGTCCTTGAACAGGGAGGTGTGTCAGTTGCTGAGATCTGCCGTGTCCTAACTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTATCATCCGTATGAAGGT CTGAGCGCGACCAAATGCCAGATCGAAAGAGGTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA AGGTGATCTGCCTATGCCAACACTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA GTATGAAGGCATCGCCGTGTCGACGCCAAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCCTGATCACCCCCGACTAA
449 ATG-5135		MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVEDGEKITTTGTLWNGNKI IDERLITPD
450 ATG-5146 (LgTrip 5146)		ATGAAACATCACCACCATCACCATCATGTCCTCACACTCGACGATTCGTTGGGACTGGGAACAGAACGCCGCT ACAACCTGGCCAAGTCCTTGAACAGGGAGGTGTGTCAGTTGCTGAGATCTGCCGTGTCCTAACTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTATCATCCGTATGAAGGT CTGAGCGCGACCAAATGCCAGATCGAAAGAGGTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA AGGTGATCTGCCTATGCCAACACTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA GTATGAAGGCATCGCCGTGTCGACGCCAAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCCTGATCGATCCCGACTAA
451 ATG-5146 (LgTrip 5146)		MKHHHHHHHVFTLDDFVGDWEQTAAYNLQVLEQGGVSSLLQNLAVSVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDHHFKVILPYGTLVIDGVTNPKNLYFGRPYEGIAVFDGKIKTTGTLWNGNKI IDERLIDPD
452 ATG-5158		ATGAAACATCACCACCATCACCATCATGTCCTCACACTCGACGATTCGTTGGGACTGGGAACAGAACGCCGCT ACAACCTGGCCAAGTCCTTGAACAGGGAGGTGTGTCAGTTGCTGAGATCTGCCGTGTCCTAACTCC GATCATGAGGATTGTCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTATCATCCGTATGAAGGT CTGAGCGCGACCAAATGCCAGATCGAAAGAGGTGTTAAGGTGGTGTACCCGTGGATGATCATCACTTA

TABLE 2-continued

		<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>
SEQ ID NO Name	Sequence	
	AGGTGATCCTGCCCTATGGCACACTGGTAATCGACGGGTTACGCCAACAAAGCTGAACATTTCGGACACCC GTATGAAGGCATGCCGTGTCACGCGAGAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCTGATCGATGACTAA	
453 ATG-5158	MKHHHHHHHVFVLDLFDVGDWEQTAAYNLQVLEQGGVSSLQLNLA SVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGLVIDGVTPNKLNYFGHPYEGIAVEDGEKI TTGTLWNGNKI IDERLIDDD	
454 ATG-5260	ATGAAACATCACCACCATCATGATTTCACACTCGACGATTTCGTTGGGACTGGAACAGACAGCCGCT ACAACCTGGACCAAGTCTTGACACAGGGAGGTGTCCAGTTGCTCAGAATCTGCCGTGCGTAACCTC GATCATGAGGATTGTCCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTCTCATCCGTATGAAGGT CTGAGCGCCGACCAAATGGCCAGATCGAAGAGGTGTTAAGGTGGTGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCATCGGCACACTGGTAATCGACGGGTTACGCCAACAGCTGAACATTTCGGACACCC GTATGAAGGCATGCCGTGTCACGCGAGAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCTGATCGATCCCGACTAA	
455 ATG-5260	MKHHHHHHHVFVLDLFDVGDWEQTAAYNLQVLEQGGVSSLQLNLA SVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPIGLVIDGVTPNKLNYFGHPYEGIAVDGEKI TTGTLWNGNKI IDERLIDPD	
456 ATG-5266	ATGAAACATCACCACCATCATGTCTTCACACTCGACGATTTCGTTGGGACTGGAACAGACAGCCGCT ACAACCTGGACCAAGTCTTGACACAGGGAGGTGTCCAGTTGCTCAGAATCTGCCGTGCGTAACCTC GATCATGAGGATTGTCCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTCTCATCCGTATGAAGGT CTGAGCGCCGACCAAATGGCCAGATCGAAGAGGTGTTAAGGTGGTGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCATCGGCACACTGGTAATCGACGGGTTACGCCAACAGCTGAACATTTCGGACACCC GTATGAAGGCATGCCGTGTCACGCGAGAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCTGATCGATCCCGACTAA	
457 ATG-5266	MKHHHHHHHVFVLDLFDVGDWEQTAAYNLQVLEQGGVSSLQLNLA SVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPIGLVIDGVTPNKLNYFGHPYEGIAVEDGEKI TTGTLWNGNKI IDERLIDPD	
458 ATG-5267	ATGAAACATCACCACCATCATGTCTTCACACTCGACGATTTCGTTGGGACTGGAACAGACAGCCGCT ACAACCTGGACCAAGTCTTGACACAGGGAGGTGTCCAGTTGCTCAGAATCTGCCGTGCGTAACCTC GATCATGAGGATTGTCCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTCTCATCCGTATGAAGGT CTGAGCGCCGACCAAATGGCCAGATCGAAGAGGTGTTAAGGTGGTGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCATCGGCACACTGGTAATCGACGGGTTACGCCAACAGCTGAACATTTCGGACACCC GTATGAAGGCATGCCGTGTCACGCGAGAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCTGATCGATCCCGACTAA	
459 ATG-5267	MKHHHHHHHVFVLDLFDVGDWEQTAAYNLQVLEQGGVSSLQLNLA SVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPIGLVIDGVTPNKLNYFGHPYEGIADFDGEKI TTGTLWNGNKI IDERLIDPD	
460 ATG-5278	ATGAAACATCACCACCATCATGTCTTCACACTCGACGATTTCGTTGGGACTGGAACAGACAGCCGCT ACAACCTGGACCAAGTCTTGACACAGGGAGGTGTCCAGTTGCTCAGAATCTGCCGTGCGTAACCTC GATCATGAGGATTGTCCGGAGCGGTGAAATGCCCTGAAGATCGACATCCATGTCTCATCCGTATGAAGGT CTGAGCGCCGACCAAATGGCCAGATCGAAGAGGTGTTAAGGTGGTGTACCCCTGTGGATGATCATCACTTTA AGGTGATCCTGCCCATCGGCACACTGGTAATCGACGGGAGACGCCAACAGCTGAACATTTCGGACACCC GTATGAAGGCATGCCGTGTCACGCGAGAAGATCACTACCACAGGGACCCGTGGAACGGCAACAAAATT ATCGACGAGCGCTGATCGATCCCGACTAA	
461 ATG-5278	MKHHHHHHHVFVLDLFDVGDWEQTAAYNLQVLEQGGVSSLQLNLA SVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPIGLVIDGVTPNKLNYFGHPYEGIADFDGEKI TTGTLWNGNKI IDERLIDPD	
462 ATG-4794	atggaaacatcaccatcaccatcatgtcttcacactcgacgatttcgttgggactggAACAGACAGCCGCT acaacacctggaccaagtcttgcacaggagggtgtgtccagttgtcagaatctccgtgtccgttaactcc gatcatgaggattgtccggagccgtaaaatgccctgaagatcgacatccatgtctcatccgtatgaaggt ctgagcgccgaccaaattggcccagatcgaaagggtgtttaaagggtgttacccctgtggatgatcatcactta agggtgatctgcctatggccactatcggtatcgacgggagacgccAACAGCTGAACATTTCGGACACCC gtatgaaggcattcgacggcggagaaatcgacgggagacgccAACAGCTGAACATTTCGGACACCC atcgacgagcgctgatcgatcccgactaa	
463 ATG-4794	MKHHHHHHHVFVLDLFDVGDWEQTAAYNLQVLEQGGVSSLQLNLA SVTPIMRIVRSGENALKIDIHVIIPYEG LSADQMAQIEEVFKVVYPVDDHHFKVILPYGLVID	
720 HALOTAG	MAEIGTGFPPDFPHYVEVLGERMHYVDVGPDRGTPVFLHGNPTSSYWRNIIPH VAPTHRCIAPD LIGMGKSD KPD LGYFFDDHVRFMADFIEALGLEEEVVLVIHDWGSALGFHWAKRNPERVKGIAFM E FIR P I P T D E W P E F A R ETPQAFRITDVGRKLIIIDQNVFIEGTLPMGVYRPLTEVMDHYREPFLNPVDR EPLWRFPNELPIAGEPANIV ALVEEYMDWLHQSPVPKLLFWGTPGVLI PPAEAARLAKSLPNCKAVD IGPGLNLLQEDNPDLIGSEIARWLST LEISG	



TABLE 2-continued

<u>Exemplary peptide, dipeptide, and polypeptide sequences.</u>		
SEQ ID NO Name	Sequence	
730ATG4551 SmTrip9 (760) - 15GS-G	MKKMLFRVTIQKWKGSGGGGGGGGSGMTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWT YDDATKTFTVTEKPEVIDASELTPAVTTYKLVLINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDD ATKTFTVTEKPEVIDASELTPAVTTYKLVLINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATK TFTVTEHHHHHH	

TABLE 3

<u>Exemplary peptide sequences.</u>		
SEQ ID NO.	Sequence	Pep ID
16	GKMLFRVTINSWK	521 (SmTrip9 Pep521)
17	VSVSGWRLFKKIS	289 (SmTrip10 Pep289; VSHiBiT)
18	VSGWRLFRRIS	691 (SmTrip10 Pep691; HW-0977)
19	VSVSGWRLFRRIS	692 (SmTrip10 Pep692; HW-1053)
20	GRMLFRVTINSWR	693 (SmTrip9 Pep693; HW- 0984 (SulfoSE-PEG3); HW-1042 (SulfoSE-PEG6))
21	GKMLFRVTINKWK	743 (SmTrip9 Pep743)
22	DKLLFTVTIEKYK	759 (SmTrip9 Pep759)
23	KKMLFRVTIQKWK	760 (SmTrip9 Pep760)
24	GRLLFVVVIERYR	895 (SmTrip9 Pep895; HW- 1010 (SulfoSE-PEG3); HW-1043 (SulfoSE-PEG6))
25	RRMLFRVTIQRWR	929 (SmTrip9 Pep929; HW- 1055 (SulfoSE-PEG3); HW-1052 (SulfoSE-PEG6))
26	VSGWRLFRRISC	937 (SmTrip9 Pep937; HW-0987)
27	GRMLFRVTINSWRC	938 (SmTrip9 Pep938; HW-0992 (TAMRA); HW-1050 (SA))
464	VSGWRLFKKIS	86
465	VSGWRLFKKI	229
466	WNNGNKIIDERLITPD	543
467	KKITTTGTWLWNGR	544

TABLE 3 -continued

Exemplary peptide sequences.		
Pep ID	SEQ ID NO.	Sequence
545	468	R PY E G I A V F D G K
591	469	G K M L F R V T I W K V S V S G W R L F K K I S
592	470	G K M L F R V T I W K V S G W R L F K K I S
593	471	G S M K F R V T I N S W K V S V S G W R L F K K I S
594	472	G S M K F R V T I N S W K V S G W R L F K K I S
595	473	G S M K F R V T I N S W K N V T G Y R L F K K I S N
596	474	G S M K F R V T I N S W K V T G Y R L F E K I S
597	475	G S M K F R V T I W K V S V S G W R L F K K I S
598	476	G S M K F R V T I W K V S G W R L F K K I S
599	477	G R M L F R V T I N S W K V S V S G W R L F K K I S
600	478	G R M L F R V T I N S W K V S G W R L F K K I S
601	479	G R M L F R V T I W K V S V S G W R L F K K I S
602	480	G R M L F R V T I W K V S G W R L F K K I S
603	481	G S M L F R V T I N S V S V S G W R L F K K I S
604	482	G S M L F K V T I N S V S V S G W R L F K K I S
605	483	G S M L F Q V T I N S V S G W R L F K K I S
606	484	G S M L F E V T I N S V S G W R L F K K I S
607	485	G S M L F N V T I N S V S G W R L F K K I S
608	486	G R P Y E G I A V F D G K K I T T T G T L
609	487	G S M K F R V T I N S W K V T G Y R L F E K E S
610	488	G S M K F R V T I N S W K V E G Y R L F E K I S
611	489	K K I T T T G T L W N G N K I I D E R L I T P D
612	490	W N G N K I I D E R L I T P D G S M L F R V T I N S
671	491	G K M L F R V T I Q K W K
668	492	G K M L F R V T I G K W K
727	493	G K M L F R V T I G R W K
669	494	G K M L F R V T I G N W K
674	495	G K M L F R V T I Q N W K
702	496	G K M L F R V T I D K W K
703	497	G K M L F R V T I E K W K
705	498	E K M L F R V T I E S W K
724	499	E K L L F R V T I E S W K
725	500	E K L L F R V T I E S Y K
730	501	G K M L F R V T I E R W K
731	502	G K M L F R V T I D R W K

TABLE 3 -continued

Exemplary peptide sequences.		
Pep ID	SEQ ID NO.	Sequence
738	503	DKMLFRVTIQQWK
739	504	DKMLFRVTIGKWK
848	505	DKMLFRVTIGRWK
740	506	DKMLFRVTIGNWK
741	507	DKMLFRVTIQNWK
732	508	DKMLFRVTIDKWK
742	509	DKMLFRVTIEKWK
735	510	DKMLFRVTIERWK
733	511	DKMLFRVTIDRWK
798	512	RPYEGIAVFDGKKITVTGTLWNGNKIIDER LITPD
849	513	EKMLFRVTIQQWK
708	514	EKMLFRVTIGKWK
709	515	EKMLFRVTIGRWK
775	516	DKMLFTVTIQQVSGWRLFKKIS
788	517	DKLLFTVTIEKVSGWRLFKKIS
789	518	DKLLFTVTIEKWVSGWRLFKKIS
790	519	DKLLFTVTIEKYVSGWRLFKKIS
792	520	DKLLFTVTIEKYVSVSGWRLFKKIS
795	521	KKMLFRVTIQQVSGWRLFKKIS
797	522	KKMLFRVTIQQVSVSGWRLFKKIS
796	523	KKMLFRVTIQQVSGWRLFKKIS
804	524	DKLLFTVTIGKVSGWRLFKKIS
805	525	DKLLFTVTIGKYVSGWRLFKKIS
806	526	DKLLFTVTIGKYVSVSGWRLFKKIS
807	527	DKLLFTVTIGKVKVSVSGWRLFKKIS
808	528	DKLLFTVTIQQVSGWRLFKKIS
813	529	KKMLFTVTIQQVSGWRLFKKIS
816	530	KKLLFRVTIQQVSGWRLFKKIS
825	531	DKLLFTVTIEKVSGWRLFKKI
826	532	DKLLFTVTIEKYVSVSGWRLFKKI
827	533	DRLLFTVTIERVSGWRLFKKIS
831	534	EKLLFTVTIEKVSGWRLFKKIS
832	535	KKLLFTVTIGKVSGWRLFKKIS
833	536	GSMRFRVTINSWRVTGYRLFERES
834	537	GSMKFRVTINSVTGYRLFEKES

TABLE 3 -continued

Exemplary peptide sequences.		
Pep ID	SEQ ID NO.	Sequence
844	538	KKIITTGTLWNGNKIID
845	539	ERLITPDGSMLFRVTINSVSGWRLFKKIS
846	540	GRPYEGIAVDFGKKITTGTLWNGNKIIDE RLITPDGSMLFRVTINSVSGWRLFKKIS
847	541	GVTPNKLNYFGRPYEGIAVDFGKKITTGTLWNGNKIIDERLITPDGSMLFRVTINSVSGWRLFKKIS
850	542	EKMLFRVTIGNWK
851	543	EKMLFRVTIQNWK
706	544	EKMLFRVTIDKWK
707	545	EKMLFRVTIEKWK
737	546	EKMLFRVTIERWK
736	547	EKMLFRVTIDRWK
852	548	KKMLFRVTIGKWK
853	549	KKMLFRVTIGRWK
854	550	KKMLFRVTIGNWK
855	551	KKMLFRVTIQNWK
856	552	KKMLFRVTIDKWK
857	553	KKMLFRVTIEKWK
858	554	KKMLFRVTIERWK
859	555	KKMLFRVTIDRWK
860	556	RKMLFRVTIQKWK
861	557	RKMLFRVTIGKWK
862	558	RKMLFRVTIGRWK
863	559	RKMLFRVTIGNWK
864	560	RKMLFRVTIQNWK
865	561	RKMLFRVTIDKWK
866	562	RKMLFRVTIEKWK
867	563	RKMLFRVTIERWK
868	564	RKMLFRVTIDRWK
656	565	EQMLFRVTINSWK
869	566	SRMLFRVTINSWK
533	567	GEMLFRTINNSWK
690	568	GKMKFRVTINNSWK
678	569	GKMLFRVKINNSWK
679	570	GKMLFRVRINNSWK
681	571	GKMLFRVDINNSWK

TABLE 3 -continued

Exemplary peptide sequences.		
Pep ID	SEQ ID NO.	Sequence
663	572	GKMLFRVTIDSWK
714	573	EKMLFKVTIQQWK
870	574	EKMLFTVTIQQWK
871	575	EKMLFKVTIDKWK
872	576	EKMLFTVTIDKWK
873	577	EKMLFKVTIGRWK
744	578	DKMLFKVTIQQWK
745	579	DKMLFTVTIQQWK
874	580	DKMLFKVTIDKWK
875	581	DKMLFTVTIDKWK
876	582	GKMLFKVTIEKWK
877	583	GKMLFTVTIEKWK
748	584	DKMLFKVTIGKWK
749	585	DKMLFTVTIGKWK
878	586	DKMLFKVTIGNWK
879	587	DKMLFKVTIQNWK
781	588	GKMLFKVTINKWK
782	589	GKMLFTVTINKWK
752	590	DKMLFKVTIEKWK
753	591	DKMLFTVTIEKWK
750	592	DKLLFKVTIGKWK
786	593	DKMLFTVTINKWK
756	594	DKLLFTVTIQQWK
757	595	DKLLFTVTIQKYK
758	596	DKLLFTVTIEKWK
793	597	DKLLFTVTIGKWK
794	598	DKLLFTVTIGKYK
799	599	DKLLFTVTINKWK
800	600	DKLLFTVTINKYK
780	601	GKMLFRVTINS
765	602	DKMLFTVTIQQK
779	603	DKMLFKVTIQQK
820	604	DKLLFTVTIGK
819	605	DKMLFTVTIGK
822	606	DKMLFTVTIEK
821	607	DKLLFTVTIEK

TABLE 3 -continued

Exemplary peptide sequences.		
Pep ID	SEQ ID NO.	Sequence
627	608	*DKMLFRVTINSWK
628	609	*EKMLFRVTINSWK
629	610	*RKMLFRVTINSWK
630	611	*KKMLFRVTINSWK
631	612	*HKMLFRVTINSWK
632	613	*GLMLFRVTINSWK
633	614	*GQMLFRVTINSWK
634	615	*GTMLFRVTINSWK
635	616	*GKLLFRVTINSWK
636	617	*GKMLFKVTINSWK
637	618	*GKMLFRVTIQSWK
638	619	*GKMLFRVTIDSWK
639	620	*GKMLFRVTIGSWK
640	621	*GKMLFRVTINTWK
641	622	*GKMLFRVTINNWK
642	623	*GKMLFRVTINQWK
643	624	*GKMLFRVTINPKW
644	625	*GKMLFRVTINKWK
645	626	*GKMLFRVTINSWQ
646	627	*GKMLFRVTINSWN
647	628	*GKMLFRVTIN SWT
648	629	*GKMLFRVTINSWH
649	630	*GKMLFRVTINSWP
650	631	*GKMLFRVTINSWR
677	632	GKMKFRVTIDSWK
680	633	GKMLFRVEINSWK
682	634	GKMLFRVQINSWK
683	635	GKMKFRVKINSWK
684	636	GKMKFRVRINSWK
685	637	GKMKFRVEINSWK
686	638	GKMKFRVDINSWK
687	639	GKMKFRVQINSWK
688	640	GKMKFRVNINSWK
689	641	GKMKFRVSINSWK
613	642	GKMLFRVNINSWK

TABLE 3 -continued

Exemplary peptide sequences.		
Pep ID	SEQ ID NO.	Sequence
614	643	GKMLFRVSINSWK
615	644	GKMLFRVWINSWK
616	645	GKMSFRVTINSWK
617	646	GKMWFRVTINSWK
618	647	GKMNFRVTINSWK
619	648	GSMLFRVTINSYK
620	649	GKMLFRVTINSYK
621	650	GKMLFRVTIKSWK
622	651	GKMLFRVTIESWK
716	652	GKMKFRVTIQSWK
717	653	GKMKFRVTIESWK
718	654	GKMKFRVTIKSWK
719	655	GKMKFRVTIRSWK
651	656	RLMLFRVTINSWK
652	657	RQMLFRVTINSWK
653	658	KLMLFRVTINSWK
654	659	KQMLFRVTINSWK
655	660	ELMLFRVTINSWK
657	661	DLMLFRVTINSWK
658	662	DQMLFRVTINSWK
659	663	DKMLFRVTINSWK
660	664	EKMLFRVTINSWK
661	665	RKMLFRVTINSWK
662	666	KKMLFRVTINSWK
665	667	GKMLFRVTIGSWK
667	668	GKMLFRVTINKWK
670	669	GKMLFRVTISWK
671	670	GKMLFRVTIQKWK
672	671	GKMLFRVTITKWK
673	672	GKMLFRVTIKWK
675	673	GKMLFKVTINSWK
676	674	RLMLFRVTIGKWK
701	675	GKMLFRVTINRWK
710	676	EKMLFTVTIGKWK
711	677	EKLLFTVTIGKWK
712	678	EKMLFTVTIGRWK

TABLE 3 -continued

Exemplary peptide sequences.		
Pep ID	SEQ ID NO.	Sequence
720	679	EKMLFTVTIEKWK
722	680	DKMLFRVTIESWK
726	681	EKLLFRVTIGKYK
746	682	DKLLFKVTIQKWK
747	683	DKLLFKVTIQKYK
751	684	DKLLFKVTIQKYK
754	685	DKLLFKVTIQKYK
755	686	DKLLFKVTIQKYK
761	687	KKLLFRVTIQRWK
762	688	DRMLFRVTIQRWR
766	689	ERMLFRVTIQRWR
768	690	GRMLFRVTINRWR
770	691	DRMLFRVTIERWR
783	692	DKMLFKVTIQKYK
784	693	DKMLFRVTINKWK
785	694	DKMLFKVTIEKYK
787	695	DKMLFKVTINKWK
693	696	GRMLFRVTINSWR
895	697	GRLLFVVVIERYR
937	698	VSGWRLFRRISC
938	699	GRMLFRVTINSWR
939	700	GRLLFTVTIERYRC
840	701	GKLLFVVVIEKYK
900	702	GKLLFVTIEKVSGWRLFKKIS

\*Terminus unblocked

TABLE 4

Exemplary luciferase base sequences.		
Pep ID	SEQ ID NO.	Sequence
LgTrip 3546 -WT strand 9-HiBiT	703	MVFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLAWSVTPIMRIVRSGENAL KIDIHVIIPYEGLSADQMAQIEEVFKVVPVDDHHFKVILPYGTLVIDGVTPNK <b>LNYFGRPYEGIAVFDGKIKTTGTLWNGNKIIDERLITPDGSMLFRVTINSVSG</b> WRLFKKIS
LgTrip 3546 -WT strand 9-SmBiT	704	MVFTLDDFVGDWEQTAAYNLQDVLEQGGVSSLQNLAWSVTPIMRIVRSGENAL KIDIHVIIPYEGLSADQMAQIEEVFKVVPVDDHHFKVILPYGTLVIDGVTPNK <b>LNYFGRPYEGIAVFDGKIKTTGTLWNGNKIIDERLITPDGSMLFRVTINSVTC</b> YRLFEEIL

TABLE 4-continued

Exemplary luciferase base sequences.		
Pep ID	SEQ ID NO.	Sequence
LgTrip 3546 (1-5)	705	MVFTLDDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVRSGENA LKIDIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTP
LgTrip 3546 (1-6)	706	MVFTLDDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVRSGENA LKIDIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTP <b>NKLNYPGRPYEGIAVEDG</b>
LgTrip 3546 (1-7)	707	MVFTLDDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVRSGENA LKIDIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTP
LgTrip 3546 (1-8)	708	MVFTLDDFVGDWEQTAAYNLDQVLEQGGVSSLQNLAVSVTPIMRIVRSGENA LKIDIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTP <b>NKLNYPGRPYEGIAVFVDGKKTTTGTLWNGNKIIDERLITPD</b>
LgTrip 3546 (strands 6-8) -WT strand 9-HiBiT	709	<b>GVTPNKLNYFGRPYEGIAVFVDGKKTTTGTLWNGNKIIDERLITPDGSMLFRV</b> TINSVSGWRLFKKIS
LgTrip 3546 (strands 7-8) -WT strand 9-HiBiT	710	KKITTGTLWNGNKIIDERLITPDGSMLFRVTINSVSGWRLFKKIS
LgTrip 3546 (strand 8)- WT strand 9 -HiBiT	711	<b>WNGNKIIDERLITPDGSMLFRVTINSVSGWRLFKKIS</b>
WT strand 9 -HiBiT	712	GSMLFRVTINSVSGWRLFKKIS
LgTrip 3546 (strands 6-8) -WT strand 9-SmBiT	713	<b>GVTPNKLNYFGRPYEGIAVFVDGKKTTTGTLWNGNKIIDERLITPDGSMLFRV</b> TINSVTGYRLFEEIL
LgTrip 3546 (strands 7-8) -WT strand 9-SmBiT	714	KKITTGTLWNGNKIIDERLITPDGSMLFRVTINSVTGYRLFEEIL
LgTrip 3546 (strand 8)- WT strand 9 -SmBiT	715	<b>WNGNKIIDERLITPDGSMLFRVTINSVTGYRLFEEIL</b>
WT strand 9 -SmBiT	716	GSMLFRVTINSVTGYRLFEEIL
β6-like	717	<b>GVTPNKLNYFGRPYEGIAVEDG</b>
β7-like	718	KKITTGTL
β8-like	719	<b>WNGNKIIDERLITPD</b>
ATG3998 [6xHis- TNFa(sol)- VS-HiBiT]	721	atggaaacatccccatccccatcatgtcagatcatttctcgaaaccccgagt acaaggctgtggccatgttgttagcaaacctcaagctgagggcagctcca gtggctgaacccggccggccatgtggccatgtggccatgtggccatgtgg gataaccagtggtggccatcagaggccgttgcacccatgtggccatgtgg tccttcattcaaggcccaaggctggccatgtggccatgtggccatgtgg catcagccatcggcgatccatccatgtggccatgtggccatgtggccatgtgg atcaaggccctggccatgtggccatgtggccatgtggccatgtggccatgtgg ggtagggccatgtggccatgtggccatgtggccatgtggccatgtggccatgtgg actcagccgtggccatgtggccatgtggccatgtggccatgtggccatgtgg caggcttacttggatcattggccatgtggccatgtggccatgtggccatgtgg gtggggggcggccatgtggccatgtggccatgtggccatgtggccatgtgg gattagctaa
ATG3998 [6xHis-	722	MKHHHHHHVRSSSRTPSDKPVAHVVANPQAEGQLQWLNRANALLANGVELR DNQLVVPSEGGLYLIYSQVLFKGQGCPSTHLLHTISRIAVSYQTKVNLSSA

TABLE 4-continued

Exemplary luciferase base sequences.		
Pep ID	SEQ ID NO.	Sequence
TNF $\alpha$ (sol)-VS-HiBiT]		IKSPQCORETPEGAEAKPWYPIYLGGVFQLEKGDRRLSAEINRPDYLDFAESGQVYFGIIALSSGGGGGGGGSGGVSVGWRLFKKIS.
ATG4002 [smTrip9 (521)-15GS- protein G- 6xHis]	723	ATGGGcaagatgctgttccgagtaaccatcaacagctggaaaggggagctccG GTGGTGGCGGGAGCGGAGGTGGAGGtcgAGCGGTATGACGTATAAGTTAAT CCTTAATGGTAAAACATTGAAGGGCAGACAACACTACTGAAGCTGTGATGCT GCTACTGCAGAAAAAGCTTCAAAACATACGCTAACGACAACGGTGTGACG GTGAATGGACTTACGACGATGCCGACGAAACCTTTACGGTCACCGAAAAACCC AGAAGTGATCGATCGCTCTGAATTAAACACCAGCCGTGACAACATTACAAACCT GTTATTAAATGGTAAAACATTGAAGGGCAGACAACACTACTGAGGCTGTGATG CTGCTACTGCAGAGAAGGTGTTCAAACAAATATGCGAATGACAACGGTGTGTTGA CGGTGAGTGGACTTACGACGATGCGACTAACGACCTTACAGTTACTGAAAAAA CCAGAAAGTGATCGATCGCTCTGAGTTAACACCAGCCGTGACAACCTTACAAAC TTGTTATTAAATGGTAAAACATTGAAGGGCAGACAACACTACTAAAGCAGTAGA CCGAGAAACTCGGGAGAGGCCTTCAAACAAATACGCTAACGACAACGGTGTGTT GATGGTGTGGACTTATGATGATGCCACAAAACCTTACGGTAACTGAGC ATCATCACCATCACCACTAA
ATG4002 [smTrip9 (52 1)-15GS- protein G- 6xHis]	724	MGKMLFRVTINSWKSSGGGGSSGGSSGMTYKLILNGKTLKGETTTEAVDA ATAEKVFKQYANDNGVDGEWTYDDATKTFVTEKEVIDASELTPAVTTYKL VINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFVTEK PEVIDASELTPAVTTYKLVINGKTLKGETTKAVDAETAEKAFKQYANDNGV DGVWTYDDATKTFVTEHHHHHH.

## SEQUENCE LISTING

Sequence total quantity: 730

SEQ ID NO: 1 moltype = AA length = 170  
 FEATURE Location/Qualifiers  
 REGION 1..170  
 note = synthetic  
 source 1..170  
 mol\_type = protein  
 organism = synthetic construct

SEQUENCE: 1  
 MFTLADFVGD WQQTAGYNQD QVLEQGGLSS LFQALGVSVT PIQKVVLSGE NGLKADIHVI 60  
 IPYEGLSGFQ MGLIEMIFKV VYPVDDHHFK IILHYGTLVII DGVTNPNMIDY FGRPYPGIAV 120  
 FDGKQITVTG TLWNGNKIYD ERLINPDGSL LFRVTINGVT GWRLCENILA 170

SEQ ID NO: 2 moltype = AA length = 147  
 FEATURE Location/Qualifiers  
 REGION 1..147  
 note = synthetic  
 source 1..147  
 mol\_type = protein  
 organism = synthetic construct

SEQUENCE: 2  
 MFTLADFVGD WQQTAGYNQD QVLEQGGLSS LFQALGVSVT PIQKVVLSGE NGLKADIHVI 60  
 IPYEGLSGFQ MGLIEMIFKV VYPVDDHHFK IILHYGTLVII DGVTNPNMIDY FGRPYPGIAV 120  
 FDGKQITVTG TLWNGNKIYD ERLINPD 147

SEQ ID NO: 3 moltype = AA length = 10  
 FEATURE Location/Qualifiers  
 REGION 1..10  
 note = synthetic  
 source 1..10  
 mol\_type = protein  
 organism = synthetic construct

SEQUENCE: 3 GSLLFRVTIN 10

SEQ ID NO: 4 moltype = AA length = 13  
 FEATURE Location/Qualifiers  
 REGION 1..13  
 note = synthetic  
 source 1..13  
 mol\_type = protein

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SEQUENCE: 4          organism = synthetic construct
GVTGWRLCEN ILA                      13

SEQ ID NO: 5          moltype = AA  length = 171
FEATURE
REGION
1..171
note = synthetic
source
1..171
mol_type = protein
organism = synthetic construct

SEQUENCE: 5
MVFTLEDFVG DWRQTAGYNL DQVLEQGGVS SLFQNLGVSV TPIQRIVLSG ENGLKIDIHV 60
IIPYEGLSGD QMGQIEKIFK VVYPVDDHHF KVILHYGTLV IDGVTPNMID YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLINPDGS LLFRVTINGV TGWRLCERIL A 171

SEQ ID NO: 6          moltype = AA  length = 148
FEATURE
REGION
1..148
note = synthetic
source
1..148
mol_type = protein
organism = synthetic construct

SEQUENCE: 6
MVFTLEDFVG DWRQTAGYNL DQVLEQGGVS SLFQNLGVSV TPIQRIVLSG ENGLKIDIHV 60
IIPYEGLSGD QMGQIEKIFK VVYPVDDHHF KVILHYGTLV IDGVTPNMID YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLINPD 148

SEQ ID NO: 7          moltype = AA  length = 11
FEATURE
REGION
1..11
note = synthetic
source
1..11
mol_type = protein
organism = synthetic construct

SEQUENCE: 7
GSLLFRTIN V                      11

SEQ ID NO: 8          moltype = AA  length = 13
FEATURE
REGION
1..13
note = synthetic
source
1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 8
GVTGWRLCER ILA                      13

SEQ ID NO: 9          moltype = AA  length = 158
FEATURE
REGION
1..158
note = synthetic
source
1..158
mol_type = protein
organism = synthetic construct

SEQUENCE: 9
MVFTLEDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLITPDGS MLFRVTIN 158

SEQ ID NO: 10         moltype = AA  length = 11
FEATURE
REGION
1..11
note = synthetic
source
1..11
mol_type = protein
organism = synthetic construct

SEQUENCE: 10
VTGYRLFEEI L                      11

SEQ ID NO: 11         moltype = AA  length = 11
FEATURE
REGION
1..11
note = synthetic
source
1..11
mol_type = protein

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SEQUENCE: 11          organism = synthetic construct
VSGWRLFKKI S                               11

SEQ ID NO: 12          moltype = AA  length = 155
FEATURE           Location/Qualifiers
REGION            1..155
note = synthetic
source             1..155
mol_type = protein
organism = synthetic construct

SEQUENCE: 12
MKHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSLQ QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDHHHKVII LPYGTLVIDG VTPNKLNYFG 120
RPyEGIAVFD GKKITTTGTL WNGNKIIDER LITPD                               155

SEQ ID NO: 13          moltype = AA  length = 11
FEATURE           Location/Qualifiers
REGION            1..11
note = synthetic
source             1..11
mol_type = protein
organism = synthetic construct

SEQUENCE: 13
GSMLFRVTIN S                               11

SEQ ID NO: 14          moltype = AA  length = 22
FEATURE           Location/Qualifiers
REGION            1..22
note = synthetic
source             1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 14
GSMLFRVTIN SVSGWRLFKK IS                           22

SEQ ID NO: 15          moltype = AA  length = 11
FEATURE           Location/Qualifiers
REGION            1..11
note = synthetic
source             1..11
mol_type = protein
organism = synthetic construct

SEQUENCE: 15
VSGWRLFKKI S                               11

SEQ ID NO: 16          moltype = AA  length = 13
FEATURE           Location/Qualifiers
REGION            1..13
note = synthetic
source             1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 16
GKMLFRVTIN SWK                               13

SEQ ID NO: 17          moltype = AA  length = 13
FEATURE           Location/Qualifiers
REGION            1..13
note = synthetic
source             1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 17
VSVSGWRLFK KIS                               13

SEQ ID NO: 18          moltype = AA  length = 11
FEATURE           Location/Qualifiers
REGION            1..11
note = synthetic
source             1..11
mol_type = protein
organism = synthetic construct

SEQUENCE: 18
VSGWRLFRRI S                               11

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SEQ ID NO: 19	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 19	
VSVSGWRLFR RIS	13
SEQ ID NO: 20	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 20	
GRMLFRVTIN SWR	13
SEQ ID NO: 21	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 21	
GKMLFRVTIN KWK	13
SEQ ID NO: 22	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 22	
DKLLFTVTIE KYK	13
SEQ ID NO: 23	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 23	
KKMLFRVTIQ KWK	13
SEQ ID NO: 24	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 24	
GRLLFVVVIE RYR	13
SEQ ID NO: 25	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 25	
RRMLFRVTIQ RWR	13
SEQ ID NO: 26	moltype = AA length = 12
FEATURE	Location/Qualifiers
REGION	1..12
source	note = synthetic
	1..12
	mol_type = protein

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SEQUENCE: 26          organism = synthetic construct
VSGWRLFRRI SC                      12

SEQ ID NO: 27          moltype = AA  length = 14
FEATURE
REGION               Location/Qualifiers
1..14
note = synthetic
source
1..14
mol_type = protein
organism = synthetic construct

SEQUENCE: 27          organism = synthetic construct
GRMLFRVTIN SWRC                      14

SEQ ID NO: 28          moltype = DNA  length = 513
FEATURE
misc_feature          Location/Qualifiers
1..513
note = synthetic
source
1..513
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 28
atgggtgttta cttggcaga ttcgttga gactggcaac agacagctgg atacaaccaa  60
gatcaagtgt tagaacaagg aggattgtct agtctgtcc aagccctggg agtgtcaagtc 120
accccaatcc agaaaagggt gctgtctggg gagaatgggt taaaagctga tattcatgtc 180
atcatccctt acggggact cagtgggtt caaatgggtc tgattgaat gatcttcaaa 240
gttggttacc cagtggatga tcataatcc aagatttattc tccattatgg tacactcg 300
attgcacggtg tgacacccaa catgttgac tactttggac gcccttaccc tggaaattgct 360
gtgtttgacg gcaaggagat cacagttact ggaactctgt ggaacggcaa caagatctat 420
gatgagcgcg cc tgatcaaccc agatggtca ctcccttcc cgcttactat caatggagtc 480
acggatggc gcctttgcga gaacatttctt gcc                      513

SEQ ID NO: 29          moltype = DNA  length = 549
FEATURE
misc_feature          Location/Qualifiers
1..549
note = synthetic
source
1..549
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 29
atggaaacatc accatcacca tcatgcgatc gccatggtct tcacactcga agattcg 60
ggggactggc gacagacagc cggttacaac ctggaccaag tccttgaaca gggagggtgt 120
tccagtttgtt ttcagaaatc cgggggtgtcc gtaactccga tccaaaggat tgcctgtggc 180
gttgaaaatg ggttggatag cgacatccat gtcatcatc cgtatggaaat tctggcgcc 240
gaccataatgg gocagatcg aaaaatttt aagggtgggtt accctgtggta tgatcatcac 300
ttaagggtg taatcgacta tggcacactg gtaatcgacg gggtaacggcc gaatcgatc 360
gactatcccg tggccggatc tgaaggatcg gccgtgttgc acggcaaaaa gatcaactgt 420
acagggaccc ttggaaacgg caaaaaattt atcgacgacg gctgtatcaa ccccgacggc 480
tcctgtgtt tccgagtaac catcaacggg gtgaccggct ggccgtgtg cgaacgcatt 540
ctggcggtt                      549

SEQ ID NO: 30          moltype = DNA  length = 495
FEATURE
misc_feature          Location/Qualifiers
1..495
note = synthetic
source
1..495
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 30
atgggtcttca cactcgaaga ttcgttggg gactgggaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggg agggtgtgtcc agtttgcgtc agaatctccg cgtgtccgt 120
actcccgatcc aaaggattgtt ccggggcggt gaaaatggcc tgaatgtcg catccatgtc 180
atcatcccgatc atgaagggtct gagccggcgc caaatggccc agatcgaga ggtgttaag 240
gttgggtacc ctgtgtggatc tcataactt aagggtgtatc tgccctatgg cacactggta 300
atcgacgggg ttacggccaa catgtgtac tatttcggac ggcgtatgaa aggcgtcgcc 360
gtgttgcacg gcaaaaatgtt actgttaaca gggacccctgt ggaacggcaa caaaaatttc 420
gacgagcgcg cc tgatcacccc cgacggctcc atgctgttcc gagtaaccat caacagccat 480
catcaccatc accac                      495

SEQ ID NO: 31          moltype = DNA  length = 33
FEATURE
misc_feature          Location/Qualifiers
1..33
note = synthetic
source
1..33
mol_type = other DNA
organism = synthetic construct

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SEQUENCE: 31
gtgaccggctt accggctgtt cgaggagatt ctg 33

SEQ ID NO: 32      moltype = DNA  length = 33
FEATURE          Location/Qualifiers
misc_feature    1..33
note = synthetic
source          1..33
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 32
gtgagcggctt ggccgtgtt caagaagatt agc 33

SEQ ID NO: 33      moltype = AA   length = 148
FEATURE          Location/Qualifiers
REGION          1..148
note = synthetic
source          1..148
mol_type = protein
organism = synthetic construct

SEQUENCE: 33
MVFTLQDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTNPMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKKII DERLITPD 148

SEQ ID NO: 34      moltype = DNA  length = 444
FEATURE          Location/Qualifiers
misc_feature    1..444
note = synthetic
source          1..444
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 34
atgggtcttca cactcgaaga ttccgttggg gactggaaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggg aggtgtgtcc agttgtctgc aqaatctcg cgtgtccgta 120
actccgatcc aaaggattgt ccggagccgg taaaatgccc tgaagatcga catccatgtc 180
atcatcccgat atgaaggctt gggccgcac caaatggccc agatcgaaga ggtgttaag 240
gtgggttacc ctgtggatga tcatacttt aagggtatcc tgccctatgg cacactgtta 300
atcgacgggg ttacggccaa catgtgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gcaaaaatg cactgttacaac gggaccctgt ggaacggcaa caaaaattatc 420
gacgagccgc tcatcacccc ccgac 444

SEQ ID NO: 35      moltype = AA   length = 155
FEATURE          Location/Qualifiers
REGION          1..155
note = synthetic
source          1..155
mol_type = protein
organism = synthetic construct

SEQUENCE: 35
MKHHHHHHHVF TLDDFVGDWE QTAAYNLQDV LEQGGVSSLQ NQLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITVTGTL WNGNKKIIDER LITPD 155

SEQ ID NO: 36      moltype = DNA  length = 465
FEATURE          Location/Qualifiers
misc_feature    1..465
note = synthetic
source          1..465
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 36
atgaaacatc accatcacca tcatgtctt acactcgaag atttcgttgg ggactggaa 60
cagacagccg cttacaaccc ggaccaagtcc cttaacagg gagggtgttc cagttgtctg 120
cagaatctcg ccgtgtccgt aactccgatc taaaatgccgatc tccggagccgg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaaggatc tgacgcggca ccaaatggcc 240
cagatcgaag aggtgtttaa ggtgggttac cctgtggatg atcatcaccc taagggtatc 300
ctggccctatg gacactcggt aatcgacggg gttacgcggca acatgttacaac 360
cgcccgatcg aaggcatcgcc cgtgttcgac ggcaaaaatg tcaactgttacaac 420
tggaacggca acaaaaattatc cgacgagccgc ctgatcaccc ccgac 465

SEQ ID NO: 37      moltype = AA   length = 148
FEATURE          Location/Qualifiers
REGION          1..148
note = synthetic
source          1..148

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mol_type = protein
organism = synthetic construct

SEQUENCE: 37
MVFTLDDFVG DWEQTAAYNL DVQLLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLITPD 148

SEQ ID NO: 38      moltype = DNA length = 444
FEATURE           Location/Qualifiers
misc_feature     1..444
note = synthetic
source            1..444
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 38
atggcgttca cactcgacga tttcggtggg gactggaa acagacgccc ctacaacctg 60
gaccaagtcc ttgaacagggg aggtgtgtcc agtttgcgtc agaatctcg cgtgtccgt 120
actccgatca tgaggattgt ccggagccgt gaaaatgcc tgaatgcga catccatgtc 180
atcatccgt atgaagggtct gagcgcgac caaatggccc agatcgaaa ggtgtttaag 240
gtgtgttacc ctgtggatga tcatacttt aagggtgtcc tgccctatgg cacactggta 300
atcgacgggg ttacgcgaa caagtcgaa tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaatggg cactgttaca gggaccctgt ggaacggcaa caaaattatc 420
gacgagcgcc tggatcacccc cgac 444

SEQ ID NO: 39      moltype = DNA length = 33
FEATURE           Location/Qualifiers
misc_feature     1..33
note = synthetic
source            1..33
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 39
ggctccatgc tggtccgagt aaccatcaac agc 33

SEQ ID NO: 40      moltype = DNA length = 33
FEATURE           Location/Qualifiers
misc_feature     1..33
note = synthetic
source            1..33
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 40
gtgagcggct ggccggctgtt caagaagatt agc 33

SEQ ID NO: 41      moltype = AA length = 148
FEATURE           Location/Qualifiers
REGION           1..148
note = synthetic
source            1..148
mol_type = protein
organism = synthetic construct

SEQUENCE: 41
MVFTLEDFFVG DWEQTAAYNL DVQLLEQGGVS SLFQNLAVSV TPIQRIVLSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEKIFK VVYPVDDHHF KVILHYGTLV IDGVTPNMIN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLITPD 148

SEQ ID NO: 42      moltype = DNA length = 444
FEATURE           Location/Qualifiers
misc_feature     1..444
note = synthetic
source            1..444
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 42
atggcgttca cactcgaa tttcggtggg gactggaa acagacgccc ctacaacctg 60
gaccaagtcc ttgaacagggg aggtgtgtcc agtttgcgtt agaatctcg cgtgtccgt 120
actccgatcc aaaggattgt cctggagccgt gaaaatgcc tgaatgcga catccatgtc 180
atcatccgt atgaagggtct gagcgcgac caaatggccc agatcgaaa aatttttaag 240
gtgtgttacc ctgtggatga tcatacttt aagggtgtcc tgccactatgg cacactggta 300
atcgacgggg ttacgcgaa catgttaca tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaatggg cactgttaca gggaccctgt ggaacggcaa caaaattatc 420
gacgagcgcc tggatcacccc cgac 444

SEQ ID NO: 43      moltype = AA length = 11
FEATURE           Location/Qualifiers
REGION           1..11

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source          note = synthetic
               1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 43
GSMLFDRVIN V                                11

SEQ ID NO: 44      moltype = DNA  length = 30
FEATURE          Location/Qualifiers
misc_feature     1..30
note = synthetic
source          1..30
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 44
ggctccatgc tggccgagt aaccatcaac                30

SEQ ID NO: 45      moltype = AA   length = 155
FEATURE          Location/Qualifiers
REGION           1..155
note = synthetic
source          1..155
mol_type = protein
organism = synthetic construct
SEQUENCE: 45
MKHHHHHHHF TLEDFVGDWE QTAAYNLQV LEQGGVSSLQ QNLAVSVTPI QRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVY PVDDHHFKVII LPYGTLVIDG VTPNMLNYFG 120
RPYEGIAVFD GKKITVTGTL WNGNKIIDER LITPD          155

SEQ ID NO: 46      moltype = DNA  length = 465
FEATURE          Location/Qualifiers
misc_feature     1..465
note = synthetic
source          1..465
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 46
atgaaacatc accatcacca tcatgtcttc acactcgaa attcgttgg ggactggaa 60
cagacagccg cctacaacct ggacaaaggc cttaacaggc gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc caaaggatttccggagccgg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaaggcc tgagcgccga ccaaattggcc 240
cagatcgaa aggtgtttaa ggtgtgtac cctgtggatg atcatcaccc taagggtatc 300
ctggccatcg gcacactgtt aatcgacggg gttacgcggg acatgtggaa ctatccgg 360
cggccgtatcg aaggcatcgc cgtgttcgac ggccaaaaga tcaactaac aggacccgt 420
tggaaacggca acaaaattat cgacgagcgc ctgatcaccc cccgac                465

SEQ ID NO: 47      moltype = DNA  length = 66
FEATURE          Location/Qualifiers
misc_feature     1..66
note = synthetic
source          1..66
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 47
ggctccatgc tggccgagt aaccatcaac agcgtgagcg gctggccgt gttcaagaag 60
attagc                                         66

SEQ ID NO: 48      moltype = AA   length = 16
FEATURE          Location/Qualifiers
REGION           1..16
note = synthetic
source          1..16
mol_type = protein
organism = synthetic construct
SEQUENCE: 48
SSWKRGSMFL RVTINS                                16

SEQ ID NO: 49      moltype = DNA  length = 48
FEATURE          Location/Qualifiers
misc_feature     1..48
note = synthetic
source          1..48
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 49
agcagctgga agcgccggctc catgtgttc cgagtaacca tcaacagc                48

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SEQ ID NO: 50      moltype = AA  length = 155
FEATURE          Location/Qualifiers
REGION           1..155
note = synthetic
source            1..155
mol_type = protein
organism = synthetic construct

SEQUENCE: 50
MKHHHHHHHFV TLDDFVG DWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKV VY PVDDHHFKV L PYGTLVIDG DTPNKLNYFG 120
R PYDGIAVFD GKKITVTGTL WNGNKIIDER LITPD 155

SEQ ID NO: 51      moltype = DNA  length = 465
FEATURE          Location/Qualifiers
misc_feature     1..465
note = synthetic
source            1..465
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 51
atgaaacatc accatcacca tcatagtcttc acactcgacg atttcgttgg ggactggaa 60
cagacacccg cttacaacct ggacaaatgc cttgaacagg gaggtgtgtc cagttgtctg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattt tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaa aggtgtttaa ggtgtgtac ctgtgttgcg atcatcaccc taagggtgtac 300
ctggccatcg gcacactgtt aatcgacccg gatacgccga acaagctgaa ctatccgaa 360
cggccgtatcg atggcatcg cgtgttcgac ggcaaaaaaa tcaactgttaac agggaccctg 420
tggAACGGCA aaaaaattat cgacgagcgc ctgtatcaccc ccggac 465

SEQ ID NO: 52      moltype = AA  length = 155
FEATURE          Location/Qualifiers
REGION           1..155
note = synthetic
source            1..155
mol_type = protein
organism = synthetic construct

SEQUENCE: 52
MKHHHHHHHFV TLDDFVG DWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKV VY PVDDHHFKV L PYGTLVIDG DTPSKLNYFG 120
R PYEGIAVFD GKKITVTGTL WNGNKIIDER LITPD 155

SEQ ID NO: 53      moltype = DNA  length = 465
FEATURE          Location/Qualifiers
misc_feature     1..465
note = synthetic
source            1..465
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 53
atgaaacatc accatcacca tcatagtcttc acactcgacg atttcgttgg ggactggaa 60
cagacacccg cttacaacct ggacaaatgc cttgaacagg gaggtgtgtc cagttgtctg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattt tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaa aggtgtttaa ggtgtgtac ctgtgttgcg atcatcaccc taagggtgtac 300
ctggccatcg gcacactgtt aatcgacccg gttacgcccga gcaagctgaa ctatccgaa 360
cggccgtatcg aaggcatcg cgtgttcgac ggcaaaaaaa tcaactgttaac agggaccctg 420
tggAACGGCA aaaaaattat cgacgagcgc ctgtatcaccc ccggac 465

SEQ ID NO: 54      moltype = AA  length = 155
FEATURE          Location/Qualifiers
REGION           1..155
note = synthetic
source            1..155
mol_type = protein
organism = synthetic construct

SEQUENCE: 54
MKHHHHHHHFV TLDDFVG DWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKV VY PVDDHHFKV L PYGTLVIDG DTPNKLNYFG 120
R PYEGFAVFD GKKITVTGTL WNGNKIIDER LITPD 155

SEQ ID NO: 55      moltype = DNA  length = 465
FEATURE          Location/Qualifiers
misc_feature     1..465
note = synthetic
source            1..465

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mol_type = other DNA
organism = synthetic construct

SEQUENCE: 55
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtc cttgaacagg gaggtgtgtc cagttgctg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgca ccaaataatggcc 240
cagatcgaaag aggtttaa ggtgtgtac cctgtggatc atcatcactt taagggtgtac 300
ctgcccattatgc acacactgggt aatcgacggg gttacgcgca acaagctgaa ctatttcgga 360
cgcccgatg aaggcttcgc cgtgttcgac ggcaaaaaga tcactgttaac agggaccctg 420
tggAACGGCA aaaaaattatcgacgacgccc ctgtatcaccccc 465

SEQ ID NO: 56      moltype = AA length = 155
FEATURE           Location/Qualifiers
REGION            1..155
note = synthetic
source             1..155
mol_type = protein
organism = synthetic construct

SEQUENCE: 56
MKHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDHHFKVII LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVCD GKKITVTGTL WNGNKIIDER LITPD 155

SEQ ID NO: 57      moltype = DNA length = 465
FEATURE           Location/Qualifiers
misc_feature       1..465
note = synthetic
source             1..465
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 57
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtc cttgaacagg gaggtgtgtc cagttgctg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgca ccaaataatggcc 240
cagatcgaaag aggtttaa ggtgtgtac cctgtggatc atcatcactt taagggtgtac 300
ctgcccattatgc acacactgggt aatcgacggg gttacgcgca acaagctgaa ctatttcgga 360
cgcccgatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactgttaac agggaccctg 420
tggAACGGCA aaaaaattatcgacgacgccc ctgtatcaccccc 465

SEQ ID NO: 58      moltype = AA length = 155
FEATURE           Location/Qualifiers
REGION            1..155
note = synthetic
source             1..155
mol_type = protein
organism = synthetic construct

SEQUENCE: 58
MKHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDHHFKVII LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKISVTGTL WNGNKIIDER LITPD 155

SEQ ID NO: 59      moltype = DNA length = 465
FEATURE           Location/Qualifiers
misc_feature       1..465
note = synthetic
source             1..465
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 59
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtc cttgaacagg gaggtgtgtc cagttgctg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgca ccaaataatggcc 240
cagatcgaaag aggtttaa ggtgtgtac cctgtggatc atcatcactt taagggtgtac 300
ctgcccattatgc acacactgggt aatcgacggg gttacgcgca acaagctgaa ctatttcgga 360
cgcccgatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactgttaac agggaccctg 420
tggAACGGCA aaaaaattatcgacgacgccc ctgtatcaccccc 465

SEQ ID NO: 60      moltype = AA length = 155
FEATURE           Location/Qualifiers
REGION            1..155
note = synthetic
source             1..155
mol_type = protein

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SEQUENCE: 60
organism = synthetic construct
MKHHHHHHVF TLDDFVGDWE QTAAYNLQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITATGTL WNGNKIIDER LITPD 155

SEQ ID NO: 61      moltype = DNA length = 465
FEATURE           Location/Qualifiers
misc_feature      1..465
note = synthetic
source            1..465
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 61
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtgc ttgaacagg gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattg tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgttac cctgtggatg atcatcacct taaggtgtac 300
ctgcccatacg gacacttgtt aatcgacggg gttacgcggc acaagctgaa ctattccga 360
cgcccgatcg aaggcatcgc cgtgttcgac ggcaaaaaga tcactgcaac agggaccctg 420
tggAACCGCA aaaaaattat cgacgagcgc ctgatcaccc ccgac 465

SEQ ID NO: 62      moltype = DNA length = 465
FEATURE           Location/Qualifiers
misc_feature      1..465
note = synthetic
source            1..465
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 62
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtgc ttgaacagg gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattg tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgttac cctgtggatg atcatcacct taaggtgtac 300
ctgcccatacg gacacttgtt aatcgacggg gttacgcggc acaagctgaa ctattccga 360
cgcccgatcg aaggcatcgc cgtgttcgac ggcaaaaaga tcactaccac agggaccctg 420
tggAACCGCA aaaaaattat cgacgagcgc ctgatcaccc ccgac 465

SEQ ID NO: 63      moltype = AA length = 149
FEATURE           Location/Qualifiers
REGION            1..149
note = synthetic
source            1..149
mol_type = protein
organism = synthetic construct

SEQUENCE: 63
MVFTLDDFVG DWEQTAAYNL DVQLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPDG 149

SEQ ID NO: 64      moltype = DNA length = 447
FEATURE           Location/Qualifiers
misc_feature      1..447
note = synthetic
source            1..447
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 64
atgggtcttca cactcgacga ttccgttggg gactgggaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacagggg aggtgtgtcc agtttgcgtc agaatctcg cgtgtccgt 120
actccgatca tgaggattgt ccggagccgt gaaaatgccg tgaagatcga catccatgtc 180
atcatccccgt atgaagggtc gagccgcac caaatggccc agatcgaaga ggtgtttaag 240
gtgggtgtacc ctgtggatga tcatcactt aaggtgtatcc tggccctatgg cacactggta 300
atcgacccggg ttacgcggc aaagtcgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gcaaaaagat cactaccaca gggaccctgt ggaacggcaa caaaaattatc 420
gacgagccgc tgatcacccc cgacggc 447

SEQ ID NO: 65      moltype = AA length = 147
FEATURE           Location/Qualifiers
REGION            1..147
note = synthetic
source            1..147
mol_type = protein
organism = synthetic construct

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SEQUENCE: 65
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITP 147

SEQ ID NO: 66      moltype = DNA  length = 441
FEATURE           Location/Qualifiers
misc_feature      1..441
                  note = synthetic
source            1..441
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 66
atggcttca cactcgacga ttccgttggg gactggaaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggg aggtgtgtcc agtttgcgtc agaatctcgc cgtgtccgtta 120
actccgatca tgaggattgt ccggagcggt gaaaatgccccc tgaagatcga catccatgtc 180
atcatcccgat  atgaaggctt gagegcgcac caaatggccc agatcgaaga ggtgtttaag 240
gttgtgtacc ctgtggatga tcataactt aagggtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcggaa caagctgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaaagat cactaccaca gggaccctgt ggaacggcaa caaaaatttac 420
gacgagcgcc tgatcacccc c 441

SEQ ID NO: 67      moltype = AA  length = 146
FEATURE           Location/Qualifiers
REGION            1..146
                  note = synthetic
source            1..146
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 67
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLIT 146

SEQ ID NO: 68      moltype = DNA  length = 438
FEATURE           Location/Qualifiers
misc_feature      1..438
                  note = synthetic
source            1..438
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 68
atggcttca cactcgacga ttccgttggg gactggaaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggg aggtgtgtcc agtttgcgtc agaatctcgc cgtgtccgtta 120
actccgatca tgaggattgt ccggagcggt gaaaatgccccc tgaagatcga catccatgtc 180
atcatcccgat  atgaaggctt gagegcgcac caaatggccc agatcgaaga ggtgtttaag 240
gttgtgtacc ctgtggatga tcataactt aagggtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcggaa caagctgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaaagat cactaccaca gggaccctgt ggaacggcaa caaaaatttac 420
gacgagcgcc tgatcaccc 438

SEQ ID NO: 69      moltype = AA  length = 150
FEATURE           Location/Qualifiers
REGION            1..150
                  note = synthetic
source            1..150
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 69
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPDGS 150

SEQ ID NO: 70      moltype = DNA  length = 450
FEATURE           Location/Qualifiers
misc_feature      1..450
                  note = synthetic
source            1..450
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 70
atggcttca cactcgacga ttccgttggg gactggaaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggg aggtgtgtcc agtttgcgtc agaatctcgc cgtgtccgtta 120
actccgatca tgaggattgt ccggagcggt gaaaatgccccc tgaagatcga catccatgtc 180
atcatcccgat  atgaaggctt gagegcgcac caaatggccc agatcgaaga ggtgtttaag 240
gttgtgtacc ctgtggatga tcataactt aagggtatcc tgccctatgg cacactggta 300

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atcgacgggg ttacgcgaa caagctgaac tatttcggac ggccgtatga aggcacatcgcc 360
gtgttcgacg gaaaaaat cactaccaca gggacctctgt ggaacggcaa caaaaattatc 420
gacgagcgcc tgatcccccc cgacggcago 450

SEQ ID NO: 71      moltype = AA  length = 164
FEATURE           Location/Qualifiers
REGION            1..164
note = synthetic
source             1..164
mol_type = protein
organism = synthetic construct

SEQUENCE: 71
MFTLEDFVGD WEQTAAYNLD QVLEQGGVSS LLQNLAVSVT PIQRIVRSGE NALKIDIHVI 60
IPIYEGLSADQM MAQIEEVFKV VYPVDDHHFKV VILPYGTLVII DGVTNPMLNY FGRPYEGIAV 120
FDGKKITVTG TLWNGNKIID ERLITPDGSM LFRVTINSHH HHHH 164

SEQ ID NO: 72      moltype = DNA  length = 495
FEATURE           Location/Qualifiers
misc_feature      1..495
note = synthetic
source             1..495
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 72
atgttccacac tcgaagattt cggtggggac tggaaacaga cagccgccta caacctggac 60
caagtccctg aacagggggg ttgttccagt ttgctgcaga atctcgccgt gtccgttaact 120
ccgatccatg gaggatgtccg gagccgttgc aatggccctgt agatcgacat ccatgtcata 180
atccccgtatg aaggatgtccg ccgcgcacca atggcccaga tgcgaagagggt gtttaagggt 240
gtgttacccctg ttggatgatca tcactttaag gtatcctgc cctatggcac actgttaact 300
gacgggggtta cgccgcacat gctgaactat ttccggacggc cgtatgcagg catggccgt 360
ttcgcacggca aaaaatgtcc tggtaacacggg accctgttgc acggcaacaa aattatcgac 420
gagccgcctgca tcaccccccga cgggtccatg ctgttccgag taaccatcaa cagccatcat 480
caccatcacc actaa 495

SEQ ID NO: 73      moltype = AA  length = 163
FEATURE           Location/Qualifiers
REGION            1..163
note = synthetic
source             1..163
mol_type = protein
organism = synthetic construct

SEQUENCE: 73
MTLEDFVGDW EQTAAYNLDQ VLEQGGVSSL LQNLAVSVTP IQRIVRSGEN ALKIDIHVII 60
IPIYEGLSADQM QAIEEVFKVV YPVDDHHFKV ILPYGTLVIDG VTNPMLNYF GRPYEGIAVF 120
DGKKITVTGT LWNGNKIIDE RLITPDGSM LFRVTINSHH HHH 163

SEQ ID NO: 74      moltype = DNA  length = 492
FEATURE           Location/Qualifiers
misc_feature      1..492
note = synthetic
source             1..492
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 74
atgacacttc aagatttcgt tggggacttg gaacagacag ccgcctacaa cctggaccaa 60
gtccttgcac aggaggatgtgt gtccagttt ctgcagaatc tgcgcgtgtc cgtaactccg 120
atccaaagga ttgtccggag cggtaaaaat gcgcctgaaga tgcacatcca tgcatacatc 180
ccgtatcaga gtctgagcgc cgaccaaataat gcgcagatcg aagagggtt taagggtgt 240
taccctgtgg atgatcatca cttaaggatgt atccctgcctt atggcacact ggtaatcgac 300
gggggttacgc cgaacatgtc gaactatggc ggacggccgt atgaaggcat cgccgtgttc 360
gacggccaaa agatcactgt aacaggaccc ctgttgcacgc gcaacaaaat tatecgacgag 420
cgccgtatca ccccccacgg ctccatgtc ttccgagtaa ccatcaacag ccatcatcac 480
catcaccact aa 492

SEQ ID NO: 75      moltype = AA  length = 162
FEATURE           Location/Qualifiers
REGION            1..162
note = synthetic
source             1..162
mol_type = protein
organism = synthetic construct

SEQUENCE: 75
MLEDFVGDWE QTAAAYNLDQV LEQGGVSSL QNLAVSVTPI QRIVRSGENA LKIDIHVIIP 60
YEGLSADQMA QIEEVFKVYY PVDDHHFKVII LPYGTLVIDG VTNPMLNYFG RPYEGIAVFD 120
GKIKITVTGTL WNGNKIIDER LITPDGSMLF RVTINSHHHH HH 162

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SEQ ID NO: 76      moltype = DNA length = 489
FEATURE          Location/Qualifiers
misc_feature     1..489
note = synthetic
source           1..489
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 76
atgcgtcaag attcgttgg ggactggaa cagacagccg cctacaacct ggaccaagt 60
cttgaacagg gaggtgtc tcaatcgatc cgatgttgcg aactccgatc 120
caaaggatcg tccggagcg taaaatgcg ctgaagatcg acatccatgt catcatccg 180
tatgaagggtc tgagcgccg cccaaatggcc cagatcgaa aggtgtttaa ggtgggtac 240
cctgtggatg atcatcaactt taagggtatc ctggccatgt gcacactgtt aatcgacggg 300
gttacgcggca acatgtgaa ctatccgga cggccgtatc aaggcatcgc cgtgttcgac 360
ggcaaaaaaa tcaactgtaa acgggatctg tggaaacggca aaaaaattat cgacgacgc 420
ctgtatcaccc ccgacggctc catgtgttc cgagtaacca tcaacagcca tcataccat 480
caccactaa                                         489

SEQ ID NO: 77      moltype = AA length = 161
FEATURE          Location/Qualifiers
REGION           1..161
note = synthetic
source           1..161
mol_type = protein
organism = synthetic construct

SEQUENCE: 77
MEDFVGDW EQTAYNLDQVL EQGGVSSLQ NLAVSVTPIQ RIVRSGENAL KIDIHVIIPY 60
EGLSADQMAQ IEEVFKVYP VDDHHFKVIL PYGTLVIDGV TPNMLNYFGR PYEGIAVFDG 120
KKITVTGTLW NGNKIIDERL ITPDGSMFLR VTINSHHHHH H                                         161

SEQ ID NO: 78      moltype = DNA length = 486
FEATURE          Location/Qualifiers
misc_feature     1..486
note = synthetic
source           1..486
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 78
atgaaagatt tcgttgggaa ctgggaacag acagccgcct acaacctgga ccaagtcctt 60
gaacaggggat gtgtgtccag tttgtgcag aatctcgccg tggccgttaac tccgatccaa 120
aggatttgcc ggagccgtga aaatgcccctg aagatcgaca tccatgtcat catccgtat 180
gaagggtctga ggcgcgacca aatggccctg atcgaagagg tggttaaggt ggtgtaccct 240
gtgtgatgtc atcaactttaa ggtgtatccctg ccctatggca cactgttataat cgacgggtt 300
acgcccgaaca tgctgtacta ttccggacgg cctgtatgaa gcatcgccgt gttcgacggc 360
aaaaagatcta ctgttaacagg gaccctgtgg aacggcaaca aattatcgta cgagcgctg 420
atcaccctccg acggctccat gctgttccga gtaaccatca acagccatca tcaccatcac 480
cactaa                                         486

SEQ ID NO: 79      moltype = AA length = 174
FEATURE          Location/Qualifiers
REGION           1..174
note = synthetic
source           1..174
mol_type = protein
organism = synthetic construct

SEQUENCE: 79
MFKKIISGSSG VFTLEDVGD WEQTAAYNLD QVLEQGGVV SLLQNLAVSVT PIQRIVRSGE 60
NALKIDHVI I PYEGLSADQ MAQIEEVFKV YVPVDDHHFKV ILVLPYGTLLV DGVTPNMLNY 120
FGPRPYEGIAV FDGKKITVTG TLWNGNKIID ERLITPDGSM LFRVTINSHHH HHHH                                         174

SEQ ID NO: 80      moltype = DNA length = 525
FEATURE          Location/Qualifiers
misc_feature     1..525
note = synthetic
source           1..525
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 80
atgttcaaga agatttagcggt ctcgacgggt gtcttcacac tcgaagattt cggtggggac 60
tgggaacaga cagccgccta caacctggac caagtccctt aacaggggagg tggatgtccagt 120
ttgctgcaga atctcgccgt tccgtactt ccgtatccaa ggattgtccg gagecggtgaa 180
aatgcccctga agatcgacat ccgtatgtc atcccgatgt aagggtctgag cgccgaccaa 240
atggccctaga tcgaagaggt gtttaaggtt gttgttccctg tggatgtatca tcactttaag 300
gtgatcctgc cctatggcac actggtaatc gacgggggtt aacggcaacat gctgaactat 360
ttcggacggc cgtatgttgg cttcgacggca aaaatgttgg tggatgtatca tcactttaag 420
accctgttggaa acggcaacaa aattatcgac gacggccgtca tcaccctccg cggctccatg 480

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ctgttccgag taaccatcaa cagccatcat caccatcacc actaa      525
SEQ ID NO: 81          moltype = AA  length = 173
FEATURE
REGION               Location/Qualifiers
1..173
note = synthetic
source
1..173
mol_type = protein
organism = synthetic construct
SEQUENCE: 81
MKKISGSSGV FTLEDVGDW EQTAAYNLQQ VLEQGGVSSL LQNLAVSVTP IQRIVRSGEN 60
ALKIDIHVIY PYEGLSADQM AQIEEVFKVV YPVDDHHFKV ILPYGTLVID GVTPNMLNYF 120
GRPYEGIAVF DGKKITVTGT LWNGNKIIDE RLITPDGSML FRVTINSHHH HHH 173

SEQ ID NO: 82          moltype = DNA  length = 522
FEATURE
misc_feature          Location/Qualifiers
1..522
note = synthetic
source
1..522
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 82
atgaagaaga tttagcggtc gagcggtgc ttcacactcg aagatttcgt tggggactgg 60
gaacagacag cccgttacaa cctggaccaa gtccttgaac agggagggtgt gtccagttg 120
ctgcagaatc tcggcggtc cgtaactccg atccaaaggaa ttgtccggag cgggtaaaaat 180
gccctgaaaga tggacatcca tgcacatcgc ccgtatgaag gtctgagcgc cggacaaaatg 240
ggccagatcg aagagggttt taagggttg taccctgtgg atgatcatca cttaagggtg 300
atccctgcct atggcacact ggtaatcgac ggggttacgc cgaacatgtt gaactattt 360
ggacggccgt atgaaggcat cggcgttgc gacggcaaaa agatcaactgt aacagggacc 420
ctgttgaacg gcaacaaaat ttcgacgac ccgtatcatca ccccccggg ctccatgtg 480
ttccgagtaa ccatcaacac ccacatcatc catcaccact aa 522

SEQ ID NO: 83          moltype = AA  length = 172
FEATURE
REGION               Location/Qualifiers
1..172
note = synthetic
source
1..172
mol_type = protein
organism = synthetic construct
SEQUENCE: 83
MKISGSSGVF TLEDVGDWE QTAAYNLQDV LEQGGVSSLI QNLAVSVTPPI QRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDHHFKVII LPYGTLVIDG VTPNMLNYFG 120
GRPYEGIAVFD GKKITVTGTL WNGNKIIDERL LITPDGSMLFR VTINSHHHH HH 172

SEQ ID NO: 84          moltype = DNA  length = 519
FEATURE
misc_feature          Location/Qualifiers
1..519
note = synthetic
source
1..519
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 84
atgaagatta gccccgtcgag cgggtgttcc acactcgaaat ttccgtgg ggactggaa 60
cagacagccg cctacaacctt ggaccaagtgc ttgttgcagg gagggtgtgc cagttgtg 120
cagaatctcc cggtgtccgt aactccgcataaaggatgg tccggagccg tgaaaatgcc 180
ctgaatgtcg acatccatgtt catcatccgc tatgaagggtc tgagcgcgc ccaaatggcc 240
cagatcgaaag aggtgtttaa ggtgtgtac cctgtggatgc atcatcactt taagggtgt 300
ctggccctatg gcacactggg aatcgacggg gttacgcgcg acatgtgaa ctatttgcga 360
cgcccgatcg aaggcatcgc cgtgttcgac ggcaaaaaaaa tcactgttaac agggaccctg 420
tggAACGGCA acaaaaattat cgacgacgcg ctgatcaccc cccggccgtc catgtgttc 480
cgatgtacca tcaacagccca tcatcacat caccactaa 519

SEQ ID NO: 85          moltype = AA  length = 171
FEATURE
REGION               Location/Qualifiers
1..171
note = synthetic
source
1..171
mol_type = protein
organism = synthetic construct
SEQUENCE: 85
MISGSSGVFT LEDFVGDW EQGGVSSLLQ NLAVSVTPIQ RIVRSGENAL 60
KIDIHVIIPY EGLSADQMAQ IEEVFKVVP VDDHHFKVIL PYGTLVIDGV TPNMLNYFGR 120
GRPYEGIAVFDG KKIKITVTGTLW NGNKIIDERL ITPDGSMLFR VTINSHHHHH H 171

SEQ ID NO: 86          moltype = DNA  length = 516
FEATURE
Location/Qualifiers

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misc_feature      1..516
                  note = synthetic
source           1..516
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 86
atgattagcg gtcgagccg tgcggcata ctcgaagatt tcgttgggaa ctggaaacag 60
acacccgcct acaacccgtt ccaaggccctt gaacaggagg gtgtgtccag tttgtgcag 120
aatctcgccg tgcgttac acgttccaa aggattgtcc ggagcggtaa aaatgccctg 180
aaatcgaca tccatgtcat ctcgttccat gaaggcttgc ggcggcacc aatggccctg 240
atcgaagagg gttttaaagggtt ggtgttccat gtcgttgcata atcaattaa ggtgttccctg 300
ccctatggca cactggtaat cgacgggggtt acggccaaata tcgttgcata tttcgacgg 360
ccgtatggaa gcatcgccgtt gtcgttgcata aaaaatggatca tcgttgcata gaccctgtgg 420
aacggcaaca aattatcgatcgacggccctg atcacccccc acggctccat gtcgttccctg 480
gtaaccatca acagccatca tcaccatca cactaa 516

SEQ ID NO: 87      moltype = AA length = 170
FEATURE          Location/Qualifiers
REGION           1..170
                  note = synthetic
source            1..170
                  mol_type = protein
                  organism = synthetic construct
SEQUENCE: 87
MSGSSGVFTL EDFVGDWEQT AAYNLDQVLE QGGVSSLQVN LAVSVTPIQR IVRSGENALK 60
IDIHVIIPYE GLSADQMAQI EEVFKVVPV DDHDFKVILP YGTLVIDGVT PNMLNYFGRP 120
YEGIAVFDGK KITVTGTLWN GNKIIDERLI TPDGSMLFRV TINSHHHHHH 170

SEQ ID NO: 88      moltype = DNA length = 513
FEATURE          Location/Qualifiers
misc_feature     1..513
                  note = synthetic
source            1..513
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 88
atgagcggctt cgagcgggtt ctgcgttccatc gaagatttcg ttggggactg ggaacagaca 60
ggccgcctaca acctggacca agtccgttccatc caggagggtt tgccgttccatc gtcgttgcata 120
ctcgccgttccatc gatccgttccatc gatccgttccatc attgttccatc ggcgttgcata tgccgttgcata 180
atcgacatccatc atgttccatc cccgttgcata ggtgttgcata ccgttgcata aatggccctg 240
gaagagggttccatc ttaagggttccatc gtaccctgttccatc gatgttgcata actttaaagggttccatc gtcgttgcata 300
tatggccacac tggatccatc cgggggttccatc ccgttgcata tgaacttccatc cggacggccctg 360
tatgaaggccatc tggccgttccatc cgacggccaaata aqatccatc taacagggttccatc cctgttgcata 420
ggcaacaataa ttatcgacca ggcgttgcata accccggaccc gtcgttgcata gttccgttccatc 480
accatcaaca gocatcatca cccatccatca taa 513

SEQ ID NO: 89      moltype = AA length = 158
FEATURE          Location/Qualifiers
REGION           1..158
                  note = synthetic
source            1..158
                  mol_type = protein
                  organism = synthetic construct
SEQUENCE: 89
MKHHHHHHHVFTL DDFVGDWE QTAAVNLDQVLE QGGVSSLQVN QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVPV PVDDHDFKVILP YGTLVIDGVT VTPNKLNYFG 120
RPyEGIAVFD GKKITTTGTL WNGNKIIDERLI LITPDGSM 158

SEQ ID NO: 90      moltype = DNA length = 477
FEATURE          Location/Qualifiers
misc_feature     1..477
                  note = synthetic
source            1..477
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 90
atgaaacatc accatccatc tcgttccatc acactcgaccc atttcgttgg ggactggaa 60
cagacagccg cctacaaccc ggaccaagtc cttgttccatc gaggtgttccatc cagttgttccatc 120
cagaatctcg ccgttccatc aactccgttccatc atgaggatttgc tccggacccg tgaaaaatggcc 180
ctgttccatc acatccatc catcatccatc tatgttccatc tgacggccca ccaaatggcc 240
cagatcgaccc aggtgttccatc ggtgttccatc cttgttccatc atcatccatc taagggttccatc 300
ctggccctatc gcacactgggttccatc aatcgacccgggttccatc gcaacccggatccatc 360
cggccgtatc aaggcatcgccgttccatc cgttccatc ggcaaaaaga tcactaccac agggaccctg 420
tgaaacggccatc aaaaaattatcgacccatc cggacggccatc catgttccatc 477

SEQ ID NO: 91      moltype = AA length = 159

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FEATURE          Location/Qualifiers
REGION          1..159
                note = synthetic
source           1..159
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 91
MKHHHHHHHV TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER LITPDGSML 159

SEQ ID NO: 92      moltype = DNA length = 480
FEATURE          Location/Qualifiers
misc_feature     1..480
                note = synthetic
source           1..480
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 92
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaaagtc cttgaacagg gaggtgtgtc cagttgctg 120
cagaatctcg ccgtgtccgt aactccgcgt atgaggatttgc tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcga ccaaataatgcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtgttgcgat atcatacc tttaagggtatc 300
ctgcctatg gcacactgggt aatcgacggg gttacgcgcga acaagctgaa ctatttcgga 360
cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaaaaatcactaccac agggaccctg 420
tggaaacggca acaaaaattat cgacgacgcgcg ctgtatcaccc cccgacggcag catgtgttaa 480

SEQ ID NO: 93      moltype = AA length = 160
FEATURE          Location/Qualifiers
REGION          1..160
                note = synthetic
source           1..160
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 93
MKHHHHHHHV TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER LITPDGSML 160

SEQ ID NO: 94      moltype = DNA length = 483
FEATURE          Location/Qualifiers
misc_feature     1..483
                note = synthetic
source           1..483
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 94
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaaagtc cttgaacagg gaggtgtgtc cagttgctg 120
cagaatctcg ccgtgtccgt aactccgcgt atgaggatttgc tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcga ccaaataatgcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtgttgcgat atcatacc tttaagggtatc 300
ctgcctatg gcacactgggt aatcgacggg gttacgcgcga acaagctgaa ctatttcgga 360
cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaaaaatcactaccac agggaccctg 420
tggaaacggca acaaaaattat cgacgacgcgcg ctgtatcaccc cccgacggcag catgtgttca 483

SEQ ID NO: 95      moltype = AA length = 152
FEATURE          Location/Qualifiers
REGION          1..152
                note = synthetic
source           1..152
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 95
MKHHHHHHHV TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER LI 152

SEQ ID NO: 96      moltype = DNA length = 459
FEATURE          Location/Qualifiers
misc_feature     1..459
                note = synthetic
source           1..459
                mol_type = other DNA

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SEQUENCE: 96          organism = synthetic construct
atgaaacatc accatcacca tcatgtcttc acactcgacg attcggtgg ggactggaa 60
cagacagccg cctacaacctt ggaccaagtc ctggAACAGG gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattg tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtggatc atcatcattt taaggtgatc 300
ctgcccatacg gcacacttgtt aatcgacggg gttacgcggc acaagctgaa ctatccgga 360
cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactaccac agggaccctg 420
tggAACCGCA aaaaaattat cgacgagcgc ctgtaa 459

SEQ ID NO: 97          moltype = AA length = 151
FEATURE               Location/Qualifiers
REGION                1..151
note = synthetic
source                1..151
mol_type = protein
organism = synthetic construct

SEQUENCE: 97
MKHHHHHHHV TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDDHHFKVII LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER L 151

SEQ ID NO: 98          moltype = DNA length = 456
FEATURE               Location/Qualifiers
misc_feature          1..456
note = synthetic
source                1..456
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 98
atgaaacatc accatcacca tcatgtcttc acactcgacg attcggtgg ggactggaa 60
cagacagccg cctacaacctt ggaccaagtc ctggAACAGG gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattg tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtggatc atcatcattt taaggtgatc 300
ctgcccatacg gcacacttgtt aatcgacggg gttacgcggc acaagctgaa ctatccgga 360
cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactaccac agggaccctg 420
tggAACCGCA aaaaaattat cgacgagcgc ctgtaa 456

SEQ ID NO: 99          moltype = AA length = 150
FEATURE               Location/Qualifiers
REGION                1..150
note = synthetic
source                1..150
mol_type = protein
organism = synthetic construct

SEQUENCE: 99
MKHHHHHHHV TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDDHHFKVII LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER L 150

SEQ ID NO: 100         moltype = DNA length = 453
FEATURE               Location/Qualifiers
misc_feature          1..453
note = synthetic
source                1..453
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 100
atgaaacatc accatcacca tcatgtcttc acactcgacg attcggtgg ggactggaa 60
cagacagccg cctacaacctt ggaccaagtc ctggAACAGG gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattg tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtggatc atcatcattt taaggtgatc 300
ctgcccatacg gcacacttgtt aatcgacggg gttacgcggc acaagctgaa ctatccgga 360
cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactaccac agggaccctg 420
tggAACCGCA aaaaaattat cgacgagcgc taa 453

SEQ ID NO: 101         moltype = AA length = 123
FEATURE               Location/Qualifiers
REGION                1..123
note = synthetic
source                1..123
mol_type = protein
organism = synthetic construct

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SEQUENCE: 101
MVAIWHEMW HEGLEEASRL YFGERNVKGM FEVLEPLHAM MERGPQLKE TSFNQAYGRD 60
LMEAQEWRK YMKGNSNVKDL TQAWDLYYHV FRRISGGSGG GGSGGSSSSGG AIVSGWRLF 120
KIS 123

SEQ ID NO: 102      moltype = DNA  length = 372
FEATURE           Location/Qualifiers
misc_feature      1..372
                  note = synthetic
source            1..372
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 102
atgggtggcca tcctctggca tgagatgtgg catgaaggcc tggaaagaggc atctcgttg 60
tactttgggg aaaggaacgt gaaaaggcatg tttgagggtgc tggagccctt gcatgctatg 120
atggaaacggg gccccccagac tctgaaggaa acatcctta atcaggccta tggtcgagat 180
ttaatggagg cccaaagagtg gtgcaggaag tacatgaaat cagggaaatgt caaggacctc 240
acccaaagcct gggacctcta ttatcatgtg ttccgacgaa tcagtggtgg ttcaagggtgt 300
ggcggggagcg gtggctcgag cagcgggtgga gcgatcgtga gcccgtggcg gctgttcaag 360
aagatttagct aa 372

SEQ ID NO: 103      moltype = AA  length = 125
FEATURE           Location/Qualifiers
REGION            1..125
                  note = synthetic
source            1..125
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 103
MVAIWHEMW HEGLEEASRL YFGERNVKGM FEVLEPLHAM MERGPQLKE TSFNQAYGRD 60
LMEAQEWRK YMKGNSNVKDL TQAWDLYYHV FRRISGGSGG GGSGGSSSSGG AIVSGWRL 120
FKKIS 125

SEQ ID NO: 104      moltype = DNA  length = 378
FEATURE           Location/Qualifiers
misc_feature      1..378
                  note = synthetic
source            1..378
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 104
atgggtggcca tcctctggca tgagatgtgg catgaaggcc tggaaagaggc atctcgttg 60
tactttgggg aaaggaacgt gaaaaggcatg tttgagggtgc tggagccctt gcatgctatg 120
atggaaacggg gccccccagac tctgaaggaa acatcctta atcaggccta tggtcgagat 180
ttaatggagg cccaaagagtg gtgcaggaag tacatgaaat cagggaaatgt caaggacctc 240
acccaaagcct gggacctcta ttatcatgtg ttccgacgaa tcagtggtgg ttcaagggtgt 300
ggcggggagcg gtggctcgag cagcgggtgga gcgatcgtta gcccgtggcg ctggcgctg 360
tcaagaaga tcaactaa 378

SEQ ID NO: 105      moltype = AA  length = 129
FEATURE           Location/Qualifiers
REGION            1..129
                  note = synthetic
source            1..129
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 105
MVAIWHEMW HEGLEEASRL YFGERNVKGM FEVLEPLHAM MERGPQLKE TSFNQAYGRD 60
LMEAQEWRK YMKGNSNVKDL TQAWDLYYHV FRRISGGSGG GGSGGSSSSGG AIVSGWRLF 120
KISHHHHHH 129

SEQ ID NO: 106      moltype = DNA  length = 390
FEATURE           Location/Qualifiers
misc_feature      1..390
                  note = synthetic
source            1..390
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 106
atgggtggcca tcctctggca tgagatgtgg catgaaggcc tggaaagaggc atctcgttg 60
tactttgggg aaaggaacgt gaaaaggcatg tttgagggtgc tggagccctt gcatgctatg 120
atggaaacggg gccccccagac tctgaaggaa acatcctta atcaggccta tggtcgagat 180
ttaatggagg cccaaagagtg gtgcaggaag tacatgaaat cagggaaatgt caaggacctc 240
acccaaagcct gggacctcta ttatcatgtg ttccgacgaa tcagtggtgg ttcaagggtgt 300
ggcggggagcg gtggctcgag cagcgggtgga gcgatcgtga gcccgtggcg gctgttcaag 360
aagatttagcc atcatcacca tcaccactaa 390

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SEQ ID NO: 107      moltype = AA  length = 131
FEATURE          Location/Qualifiers
REGION           1..131
note = synthetic
source            1..131
mol_type = protein
organism = synthetic construct

SEQUENCE: 107
MVAAILWHEMW HEGLEEAASRL YFGERNVKGM FEVLEPLHAM MERGPQLKE TSFNQAYGRD 60
LMEAQEWCRK YMKSgnVKDL TQAWDLYYHV FRRISGGSGG GGSGGSSSSG AIVSVSGWRL 120
FKKISHHHHH H 131

SEQ ID NO: 108      moltype = DNA  length = 396
FEATURE          Location/Qualifiers
misc_feature     1..396
note = synthetic
source            1..396
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 108
atgggtggcoca tcctctggca tgagatgtgg catgaaggcc tggaaaggccc atctcgttt 60
tactttgggg aaaggAACgt gaaaaggcatg ttggagggtgc ttggagccctt gcatgctatg 120
atggaaacggg gccccccagac tctgaaggaa acatccctta atcaggccctt tggtcgagat 180
ttaatggagg cccaaagagtg gtgcaggaag tacatgaat caggaaatgt caaggaccc 240
acccaaaggctt gggacccctta ttatcatgtg ttccgacgaa tcagtggtgg ttcaagggtt 300
ggggggagcg ctgggctcgag cagcgggtgg gcatcgatc gggtggccgg ctggccggctg 360
ttcaagaaga ttagccatca tcaccatcac cactaa 396

SEQ ID NO: 109      moltype = AA  length = 118
FEATURE          Location/Qualifiers
REGION           1..118
note = synthetic
source            1..118
mol_type = protein
organism = synthetic construct

SEQUENCE: 109
MKHIIHHHHVVA ILWHEMWHEG LEEASRLYFG ERNVKGMPFEV LEPLHAMMER GPQLKETSF 60
NQAYGRDLME AQEWCRKYMKA SGNVKDLTQA WDLYYHVFR ISGGSGGVSG WRLPKKIS 118

SEQ ID NO: 110      moltype = DNA  length = 357
FEATURE          Location/Qualifiers
misc_feature     1..357
note = synthetic
source            1..357
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 110
atgaaaacatc accatcacca tcatgtggcc atcctctggc atgagatgtg gcatgaaggc 60
ctggaaaggagg catctcggtt gtactttggg gaaaggAACgt tgaaaggcat gtttgaggtg 120
ctggagccct tgcatgtcat gatggAACCG gggccccccaga ctctgaaggaa aacatccctt 180
aatcaggccat atggtcgaga ttaatgggg gcccaagagt ggtgcaggaa gtatcatgaaa 240
tcaggaaatg tcaaggaccc cacccaaaggcc tgggacccctt attatcatgtt gttccgacca 300
atcagtggtt gttcagggtgg tggcggctgt tcaagaagat tagctaa 357

SEQ ID NO: 111      moltype = AA  length = 123
FEATURE          Location/Qualifiers
REGION           1..123
note = synthetic
source            1..123
mol_type = protein
organism = synthetic construct

SEQUENCE: 111
MKHIIHHHHVVA ILWHEMWHEG LEEASRLYFG ERNVKGMPFEV LEPLHAMMER GPQLKETSF 60
NQAYGRDLME AQEWCRKYMKA SGNVKDLTQA WDLYYHVFR ISGGSGGGGS GGVSGWRLFK 120
KIS 123

SEQ ID NO: 112      moltype = DNA  length = 372
FEATURE          Location/Qualifiers
misc_feature     1..372
note = synthetic
source            1..372
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 112
atgaaaacatc accatcacca tcatgtggcc atcctctggc atgagatgtg gcatgaaggc 60

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ctggaagagg catctcggtt gtactttggg gaaaggaacg tgaaaggcat gtttgaggtg 120
ctggagccct tgcatgttat gatggAACGG ggcccccaga ctctgaagga aacatccccc 180
aatcaggcct atggtcgaga tttaatggag gcccaagagt ggtgcaggaa gtacatgaaa 240
tcagggaaatg tcaaggaccc cacccaaGCC tgggaccctt attatcatgt gttccgacga 300
atcagtggtg gttcaggtgg tggcgggago ggtggcgtga gcggctggcg gctgttcaag 360
aagattagct aa 372

SEQ ID NO: 113      moltype = AA length = 128
FEATURE           Location/Qualifiers
REGION            1..128
note = synthetic
source             1..128
mol_type = protein
organism = synthetic construct

SEQUENCE: 113
MKHHHHHHVA ILWHEMWHEG LEEASRLYFG ERNVKGMPEV LEPLHAMMER GPQTLKETSF 60
NQAYGRDLME AQEWCRKYMK SGNVKDLTQA WDLYYHVFRR ISGGSGGGGS GGSSSGGVSG 120
WRLFKKIS 128

SEQ ID NO: 114      moltype = DNA length = 387
FEATURE           Location/Qualifiers
misc_feature       1..387
note = synthetic
source             1..387
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 114
atgaaacatc accatcacca tcatgtggcc atcctctggc atgagatgtg gcatgaaggc 60
ctggaagagg catctcggtt gtactttggg gaaaggaacg tgaaaggcat gtttgaggtg 120
ctggagccct tgcatgttat gatggAACGG ggcccccaga ctctgaagga aacatccccc 180
aatcaggcct atggtcgaga tttaatggag gcccaagagt ggtgcaggaa gtacatgaaa 240
tcagggaaatg tcaaggaccc cacccaaGCC tgggaccctt attatcatgt gttccgacga 300
atcagtggtg gttcaggtgg tggcgggago ggtggcgtga gcagcgggtgg agttagccgc 360
tggcggctgt tcaagaatg tagctaa 387

SEQ ID NO: 115      moltype = AA length = 120
FEATURE           Location/Qualifiers
REGION            1..120
note = synthetic
source             1..120
mol_type = protein
organism = synthetic construct

SEQUENCE: 115
MKHHHHHHVA ILWHEMWHEG LEEASRLYFG ERNVKGMPEV LEPLHAMMER GPQTLKETSF 60
NQAYGRDLME AQEWCRKYMK SGNVKDLTQA WDLYYHVFRR ISGGSGGVSV SGWRLFKKIS 120

SEQ ID NO: 116      moltype = DNA length = 363
FEATURE           Location/Qualifiers
misc_feature       1..363
note = synthetic
source             1..363
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 116
atgaaacatc accatcacca tcatgtggcc atcctctggc atgagatgtg gcatgaaggc 60
ctggaagagg catctcggtt gtactttggg gaaaggaacg tgaaaggcat gtttgaggtg 120
ctggagccct tgcatgttat gatggAACGG ggcccccaga ctctgaagga aacatccccc 180
aatcaggcct atggtcgaga tttaatggag gcccaagagt ggtgcaggaa gtacatgaaa 240
tcagggaaatg tcaaggaccc cacccaaGCC tgggaccctt attatcatgt gttccgacga 300
atcagtggtg gttcaggtgg tggtagcgtt aegggctggc gctgttcaa gaagatcgc 360
taa 363

SEQ ID NO: 117      moltype = AA length = 125
FEATURE           Location/Qualifiers
REGION            1..125
note = synthetic
source             1..125
mol_type = protein
organism = synthetic construct

SEQUENCE: 117
MKHHHHHHVA ILWHEMWHEG LEEASRLYFG ERNVKGMPEV LEPLHAMMER GPQTLKETSF 60
NQAYGRDLME AQEWCRKYMK SGNVKDLTQA WDLYYHVFRR ISGGSGGGGS GGVSVSGWRL 120
FKKIS 125

SEQ ID NO: 118      moltype = DNA length = 378
FEATURE           Location/Qualifiers

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misc_feature          1..378
                      note = synthetic
source               1..378
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 118
atgaaacatc accatcacca tcatgtggcc atcctctggc atgagatgtg gcatgaaggc 60
cttggaaaggc catctcggtt gtactttggg gaaaggaacg tgaaaggcat gtttgagggtg 120
ctggagccct tgcgtat gatggAACGG ggcccccaga ctctgaagga aacatccccc 180
aatcaggcct atggtcgaga ttatggag gcccaagagt ggtgcaggaa gtacatgaaa 240
tcaggaaatg tcaaggaccc caccacccggg tgggacccctt attatcatgt gttccgacga 300
atcagtgggtg gttcagggtgg tggcggggc ggtggcgtta gcgttagcgg ctggcgctg 360
ttcaagaaga tcagctaa                                         378

SEQ ID NO: 119      moltype = AA  length = 130
FEATURE             Location/Qualifiers
REGION              1..130
                      note = synthetic
source               1..130
                      mol_type = protein
                      organism = synthetic construct
SEQUENCE: 119
MKHHHHHHVVA ILWHEMWHEG LEEASRLYFG ERNVKGMFEV LEPLHAMMER GPQTLKETSF 60
NQAYGRDLME AQEWCRKYMK SGNVKDLTQA WDLYYHVPRR ISGGSGGGGS GGSSSGGVSV 120
SGWRLFKKIS                                         130

SEQ ID NO: 120      moltype = DNA  length = 393
FEATURE             Location/Qualifiers
misc_feature         1..393
                      note = synthetic
source               1..393
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 120
atgaaacatc accatcacca tcatgtggcc atcctctggc atgagatgtg gcatgaaggc 60
cttggaaaggc catctcggtt gtactttggg gaaaggaacg tgaaaggcat gtttgagggtg 120
ctggagccct tgcgtat gatggAACGG ggcccccaga ctctgaagga aacatccccc 180
aatcaggcct atggtcgaga ttatggag gcccaagagt ggtgcaggaa gtacatgaaa 240
tcaggaaatg tcaaggaccc caccacccggg tgggacccctt attatcatgt gttccgacga 300
atcagtgggtg gttcagggtgg tggcggggc ggtggcgtta gcagcggcgg agtttagcg 360
agcggctggc gctgttcaa gaatcagcgtaa                                         393

SEQ ID NO: 121      moltype = AA  length = 134
FEATURE             Location/Qualifiers
REGION              1..134
                      note = synthetic
source               1..134
                      mol_type = protein
                      organism = synthetic construct
SEQUENCE: 121
MGSMMLFRVTI NSSSSGGGGS GGGSSGGGVQ VETISPGDGR TFPKRGQTCV VHYTGMLEDG 60
KKFDSRDRN KPKFMLGKQ EVIRGWEVG AQMSVGQRAK LTISPDYAYG ATGHPGIIPP 120
HATLVDVEL LKLE                                         134

SEQ ID NO: 122      moltype = DNA  length = 405
FEATURE             Location/Qualifiers
misc_feature         1..405
                      note = synthetic
source               1..405
                      mol_type = other DNA
                      organism = synthetic construct
SEQUENCE: 122
atgggctcca tgctgttccg agtaaccatc aacagctcgat gttcagggtgg tggcggggc 60
ggggggggc gcaaggcggtgg aggaggatcgat gttggaaacca tctccccagg agacggggc 120
accttccccca agcgccggca gaccctcgat gtgcactatc ccgggatgt tgaatggaa 180
aagaaattttt atccctcccg ggacagaaaa acggcccttta agtttatgtt aggaacgg 240
gagggtatcc gaggctggga agaagggtt gcccagatgat gttgggtca gagagccaaa 300
ctgactatata ctccagatta tgcctatgtt gccactggc acccaggcat catccacca 360
catgccactc tcgttccgat tttttttttt aataa                                         405

SEQ ID NO: 123      moltype = AA  length = 136
FEATURE             Location/Qualifiers
REGION              1..136
                      note = synthetic
source               1..136
                      mol_type = protein

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SEQUENCE: 123          organism = synthetic construct
MGVQVETISP GDGRTFPKRG QTCVVHYTGM LEDGKKFDSS RDRNPKFKM LGKQE VIRGW 60
EEGVAQMSVG QRAKLTISPD YAYGATGHPG IIPPHATLVF DVELLKLEGG SGGGSGGSS 120
SGGAIGSMLF RVTINS   136

SEQ ID NO: 124          moltype = DNA length = 408
FEATURE
misc_feature           Location/Qualifiers
1..408
note = synthetic
source
1..408
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 124
atgggagatgc aggtggaaac catctccca ggagacgggc gcacccccc caagcggc 60
caaacctcg tggtcacta caccggatg cttaaaggatg gaaaaggatt tgattcc 120
cgggacagaa acaaggccctt taatgtttatg cttagtcaagg aggaggatgtat ccgaggctgg 180
gaagaagggg ttgccccatg gatgttgggt cagagagcca aactgtat atctccagat 240
tatgcctatg ttgcactatg gcaccaggcc atcatccac cacatgcac tctgtcttc 300
gatgtggagc ttctaaaactt ggaagggtgtt tcaggtggt ccggggacggc tggctcgac 360
agcgggtggag cgtatggctc catgtgttc cgagtaacc acaacagc 408

SEQ ID NO: 125          moltype = AA length = 165
FEATURE
REGION
1..165
note = synthetic
source
1..165
mol_type = protein
organism = synthetic construct

SEQUENCE: 125
MVFTLEDVFG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTIV IDGVTPNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLITPDGS MLFRVTINSH HHHHHH 165

SEQ ID NO: 126          moltype = DNA length = 498
FEATURE
misc_feature           Location/Qualifiers
1..498
note = synthetic
source
1..498
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 126
atgtcttca cactcgaaga ttccgttggg gactggaaac agacagccgc ctacaacctg 60
gaccaaggcc ttgaacaggg aggtgtgtcc agtggatcg acaaattccgc cgtgtccgt 120
actccgatcc aaaggatgt ccggagccgt gaaaatgcc tgaatgtca catccatgc 180
atcatcccgat atgaaggatct gagcgcgcac caaatggccc agatcaaga ggtgttaag 240
gttgttacc ctgttgatcc tcataactt aaggtgtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcggaa catgtgaad tatttcggac ggccgtatgaa aggcatcgcc 360
gtgttcacgc gaaaaaaatgaa cactgtaca gggacccatg ggaacggccaa caaaattatc 420
gacgagccgc tgatcacccc cgacggctcc atgctgttcc gagtaaccat caacagccat 480
catcaccatc accactaa 498

SEQ ID NO: 127          moltype = AA length = 13
FEATURE
REGION
1..13
note = synthetic
source
1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 127
NVSGWRLFKK ISN                                                 13

SEQ ID NO: 128          moltype = AA length = 13
FEATURE
REGION
1..13
note = synthetic
source
1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 128
NVTGYRLFKK ISN                                                 13

SEQ ID NO: 129          moltype = AA length = 12
FEATURE
REGION
1..12
note = synthetic

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source	1..12
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 129	
VSGWRLFKKI SN	12
SEQ ID NO: 130	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
	note = synthetic
source	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 130	
SGWRLFKKIS N	11
SEQ ID NO: 131	moltype = AA length = 10
FEATURE	Location/Qualifiers
REGION	1..10
	note = synthetic
source	1..10
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 131	
GWRLFKKISN	10
SEQ ID NO: 132	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
	note = synthetic
source	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 132	
VTGYRLPEKI S	11
SEQ ID NO: 133	moltype = AA length = 10
FEATURE	Location/Qualifiers
REGION	1..10
	note = synthetic
source	1..10
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 133	
SGWRLFKKIS	10
SEQ ID NO: 134	moltype = AA length = 6
FEATURE	Location/Qualifiers
REGION	1..6
	note = synthetic
source	1..6
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 134	
VSGWRL	6
SEQ ID NO: 135	moltype = AA length = 7
FEATURE	Location/Qualifiers
REGION	1..7
	note = synthetic
source	1..7
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 135	
VSGWRLF	7
SEQ ID NO: 136	moltype = AA length = 8
FEATURE	Location/Qualifiers
REGION	1..8
	note = synthetic
source	1..8
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 136	
VSGWRLFK	8

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SEQ ID NO: 137	moltype = AA length = 9
FEATURE	Location/Qualifiers
REGION	1..9
source	note = synthetic
	1..9
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 137	
VSGWRLFKK	9
SEQ ID NO: 138	moltype = AA length = 10
FEATURE	Location/Qualifiers
REGION	1..10
source	note = synthetic
	1..10
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 138	
VSGWRLFKKI	10
SEQ ID NO: 139	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 139	
VSGWRLYKKI S	11
SEQ ID NO: 140	moltype = AA length = 22
FEATURE	Location/Qualifiers
REGION	1..22
source	note = synthetic
	1..22
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 140	
GSMLFRVTIN SVSGWALFKK IS	22
SEQ ID NO: 141	moltype = AA length = 22
FEATURE	Location/Qualifiers
REGION	1..22
source	note = synthetic
	1..22
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 141	
GSMLFRVTIN SVTGYRLFEE IL	22
SEQ ID NO: 142	moltype = AA length = 16
FEATURE	Location/Qualifiers
REGION	1..16
source	note = synthetic
	1..16
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 142	
GSMLFRVTIN SSSWKR	16
SEQ ID NO: 143	moltype = AA length = 14
FEATURE	Location/Qualifiers
REGION	1..14
source	note = synthetic
	1..14
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 143	
VSGVSGWRLF KKIS	14
SEQ ID NO: 144	moltype = AA length = 12
FEATURE	Location/Qualifiers
REGION	1..12
source	note = synthetic
	1..12
	mol_type = protein

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SEQUENCE: 144 VVSGWRLFKK IS	organism = synthetic construct	
		12
SEQ ID NO: 145 FEATURE REGION	moltype = AA length = 15 Location/Qualifiers 1..15	
source	note = synthetic 1..15 mol_type = protein organism = synthetic construct	
SEQUENCE: 145 SSWKRSMLFR VTINS		15
SEQ ID NO: 146 FEATURE REGION	moltype = AA length = 14 Location/Qualifiers 1..14	
source	note = synthetic 1..14 mol_type = protein organism = synthetic construct	
SEQUENCE: 146 SSWKRMLFRV TINS		14
SEQ ID NO: 147 FEATURE REGION	moltype = AA length = 17 Location/Qualifiers 1..17	
source	note = synthetic 1..17 mol_type = protein organism = synthetic construct	
SEQUENCE: 147 SSWKRDGSML PRVTINS		17
SEQ ID NO: 148 FEATURE REGION	moltype = AA length = 18 Location/Qualifiers 1..18	
source	note = synthetic 1..18 mol_type = protein organism = synthetic construct	
SEQUENCE: 148 SSWKRPDGSM LFRVTINS		18
SEQ ID NO: 149 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16	
source	note = synthetic 1..16 mol_type = protein organism = synthetic construct	
SEQUENCE: 149 SSWKRSMLFR VTINSV		16
SEQ ID NO: 150 FEATURE REGION	moltype = AA length = 15 Location/Qualifiers 1..15	
source	note = synthetic 1..15 mol_type = protein organism = synthetic construct	
SEQUENCE: 150 SSWKRMLFRV TINSV		15
SEQ ID NO: 151 FEATURE REGION	moltype = AA length = 18 Location/Qualifiers 1..18	
source	note = synthetic 1..18 mol_type = protein organism = synthetic construct	
SEQUENCE: 151 SSWKRDGSML PRVTINSV		18
SEQ ID NO: 152 FEATURE	moltype = AA length = 19 Location/Qualifiers	

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REGION	1..19	
source	note = synthetic	
	1..19	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 152		
SSWKRPDGSM LFRVTINSV		19
SEQ ID NO: 153	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = synthetic	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 153		
SSWKRSMLFR VTINSVS		17
SEQ ID NO: 154	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
REGION	1..16	
source	note = synthetic	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 154		
SSWKRMFLRV TINSVS		16
SEQ ID NO: 155	moltype = AA length = 19	
FEATURE	Location/Qualifiers	
REGION	1..19	
source	note = synthetic	
	1..19	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 155		
SSWKRDGSML PRVTINSVS		19
SEQ ID NO: 156	moltype = AA length = 20	
FEATURE	Location/Qualifiers	
REGION	1..20	
source	note = synthetic	
	1..20	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 156		
SSWKRPDGSM LFRVTINSV		20
SEQ ID NO: 157	moltype = AA length = 15	
FEATURE	Location/Qualifiers	
REGION	1..15	
source	note = synthetic	
	1..15	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 157		
SSWKRGSMMLF RVTIN		15
SEQ ID NO: 158	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
REGION	1..14	
source	note = synthetic	
	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 158		
SSWKRGSMMLF RVTI		14
SEQ ID NO: 159	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
REGION	1..14	
source	note = synthetic	
	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 159		

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SSWKRSMLFR VTIN	14
SEQ ID NO: 160 FEATURE REGION source SEQUENCE: 160 SSWKMLFRV TIN	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 161 FEATURE REGION source SEQUENCE: 161 SSWKRDGSML FRVTIN	moltype = AA length = 16 Location/Qualifiers 1..16 note = synthetic 1..16 mol_type = protein organism = synthetic construct
SEQ ID NO: 162 FEATURE REGION source SEQUENCE: 162 SSWKRPDGSM LFRVTIN	moltype = AA length = 17 Location/Qualifiers 1..17 note = synthetic 1..17 mol_type = protein organism = synthetic construct
SEQ ID NO: 163 FEATURE REGION source SEQUENCE: 163 SSWKRSMLFR VTI	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 164 FEATURE REGION source SEQUENCE: 164 SSWKMLFRV TI	moltype = AA length = 12 Location/Qualifiers 1..12 note = synthetic 1..12 mol_type = protein organism = synthetic construct
SEQ ID NO: 165 FEATURE REGION source SEQUENCE: 165 SSWKRDGSML FRVTI	moltype = AA length = 15 Location/Qualifiers 1..15 note = synthetic 1..15 mol_type = protein organism = synthetic construct
SEQ ID NO: 166 FEATURE REGION source SEQUENCE: 166 SSWKRPDGSM LFRVTI	moltype = AA length = 16 Location/Qualifiers 1..16 note = synthetic 1..16 mol_type = protein organism = synthetic construct
SEQ ID NO: 167 FEATURE REGION	moltype = AA length = 15 Location/Qualifiers 1..15 note = synthetic

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source	1..15	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 167		
VSGWRLFKKI SVFTL		15
SEQ ID NO: 168	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
REGION	1..14	
source	note = synthetic	
	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 168		
VSGWRLFKKI SVFT		14
SEQ ID NO: 169	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 169		
VSGWRLFKKI SVF		13
SEQ ID NO: 170	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
source	note = synthetic	
	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 170		
VSGWRLFKKI SV		12
SEQ ID NO: 171	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
source	note = synthetic	
	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 171		
VSGWRLCKKI S		11
SEQ ID NO: 172	moltype = AA length = 22	
FEATURE	Location/Qualifiers	
REGION	1..22	
source	note = synthetic	
	1..22	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 172		
VSGWRLFKKI SGSMMLFRVTI NS		22
SEQ ID NO: 173	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 173		
SSWKRLFRVT INS		13
SEQ ID NO: 174	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
source	note = synthetic	
	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 174		
SSWKRFRVTI NS		12

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SEQ ID NO: 175	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 175	
SSWKRRVTIN S	11
SEQ ID NO: 176	moltype = AA length = 19
FEATURE	Location/Qualifiers
REGION	1..19
source	note = synthetic
	1..19
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 176	
SSWKRTPDGS MLFRVTINS	19
SEQ ID NO: 177	moltype = AA length = 20
FEATURE	Location/Qualifiers
REGION	1..20
source	note = synthetic
	1..20
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 177	
SSWKRITPDG SMLFRVTINS	20
SEQ ID NO: 178	moltype = AA length = 21
FEATURE	Location/Qualifiers
REGION	1..21
source	note = synthetic
	1..21
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 178	
SSWKRLITPD GSMLFRVTIN S	21
SEQ ID NO: 179	moltype = AA length = 16
FEATURE	Location/Qualifiers
REGION	1..16
source	note = synthetic
	1..16
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 179	
SSRGSMFLFRV TINSWK	16
SEQ ID NO: 180	moltype = AA length = 16
FEATURE	Location/Qualifiers
REGION	1..16
source	note = synthetic
	1..16
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 180	
SKRGSMFLFRV TINSWS	16
SEQ ID NO: 181	moltype = AA length = 14
FEATURE	Location/Qualifiers
REGION	1..14
source	note = synthetic
	1..14
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 181	
SWRGSMFLFRV TINS	14
SEQ ID NO: 182	moltype = AA length = 14
FEATURE	Location/Qualifiers
REGION	1..14
source	note = synthetic
	1..14
	mol_type = protein

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SEQUENCE: 182 SSRGSMFLRV TIWK	organism = synthetic construct	
		14
SEQ ID NO: 183 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16	
source	note = synthetic 1..16 mol_type = protein	
SEQUENCE: 183 SSWKRGSMLY RVTINS	organism = synthetic construct	
		16
SEQ ID NO: 184 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16	
source	note = synthetic 1..16 mol_type = protein	
SEQUENCE: 184 SSWKRGSMWL RVTINS	organism = synthetic construct	
		16
SEQ ID NO: 185 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16	
source	note = synthetic 1..16 mol_type = protein	
SEQUENCE: 185 SSWKRGSMRH RVTINS	organism = synthetic construct	
		16
SEQ ID NO: 186 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16	
source	note = synthetic 1..16 mol_type = protein	
SEQUENCE: 186 SSWKRGSLLF RVTINS	organism = synthetic construct	
		16
SEQ ID NO: 187 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16	
source	note = synthetic 1..16 mol_type = protein	
SEQUENCE: 187 SSWKRGSKLF RVTINS	organism = synthetic construct	
		16
SEQ ID NO: 188 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16	
source	note = synthetic 1..16 mol_type = protein	
SEQUENCE: 188 SSWKRGSRLF RVTINS	organism = synthetic construct	
		16
SEQ ID NO: 189 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16	
source	note = synthetic 1..16 mol_type = protein	
SEQUENCE: 189 SSWKRGSLFLF RVTINS	organism = synthetic construct	
		16
SEQ ID NO: 190 FEATURE	moltype = AA length = 16 Location/Qualifiers	

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REGION	1..16	
source	note = synthetic	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 190		
SSWKRGSWLF RVTINS		16
SEQ ID NO: 191	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
REGION	1..16	
source	note = synthetic	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 191		
SSWKRGSMLF RVINS		16
SEQ ID NO: 192	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
REGION	1..16	
source	note = synthetic	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 192		
SSWKRGSMLF RVQINS		16
SEQ ID NO: 193	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
REGION	1..16	
source	note = synthetic	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 193		
SSWKRGSMLF RVNINS		16
SEQ ID NO: 194	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = synthetic	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 194		
SSWKRGSMLF RVTINSC		17
SEQ ID NO: 195	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
source	note = synthetic	
	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 195		
CVSGWRLFKK IS		12
SEQ ID NO: 196	moltype = AA length = 17	
FEATURE	Location/Qualifiers	
REGION	1..17	
source	note = synthetic	
	1..17	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 196		
SSWKRGSMLF RVTINSK		17
SEQ ID NO: 197	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
source	note = synthetic	
	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 197		

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KVSGWRLFKK IS		12
SEQ ID NO: 198	moltype = AA length = 23	
FEATURE	Location/Qualifiers	
REGION	1..23	
source	note = synthetic	
	1..23	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 198		
GSLLFRVTIN GVTGWRLCEN ILA		23
SEQ ID NO: 199	moltype = AA length = 24	
FEATURE	Location/Qualifiers	
REGION	1..24	
source	note = synthetic	
	1..24	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 199		
GSLLFRVTIN VGVGTGWRLC E RILA		24
SEQ ID NO: 200	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
source	note = synthetic	
	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 200		
SVSGWRLFKK IS		12
SEQ ID NO: 201	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 201		
NSVSGWRLFK KIS		13
SEQ ID NO: 202	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
REGION	1..9	
source	note = synthetic	
	1..9	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 202		
GWRLFKKIS		9
SEQ ID NO: 203	moltype = DNA length = 501	
FEATURE	Location/Qualifiers	
misc_feature	1..501	
source	note = synthetic	
	1..501	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 203		
atgttgagcg gttcaagaag attagccacc atcaccatca ccatcatcac	60	
tccacactcg acgattcgt tgggactgg gaacagacag cgcctacaa cctggaccaa	120	
gtccttgaac agggagggtgt gtccagttt ctgcagaatc tcgcccgttc cgtaactccg	180	
atcatgagga ttgtccggag cgggtaaaaat gcccctgaaga tcgcacatcca tgcatcatc	240	
ccgtatgaaag gtctgagcgc cgaccaaatg cggcagatcg aagagggttt taagggtgt	300	
taccctgtgg atgatcatca ctttaagggtg atccctgcctt atggcacact ggtaatcgac	360	
ggggttacgc cgaacaagct gaactatttc ggacggccgt atgaaggcat cgccgtttc	420	
gacggcaaaa agatcaactac cacagggacc ctgtggaacg gcaacaaaat tatcgacgag	480	
cgcctgatca ccccccacta a	501	
SEQ ID NO: 204	moltype = AA length = 166	
FEATURE	Location/Qualifiers	
REGION	1..166	
source	note = synthetic	
	1..166	
	mol_type = protein	

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SEQUENCE: 204          organism = synthetic construct
MVSGWRLFKK ISHHHHHHHH FTLDLDFVGDW EQTAAYNLDDQ VLEQGGVSSL LQNLAVSVTP 60
IMRIVRSGEN ALKIDIHVII PYEGLSADQM AQIEEVFKVV YPVDDHHFKV ILPYGTLVID 120
GVTPNKLNYF GRPYEGIAVF DGKKITTTGT LWNGNKNIIDE RLITPD 166

SEQ ID NO: 205          moltype = DNA length = 510
FEATURE
misc_feature           Location/Qualifiers
1..510
note = synthetic
source
1..510
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 205
atgaaacatc accatcacca tcatgtgagc ggctggcgcc tgttcaagaa gattagccgc 60
agtcctcggtt tcacactcga cgatttcgtt qgggactggg aacagacagc cgcctacaac 120
ctggaccaag tccttgaaca gggaggtgtc tccagttgc tgcagaatct cgcctgtcc 180
gttaactccga tcatgaggat tgcggggcggc ggtgaaaatgg ccctgaatgt cgacatccat 240
gtcatacatcc cgtatgggg tctgacgcgc gaccaaattgg cccagatcga agaggtgttt 300
aagggtgtgt accctgttgg tgcatacatc ttaagggtga ttctgcctca tggcacactg 360
gtaatcgacg gggttacggc gaacaagctg aactatttcg gacggccgtg tgaaggcatac 420
gcctgttgc acggcaaaaa gatcactacc acaggggaccg tgtggAACCGG caacaaaatt 480
atcgacgagc gcctgatcac ccccgactaa 510

SEQ ID NO: 206          moltype = AA length = 169
FEATURE
REGION
1..169
note = synthetic
source
1..169
mol_type = protein
organism = synthetic construct

SEQUENCE: 206
MKHHHHHHHS GWRLFKKISG SSGFTLDDFV GDWEQTAAYN LDQVLEQGGV SSLQLQNLAVS 60
VTPIMRIVRS GENALKIDIH VIIPYEGLSA DQMAQIEEVF KVYPVDDHH FKVILPYGTL 120
VIDGVTPNKL NYFGGRPYEGI AVFDGKKITT TGTLWNGNKNI IDERLITPD 169

SEQ ID NO: 207          moltype = DNA length = 366
FEATURE
misc_feature           Location/Qualifiers
1..366
note = synthetic
source
1..366
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 207
atgtggcoca ttctctggca tgagatgtgg catgaaggcc tggaaagggc atctcggttg 60
tactttgggg aaaggaacgt gaaaggcatg tttgagggtgc tggagccctt gcatgctatg 120
atggaacggg gccccccagac tctgaaggaa acatccctta atcaggcccta tggtcgagat 180
ttaatgggg cccaagagt gtgcaggaa tacatggaaat caggaaatgt caaggacctc 240
acccaaacgt gggacctcta ttatcatgtt ttccgacgaa tcagtggtgg ttcaggttgt 300
ggcggggcgc gtggctcgag cagcggtgg a tgcggcgtt ggccgtgtt caagaagatt 360
agctaa 366

SEQ ID NO: 208          moltype = AA length = 121
FEATURE
REGION
1..121
note = synthetic
source
1..121
mol_type = protein
organism = synthetic construct

SEQUENCE: 208
MVAIWHHEMW HEGLEEASRL YFGERNVKGM FEVLEPLHAM MERGPQTLKE TSFNQAYGRD 60
LMEAQEWCRK YMKGNSNVKDL TQAWDLYYHV FRRISGGSGG GGSGGSSSSGG VSGWRLFKKI 120
S 121

SEQ ID NO: 209          moltype = DNA length = 372
FEATURE
misc_feature           Location/Qualifiers
1..372
note = synthetic
source
1..372
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 209
atgtggcoca ttctctggca tgagatgtgg catgaaggcc tggaaagggc atctcggttg 60
tactttgggg aaaggaacgt gaaaggcatg tttgagggtgc tggagccctt gcatgctatg 120
atggaacggg gccccccagac tctgaaggaa acatccctta atcaggcccta tggtcgagat 180
ttaatgggg cccaagagt gtgcaggaa tacatggaaat caggaaatgt caaggacctc 240

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acccaagcct gggacctcta ttatcatgtg ttccgacgaa tcagtgggg ttcagggtgt 300
ggggggagcg gtggctcgag cagcggtgga gttagcgta gcggctggcg cctgttcaag 360
aagatcagct aa 372

SEQ ID NO: 210      moltype = AA length = 123
FEATURE           Location/Qualifiers
REGION            1..123
note = synthetic
source             1..123
mol_type = protein
organism = synthetic construct

SEQUENCE: 210
MVAILEWHEMW HEGLEEAASRL YFGERNVKGM FEVLEPLHAM MERGPQLKE TSFNQAYGRD 60
LMEAQEWCRK YMKGNSNVKDL TQAWDLYYHV FRRISGGSGG GGSGGSSSSGG VSVSGWRLFK 120
KIS 123

SEQ ID NO: 211      moltype = DNA length = 369
FEATURE           Location/Qualifiers
misc_feature      1..369
note = synthetic
source             1..369
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 211
atgggagatgc aggtggaaac catctccccaa ggagacgggg gcacccccc caagcgccgc 60
cagacacctcg tgggtgacta cacccggatg ctggaaatg gaaagaatt tgattccccc 120
cgggacagaaa acaagccctt taagttatg ctggcaagc aggagggtat ccggggctgg 180
gaagaagggg ttgccccatg gagttgggtt cagagagccaa aactgactat atctccagat 240
tatgcctatg gtgccactgg gcacccggc atcatccccac cacatgocac tctcgcttc 300
gatgtggagc ttctaaact ggaagggtgtt tcaggtgggtt gcggggagccgg tggctcgagc 360
agcggtgga 369

SEQ ID NO: 212      moltype = AA length = 123
FEATURE           Location/Qualifiers
REGION            1..123
note = synthetic
source             1..123
mol_type = protein
organism = synthetic construct

SEQUENCE: 212
MGVQVETISP GDGRTFPKRG QTCVVHYTGM LEDGKKFDSS RDRNKPDKFM LGKQE VIRGW 60
EEGVAQMSVG QRALKTISPD YAYGATGHPG IIPPHATLVF DVELLKLEGG SGGGGGGGSS 120
SGG 123

SEQ ID NO: 213      moltype = AA length = 12
FEATURE           Location/Qualifiers
REGION            1..12
note = synthetic
source             1..12
mol_type = protein
organism = synthetic construct

SEQUENCE: 213
GSMLFRTIN SV 12

SEQ ID NO: 214      moltype = AA length = 13
FEATURE           Location/Qualifiers
REGION            1..13
note = synthetic
source             1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 214
GSMLFRTIN SVS 13

SEQ ID NO: 215      moltype = AA length = 12
FEATURE           Location/Qualifiers
REGION            1..12
note = synthetic
source             1..12
mol_type = protein
organism = synthetic construct

SEQUENCE: 215
MLFRVTINSV SG 12

SEQ ID NO: 216      moltype = AA length = 13
FEATURE           Location/Qualifiers

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REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 216		
MLFRVTINSV SGW		13
SEQ ID NO: 217	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
REGION	1..14	
source	note = synthetic	
	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 217		
MLFRVTINSV SGWK		14
SEQ ID NO: 218	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
REGION	1..14	
source	note = synthetic	
	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 218		
MLFRVTINSV SGWR		14
SEQ ID NO: 219	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
REGION	1..14	
source	note = synthetic	
	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 219		
GSMMLFRVTIN SVSG		14
SEQ ID NO: 220	moltype = AA length = 15	
FEATURE	Location/Qualifiers	
REGION	1..15	
source	note = synthetic	
	1..15	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 220		
GSMMLFRVTIN SVSGW		15
SEQ ID NO: 221	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
REGION	1..16	
source	note = synthetic	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 221		
GSMMLFRVTIN SVSGWR		16
SEQ ID NO: 222	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
REGION	1..16	
source	note = synthetic	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 222		
GSMMLFRVTIN SVSGWK		16
SEQ ID NO: 223	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
source	note = synthetic	
	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 223		

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GSMFLFRVTIWK	11
SEQ ID NO: 224 FEATURE REGION source SEQUENCE: 224 GSMFLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 225 FEATURE REGION source SEQUENCE: 225 MLFRVTINSW K	13
SEQ ID NO: 226 FEATURE REGION source SEQUENCE: 226 MLFRVTINSW S	moltype = AA length = 11 Location/Qualifiers 1..11 note = synthetic 1..11 mol_type = protein organism = synthetic construct
SEQ ID NO: 227 FEATURE REGION source SEQUENCE: 227 MLFRVTIWS	11
SEQ ID NO: 228 FEATURE REGION source SEQUENCE: 228 MLFRVTIWK	moltype = AA length = 9 Location/Qualifiers 1..9 note = synthetic 1..9 mol_type = protein organism = synthetic construct
SEQ ID NO: 229 FEATURE REGION source SEQUENCE: 229 MLFRVKINS	9
SEQ ID NO: 230 FEATURE REGION source SEQUENCE: 230 GSMFLFRVTIN SWS	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 231 FEATURE REGION	13
	moltype = AA length = 11 Location/Qualifiers 1..11 note = synthetic

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source	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 231	
GSMLFRVKIN S	11
SEQ ID NO: 232	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
	note = synthetic
source	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 232	
GSMLFRVTIW S	11
SEQ ID NO: 233	moltype = AA length = 9
FEATURE	Location/Qualifiers
REGION	1..9
	note = synthetic
source	1..9
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 233	
MLFRVNINS	9
SEQ ID NO: 234	moltype = AA length = 9
FEATURE	Location/Qualifiers
REGION	1..9
	note = synthetic
source	1..9
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 234	
MLFRVWINS	9
SEQ ID NO: 235	moltype = AA length = 9
FEATURE	Location/Qualifiers
REGION	1..9
	note = synthetic
source	1..9
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 235	
LLFRVKINS	9
SEQ ID NO: 236	moltype = AA length = 9
FEATURE	Location/Qualifiers
REGION	1..9
	note = synthetic
source	1..9
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 236	
FLFRVTINS	9
SEQ ID NO: 237	moltype = AA length = 17
FEATURE	Location/Qualifiers
REGION	1..17
	note = synthetic
source	1..17
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 237	
SSWKRGSMLF RVTINSV	17
SEQ ID NO: 238	moltype = AA length = 18
FEATURE	Location/Qualifiers
REGION	1..18
	note = synthetic
source	1..18
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 238	
SSWKRGSMLF RVTINSVS	18

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SEQ ID NO: 239	moltype = AA length = 17
FEATURE	Location/Qualifiers
REGION	1..17
source	note = synthetic
	1..17
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 239	
SSWKRMLFRV TINSVSG	17
SEQ ID NO: 240	moltype = AA length = 18
FEATURE	Location/Qualifiers
REGION	1..18
source	note = synthetic
	1..18
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 240	
SSWKRMLFRV TINSVSGW	18
SEQ ID NO: 241	moltype = AA length = 19
FEATURE	Location/Qualifiers
REGION	1..19
source	note = synthetic
	1..19
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 241	
SSWKRMLFRV TINSVSGWR	19
SEQ ID NO: 242	moltype = AA length = 19
FEATURE	Location/Qualifiers
REGION	1..19
source	note = synthetic
	1..19
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 242	
SSWKRMLFRV TINSVSGWK	19
SEQ ID NO: 243	moltype = AA length = 14
FEATURE	Location/Qualifiers
REGION	1..14
source	note = synthetic
	1..14
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 243	
MLFRVTINSV SGWK	14
SEQ ID NO: 244	moltype = AA length = 19
FEATURE	Location/Qualifiers
REGION	1..19
source	note = synthetic
	1..19
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 244	
SSWKRGSMLF RVTINSVSG	19
SEQ ID NO: 245	moltype = AA length = 20
FEATURE	Location/Qualifiers
REGION	1..20
source	note = synthetic
	1..20
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 245	
SSWKRGSMLF RVTINSVSGW	20
SEQ ID NO: 246	moltype = AA length = 21
FEATURE	Location/Qualifiers
REGION	1..21
source	note = synthetic
	1..21
	mol_type = protein

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SEQUENCE: 246          organism = synthetic construct
SSWKRGSMLF RVTINSVSGW R           21

SEQ ID NO: 247          moltype = AA  length = 21
FEATURE          Location/Qualifiers
REGION          1..21
note = synthetic
source          1..21
mol_type = protein
organism = synthetic construct

SEQUENCE: 247          organism = synthetic construct
SSWKRGSMLF RVTINSVSGW K           21

SEQ ID NO: 248          moltype = AA  length = 16
FEATURE          Location/Qualifiers
REGION          1..16
note = synthetic
source          1..16
mol_type = protein
organism = synthetic construct

SEQUENCE: 248          organism = synthetic construct
SSWKRGSYLF RVTINS                 16

SEQ ID NO: 249          moltype = AA  length = 16
FEATURE          Location/Qualifiers
REGION          1..16
note = synthetic
source          1..16
mol_type = protein
organism = synthetic construct

SEQUENCE: 249          organism = synthetic construct
SSWKRGSMLF RVKINS                 16

SEQ ID NO: 250          moltype = AA  length = 16
FEATURE          Location/Qualifiers
REGION          1..16
note = synthetic
source          1..16
mol_type = protein
organism = synthetic construct

SEQUENCE: 250          organism = synthetic construct
SSWKRGSMLF RVRINS                 16

SEQ ID NO: 251          moltype = AA  length = 16
FEATURE          Location/Qualifiers
REGION          1..16
note = synthetic
source          1..16
mol_type = protein
organism = synthetic construct

SEQUENCE: 251          organism = synthetic construct
SSWKRGSMLF RVWINS                 16

SEQ ID NO: 252          moltype = AA  length = 16
FEATURE          Location/Qualifiers
REGION          1..16
note = synthetic
source          1..16
mol_type = protein
organism = synthetic construct

SEQUENCE: 252          organism = synthetic construct
SSKGSMMLFR VTIWSV                  16

SEQ ID NO: 253          moltype = AA  length = 17
FEATURE          Location/Qualifiers
REGION          1..17
note = synthetic
source          1..17
mol_type = protein
organism = synthetic construct

SEQUENCE: 253          organism = synthetic construct
SSKGSMMLFR VTIWSVS                 17

SEQ ID NO: 254          moltype = AA  length = 15
FEATURE          Location/Qualifiers

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REGION	1..15	
source	note = synthetic	
	1..15	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 254		
SSWRGSMLFR VTIKS		15
SEQ ID NO: 255	moltype = AA length = 15	
FEATURE	Location/Qualifiers	
REGION	1..15	
source	note = synthetic	
	1..15	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 255		
KRSSGSMLFR VTIWS		15
SEQ ID NO: 256	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 256		
SSKRMLFRVT IWS		13
SEQ ID NO: 257	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 257		
KRSSMLFRVT IWS		13
SEQ ID NO: 258	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 258		
GSMKFRVTIN SWK		13
SEQ ID NO: 259	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 259		
GSMLFRKTIN SWK		13
SEQ ID NO: 260	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 260		
GSMLFRVTKN SWK		13
SEQ ID NO: 261	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
source	note = synthetic	
	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 261		

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GKMLFRVTIW K	11
SEQ ID NO: 262 FEATURE REGION source SEQUENCE: 262 GSMKFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 263 FEATURE REGION source SEQUENCE: 263 GSMKFRVTIW K	moltype = AA length = 11 Location/Qualifiers 1..11 note = synthetic 1..11 mol_type = protein organism = synthetic construct
SEQ ID NO: 264 FEATURE REGION source SEQUENCE: 264 GRMLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 265 FEATURE REGION source SEQUENCE: 265 GRMLFRVTIW K	moltype = AA length = 11 Location/Qualifiers 1..11 note = synthetic 1..11 mol_type = protein organism = synthetic construct
SEQ ID NO: 266 FEATURE REGION source SEQUENCE: 266 GSMRFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 267 FEATURE REGION source SEQUENCE: 267 GSMRFRVTIW K	moltype = AA length = 11 Location/Qualifiers 1..11 note = synthetic 1..11 mol_type = protein organism = synthetic construct
SEQ ID NO: 268 FEATURE REGION source SEQUENCE: 268 GDMLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 269 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11 note = synthetic

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source	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 269	
GDMFLFRVTIW K	11
SEQ ID NO: 270	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 270	
GSMDFRVTIN SWK	13
SEQ ID NO: 271	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 271	
GSMDFRVTIW K	11
SEQ ID NO: 272	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 272	
GEMLFRVTIN SWK	13
SEQ ID NO: 273	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 273	
GSMEFRVTIN SWK	13
SEQ ID NO: 274	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 274	
GSMEFRVTIW K	11
SEQ ID NO: 275	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 275	
GSMLFRVTIW KVK	13
SEQ ID NO: 276	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 276	
GSMLFRVTIW SVK	13

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SEQ ID NO: 277	moltype = AA length = 12
FEATURE	Location/Qualifiers
REGION	1..12
source	note = synthetic
	1..12
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 277	
GSMLFRVTIW SK	12
SEQ ID NO: 278	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 278	
GSMLFRVTIW KWK	13
SEQ ID NO: 279	moltype = AA length = 12
FEATURE	Location/Qualifiers
REGION	1..12
source	note = synthetic
	1..12
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 279	
GSMLFRVTIW KK	12
SEQ ID NO: 280	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 280	
GSMLFRVTIN S	11
SEQ ID NO: 281	moltype = AA length = 9
FEATURE	Location/Qualifiers
REGION	1..9
source	note = synthetic
	1..9
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 281	
MLFRVTINS	9
SEQ ID NO: 282	moltype = AA length = 9
FEATURE	Location/Qualifiers
REGION	1..9
source	note = synthetic
	1..9
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 282	
MLFVTINSV	9
SEQ ID NO: 283	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 283	
MLFRVTINSV S	11
SEQ ID NO: 284	moltype = AA length = 10
FEATURE	Location/Qualifiers
REGION	1..10
source	note = synthetic
	1..10
	mol_type = protein

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SEQUENCE: 284 GSMLFRVTIN	organism = synthetic construct	
		10
SEQ ID NO: 285 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9	
source	note = synthetic 1..9 mol_type = protein	
SEQUENCE: 285 GSMLFRVTI	organism = synthetic construct	
		9
SEQ ID NO: 286 FEATURE REGION	moltype = AA length = 9 Location/Qualifiers 1..9	
source	note = synthetic 1..9 mol_type = protein	
SEQUENCE: 286 SMLFRVTIN	organism = synthetic construct	
		9
SEQ ID NO: 287 FEATURE REGION	moltype = AA length = 8 Location/Qualifiers 1..8	
source	note = synthetic 1..8 mol_type = protein	
SEQUENCE: 287 MLFRVTIN	organism = synthetic construct	
		8
SEQ ID NO: 288 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7	
source	note = synthetic 1..7 mol_type = protein	
SEQUENCE: 288 MLFRVTI	organism = synthetic construct	
		7
SEQ ID NO: 289 FEATURE REGION	moltype = AA length = 15 Location/Qualifiers 1..15	
source	note = synthetic 1..15 mol_type = protein	
SEQUENCE: 289 SSKRGSMLFR VTIWS	organism = synthetic construct	
		15
SEQ ID NO: 290 FEATURE REGION	moltype = AA length = 23 Location/Qualifiers 1..23	
source	note = synthetic 1..23 mol_type = protein	
SEQUENCE: 290 GSMLFRVTIN SGVSGWALFK KIS	organism = synthetic construct	
		23
SEQ ID NO: 291 FEATURE REGION	moltype = AA length = 23 Location/Qualifiers 1..23	
source	note = synthetic 1..23 mol_type = protein	
SEQUENCE: 291 GSMLFRVTIN SGVSGWRLFK KIS	organism = synthetic construct	
		23
SEQ ID NO: 292 FEATURE	moltype = AA length = 11 Location/Qualifiers	

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REGION          1..11
source          note = synthetic
                1..11
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 292
VSGWALFKKI S                                         11

SEQ ID NO: 293          moltype = AA  length = 25
FEATURE          Location/Qualifiers
REGION          1..25
source          note = synthetic
                1..25
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 293
GSMLFRVTIN SVSGVSGWRL FKKIS                                         25

SEQ ID NO: 294          moltype = AA  length = 148
FEATURE          Location/Qualifiers
REGION          1..148
source          note = synthetic
                1..148
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 294
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV  60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPD                                         148

SEQ ID NO: 295          moltype = DNA  length = 444
FEATURE          Location/Qualifiers
misc_feature    1..444
source          note = synthetic
                1..444
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 295
atgggtctca cactcgacga ttteggttggg gactgggaac agacagccgc ctacaacctg  60
gaccaagtcc ttgaacaggg agggtgtgtc agtttgctgc agaatctcgc cgtgtccgtta 120
actccgatca tgaggattgt ccggagccgtt gaaaatgccc tgaagatcga catccatgtc 180
atcatcccgatc atgaagggtct gagcgcgcac caaatggccc agatcgaaga ggtgtttaag 240
gtgggttacc ctgtggatca tcatacactt aaggtgtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcggaa caagctgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaaagat cactaccaca gggaccctgt ggaacggcaa caaaattatc 420
gacgagcgcc tcgtatcccccc cgac                                         444

SEQ ID NO: 296          moltype = AA  length = 148
FEATURE          Location/Qualifiers
REGION          1..148
source          note = synthetic
                1..148
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 296
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV  60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLITPD                                         148

SEQ ID NO: 297          moltype = DNA  length = 444
FEATURE          Location/Qualifiers
misc_feature    1..444
source          note = synthetic
                1..444
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 297
atgggtctca cactcgaaga ttteggttggg gactgggaac agacagccgc ctacaacctg  60
gaccaagtcc ttgaacaggg agggtgtgtc agtttgctgc agaatctcgc cgtgtccgtta 120
actccgatca aaaggattgt ccggagccgtt gaaaatgccc tgaagatcga catccatgtc 180
atcatcccgatc atgaagggtct gagcgcgcac caaatggccc agatcgaaga ggtgtttaag 240
gtgggttacc ctgtggatca tcatacactt aaggtgtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcggaa catgtgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaaagat cactgtaaaca gggaccctgt ggaacggcaa caaaattatc 420
gacgagcgcc tcgtatcccccc cgac                                         444

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SEQ ID NO: 298	moltype = AA length = 12
FEATURE	Location/Qualifiers
REGION	1..12
source	note = synthetic
	1..12
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 298	
SVSGWRLFKK IS	12
SEQ ID NO: 299	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 299	
NSVSGWRLFK KIS	13
SEQ ID NO: 300	moltype = AA length = 9
FEATURE	Location/Qualifiers
REGION	1..9
source	note = synthetic
	1..9
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 300	
GWRLFKKIS	9
SEQ ID NO: 301	moltype = AA length = 23
FEATURE	Location/Qualifiers
REGION	1..23
source	note = synthetic
	1..23
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 301	
GSMLFRVTIN SGVSGWRLFK KIS	23
SEQ ID NO: 302	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 302	
GSMLFRVTIN SWK	13
SEQ ID NO: 303	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 303	
GSMLFRVTIN SWK	13
SEQ ID NO: 304	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 304	
GSMLFRVTIN SWK	13
SEQ ID NO: 305	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein

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SEQUENCE: 305 GSMLFRVTIN KWK	organism = synthetic construct	
		13
SEQ ID NO: 306 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 306 GSMLFRVTIK SWK	organism = synthetic construct	
		13
SEQ ID NO: 307 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 307 GSMLFRVTIN RWK	organism = synthetic construct	
		13
SEQ ID NO: 308 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 308 GSMLFRVTIR SWK	organism = synthetic construct	
		13
SEQ ID NO: 309 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 309 GSMLFRVTIN DWK	organism = synthetic construct	
		13
SEQ ID NO: 310 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 310 GSMLFRVTID SWK	organism = synthetic construct	
		13
SEQ ID NO: 311 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 311 GSMLFRVTIN EWK	organism = synthetic construct	
		13
SEQ ID NO: 312 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 312 GSMLFRVTIE SWK	organism = synthetic construct	
		13
SEQ ID NO: 313 FEATURE	moltype = AA length = 13 Location/Qualifiers	

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REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 313	
GSMRFRVTIN SWK	13
SEQ ID NO: 314	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 314	
GSMDFRVTIN SWK	13
SEQ ID NO: 315	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 315	
GSMEFRVTIN SWK	13
SEQ ID NO: 316	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 316	
GSMLFRRTIN SWK	13
SEQ ID NO: 317	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 317	
GSMLFRDTIN SWK	13
SEQ ID NO: 318	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 318	
GSMLFRETIN SWK	13
SEQ ID NO: 319	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 319	
GSMLFRVTDN SWK	13
SEQ ID NO: 320	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 320	

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GSMFLFRVTEN SWK	13
SEQ ID NO: 321	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 321	
GSMKFRVTIN SWK	13
SEQ ID NO: 322	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 322	
GSMFLFRKTIN SWK	13
SEQ ID NO: 323	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 323	
GSMFLFRVTKN SWK	13
SEQ ID NO: 324	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 324	
GSMFLFRVTIN S	11
SEQ ID NO: 325	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 325	
GSMFLFRVSIN S	11
SEQ ID NO: 326	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 326	
GSMFLFRVNIN S	11
SEQ ID NO: 327	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 327	
GSKLFRVTIN S	11
SEQ ID NO: 328	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic

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source          1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 328
GSRLFRVTIN S                                         11

SEQ ID NO: 329          moltype = AA  length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source          1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 329
GSMWFRVTIN S                                         11

SEQ ID NO: 330          moltype = AA  length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source          1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 330
GSMSFRVTIN S                                         11

SEQ ID NO: 331          moltype = AA  length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source          1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 331
GSMNFRVTIN S                                         11

SEQ ID NO: 332          moltype = AA  length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source          1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 332
GSMKFRVTIN S                                         11

SEQ ID NO: 333          moltype = AA  length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source          1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 333
GSMLFRWTIN S                                         11

SEQ ID NO: 334          moltype = AA  length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source          1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 334
GSMLFRSTIN S                                         11

SEQ ID NO: 335          moltype = AA  length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source          1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 335
GSMLFRNTIN S                                         11

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SEQ ID NO: 336      moltype = AA length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source            1..11
mol_type = protein
organism = synthetic construct
SEQUENCE: 336
GSMLFRKTIN S                               11

SEQ ID NO: 337      moltype = AA length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source            1..11
mol_type = protein
organism = synthetic construct
SEQUENCE: 337
GSMLFRVTWN S                               11

SEQ ID NO: 338      moltype = AA length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source            1..11
mol_type = protein
organism = synthetic construct
SEQUENCE: 338
GSMLFRVTSN S                               11

SEQ ID NO: 339      moltype = AA length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source            1..11
mol_type = protein
organism = synthetic construct
SEQUENCE: 339
GSMLFRVTNN S                               11

SEQ ID NO: 340      moltype = AA length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source            1..11
mol_type = protein
organism = synthetic construct
SEQUENCE: 340
GSMLFRVTKN S                               11

SEQ ID NO: 341      moltype = AA length = 11
FEATURE          Location/Qualifiers
REGION           1..11
note = synthetic
source            1..11
mol_type = protein
organism = synthetic construct
SEQUENCE: 341
GSMLFRVTIK S                               11

SEQ ID NO: 342      moltype = AA length = 634
FEATURE          Location/Qualifiers
REGION           1..634
note = synthetic
source            1..634
mol_type = protein
organism = synthetic construct
SEQUENCE: 342
MKHHHHHHHVS KGEELIKENN RSKLYLEGSV NGHQFKCTHE GEGKPYEGKQ TNRIKVVEGG 60
PLPFAFDILA THFMYGSKVF IKYPADLPDY FKQSFPEGFT WERVMVFEDG GVLTATQDTS 120
LQDGELIYNV KVRGVNFPAN GPVMQKKTLG WEPSTETMYP ADGGLEGRCD KALKLVGGGH 180
LHVNFKTTYK SKKPVKMPGV HYVDRRLERI KEADNETYVE QYEHAVARYS NLGGGFTLED 240
FVGDWWRQTAG YNLDQVLEQQ GVSSLFQNLG VSVTPIQRIV LSGENGLKID IHVIIPYEGL 300
SGDQMGQIEK IFKVVYPVDD HHFKVILHYG TLVIDGVTPN MIDYFGRPYE GIAVFDGKKI 360
TVTGTLWNGN KIIDERLNP DGSLLFRTVI NGVTGWRLCE RILARHELIK ENMRSKLYLE 420
GSVNGHOFKC THEGEGKPYE GKQTNRIKVV EGGPLPFADF ILATHFMYGS KVFIKYPADL 480

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PDYFKQSFPE GFTWERVMVF EDGGVLTATQ DTSLQDGELI YNVKVRGVNF PANGPVMQKK	540
TLGWEPTET MYPADGGLEG RCDKALKLVG GGHHLHVNFKT TYKSKKPVKM PGVHYVDRRL	600
ERIKEADNET YVEQYEHAVA RYSNLGGGMD ELYK	634

SEQ ID NO: 343	moltype = DNA length = 1902
FEATURE	Location/Qualifiers
misc_feature	1..1902
	note = synthetic
source	1..1902
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 343	
atgaaacatc accatcacca tcatgtgago aagggagaag aacttataaa agaaaacatg	60
cggcttaaac tgtacctcg agggtccgtc aatggcacc agtttaagtg taccacagag	120
ggtgaggagaa agccctatga ggggaagcag acaaaccgc tcaaggctgt cgaaggggaa	180
ccccctcccg ttcgtttga tatcttgct actcactta tgcgtggaa caaagtttc	240
ataaaagtata ctgcggaccc tcctgattat tttaaacagt catttcccg agggtttcaca	300
tgggaaaggg tcatgtgtt tgaggatgtt ggcgtgtc ctcgaactca ggacacctca	360
ctgcaggacg cgcgcgtat ctacaatgtt aagggtccgg gtgttaaactt ccctgccaac	420
gggcctgtt aa tgcagaagaa gaccctggg tgggagccgt ccacccaaac catgtaccc	480
gctgtatgtt ggctggaggg ccgcgtgtac aaggctctgt a gctgttgg aggtggcat	540
ttgcacgtaa atttcaagac aacttacaaag agcaaaaaac ccgtaaaaat gcccgggtt	600
cattacgtt acagaaggctt tgaacgcata aaggaaagctg ataacgcagc atacgtggag	660
cagtacgacg a cgcgcgttgc ccgcgtactca aaccctggggg tgggttttac actggaggat	720
tttggggat attggagaca gacagccggc tacaatctgg atcagggtct ggaacaagga	780
ggagtgtttt ctctgttca gaatctggg tgcgtgtga caccatccca gaggatctg	840
ctgtctggc agaatggact gaagatcgat attcaacgtga tcatcccta cgaaggctg	900
tctggagacc agatggccca gatttggaaatccatccaaatgggtatcc tttggacat	960
caccacttca aggtgtatcc gcactacccg accctgggtt ttgatggagt gacaccta	1020
atgatcgact atctccggaa accttacccg ggaatccggc tttggacccgg aaagaagatc	1080
accgtgcacg aacactgtt gatggaaatc aagatcatcg acggcggct gatcaaccct	1140
atggatctt tgcgtgttgc agtggaccatc aacgggtgtt caggatggag actgtgcgag	1200
agaattctgg cttagacatga gctaatacg gaaaatatga gaagtaagct atacccat	1260
gggtccgtca acgggtccca gtttaaatgc actcatgaatg gtgaggggaa accttatgaa	1320
gtaaagcaga ctaatcgat aaaaatgggtt gggggccgtt ctctggccatt cgcttccat	1380
attctggcca ctaactttat gtatgggtt ttaataatccc cgctgatttgc	1440
ccagactact ttaaacatgc ctccctgaa ggattccatc gggagccgg gatgggttgc	1500
gaggatggg ggcgttttac tgcaactcg gataacttcc tgcgtgttgc ggaactgtat	1560
tacaacgtt aggtggccgg cgtcaatcc ccagccatcc gtcgtgtat gcaaaagaaa	1620
accttgggtt gggagccctt aacggagaca atgttcccg cggacccggg gtttggggat	1680
agatgtata aaggatgtt aactcgccgg gggggccacc ttcatgttca tttcaagact	1740
acatataaaa gtaaaaaacc agtcaagatg cctggagtgc actacgttgc tcgttaggtt	1800
gagaggatata aagaagccga caacggaaact tatgtatgtt aatatgttgc cggccgttgc	1860
cgttatttca acttggccgg aggaatggat gaaatgttaca ag	1902
SEQ ID NO: 344	moltype = AA length = 622
FEATURE	Location/Qualifiers
REGION	1..622
	note = synthetic
source	1..622
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 344	
MKHHHHHHHS KGEELIKENM RSKLYLEGSV NGHQFKCTHE GEGKPYEGKQ TNRIKVVEGG	60
PLPFAFDILA THFMYGSVKV IKYPADLPDY FKQSFPEGFT WERVMVFEDG GVLTTATQDTS	120
LQDGELIYNV KVRGVNFSPAN GPVQMKKTLG WEPSTETMYP ADGGLEGRCRCD KALKLVGGH	180
LHVNFKTYK SKKPKVKMPGV HYVDRRLERI KEADNETYVE QYEHAVARYS NLGGGFTLED	240
FVGDWEQTA YNLDQVLEQG GVSSLQNL A VSVTPIQRIV RSGENALKID IHVIIIPYEGL	300
SADQMAQIEE VFKVVVPVDD HHFKVILPYG TLVIDGVTPN MLNYFGRPYE GIAVFDGKKI	360
TVTGTLWNGN KIIDERLITP DGSMFLFRVTI NSRHELIKEN MRSKLYLEGS VNQHQFKCTH	420
EGERGKPYEGK QTNRKVKVEG PLPFAFDIL ATHFMYGSVKV FIKYPADLPD YFKQSFPEGF	480
TWERVMVFED GGVLTATQDT SLQDGELIYN VKRGVNFPA NGPVMQKTL GWEPESTETMY	540
PADGGLEGRC DKALKLVGGG HLHVNFKTY KSKPKVKMPG VHYZVDRRLER IKEADNETYV	600
EQYEHAVARY SNLGGGMD EL YK	622
SEQ ID NO: 345	moltype = DNA length = 1866
FEATURE	Location/Qualifiers
misc_feature	1..1866
	note = synthetic
source	1..1866
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 345	
atgaaacatc accatcacca tcatgtgago aagggagaag aacttataaa agaaaacatg	60
cggcttaaac tgtacctcg agggtccgtc aatggcacc agtttaagtg taccacagag	120
ggtgaggagaa agccctatga ggggaagcag acaaaccgc tcaaggctgt cgaaggggaa	180

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ccctcccg	ttgccttga	tatctggct	actcaactta	tgtacggaag	caaagtttc	240
ataaagtatc	tcgcgac	tcctgattat	ttaaacagt	catttccga	gggttcaca	300
tggaaagg	tcatggtt	tgaggatgga	ggcgtgc	ctgcaactca	ggacacctca	360
ctgcaggac	gogagctat	ctacaatgt	aaggccgg	gtgtaaactt	ccctgccaac	420
gggcctgtaa	tgcagaagaa	gaccctggga	tggagccgt	ccaccgaaac	catgtaccct	480
gtctgatgg	ggctggaggg	ccgatgtgac	aaggctgtga	agctcg	tggtgtcat	540
ttgcacgtaa	attcaagac	aacttacaag	agoaaaaaaac	ccgtaaaat	gcccgggg	600
cattacgtt	acagaaggct	tgaacgcata	agggaaactg	ataacgagac	atacggttag	660
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ttcggtgg	actggaaaca	gacacgc	tacaacctgg	accaggct	tgaacaggga	780
gtgtgtgtca	gtttgtgtca	gaatctcg	gtgtcgat	ccatccatca	aggattgtc	840
cgagcgg	aaaatggcc	gaatgtc	atccatgtca	tcatcccgta	tgaaggctg	900
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catcaactt	aggatgtc	gccctatgg	acactgtt	tgcacgggt	tacgcgaaac	1020
atgtgtca	atttcggac	gcccgtat	ggtatcg	tttgcacgg	aaaaagatc	1080
actgtta	acag	gacacgc	aaaaatatcg	acgacgc	gatcacc	1140
gacggctca	tgctgttcc	agtaaccatc	aacagcagac	atgatcta	caaggaaat	1200
atgagaagta	actataactt	agaggggtcc	gtcaacgc	accagg	tttgcactat	1260
gaaggtgagg	ggaaacctt	tgaatcg	cataacta	gaataaaat	gttcgagg	1320
gttcctctgc	cattcgctt	cgatattctg	gcccactact	ttatgtat	gtctaaagg	1380
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gtgcactac	ttgtatcg	tttgcaggg	ataaaagaa	ccgacaa	actatgt	1800
gagcaat	atgcacgc	ggctcg	tccaa	tttgc	ggat	1860
tacaag						1866

SEQ ID NO: 346	moltype = AA	length = 611
FEATURE	Location/Qualifiers	
REGION	1..611	
note = synthetic		
source	1..611	
mol_type = protein		
organism = synthetic construct		
SEQUENCE: 346		
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PLPFAFDILA THFMYGSKVF IKYPADLPDY FKQSFPPEGFT WERVMVFEDG GVLTATQDTS	120	
LQDGELIYNV KVGVNFPAN GPVMQKKTLG WEPSTETMYP ADGGLEGRCD KALKLVGGH	180	
LHVNFKTTYK SKPKVKMPGV HYVDRRLERI KEADNETYVE QEHAVARYS NLGGGFTLDD	240	
FVGDWEQTAA YNLDQVLEQGV GSLLQNLAVS VSVTPIMRIV RSGENALKID IHVITPYEGL	300	
SADQMAQIEE VFVWVVPDD HHFKVLPYQ TLVIDGVTPC KLNYFGRPYE GIAVFDGKKI	360	
TTTGTLWNNG KIIDERLITP DRHELIKEM RSKLYLEGSV NGHQFKCTHE GEGKPYEGKQ	420	
TNRIKVVEGG PLPFAFDILA THFMYGSKVF IKYPADLPDY FKQSFPPEGFT WERVMVFEDG	480	
GVLTATQDTS LQDGELIYNV KVGVNFPAN GPVMQKKTLG WEPSTETMYP ADGGLEGRCD	540	
KALKLVGGH LHVNFKTTYK SKPKVKMPGV HYVDRRLERI KEADNETYVE QEHAVARYS	600	
NLGGGMDELY K	611	

SEQ ID NO: 347	moltype = DNA	length = 1833				
FEATURE	Location/Qualifiers					
misc_feature	1..1833					
note = synthetic						
source	1..1833					
mol_type = other DNA						
organism = synthetic construct						
SEQUENCE: 347						
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cggctctaaac tgcacgtca gggtccgtc	aatgggc	cacc agtggtaatgt	120			
gggtgaggaa	agccctatga	ggggaaacgac	acaaacccgca	tcaaggctgt	cgaagggg	180
ccctcccg	ttgccttga	tatctggct	actcaactta	tgtacggaag	caaagt	240
ataaagtatc	ctgcgcac	tcctgattat	ttaaacagt	catttccga	gggttcaca	300
tggaaagg	tcatgttgc	tgaggatgca	ggcgtgc	ctgcaactca	ggacac	360
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gggcctgtaa	tgcagaagaa	gaccctgg	tggagccgt	ccaccgaaac	catgtac	480
gtctgatgg	ggctggaggg	ccgatgtgac	aaggctgt	agctcg	ttggatgtcat	540
ttgcacgtaa	atttcaagac	aacttacaag	agcaaaaaac	ccgtaaaat	ccccggg	600
cattacgtt	acagaaggct	tgaacgcata	aaggaa	actatgc	atacgtgg	660
cagtacgac	acgcgttgc	ccgtactca	aaactgggg	gtggctcac	actcgcac	720
ttcggtgg	actggaaaca	gacacgc	tacaac	ccatgttgc	tgaacagg	780
gtgtgttca	gtttgtgtca	gaatctcg	gtgtcgat	ccatccat	gaggatgt	840
cgagcgg	aaaatggcc	gaagatgc	atccatgtca	tcatcccgta	tgaagg	900
agcgcgacc	aatatggcc	gatcgaagag	gtgtttaagg	tggtgttac	tgtggat	960
catcaactt	aggatgtc	gccctatgg	acactgtt	tgcacgg	tacgcgaa	1020
aagctgaaact	atttcgac	ggcgtat	ggcgtat	ccccgg	aaaaagatc	1080

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actaccacag ggacctgtg gaacggcaac aaaattatcg acgagcgcct gatcacccccc 1140
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actcaactta tgtatgggtc taaggctttt attaaatacc ccgctgattt gccagactac 1380
ttaaaacagt cttccctga aggattcaca tgggagccgg tgatgtgtt cgaggatgg 1440
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aaggcccgcc ggtcaattt cccagccaa ggtccatgtg tgcagaaagaa aaccttgggg 1560
tgggagccct caacggagac aatgtaccct gccgacggcc ggcttgagg tagatgtat 1620
aaggcattga aactcgctgg gggagccca cttcatgtg atttcaagac tacatataaa 1680
agtaaaaaaac cgtcaagat gcttgagggt cactacgtg atcgttaggtt ggagaggata 1740
aaagaagccg acaacgaaac ttatgttagag caatatgacg acggcgtggc tcgttattcc 1800
aacttggcg gaggatggg tgaactgtac aag 1833

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SEQ ID NO: 348      moltype = AA length = 401
FEATURE          Location/Qualifiers
REGION           1..401
note = synthetic
source            1..401
mol_type = protein
organism = synthetic construct
SEQUENCE: 348
MKHHHHHHFT LEDFVGDWEQ TAAYNLDQVL EQGGVSSLQ NLAVSVTPIQ RIVRSGENAL 60
KIDIHVIIIPY EGLSADQMAQ IEEVFKVVP VDDHHFKVIL PYGTLVIDGV TPNNMLNYFGR 120
PYEGIAVFDG KKITVTGTWL NGNKIIDERL ITPDGSMLFR VTINSGSSG SSGELIKENM 180
RSKLYLEGSV NGHQFKCTHE GEGKPYEGKQ TNRIKVVEGG PLPFADILIA THFMYGSKVF 240
IKYPADLPDY FKQSFPEGFT WERVMVFPEDG GVLTATQDTS LDGELIYNV KVRGBVNFPAN 300
GPVMQKKTLG WEPSTETMYP ADGGLERCD KALKLVGGHH LHVNFKTTYK SKKPVKMPGV 360
HYVDRRLERI KEADNEYVE QYEHAVARYS NLGGGMDELY K 401

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SEQ ID NO: 349      moltype = DNA length = 1203
FEATURE          Location/Qualifiers
misc_feature     1..1203
note = synthetic
source            1..1203
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 349
atgaaacatc accatcacca tcatttaca ctogaagatt tcgttgggg ctggaaacag 60
acagccgcct acaacatggg ccaagtccctt gaacaggagat tggtgtccag tttgtgcag 120
aatctcgccg tgcgttacac tccgttccaa aggattgtcc ggagccgtt aaatgcctg 180
aagatcgaca tccatgtcat catccgtat gaaggttca ggcgcacca aatggccag 240
atcgaagagg tggttttaggtt ggttacccctt gtggatgtatc atcactttaa ggtgatctg 300
ccctatggca cactggtaat cgacgggggtt acgcggaaacta tggtgaacta ttccggacgg 360
ccgtatgaag gatcgccgtt gttcgacggc aaaaatgtca ctgttaacagg gaccctgtgg 420
aacggcaaca aattatcgaa cgagccctgtt atcacccttcc acggctccat gctgtccga 480
gttaccatca acagccgggg ctcaatgttca tcccttgggtt agttaatcaa ggaaatatg 540
agaagtaaagc tatacttaga ggggtccgtt aacggtcacc agttttaaatg cactatgaa 600
gggtgaggggaa aaccttatgtt aggttaagcacta atcacttgc taaaatgtgtt cgaggccgtt 660
cctctgecat tgcgttgcgtt tattctggcc actcacttta tgcgttggcc taaggctttt 720
attaaatacc cccgttgcattt gccagactac tttaaaatgtt cttcccttgc aggttccaca 780
tgggagccggg tgatgtgtt cgaggatggt ggcgttcttca ctgcaactca ggatactcc 840
ttgcaagacg gggactgtat ctacaacgtt aagggtccgtt ggcgtcaattt cccagccaa 900
ggtccactgtt tgcagaagaa aaccttgggg tgggagccctt caacggagac aatgtaccct 960
ggcgacggcc ggcttgggg tagatgtgtt aagggttccgtt aactcgctgg gggccggccac 1020
cttcatgttca atttcaagac tacatataaa agttaaaaaaac cgtcaagat gcttgagggt 1080
caactacgtgg atcgttaggtt ggagaggata aaaaagccg acaacgaaac ttatgttagag 1140
caatatatgacg acggcgtggc tcgttattcc aacttggccg gaggatggt tgaactgtac 1200
aag 1203

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SEQ ID NO: 350      moltype = AA length = 395
FEATURE          Location/Qualifiers
REGION           1..395
note = synthetic
source            1..395
mol_type = protein
organism = synthetic construct
SEQUENCE: 350
MKHHHHHHFT LEDFVGDWEQ TAAYNLDQVL EQGGVSSLQ NLAVSVTPIQ RIVRSGENAL 60
KIDIHVIIIPY EGLSADQMAQ IEEVFKVVP VDDHHFKVIL PYGTLVIDGV TPNNMLNYFGR 120
PYEGIAVFDG KKITVTGTWL NGNKIIDERL ITPDGSMLFR VTINSRHEL KENMRSKYL 180
EGSVNGHOFK CTHEGEKGPKY EGKQTNRKIV VEGGPLPFAF DILATHFMYG SKVFIKYPAD 240
LPDYFKQSFPE GFTWERMV FEDGGVLTAT QDTSLQDGEL IYNVKVRGVN FPANGPVMMQK 300
KTLGWEPESTE TMYPADGGL GRCDKALKLV GGGHLHVNFK TTYKSKKPKV MPGVHYVDR 360
LERIKEADNE TYVEQYEHAR ARYSNLGGGM DELYK 395

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SEQ ID NO: 351	moltype = DNA length = 1185	
FEATURE	Location/Qualifiers	
misc_feature	1..1185	
	note = synthetic	
source	1..1185	
	mol_type = other DNA	
	organism = synthetic construct	
<b>SEQUENCE: 351</b>		
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acagccgcct acaaacttggc ccaagtccctt gaacaggggag gtgtgtccag tttgtgcag	120	
aatctcgccg tgccgttaac tccgatccaa aggattgtcc ggagccgtga aaatgccctg	180	
aaagatcaca tccatgtcat catccccat gaaggtctga ggcgcacca aatggccag	240	
atcgaagagg tggttaaggt ggtgtaccct gtggatgtc atcactttaa ggtgtatctg	300	
ccctatggca cactggtaat cgacggggtt acgcccgaaca tgctgaacta ttccggacgg	360	
ccgtatggc gcatcgccgt ttccgacggc aaaaagatcata ctgtacacagg gaccctgtgg	420	
aacggcaaca aattatcgat ccagccctg atcacccccc acggctccat gctgtccga	480	
gttaccatca acagcagaca tgagcta atc aaggaaaata tgagaagtaa gctataactt	540	
gagggggtcc tcaacggtca ccagttaaa tgcactatc aagggtgagg gaaaccttat	600	
gaaggttaaagc agactaatcg aataaaatgg tgcgaggggcg gtcctctgcc attcgcttc	660	
gtatattctgg ccactactt tatgtatggg tctaagggtt ttatataata ccccgctgt	720	
tttccagact actttaaaca gtccttcctt gaaggattca catgggagcg ggtgtatgt	780	
tttccaggatc gaggcggtt tactgtcaat caggatactt ctttgcaga cggggactg	840	
atctacaatcg ttaagggtcc cgccgtcaat ttcccgatcc atggtccatg gatcgagaa	900	
aaaacccctgg ggtggagcc ctcaacggag acaatgtacc ctgcggacgg cgggttgag	960	
ggtagatgtg ataaggcatt gaaactcgatc gggggccggc accttcatgt gaatttcaag	1020	
actacatata aagtaaaaaa accagtcaag atgcctggatc tgcaactatgt ggatcgtag	1080	
tttccaggatc taaaagaagc cgacaacgaa acttatgtatc agcaatataa gcaacggctg	1140	
gttcgttatt ccaacttggg cggaggaatc gatgtactt acaag	1185	
SEQ ID NO: 352	moltype = AA length = 390	
FEATURE	Location/Qualifiers	
REGION	1..390	
	note = synthetic	
source	1..390	
	mol_type = protein	
	organism = synthetic construct	
<b>SEQUENCE: 352</b>		
MKIHIIHHHIFT LDDFVGDWEQ	TAAYNLDQVL EQGGVSSLQ NLAVSVTPIM RIVRSGENAL	60
KIDIHVIIPIY EGLSADQMAQ	IIEEVFKVVYP VDDHHFKVIL PYGTLVIDGV TPNLKNYFGR	120
PYEGIAVFDG KKITTTGTLW NGNKIIDRL ITPDGGSGGS SGELIKEINMR SKLYLEGSVN	180	
GHQFKCTHEG EGKPYEGKQT NRIKVVEGGP LPPAFDILAT HFMYGSKVFI KYPADLPDYF	240	
KQSFPEGTWT ERVMVFEDGG VLTTATQDTSL QDGELIYNVK VRGVNFPPANG PVMQKKTLLW	300	
EPSTETMWPYD DGGLEGRCDK ALKLVGGGHL HVNFKTTYKS KKPVKMPGVH YVDRRLERIK	360	
EADNETYVEQ YEHAVARYSN LGGGMDELYK	390	
SEQ ID NO: 353	moltype = DNA length = 1170	
FEATURE	Location/Qualifiers	
misc_feature	1..1170	
	note = synthetic	
source	1..1170	
	mol_type = other DNA	
	organism = synthetic construct	
<b>SEQUENCE: 353</b>		
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acagccgcct acaaacttggc ccaagtccctt gaacaggggag gtgtgtccag tttgtgcag	120	
aatctcgccg tgccgttaac tccgatccatc aggattgtcc ggagccgtga aaatgccctg	180	
aaagatcaca tccatgtcat catccccat gaaggtctga ggcgcacca aatggccag	240	
atcgaagagg tggttaaggt ggtgtaccct gtggatgtc atcactttaa ggtgtatctg	300	
ccctatggca cactggtaat cgacggggtt acgcccgaaca agctgaacta ttccggacgg	360	
ccgtatggc gcatcgccgt ttccgacggc aaaaagatcata ctggacagg gaccctgtgg	420	
aacggcaaca aattatcgat ccagccctg atcacccccc acggggctc aggtggatcc	480	
tcagggtgac taatcaagga aaatatgaga agtaagctat acttagaggg ttccgtcaac	540	
ggtcaccatc taaaatgcac tcataatgtt gaggggaaaat ttatgtatc taagcagact	600	
aatcgaataa aagtggtcg gggcggtt ctggccatcc ctttgcataat tctggccact	660	
cactttatgtt atgggtctaa ggtttttttaa aataatcccg ctgtatggcc agactactt	720	
aaacagttct tccctgttggg attacatgg gacgggggtga ttgtgttca ggttggggc	780	
gttcttactg caactcagga tacttcctt caagacgggg aactgtatca caacgttaag	840	
gttccggccg tcaattttcc agccaatgtt ccagtgtatc agaagaaaac ttgggggtgg	900	
gacccctcaa cggagacaaat gtaccctgg gacggcgccg ttgggggttag atgtgataag	960	
gcattgaaac tcgtcgccggg cggccacccat catgtgatcc tcaagactac atataaaatgt	1020	
aaaaaaacccatg tcaagatgtcc tgggtgtac tacgtggatc gttaggttga gaggataaaa	1080	
gaagccgaca acgaaactta tttttttttttt tttttttttttt tttttttttttt tttttttttttt	1140	
tttggggccgg gaaatggatca actgtacaa	1170	
SEQ ID NO: 354	moltype = AA length = 384	
FEATURE	Location/Qualifiers	

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REGION          1..384
                note = synthetic
source          1..384
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 354
MKHHHHHHHFT LDDFVGDWEQ TAAYNLDQVL EQGGVSSLQ NLAVSVTPI RIVRSGENAL 60
KIDIHVIIIPY EGLSADQMAQ IEEVFVKVVP VDDHHFKVIL PYGTLVIDGV TPNKLNYFGR 120
PYEGIAVFDG KKITTGTGLW NGNKIIDERL ITPDRHELIK ENMRSKLYLE GSVNGHQFKC 180
THEGEGKPYE GKQTNRKVY EGGPLPFAFD ILATHFMYGS KVFICKYPADL PDYFKQSFP 240
GFTWERVMVF EDGGVLTATQ DTSIQDGEELI YNVKVRGVNF PANGPMQKK TLGWEPSSTET 300
MYPADGGLEG RCDKALKLVG GGHLHVNFKT TYKSKKPVKM PGVHYVDRRL ERIKEADNET 360
YVEQYEHAVA RYSNLGGGM 384

SEQ ID NO: 355      moltype = DNA length = 1152
FEATURE           Location/Qualifiers
misc_feature      1..1152
                note = synthetic
source            1..1152
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 355
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acagccgcct acaaactgg  ccaagtccctt gaacaggagg gtgtgtccag tttgtgcag 120
aatctcgccg tgcgtttaac tccgcattat aggttgtcc ggagcggtaa aaatgcctg 180
aaatcgacata ccatgtcat cattccgtat gaaggctgtc ggcgcgacca aatggccag 240
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ccctatggca cactggtaat cgacgggggtt acggcgaaca agctgaacta tttcgacgg 360
ccgtatcgaa gcatcgccgt gtgcacccgtt aaaaagatca ctaccacagg gaccctgtgg 420
aacggcaaca aatttatcg  cgacggccgtg atcacccccgg acagacatga gctaatacg 480
gaaaatcgaa gaagtagt  atacttagat gggatcgatca acggteacca gtttaaatgc 540
actcatcgaa gtgaggggaa accttgcgg  ggttgcggatcataatcgataaaatgc 600
gaggccgtt ctctgcattt cgcttcgtat attctggcca ctcactttat gtatgggtct 660
aaggcttta ttaataatccc cgctgtttt ccagactact ttaaacatgc cttccctgaa 720
ggattccatcat gggaggccgtt gatgtgttccat gggatgtggag gctgttttac tgcaactcag 780
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cctggatgtc actacgtgg  tctgttgcgg gagaggatca aagaaggccg caacgaaact 1080
tatgttagacg aatatgacca cggccgtggatc cgttattccca acttggccgg aggaatggat 1140
gaactgtaca ag 1152

SEQ ID NO: 356      moltype = AA length = 155
FEATURE           Location/Qualifiers
REGION          1..155
                note = synthetic
source            1..155
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 356
MKHHHHHHHVF TLEDVGDWE QTAAYNLDQV LEQGGVSSLQ QNLAVSVTPI LRIVRSGENA 60
LKIDIHVIIIP YEGLSADQMA QIEEVFKVVP PVDHHFKVIL LPYGTLVIDGV VTPNMLNYFG 120
RPYEGIAVFD GKKITVTGTL WNGNKIIDERL LITPD 155

SEQ ID NO: 357      moltype = DNA length = 465
FEATURE           Location/Qualifiers
misc_feature      1..465
                note = synthetic
source            1..465
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 357
atgaaacatc accatcacca tcatgttcc acactcgaaat tttcggtgg ggactggaa 60
cagaccgcgc cttacaaccc ggaccaatgc ctggaaacagg gagggtgttc cagttgtct 120
cagaatctcg ccgtgtccgt aactccgatc ctaaggatgg tccggacgg tgaaaatgcc 180
ctgaatgtc acatccatgt catcatcccg tatgaagggtc tgagcgcgca ccaaattggcc 240
cagatcgaaag aggtgtttaa ggtgtgtac cctgtggatc atcatcactt taagggtatc 300
ctggccctatg gcacactggat aatcgacggg gttacgcggg acatgtgaa ctatccgg 360
cggccgtatg aaggcatcgc cgtgttgcac ggcaaaaaga tcaactgtaa aggacccgt 420
ttgaacggca acaaattatcg cggccgtggatc cttttccca cccgg 465

SEQ ID NO: 358      moltype = DNA length = 396
FEATURE           Location/Qualifiers
misc_feature      1..396
                note = synthetic

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source          1..396
               mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 358
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cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgggttac cctgtggatg atcatcactt taagggtgatc 300
ctgccctatg gcacactggt aatcgacggg gttacgcggc acaagctgaa ctatattcgga 360
cggccgtatg aaggcatcgc cgtgttcgac ggctaa                                         396

SEQ ID NO: 359      moltype = AA  length = 131
FEATURE           Location/Qualifiers
REGION            1..131
note = synthetic
source             1..131
mol_type = protein
organism = synthetic construct

SEQUENCE: 359
MKHHHHHHVFP TLDDDFVGDWE QTAAYNLDQV LEQGGVSSLQ QNLAVSVTPI MRIVRSGENA 60
LIKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDDHHFKVII LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD G                                         131

SEQ ID NO: 360      moltype = DNA  length = 654
FEATURE           Location/Qualifiers
misc_feature       1..654
note = synthetic
source              1..654
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 360
gggagcctcg gtgggtggccg gagegggggt ggagggtctga gcgggttatgac gtataaggta 60
atccttaatg gtaaaacatt gaaaggcgag acaactactg aagctgttga tgctgtctact 120
gcagaaaaag tcttcaaca atacgctaacc gacaacgggtt tgacgggtga atggacttac 180
gacgatcgca cggaaacattt tacggtcacc gaaaacccagg aagtgtatcgatc tgctgtctgaa 240
ttAACACCCAG CGGTGACAAC ttacaaacctt gttattaaatgt gtaaaaacattt gaaaggcgaa 300
acaactactg aggctgttga tgctgtctact gcagagaagg tgttcaaaaca atatgcgaat 360
gacaacgggtt tgacgggtt tgacggacttac gacgatcgca ctaagactt tacaggacttac 420
gaaaacccagg aagtgtatcgatc tgctgtctgatc ttacacccggc gacgatcacc ttacaaacctt 480
gttattaaatgt gtaaaaacattt gaaaggcgaa acaactacta aagcgtatcgatc cggcggaaact 540
gcggagaagg ctttcaaca atacgctaacc gacaacgggtt tgatgggtt ttggacttac 600
gtatcgatcacc caaaaacattt tacggtaact gacgatcacc accatcacca cttaa                                         654

SEQ ID NO: 361      moltype = AA  length = 217
FEATURE           Location/Qualifiers
REGION            1..217
note = synthetic
source             1..217
mol_type = protein
organism = synthetic construct

SEQUENCE: 361
GSSGGGGGGG GGSSGMTYKL ILNGKTLKGE TTTEAVDAAT AEKVFQYAN DNGVDGEWTY 60
DDATKTFVT EKPEVIDASE LTPAVTTYKL VINGKTLKGE TTTEAVDAAT AEKVFQYAN 120
DNGVDGEWTY DDATKTFVT EKPEVIDASE LTPAVTTYKL VINGKTLKGE TTTKAVDAET 180
AEKAFKQYAN DNGVDGVWTY DDATKTFVT EHHHHHHH                                         217

SEQ ID NO: 362      moltype = DNA  length = 363
FEATURE           Location/Qualifiers
misc_feature       1..363
note = synthetic
source              1..363
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 362
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtc cttaaacagg gagggtgtgc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgggttac cctgtggatg atcatcactt taagggtgatc 300
ctgccctatg gcacactggt aatcgacggg gttacgcggc acaagctgaa ctatattcgga 360
taa                                         363

SEQ ID NO: 363      moltype = AA  length = 120
FEATURE           Location/Qualifiers
REGION            1..120

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source          note = synthetic
               1..120
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 363
MKHHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120

SEQ ID NO: 364      moltype = DNA length = 396
FEATURE           Location/Qualifiers
misc_feature      1..396
note = synthetic
source            1..396
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 364
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtgc ttgaacagg gaggtgtgtc cagttgctg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catatcccg tatgaaggtc tgagcccgca ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtggatc atcatcactt taagggtgatc 300
ctgccctatg gcacactgggt aatcgacggg gttacgcggca acaagctgaa ctattcgga 360
cggccgtatg aaggcatcgc cgtgttcgac ggctaa 396

SEQ ID NO: 365      moltype = AA length = 131
FEATURE           Location/Qualifiers
REGION            1..131
note = synthetic
source            1..131
mol_type = protein
organism = synthetic construct
SEQUENCE: 365
MKHHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD G 131

SEQ ID NO: 366      moltype = DNA length = 423
FEATURE           Location/Qualifiers
misc_feature      1..423
note = synthetic
source            1..423
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 366
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtgc ttgaacagg gaggtgtgtc cagttgctg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catatcccg tatgaaggtc tgagcccgca ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtggatc atcatcactt taagggtgatc 300
ctgccctatg gcacactgggt aatcgacggg gttacgcggca acaagctgaa ctattcgga 360
cggccgtatg aaggcatcgc cgtgttcgac ggcaaaaaga tcactaccac agggaccctg 420
taa 423

SEQ ID NO: 367      moltype = AA length = 140
FEATURE           Location/Qualifiers
REGION            1..140
note = synthetic
source            1..140
mol_type = protein
organism = synthetic construct
SEQUENCE: 367
MKHHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL 140

SEQ ID NO: 368      moltype = DNA length = 432
FEATURE           Location/Qualifiers
misc_feature      1..432
note = synthetic
source            1..432
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 368
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacct ggaccaagtgc ttgaacagg gaggtgtgtc cagttgctg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaatgcc 180

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ctgaagatcg acatccatgt catcatcccg tatgaaggtc tgagcgcga ccaaattgcc 240
cagatcaag aggtgtttaa ggtgtgtac cctgtggatc atcatcactt taaggtgatc 300
ctgcccatacg gcacactggt aatcgacggg gttacgcga acaagctgaa ctatccgga 360
cggccgtatcg aaggcatcgc cgtgttcgac ggcaaaaaga tcactaccac agggaccctg 420
tggAACGGCTT aa 432

SEQ ID NO: 369 moltype = AA length = 143
FEATURE Location/Qualifiers
REGION 1..143
note = synthetic
source 1..143
mol_type = protein
organism = synthetic construct

SEQUENCE: 369
MKHHHHHHVF TLDDFVGDWE QTAAYNLQDV LEQGVVSSLL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDHHFKVII LPYGTIVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNG 143

SEQ ID NO: 370 moltype = DNA length = 483
FEATURE Location/Qualifiers
misc_feature 1..483
note = synthetic
source 1..483
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 370
atggtttccg tgagcggctg gccgtgttc aagaagatggatc gttcacact cgacgattc 60
gttggggact ggaaacagac agccgcctac aacctggacc aagtccctga acagggaggt 120
gtgtccagg tgcgtcagaa tctcgccgtg tccgttaactc cgatcatgag gattgtccgg 180
agcggtgaaa atgcccgtaa gatcgacatc catgtcatca tcccgatgaa aggtctgagc 240
ggcgacccaaa tggcccgatg cgaagagggtg ttaagggtgg ttttacccgtt ggatgtatcat 300
cactttaaagg tgatccgtcc ctatggcaca ctggtaatcg acggggttac gcccgaacaag 360
ctgaactatt tcggacggcc gtatgaaatcg atcgccgtgt tcgacggccaa aaagatcaat 420
accacagggaa ccctgtggaa cggcaacaaa attatcgacg agcgccgtat cacccccgac 480
taa 483

SEQ ID NO: 371 moltype = AA length = 160
FEATURE Location/Qualifiers
REGION 1..160
note = synthetic
source 1..160
mol_type = protein
organism = synthetic construct

SEQUENCE: 371
MVSVSGWRLF KKISFTLDDF VGDWEQTAAY NLDQVLEQGG VSSLQLNLAV SVTPIMRIVR 60
SGENALKIDI HVIIPYEGLS ADQMAQIEEV FKVVYPVDDH HFKVILPYGT LVIDGVTPNK 120
LYNFGRPYEG IAVFDGKKIT TTGTLWNGNK IIDERLITPD 160

SEQ ID NO: 372 moltype = DNA length = 495
FEATURE Location/Qualifiers
misc_feature 1..495
note = synthetic
source 1..495
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 372
atggtttccg tgagcggctg gccgtgttc aagaagatggatc gccggcagctc cggtttcaca 60
ctcgacgatt tcgttggga ctggaaacag acagccgcctc acaacctgga ccaagtctt 120
gaacaggaggatgtgtccag tttgtgtcag aatctcgccg tgcgttgcac tccgtatcatg 180
aggattgtcc ggacggctgaa aatgtccctg aagatcgacatc tccatgtcatc catccgtat 240
gaagggtctgaa gccgcgcacca aatggcccgatg atcgaaagggttggatgtacccct 300
gtggatgtatc actactttaa ggtgttgcctg ccctatggca cactggtaat cgacggggtt 360
acgcccgaaca agctgaacta ttccggacgg ccgtatggaa gcatcgccgt gttcgacggc 420
aaaaagatca ctaccacagg gaccctgtgg aacggcaaca aaattatcgaa cgacggcctg 480
atcacccttccg actaa 495

SEQ ID NO: 373 moltype = AA length = 164
FEATURE Location/Qualifiers
REGION 1..164
note = synthetic
source 1..164
mol_type = protein
organism = synthetic construct

SEQUENCE: 373
MVSVSGWRLF KKISGSSGFT LDDFVGDWEQ TAAYNLQDVLEQGGVSSLLQ NLAVSVTPI 60
RIVRSGENAL KIDIHVIIPY EGGLSADQMAQ IEEVFKVVYV PVDHHFKVIL PYGTLVIDGV 120

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TPNKLNYFGR PYEGIAVFDG KKITTGTLW NGNKIIIDERL ITPD               164

SEQ ID NO: 374      moltype = DNA length = 507
FEATURE          Location/Qualifiers
misc_feature    1..507
note = synthetic
source          1..507
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 374
atggtttccg tgagcggctg gcccgtgttc aagaagatta gggctcgag cggggctcg 60
agcggttcca cactcgacgt ttcgttggg gactggaaac agacagccgc ctacaacctg 120
gaccaagtcc ttgaacaggg aggtgtgtcc agtttgctgc agaatctcg cgtgtccgt 180
actccgatca tgaggattgt ccggagcggt gaaaatgcc tgaatcgca catccatgtc 240
atcatccccgt atgaagggtct gagcgcgcac caaatggccc agatcgaaaga ggtgtttaag 300
gtgtgttacc ctgtgttatgt tcataactt aagggtatcc tgcctatgg cacactggta 360
atcgacgggg ttacgcgaa caagctgaaac tatttcggac ggccgtatga aggcatcgcc 420
gtgttgcacg gaaaaaagat cactaccaca gggaccctgt ggaacggcaa caaaaattatc 480
gacgagcgcg tgcgtatcccg cgactaa                                507

SEQ ID NO: 375      moltype = AA length = 168
FEATURE          Location/Qualifiers
REGION           1..168
note = synthetic
source          1..168
mol_type = protein
organism = synthetic construct

SEQUENCE: 375
MVSVSGWRLF KKISGSSGGS SGFTLDDFVG DWEQTAAYNL DVQLEQGGVS SLLQNLAVSV 60
TPIMRIVRSG ENALKIDIHV IIPIYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV 120
IDGVTPNKLN YFGRPYEGIA VFDGKKITTT GTLWNGNKII DERLITPD               168

SEQ ID NO: 376      moltype = DNA length = 519
FEATURE          Location/Qualifiers
misc_feature    1..519
note = synthetic
source          1..519
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 376
atggtttccg tgagcggctg gcccgtgttc aagaagatta gggctcgag cggggctcg 60
agcggttcca cggcggttt cacactcgac gatttcgttg gggactggga acagacagcc 120
gcctacaaacc tggaccaagt ccttggaaacag ggaggtgtgt ccagtttgt gcagaatctc 180
gcgtgttcg taactccgat gtcggaggt gtggggagcg gtggaaatgc cctgaagatc 240
gacatccatc tcatcatccc tggatgggt ctggggcccg accaaaatggc ccagatcgaa 300
gggtgttta aggtgtgtta ccctgtggat gatcatcaactttaagggtat cctggccat 360
ggcacactgg taatcgacgg gggttacccg aacaagctgaa actatttccg acggccgtat 420
gaaggcatcg cctgtgtcg cggcaaaaag atactaccaca caggggacctt gggaaacggc 480
acaaaatcgatcg cctgtatcccg cggcaaaaatcgatcg cccgactaa                                519

SEQ ID NO: 377      moltype = AA length = 172
FEATURE          Location/Qualifiers
REGION           1..172
note = synthetic
source          1..172
mol_type = protein
organism = synthetic construct

SEQUENCE: 377
MVSVSGWRLF KKISGSSGGS SGGSSSGFTLD DFVGDWEQTA AYNLDQVLEQ GGVSSLQNL 60
AVSVTPIMRI VRSGENALKI DIHVIIPYEG LSADQMAQIE EVFKVVYPVD DHHKVILPY 120
GTLVIDGVTP NKLNYFGRPY EGIAVFDGKK ITTTGTLWNG NKIIIDERLIT PD               172

SEQ ID NO: 378      moltype = DNA length = 531
FEATURE          Location/Qualifiers
misc_feature    1..531
note = synthetic
source          1..531
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 378
atggtttccg tgagcggctg gcccgtgttc aagaagatta gggctcgag cggggctcg 60
agcggttcca cggcggtgg ctcgagcgggt ttcacactcg acgatttctgt tggggactgg 120
gacacagacag ccgcctacaa cctggaccaa gtccttgaac agggaggtgt gtccagttt 180
ctgcagaatc tcgcccgtgtc cgtaactccg atcatgagga ttgtccggag cggtgaaaat 240
gcctgttcaaga tcgcacatcca tgcgtatccca cctgtatcgaa gtctgagcgc cggccaaatg 300
gcggcggatcg aagggatcg ttaagggtgtt taccctgtgtt atgatcatca cttaagggtg 360

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atccctgcctt atggcacact ggtaatcgac ggggttacgc cgaacaagct gaactattc 420
ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcaactac cacagggacc 480
ctgtgaaacg gcaacaaaat tatcgacgag cgccgtatca cccccgacta a 531

SEQ ID NO: 379      moltype = AA length = 176
FEATURE           Location/Qualifiers
REGION            1..176
note = synthetic
source             1..176
mol_type = protein
organism = synthetic construct

SEQUENCE: 379
MVSVSGWRLF KKISGSSGGS SGGSSGGSSG FTLDDFVGDW EQTAAYNLDQ VLEQGGVSSL 60
LQLNLAVSVTP IMRIVRSGEN ALKIDIHVII PYEGLSADQM AQIEEVFKVV YPVDDHHFKV 120
ILPYGTLVID GTVPNKLNYF GRPYEGIAVF DGKKITTTGT LWNGNKNIIDE RLITPD 176

SEQ ID NO: 380      moltype = DNA length = 543
FEATURE           Location/Qualifiers
misc_feature       1..543
note = synthetic
source             1..543
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 380
atggtttccg tgagcggctg gccgtgttc aagaagatta gggctcgag cgggtggctcg 60
agcgggtgct cgagcggctg ctgcagcgtt ggctcgagcg gtttcaactc cgacgatttc 120
gttggggact gggaaacagac agccgcctac aacctggac aagtcttgc acagggaggt 180
gtgtccaggc tgctgcagaa tctcgccgtg tccgtaaactc cgatcatcg gattgtccgg 240
agcggtaaaa atgcctgtaa gategacatc catgtcatca tcccgtatga aggtctgagc 300
ggcgaccaaa tggcccaagat cgaagagggtg tttaagggtg tgtaccctgt ggatgtatcat 360
cactttaagg tgatcctgcg ctatggcaca ctggtaatcg acgggttac gccgaacaag 420
ctgaaacttccg tggacggcc gtatgacggc atcggctgt tcgacggcaa aaagatcact 480
accacaggaa ccctgtggaa cggcaacaaa attatcgacg agccgtat caccggac 540
taa 543

SEQ ID NO: 381      moltype = AA length = 180
FEATURE           Location/Qualifiers
REGION            1..180
note = synthetic
source             1..180
mol_type = protein
organism = synthetic construct

SEQUENCE: 381
MVSVSGWRLF KKISGSSGGS SGGSSGGSSG GSSGFTLDDF VGDWEQTAAY NLDQVLEQGG 60
VSSLNLQNLAV SVTPIMRIVR SGENALKIDI HVIIIPYEGLS ADQMAQIEEV FKVVYPVDDH 120
HFKVILPYGT LVIDGVTPNK LNYFGRPYEG IAVFDGKKIT TTGTLWNGNK IIDERLITPD 180

SEQ ID NO: 382      moltype = DNA length = 537
FEATURE           Location/Qualifiers
misc_feature       1..537
note = synthetic
source             1..537
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 382
atggtgagcg gctggggctt gttcaagaag attagcggtt cgacgggtgg ctgcagcgtt 60
ggctcgacgc gtggctcgag cgggtgctcg a cactcgacga ttgcgttggg 120
gactggaaac agacagccgc ctacaacctg gaccaagtcc ttgaacaggg aggtgtgtcc 180
agtttgcgcg a gaaatctgcg cgtgtccgtt actccgtatc tgaggattgt ccggagccgt 240
gaaatggccc tgaatggcc catccatgtc atcateccgtt atgaaggctt gagcggccgac 300
caaatggccc agatcgaa ggtgtttaa gttgtgttcc ctgtggatga tcatcacttt 360
aagggtgttcc tggccatgttcc cacactggta atcgacgggg ttacgcgaa caagtcgaa 420
tatttcggac ggccgttatgaa aggcatcgcc gtgttcgacg gaaaaagat cactaccaca 480
gggaccctgtt ggaacggcaa caaaaattatc gacgacggcc tgatcaccggc cgactaa 537

SEQ ID NO: 383      moltype = AA length = 178
FEATURE           Location/Qualifiers
REGION            1..178
note = synthetic
source             1..178
mol_type = protein
organism = synthetic construct

SEQUENCE: 383
MVSVSGWRLF KKISGSSGGS SGGSSGGSSG SGFTLDDFVG DWEQTAAYNL DVQVLEQGGVS 60
SLLQNLAVSV TPIMRIVRSG ENALKIDIHV IIIPYEGLSAD QMAQIEEVFK VVYPVDDHHF 120
KVLVILPYGT LVIDGVTPNK LNYFGRPYEGIA VFDGKKITTT GTLWNGNKKII DERLITPD 178

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SEQ ID NO: 384      moltype = DNA length = 486
FEATURE           Location/Qualifiers
misc_feature      1..486
                  note = synthetic
source            1..486
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 384
atgggtcttca cactcgacga tttcggttggg gactgggaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacagggg agggtgttcc agtgggtgtc aaaaatccgc cgtgtccgt 120
actccgatca tgaggattgt ccggagcgggt gaaaatgccc tgaagatcga catccatgtc 180
atcatcccgatca tgaggattgtt ccggagcgggt gaaaatgccc agatcgaaga ggtgtttaag 240
gtgggttacc ctgtggatgt tcatactttt aagggtgtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcccga caagctgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaaaatg cactaccaca gggaccctgt ggaacggcaa caaaaattatc 420
gacgagccgc ttacgcccga cgacgtttcc gtgagccgtt ggccgtgtt caagaagatt 480
agctaa                                         486

SEQ ID NO: 385      moltype = AA length = 161
FEATURE           Location/Qualifiers
REGION            1..161
                  note = synthetic
source            1..161
                  mol_type = protein
                  organism = synthetic construct
SEQUENCE: 385
MVFTLDDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPDVS VSGWRLFKKI S 161

SEQ ID NO: 386      moltype = DNA length = 498
FEATURE           Location/Qualifiers
misc_feature      1..498
                  note = synthetic
source            1..498
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 386
atgggtcttca cactcgacga tttcggttggg gactgggaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacagggg agggtgttcc agtgggtgtc aaaaatccgc cgtgtccgt 120
actccgatca tgaggattgt ccggagcgggt gaaaatgccc tgaagatcga catccatgtc 180
atcatcccgatca tgaggattgtt ccggagcgggt gaaaatgccc agatcgaaga ggtgtttaag 240
gtgggttacc ctgtggatgt tcatactttt aagggtgtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcccga caagctgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaaaatg cactaccaca gggaccctgt ggaacggcaa caaaaattatc 420
gacgagccgc ttacgcccga cgacgttcc cgacgtgtt ccgtgagccg ctggccgt 480
ttcaagaaga tttagctaa                                         498

SEQ ID NO: 387      moltype = AA length = 165
FEATURE           Location/Qualifiers
REGION            1..165
                  note = synthetic
source            1..165
                  mol_type = protein
                  organism = synthetic construct
SEQUENCE: 387
MVFTLDDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPDGS SGVSWSGWRL FKKIS 165

SEQ ID NO: 388      moltype = DNA length = 510
FEATURE           Location/Qualifiers
misc_feature      1..510
                  note = synthetic
source            1..510
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 388
atgggtcttca cactcgacga tttcggttggg gactgggaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacagggg agggtgttcc agtgggtgtc aaaaatccgc cgtgtccgt 120
actccgatca tgaggattgt ccggagcgggt gaaaatgccc tgaagatcga catccatgtc 180
atcatcccgatca tgaggattgtt ccggagcgggt gaaaatgccc agatcgaaga ggtgtttaag 240
gtgggttacc ctgtggatgt tcatactttt aagggtgtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcccga caagctgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaaaatg cactaccaca gggaccctgt ggaacggcaa caaaaattatc 420

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gacgagcgcc tgatcacccc cgacggctcg agcggtggtt cgagcggtgt ttccgtgagc 480
ggctggcgcc tggtaagaa gattagctaa 510

SEQ ID NO: 389      moltype = AA length = 169
FEATURE           Location/Qualifiers
REGION            1..169
note = synthetic
source             1..169
mol_type = protein
organism = synthetic construct

SEQUENCE: 389
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPDGS SGSSSGVSVS GWRLFKKIS 169

SEQ ID NO: 390      moltype = DNA length = 504
FEATURE           Location/Qualifiers
misc_feature       1..504
note = synthetic
source             1..504
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 390
atgggtttca cactcgacga ttgcgttggg gactgggaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacagggg aggtgtgtcc agtttgcgtc agaatctcgc cgtgtccgt 120
actccgatca tgaggattgt ccggagcgtt gaaaatgccc tgaagatcga catccatgtc 180
atcatccgtt atgaagggtt gagcggccgac caaatggcc agatcgaaga ggtgtttaag 240
gtgggtgtacc ctgtggatga tcatacattt aagggtatcc tggccctatgg cacactggta 300
atcgacgggg ttacgcccga caauctgaac tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gaaaaaaagat cactaccaca gggaccctgtt ggaacggccaa caaaaattatc 420
gacgagcgcc tgatcacccc cgacggctcg agcggtggtt cgagcggtgtt gaggcggtgg 480
cggtgttca agaagattag ctta 504

SEQ ID NO: 391      moltype = AA length = 167
FEATURE           Location/Qualifiers
REGION            1..167
note = synthetic
source             1..167
mol_type = protein
organism = synthetic construct

SEQUENCE: 391
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPDGS SGSSSGVSGW RLFKKIS 167

SEQ ID NO: 392      moltype = DNA length = 501
FEATURE           Location/Qualifiers
misc_feature       1..501
note = synthetic
source             1..501
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 392
atgggtttccg tgacggctg ggggtgttc aagaagatta gtttcacact cgacgatttc 60
gtggggact gggaaacagac agccgcctac aacctggacc aagtccatgg acaggagggt 120
gtgtcccgat ttgtcgatcc ttcgtggatcc tccgttaactt cgatcatgatg gattgtccgg 180
agcggtaaa atgcctgtaa gatecgcacatc catgtcatca tcccgatata aggtctgagc 240
ggccacccaa tggcccgat cgaagagggtt ttaagggtt gttaccctgtt ggatgatcat 300
cactttaagg tgatctggcc ctatggcaca ctggtaatcc acggggttac gccgaacaag 360
ctgaaactt tggacggcc gatggaaatc atcgcctgtt tccggccaa aaagatcact 420
accacaggga ccctgtggaa cggcaacaaa attatcgacg agcgcctgtt caccggccac 480
catcaccatc accatcattaa a 501

SEQ ID NO: 393      moltype = AA length = 166
FEATURE           Location/Qualifiers
REGION            1..166
note = synthetic
source             1..166
mol_type = protein
organism = synthetic construct

SEQUENCE: 393
MVSVSGWRLF KKISFTLDDF VGDWEQTAAY NLDQVLEQGG VSSLLQNLAV SVTPIMRIVR 60
SGENALKIDI HVIIPYEGLS ADQMAQIEEV FKVVYPVDDH HFKVILPYGT LVIDGVTPNK 120
LNYFGRPYEG IAVFDGKKIT TTGTLWNGNK IIDERLITPD HHHHHHHH 166

SEQ ID NO: 394      moltype = DNA length = 513

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FEATURE                               Location/Qualifiers
misc_feature                         1..513
                                      note = synthetic
source                                1..513
                                      mol_type = other DNA
                                      organism = synthetic construct
SEQUENCE: 394
atgggttccg tgagcggctg gccgcgttca aagaagatta gcggcagctc cggtttcaca 60
ctcgacgatt tcgttgggga ctggaaacag acagccgcct acaacctgga ccaagtctt 120
gaacaggaggatgtgtccag tttctgtcag aatctcgccc tggccgttaac tccgatcatg 180
aggattgtccgagccatggatgtccaaatggccctg aagatcgacaa tccatgtcat catccgtat 240
gaagggtctgaa ggcggccacca aatggccctg atcgaagagg tggtaaagggt ggtgtaccct 300
gtggatgtatc atcactttaa ggtgtatctg ccctatggca cactgttaat cgacgggtt 360
acgcccgaaca agctgtacta ttccggacgg ccgtatgtaa gcatcgccgt gttcgacggc 420
aaaagatgtttttttccacagg gacccgttgg aacggcaaca aaattatcgaa cgagcgctg 480
atccccccca accatcacca tcaccatcat taa                                         513

SEQ ID NO: 395      moltype = AA length = 170
FEATURE                               Location/Qualifiers
REGION                                1..170
                                      note = synthetic
source                                1..170
                                      mol_type = protein
                                      organism = synthetic construct
SEQUENCE: 395
MVSVSGWRLF KKISGSSGFT LDDFVGDWEQ TAAYNLQDQL EQGGVSSLQ NLAVSVTPIM 60
RIVRSGENAL KIDIHVIIPY EGLSADQMAQ IEEVFVKVYP VDDHHFKVIL PYGTLVIDGV 120
TPNKLNYFGR PYEGIAVFDG KKITTGTIW NGNKIIDERL ITPDHHHHHHH 170

SEQ ID NO: 396      moltype = DNA length = 525
FEATURE                               Location/Qualifiers
misc_feature                         1..525
                                      note = synthetic
source                                1..525
                                      mol_type = other DNA
                                      organism = synthetic construct
SEQUENCE: 396
atgggttccg tgagcggctg gccgcgttca aagaagatta gcggcgtcggc cggtggctcg 60
agccgggttcc cactcgacca ttctgttggg gactggaaac agacagccgc ctacaacctg 120
gaccaaggatccatgtgtccaaatggccctg agtttgcgtc aagatctcgcc cgtgtccgta 180
actccgtatca tgaggattgt ccggagccgtt gaaaatgcc tgaagatcgaa catccatgtc 240
atcatcccgatgtgttggatgtccactttaatggatgttccatgttggccatgttggatgttgg 300
gtgtgttggatgtgttggatgtccactttaatggatgttccatgttggccatgttggatgttgg 360
atcgacggggatgtgttggatgtccactttaatggatgttccatgttggccatgttggatgttgg 420
gtgttgcgtccatgttggatgtccactttaatggatgttccatgttggccatgttggatgttgg 480
gacccgttggatgtgttggatgtccactttaatggatgttccatgttggccatgttggatgttgg 525

SEQ ID NO: 397      moltype = AA length = 174
FEATURE                               Location/Qualifiers
REGION                                1..174
                                      note = synthetic
source                                1..174
                                      mol_type = protein
                                      organism = synthetic construct
SEQUENCE: 397
MVSVSGWRLF KKISGSSGGS SGFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV 60
TPIMRIVRSG ENALKIDIHV IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV 120
IDGVTPNKLNYFGR YFGRPYEGIA VFDGKKITTT GTLWNGNKII DERLITPDHH HHHH 174

SEQ ID NO: 398      moltype = DNA length = 537
FEATURE                               Location/Qualifiers
misc_feature                         1..537
                                      note = synthetic
source                                1..537
                                      mol_type = other DNA
                                      organism = synthetic construct
SEQUENCE: 398
atgggttccg tgagcggctg gccgcgttca aagaagatta gcggcgtcggc cggtggctcg 60
agccgggttcc cactcgacca ttctgttggg gactggaaac agacagccgc ctacaacctg 120
gaccaaggatccatgtgtccaaatggccctg agtttgcgtc aagatctcgcc cgtgtccgta 180
actccgtatca tgaggattgt ccggagccgtt gaaaatgcc tgaagatcgaa catccatgtc 240
gacatccatgtcatcatccc gtatgttggatgtccactttaatggatgttccatgttggatgttgg 300
gagggtgtttatgtgttggatgtccactttaatggatgttccatgttggatgttggatgttggatgttgg 360
ggcacactgg taatcgacgg ggttacggcc aacaagctga actatgttggccatgttggatgttggatgttgg 420
gaaggcatcg ccgtgttgcg cggaaaaaag atcactacca caggacccgtt gttggacggc 480
aacaaaatattatgtgttggatgtccactttaatggatgttccatgttggatgttggatgttggatgttgg 537

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SEQ ID NO: 399      moltype = AA length = 178
FEATURE          Location/Qualifiers
REGION           1..178
note = synthetic
source            1..178
mol_type = protein
organism = synthetic construct

SEQUENCE: 399
MVSVSGWRLF KKISGSSGGS SGGSSGFTLD DFVGDWEQTA AYNLDQVLEQ GGVSSLQLNL 60
AVSVTPIMRI VRSGENALKI DHVIIPYEG LSADQMAQIE EVFKVVYPVD DHHFKVILPY 120
GTLVIDGVTP NKLNYFGRPY EGIAVFDGKK ITTGTWLNG NKİİDERLIT PDHHHHHHH 178

SEQ ID NO: 400      moltype = DNA length = 549
FEATURE          Location/Qualifiers
misc_feature     1..549
note = synthetic
source            1..549
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 400
atgggtttccg tgagcggctg gccgcgttgc aagaagatta gcggcgtcgag cggtggtctcg 60
agcgggtggct cgagcggctgg ctgcacactcg acgatttcgt tggggactgg 120
gaacagacag cggccatcaa ctgcggacaa gtcctttaac agggagggtgt gtccaggttg 180
ctgcagaatc tcgcgtgtc cgtaactccg atcatgagga ttgtccggag cggtgaaaat 240
gccctgaaga tcgacatcca tgcatacatc ccgtatgaag gtctgagcgc cgaccaaatg 300
gcccagatcg aagggtgtt taagggtgtt taccctgtgtg atgatcatca cttaagggtg 360
atccctgcct atggcacact ggtaatcgac ggggttacgc cgaacaagct gaactattc 420
ggacggccgt atgaaggcat cgccgtgttc gacggcaaaa agatcactac cacagggacc 480
ctgtggaaacg gcaacaaaat tatcgacgag cgccgtatca ccccccggacca tcaccatcac 540
catcattaa                                         549

SEQ ID NO: 401      moltype = AA length = 182
FEATURE          Location/Qualifiers
REGION           1..182
note = synthetic
source            1..182
mol_type = protein
organism = synthetic construct

SEQUENCE: 401
MVSVSGWRLF KKISGSSGGS SGGSSGGSSG FTLDDFVGDW EQTAAYNLDQ VLEQGGVSSL 60
LQNLAWSVTP IMRIVRSGEN ALKIDIHVII PYEGLSADQM AQIEEVFKVV YPVDDHFKV 120
ILPYGTLVID GVTPNKLNYF GRPYEGIAVF DGKKITTGT LWNGNKIIDE RLITPDHHHH 180
HH                                         182

SEQ ID NO: 402      moltype = DNA length = 555
FEATURE          Location/Qualifiers
misc_feature     1..555
note = synthetic
source            1..555
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 402
atggtgagcg gtcggcgct gttcaagaag attagcggtt cgagcgggtt ctgcagcggt 60
ggctcggacg ctgggtcgag cggtggctcg agcgggttca cactcgacga ttgcgttggg 120
gactggaaac agacagccgc ctacaacccg cacaaggctt ttgaacaggg aggtgtgtcc 180
agtttgcgtc agaatctcg cgtgtccgtt actccgtatc tgaggattgtt ccggagccgt 240
gaaaatggcc tgaatcgatc catccatgtc atcatccgtt atgaagggtt gagcggccac 300
caaatggccc agategaaga ggtgtttaag gtgtgttacc ctgtggatga tcatcatctt 360
aagggtgatcc tgccctatgg cacactggta atcgacgggg ttaccccgaaa caagctgaac 420
tatttggac ggccgtatga aggatccgcg gtgttcgacg gcaaaaaatg cactaccaca 480
gggaccctgt ggaacggcaa caaaaattatc gacgagcgcc tgcgttccccc cgaccatcac 540
catcaccatc attaa                                         555

SEQ ID NO: 403      moltype = AA length = 184
FEATURE          Location/Qualifiers
REGION           1..184
note = synthetic
source            1..184
mol_type = protein
organism = synthetic construct

SEQUENCE: 403
MVSGWRLFKK ISGGSSGGSS GSSGGSSGGS SGFTLDDFVG DWEQTAAYNL DVQVLEQGGVS 60
SLLQNLAVSV TPIMRIVRSG ENALKIDIHV IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF 120
KILPYGTLV IDGVTPNKLN YFGRPYEGIA VFDGKKITT GTLWNGNKKII DERLITPDHH 180
HHHH                                         184

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SEQ ID NO: 404      moltype = DNA  length = 561
FEATURE          Location/Qualifiers
misc_feature     1..561
                  note = synthetic
source           1..561
                  mol_type = other DNA
organism         synthetic construct

SEQUENCE: 404
atgggttccg tgagcggctg gcccgtgtt aagaagatta gggctcgag cggggctcg 60
aggcgggtgc ctgcggctgg ctcgagcggt gggtcgacgt gttcacact cgacgattc 120
gttggggact gggaaacagac agccgcctac aacctggacc aagtccatgt acaaggagg 180
gtgtccagg tgcgtcgagaa tctcgccgtg tccgttaactc cgatcatgag gattgtccgg 240
agccggtaaa atgcctgtggat gatgcacatc catgtcatca tcccgatata aggtctgac 300
gcccggccatggat tggcccgat cgaagagggtg ttaagggtgg tgcgttgcgtt ggatgtat 360
cactttaagg tgatcctgcctatggcaca ctggtaatcg acggggttac qccaaacaag 420
ctgaactatt tcggacggcc gtatgaaggc atcggcgatgc tgcacggcaa aaagatcact 480
accacaggga ccctgtggaa cggcaacaaa attatcgacg agccgcgtat caccccgac 540
catcaccatc accatcattaa a 561

SEQ ID NO: 405      moltype = AA  length = 186
FEATURE          Location/Qualifiers
REGION           1..186
                  note = synthetic
source           1..186
                  mol_type = protein
organism         synthetic construct

SEQUENCE: 405
MVSVSGWRLF KKISGSSGGSG SGGSSGGSSG GSSGFTLDDF VGDWEQTAAY NLDQVLEQGG 60
VSSLNLQNLAV SVTPIMRIVR SGENALKIDI HVIIPYEGLS ADQMAQIEEV FKVVYPVDDH 120
HFKVILPYGT LVIDGVTPNK LNYFGGRPKIT TTGTLWNGNK IIDERLITPD 180
HHHHHHH 186

SEQ ID NO: 406      moltype = DNA  length = 507
FEATURE          Location/Qualifiers
misc_feature     1..507
                  note = synthetic
source           1..507
                  mol_type = other DNA
organism         synthetic construct

SEQUENCE: 406
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcggtgg ggactggaa 60
cagacagccg cctacaaccccttggaaacaggcggatgggtgtgtc cagttgtgtc 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatgg tccggagccgg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcga ccaaatggcc 240
cagatcgaag aggtgtttaa ggtgggtgtac cctgtggatgc atcatcactt taagggtatc 300
ctggccatcgatc aacactcgatc aatcgacgggg gttacgcggca acaagctgaa ctatccgaa 360
cggccgtatcgatc aaggcatcgatc cgtgttcgac ggcaaaaaga tcaactaccac agggacccgt 420
tggaaacggca aaaaaattat cgaacgcgcgtatcgatcaccac ccgacgttccgtggc 480
tggcggtgttcaagaatgt tagctaa 507

SEQ ID NO: 407      moltype = AA  length = 168
FEATURE          Location/Qualifiers
REGION           1..168
                  note = synthetic
source           1..168
                  mol_type = protein
organism         synthetic construct

SEQUENCE: 407
MKHHHHHHVF TLDDFVGDW QTAAYNLDQV LEQGGVSSLL QNLAVSVTPI MRIVRSGENA 60
LIKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVII LPYGTLLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER LITPDVSVSG WRLFKKIS 168

SEQ ID NO: 408      moltype = DNA  length = 519
FEATURE          Location/Qualifiers
misc_feature     1..519
                  note = synthetic
source           1..519
                  mol_type = other DNA
organism         synthetic construct

SEQUENCE: 408
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcggtgg ggactggaa 60
cagacagccg cctacaaccccttggaaacaggcggatgggtgtgtc cagttgtgtc 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatgg tccggagccgg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcga ccaaatggcc 240
cagatcgaag aggtgtttaa ggtgggtgtac cctgtggatgc atcatcactt taagggtatc 300

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ctggccctatg gcacactggc aatcgacggg gttacgccc acaagctgaa ctatccgga 360
cgccgcgtatg aaggcatcgc cgtgtcgac ggcaaaaaa gtaactaccac agggacctg 420
tggAACGGCA acaaattat cgacgagcgc ctgatcaccc ccgacggctc gagcgggtt 480
tccgtgagcg gtcggcgct gttcaagaag attagctaa 519

SEQ ID NO: 409      moltype = AA length = 172
FEATURE           Location/Qualifiers
REGION            1..172
note = synthetic
source             1..172
mol_type = protein
organism = synthetic construct

SEQUENCE: 409
MKHHHHHHHF TLDDFVGDWE QTAAYNLQV LEQGGVSSLQ QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKIKTTGTL WNGNKIIDER LITPDGSSGG SVSGWRLFKK IS 172

SEQ ID NO: 410      moltype = DNA length = 525
FEATURE           Location/Qualifiers
misc_feature       1..525
note = synthetic
source             1..525
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 410
atgaaacatc accatcacca tcatgtcttc acactcgacg attcgttgg ggactggaa 60
cagacagcgc cttacaacct ggaccaagtgc ctggaaacagg gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttccggagccgg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcg ccaaatggcc 240
cagatcgaag aggtgtttaa ggtgtgttac cctgtggatc atcatcaccc taagggtgtc 300
ctggccctatg gcacactggc aatcgacggg gttacgccc acaagctgaa ctatccgga 360
cggccgtatg aaggcatcgc cgtgtcgac ggcaaaaaa gtaactaccac agggacctg 420
tggAACGGCA acaaattat cgacgagcgc ctgatcaccc ccgacggctc gagcgggtt 480
tcgagcggctg tgagcggctg gccggctt aagaagatta gctaa 525

SEQ ID NO: 411      moltype = AA length = 174
FEATURE           Location/Qualifiers
REGION            1..174
note = synthetic
source             1..174
mol_type = protein
organism = synthetic construct

SEQUENCE: 411
MKHHHHHHHF TLDDFVGDWE QTAAYNLQV LEQGGVSSLQ QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKIKTTGTL WNGNKIIDER LITPDGSSGG SSGVSGWRLF KKIS 174

SEQ ID NO: 412      moltype = DNA length = 531
FEATURE           Location/Qualifiers
misc_feature       1..531
note = synthetic
source             1..531
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 412
atgaaacatc accatcacca tcatgtcttc acactcgacg attcgttgg ggactggaa 60
cagacagcgc cttacaacct ggaccaagtgc ctggaaacagg gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttccggagccgg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcg ccaaatggcc 240
cagatcgaag aggtgtttaa ggtgtgttac cctgtggatc atcatcaccc taagggtgtc 300
ctggccctatg gcacactggc aatcgacggg gttacgccc acaagctgaa ctatccgga 360
cggccgtatg aaggcatcgc cgtgtcgac ggcaaaaaa gtaactaccac agggacctg 420
tggAACGGCA acaaattat cgacgagcgc ctgatcaccc ccgacggctc gagcgggtt 480
tcgagcggctg ttccgttag cggctggcg ctgttcaaga agattagcta a 531

SEQ ID NO: 413      moltype = AA length = 176
FEATURE           Location/Qualifiers
REGION            1..176
note = synthetic
source             1..176
mol_type = protein
organism = synthetic construct

SEQUENCE: 413
MKHHHHHHHF TLDDFVGDWE QTAAYNLQV LEQGGVSSLQ QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVY PVDDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKIKTTGTL WNGNKIIDER LITPDGSSGG SSGVSGWRLF LFKKIS 176

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SEQ ID NO: 414      moltype = DNA length = 498
FEATURE          Location/Qualifiers
misc_feature     1..498
                  note = synthetic
source           1..498
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 414
atgggtttca cactcgaaga ttctgttgg gactggaaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggg agggtgtc agttgtgc aaaaatccgc cgtgtccgt 120
actcccgatcc aaaggattgt ccggagccgt gaaaatgccc tgaagatcga catccatgc 180
atcatcccgatcc aaagggtct gagcgcgcac caaatggccc agatcgaaga ggtgttaag 240
gttgtgtacc ctgtggatcc tcataactt aagggtgatcc tgccctatgg cacactggta 300
atcgcacgggg ttacgcgcga catgtgaac tatttcggac ggccgtatga aggcacgc 360
gttgtcgacg qaaaaaaatgactgtaaaca gggacccctgt ggaacgcacaa caaaattatc 420
gacgagcgcgcc tgatcacccc cgacggctcc atgctgttcc gagtaaccat caacagccat 480
catcaccatc accactaa                                         498

SEQ ID NO: 415      moltype = AA length = 165
FEATURE          Location/Qualifiers
REGION           1..165
                  note = synthetic
source           1..165
                  mol_type = protein
                  organism = synthetic construct
SEQUENCE: 415
MVTLEDFVQ DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLITPDGS MLPRVTINSH HHHHHH 165

SEQ ID NO: 416      moltype = DNA length = 501
FEATURE          Location/Qualifiers
misc_feature     1..501
                  note = synthetic
source           1..501
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 416
atggtgagcg gctggcggtt gttcaagaag attagccacc atcaccatca ccatcatcac 60
ttcacactcg acgattcgt tggggactgg gaacagacag ccgcctacaa cctggaccaa 120
gtcccttgaac aaggagggtgt gtccagttt ctgcagaatc tcgcgtgtc cgtaactccg 180
atcatggaga ttgtccggag cgggtggaaat gcccgtaaaga tcgcacatcca tgcacatc 240
ccgtatggaaatgtctgagcc cgaccaatgg cccagatgg aagggtgtt taagggtgt 300
taccctgtgg atgatcatca cttaagggtg atcctgcctt atggcacact ggtaaatcgac 360
gggggttacgc cgaacaagct gaactatttc ggacggccgt atgaaggcat cggcgtttc 420
gacggcaaaa agatcactac cacagggacc ctgtggaaac gcaacaaaat tatcgacgag 480
cgccctgtatca cccccgacta a                                         501

SEQ ID NO: 417      moltype = AA length = 166
FEATURE          Location/Qualifiers
REGION           1..166
                  note = synthetic
source           1..166
                  mol_type = protein
                  organism = synthetic construct
SEQUENCE: 417
MVGWRLFKK ISHHHHHHHH FTLDLDFVGDW EQTAAYNLQD VLEQGGVSSL LQNLAVSVTP 60
IMRIVRSGEN ALKIDIHVII PYEGLSADM AQIEEVFKV YPVDDHHFKV ILPYGTLVID 120
GVTPNKLNYF GRPYEGIAVF DGKKITTTGT LWNGNKIIDE RLITPD 166

SEQ ID NO: 418      moltype = DNA length = 510
FEATURE          Location/Qualifiers
misc_feature     1..510
                  note = synthetic
source           1..510
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 418
atgaaacatc accatcacca tcatgtgago ggctggcggtt gttcaagaa gattagccgc 60
agtcgtccgtt tcacactcgaa cgatttcgtt ggggactggg aacagacagc ccgcctacac 120
ctggaccaag tccttgaaca gggaggtgtg tccagttgc tcgcagaatct cggcgtgtcc 180
gtaaatccga tcatgaggat tgcgtccggac ggtgaaaatgg ccctgaagat cgacatccat 240
gtcatcatcc cgatgtgagg tctgagccgc gaccaatgg cccagatcga agagggtttt 300
aagggtgtgtt accctgtggaa tgatcatc tttaaagggtga tccgtccctt tggcacactg 360
gtaaatcgacg ggggttacgc gacaaagctg aactatttcg gacggccgtt gtaaggcatc 420

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gccgtgttcg acggcaaaaa gatcaactacc acagggaccc tgtggaacgg caacaaaatt 480
atcgacgagc gctgtatcac ccccgactaa 510

SEQ ID NO: 419      moltype = AA length = 169
FEATURE          Location/Qualifiers
REGION           1..169
note = synthetic
source            1..169
mol_type = protein
organism = synthetic construct

SEQUENCE: 419
MKHHHHHHVWS GWRLFKKISG SSGFTLDDFV GDWEQTAAYN LDQVLEQGGV SSLLQNLAVS 60
VTPIMRIVRS GENALKIDIH VIIPYEGLSA DQMAQIEEVF KVVPVDDHH FKVILPYGTL 120
VIDGVTPNKL NYFGRPYEGI AVFDGKKITT TGTLWNNGNKI IDERLITPD 169

SEQ ID NO: 420      moltype = DNA length = 507
FEATURE          Location/Qualifiers
misc_feature     1..507
note = synthetic
source            1..507
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 420
atgggtgacgc gttcaagaag attagccgca gtcgggtt cacactcgac 60
gatttcgttg gggactggga acagacagcc gcctacaacc tggaccaagt ccttgaacag 120
ggagggtgtt ccagttgtc gcagaatctc gccgtgtccg taactccgt catgaggatt 180
gtccggacgc gtgaaaatgc cctgaaagatc gacatccatc ttatcatccc gtatgaaagg 240
cttgagccgc accaaatggc ccagatcgaa gaggtgtta aggtgggtta ccctgtggat 300
gatcatcaact ttaagggtat cctgcccata ggcacactgg taatcgacgg ggttacccgg 360
aacaagctga actatccgg acggccgtat gaaggcatcg ccgtgttcga cggcaaaaag 420
atcaactacca cagggacccct gtggaaacggc aacaaaattt tcgacgagcg cctgatcacc 480
ccggaccatc accatcacca tcattaa 507

SEQ ID NO: 421      moltype = AA length = 168
FEATURE          Location/Qualifiers
REGION           1..168
note = synthetic
source            1..168
mol_type = protein
organism = synthetic construct

SEQUENCE: 421
MWSGWRLFKK ISGSSGFTLD DFVGDWEQTA AYNLDQVLEQ GGVSSLQLNL AVSVTPIMRI 60
VRSGENALKI DIHVIIPYEG LSADQMAQIE EVFKVVYPVD DHHFKVILPY GTLVIDGVTP 120
NKLNYFGRPY EGIAVFDGKK ITTTGTWLNG NKİIDERLİT PDHHHHHH 168

SEQ ID NO: 422      moltype = DNA length = 498
FEATURE          Location/Qualifiers
misc_feature     1..498
note = synthetic
source            1..498
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 422
atggtcttca cactcgaaga ttctgtggg gactggaaac agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggc aggttgtcgc agaatctccg cgtgtccgtt 120
actcccgatcc aaagggtgtt cccggacggc gaaaatggcc tgaagatcga catccatgtc 180
atcatcccgatcc atgaagggtt gacggccgcac caaatggccc agatcgaaga ggtgtttag 240
gtgtgttacc ctgtggatga ttatcatctt aagggtgatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcccac catgtgaac tatttccggac ggccgtatga aggcatcgcc 360
gtgttcgacgc gcaaaaatggcactgtgaaca gggaccctgtt ggaacgagaa caaaatttac 420
gacgagccgc tgatcaccccg cgacggctcc atgctgttcc gagtaaccat caacagccat 480
catcaccatc accactaa 498

SEQ ID NO: 423      moltype = AA length = 165
FEATURE          Location/Qualifiers
REGION           1..165
note = synthetic
source            1..165
mol_type = protein
organism = synthetic construct

SEQUENCE: 423
MVFTLEDVFV DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRIVRSG ENALKIDIH 60
IIIPYEGLSAD QMAQIEEVFK VVVPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNENKII DERLITPDGS MLFRVTINSH HHHHH 165

SEQ ID NO: 424      moltype = DNA length = 498

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FEATURE Location/Qualifiers  
 misc\_feature 1..498  
     note = synthetic  
 source 1..498  
     mol\_type = other DNA  
     organism = synthetic construct

SEQUENCE: 424  
 atggcattca cactcgaa gtttgcgtgg gactggaa acgacagccgc ctacaacctg 60  
 gaccaagtcc ttgaacaggg aggttgtgtcc agtttgcgtc agaatctcg cgtgtccgt 120  
 actccgatcc aaaggatgtt ccggagccgt gaaaatgccc tgaagatcga catccatgtc 180  
 atcatcccgatcc aaaggatgtt ccggagccgt gaaaatgccc tgaagatcga catccatgtc 240  
 gtgtgttacc ctgtggatga tcataactt aagggtgtcc tgccctatgg cacactggta 300  
 atcgacgggg ttacggccaa catgtgaac tatttcggac ggccgtatga aggcatcgcc 360  
 gtgttcgacg gaaaaaagat cactgtaaaca gggaccctgtt ggaacggcgt taaaattatc 420  
 gacgagccgc tgatcaccccc cgacggctcc atgctgttcc gagtaaccat caacagccat 480  
 catcaccatc accactaa 498

SEQ ID NO: 425 moltype = AA length = 165  
 FEATURE Location/Qualifiers  
 REGION 1..165  
     note = synthetic  
 source 1..165  
     mol\_type = protein  
     organism = synthetic construct

SEQUENCE: 425  
 MVFTLEDVFG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRIVRSG ENALKIDIHV 60  
 IIIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA 120  
 VFDGKKITVT GTLWNGVKII DERLITPDGS MLFRVTINSH HHHHHH 165

SEQ ID NO: 426 moltype = DNA length = 498  
 FEATURE Location/Qualifiers  
 misc\_feature 1..498  
     note = synthetic  
 source 1..498  
     mol\_type = other DNA  
     organism = synthetic construct

SEQUENCE: 426  
 atggcattca cactcgaa gtttgcgtgg gactggaa acgacagccgc ctacaacctg 60  
 gaccaagtcc ttgaacaggg aggttgtgtcc agtttgcgtc agaatctcg cgtgtccgt 120  
 actccgatcc aaaggatgtt ccggagccgt gaaaatgccc tgaagatcga catccatgtc 180  
 atcatcccgatcc aaaggatgtt ccggagccgt gaaaatgccc tgaagatcga catccatgtc 240  
 gtgtgttacc ctgtggatga tcataactt aagggtgtcc tgccctatgg cacactggta 300  
 atcgacgggg ttacggccaa catgtgaac tatttcggac ggccgtatga aggcatcgcc 360  
 gtgttcgacg gaaaaaagat cactgtaaaca gggaccctgtt ggaacggcgt caaaattatc 420  
 gacgagccgc tgatcaccccc cgacggctcc atgctgttcc gagtaaccat caacagccat 480  
 catcaccatc accactaa 498

SEQ ID NO: 427 moltype = AA length = 165  
 FEATURE Location/Qualifiers  
 REGION 1..165  
     note = synthetic  
 source 1..165  
     mol\_type = protein  
     organism = synthetic construct

SEQUENCE: 427  
 MVFTLEDVFG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRMRVRS ENALKIDIHV 60  
 IIIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA 120  
 VFDGKKITVT GTLWNGNKII DERLITPDGS MLFRVTINSH HHHHHH 165

SEQ ID NO: 428 moltype = DNA length = 498  
 FEATURE Location/Qualifiers  
 misc\_feature 1..498  
     note = synthetic  
 source 1..498  
     mol\_type = other DNA  
     organism = synthetic construct

SEQUENCE: 428  
 atggcattca cactcgaa gtttgcgtgg gactggaa acgacagccgc ctacaacctg 60  
 gaccaagtcc ttgaacaggg aggttgtgtcc agtttgcgtc agaatctcg cgtgtccgt 120  
 actccgatcc aaaggatgtt ccggagccgt gaaaatgccc tgaagatcga catccatgtc 180  
 atcatcccgatcc aaaggatgtt ccggagccgt gaaaatgccc tgaagatcga catccatgtc 240  
 gtgtgttacc ctgtggatga tcataactt aagggtgtcc tgccctatgg cacactggta 300  
 atcgacgggg ttacggccaa catgtgaac tatttcggac ggccgtatga aggcatcgcc 360  
 gtgttcgacg gaaaaaagat cactgtaaaca gggaccctgtt ggaacggcgt caaaattatc 420  
 gacgagccgc tgatcaccccc cgacggctcc atgctgttcc gagtaaccat caacagccat 480  
 catcaccatc accactaa 498

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SEQ ID NO: 429      moltype = AA  length = 165
FEATURE          Location/Qualifiers
REGION           1..165
note = synthetic
source            1..165
mol_type = protein
organism = synthetic construct

SEQUENCE: 429
MVFTLEDFVG DWKQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRMVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLITPDGS MLFRVTINSH HHHHHH 165

SEQ ID NO: 430      moltype = DNA  length = 498
FEATURE          Location/Qualifiers
misc_feature     1..498
note = synthetic
source            1..498
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 430
atgggtcttca cactcgaaga ttccgttggg gactggaagc agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggg agggtgttcc agtttgcgtc aqaatctcg cgtgtccgt 120
actccgatcc aaaggatggt ccggagccgtt gaaaatgcc tgaagatcga catccatgtc 180
atcatcccgatcc atgaagggtct gagcgccgac caaatggccc agatcgaaga ggtgttaag 240
gtgggttacc ctgtggatga tcatacactt aagggtgttcc tgccctatgg cacactggta 300
atcgacgggg ttacgcccga catgtgaad tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gcaaaaagat cactgtaaaca gggaccctgtt ggaacgacgt caaaattatc 420
gacgagccgc tgatcaccccc cgacggctcc atgtcgttcc gagtaaccat caacagccat 480
catcaccatc accactaa 498

SEQ ID NO: 431      moltype = AA  length = 165
FEATURE          Location/Qualifiers
REGION           1..165
note = synthetic
source            1..165
mol_type = protein
organism = synthetic construct

SEQUENCE: 431
MVFTLEDFVG DWKQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRMVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNDVKII DERLITPDGS MLFRVTINSH HHHHHH 165

SEQ ID NO: 432      moltype = DNA  length = 498
FEATURE          Location/Qualifiers
misc_feature     1..498
note = synthetic
source            1..498
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 432
atgggtcttca cactcgaaga ttccgttggg gactggaagc agacagccgc ctacaacctg 60
gaccaagtcc ttgaacaggg agggtgttcc agtttgcgtc aqaatctcg cgtgtccgt 120
actccgatcc aaaggatggt ccggagccgtt gaaaatgcc tgaagatcga catccatgtc 180
atcatcccgatcc atgaagggtct gagcgccgac caaatggccc agatcgaaga ggtgttaag 240
gtgggttacc ctgtggatga tcatacactt aagggtgttcc tgccctatgg cacactggta 300
atcgacgggg ttacgcccga catgtgaad tatttcggac ggccgtatga aggcatcgcc 360
gtgttcgacg gcaaaaagat cactgtaaaca gggaccctgtt ggaacgacgt caaaattatc 420
gacgagccgc tgatcaccccc cgacggctcc atgtcgttcc gagtaaccat caacagccat 480
catcaccatc accactaa 498

SEQ ID NO: 433      moltype = AA  length = 165
FEATURE          Location/Qualifiers
REGION           1..165
note = synthetic
source            1..165
mol_type = protein
organism = synthetic construct

SEQUENCE: 433
MVFTLEDFVG DWKQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRMVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNDVKII DERLITPDGS MSFRVTINSH HHHHHH 165

SEQ ID NO: 434      moltype = DNA  length = 498
FEATURE          Location/Qualifiers
misc_feature     1..498

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source          note = synthetic
               1..498
               mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 434
atgggtcttc cactcgaaga ttccgttggg gactggaagc agacagccgc ctacaacctg  60
gaccaagtcc ttgaacaggg aggttgtgtcc agtttgcgtc aqaatctcg cgtgtccgt 120
actccgatcc aaaggatggt ccggagccgt gaaaatgcc tgaagatcga catccatgtc 180
atcatcccgatgtc atgaagggtct gagcgcgcac caaatggccc agatcgaaga ggtgttaag 240
gtgggttacc ctgtgttatgt tcatactttt aqgtgtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcgaa catgtgaac gggacccgtt ggaacggcaa caaaattatc 360
gtgttcgacg gaaaaaaagat cactgtaaaca gggacccgtt ggaacggcaa caaaattatc 420
gacgagccgc tgatcacccc cgacggctcc atgtccttcc gagtaaccat caacagccat 480
catcaccatc accactaa                                         498

SEQ ID NO: 435      moltype = AA  length = 165
FEATURE           Location/Qualifiers
REGION            1..165
source          note = synthetic
               1..165
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 435
MVTLEDFVG DWKQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRMRSG ENALKIDIHV  60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGNKII DERLITPDGS MSFRVTINSH HHHHHH                         165

SEQ ID NO: 436      moltype = DNA  length = 498
FEATURE           Location/Qualifiers
misc_feature      1..498
source          note = synthetic
               1..498
               mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 436
atgggtcttc cactcgaaga ttccgttggg gactggaagc agacagccgc ctacaacctg  60
gaccaagtcc ttgaacaggg aggttgtgtcc agtttgcgtc aqaatctcg cgtgtccgt 120
actccgatcc aaaggatggt ccggagccgt gaaaatgcc tgaagatcga catccatgtc 180
atcatcccgatgtc atgaagggtct gagcgcgcac caaatggccc agatcgaaga ggtgttaag 240
gtgggttacc ctgtgttatgt tcatactttt aqgtgtatcc tgccctatgg cacactggta 300
atcgacgggg ttacgcgaa catgtgaac gggacccgtt ggaacggcaa caaaattatc 360
gtgttcgacg gaaaaaaagat cactgtaaaca gggacccgtt ggaacggcaa caaaattatc 420
gacgagccgc tgatcacccc cgacggctcc atgtccttcc gagtaaccat caacagccat 480
catcaccatc accactaa                                         498

SEQ ID NO: 437      moltype = AA  length = 165
FEATURE           Location/Qualifiers
REGION            1..165
source          note = synthetic
               1..165
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 437
MVTLEDFVG DWKQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRMRSG ENALKIDIHV  60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA 120
VFDGKKITVT GTLWNGVKII DERLITPDGS MSFRVTINSH HHHHHH                         165

SEQ ID NO: 438      moltype = DNA  length = 468
FEATURE           Location/Qualifiers
misc_feature      1..468
source          note = synthetic
               1..468
               mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 438
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa  60
cagacagccg cctacaacct ggacaaagtc cttgaacagg gaggtgtgtc cagttgtct 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatgttccggagccgg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgggttac cctgtgttatgt atcatcattt taagggtatc 300
ctgcccatacg gcacactgggt aatcgacggg gttacgcgcga acaagctgaa ctatccgg 360
caccctgtatc aaggcatcgc cgtgtcgac ggcaaaaaga tcactaccac agggaccctg 420
tggaacggca acaaattatc cgacgagccgcttcatgtcaccc ccgactaa                                         468

SEQ ID NO: 439      moltype = AA  length = 155
FEATURE           Location/Qualifiers

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REGION          1..155
                note = synthetic
source          1..155
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 439
MKHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSLQ NLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER LITPD 155

SEQ ID NO: 440      moltype = DNA length = 468
FEATURE          Location/Qualifiers
misc_feature    1..468
                note = synthetic
source          1..468
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 440
atgaaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cttacaacctt ggaccaagtc ctgttgcagg gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc ttccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcga ccaaattggcc 240
cagatcgaaag aggtgtttaa ggtgggttac cctgtggatc atcatcacatttgc taaggtgtac 300
ctgcccatacg gcacactgggt aatcgacggg gttacgcgcga acaagctgaa ctatccggaa 360
cgcccgatcg aaggcatcgccgttgcac ggccgagaaga tcactaccac agggaccctg 420
tggaaacggca aaaaaattatcgacgacgcccctgtatccggactaa 468

SEQ ID NO: 441      moltype = AA length = 155
FEATURE          Location/Qualifiers
REGION          1..155
                note = synthetic
source          1..155
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 441
MKHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSLQ NLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GEKITTTGTL WNGNKIIDER LITPD 155

SEQ ID NO: 442      moltype = DNA length = 468
FEATURE          Location/Qualifiers
misc_feature    1..468
                note = synthetic
source          1..468
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 442
atgaaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cttacaacctt ggaccaagtc ctgttgcagg gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc ttccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgcga ccaaattggcc 240
cagatcgaaag aggtgtttaa ggtgggttac cctgtggatc atcatcacatttgc taaggtgtac 300
ctgcccatacg gcacactgggt aatcgacggg gttacgcgcga acaagctgaa ctatccggaa 360
cgcccgatcg aaggcatcgccgttgcac ggccgaaaaga tcactaccac agggaccctg 420
cttaaacggca aaaaaattatcgacgacgcccctgtatccggactaa 468

SEQ ID NO: 443      moltype = AA length = 155
FEATURE          Location/Qualifiers
REGION          1..155
                note = synthetic
source          1..155
                mol_type = protein
                organism = synthetic construct
SEQUENCE: 443
MKHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSLQ NLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL PNGNKIIDER LITPD 155

SEQ ID NO: 444      moltype = DNA length = 468
FEATURE          Location/Qualifiers
misc_feature    1..468
                note = synthetic
source          1..468
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 444

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```
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacctt ggaccaagtcc ttgaacagg gaggtgtgtc cagtttgcgt 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattt tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaaag aggtgtttaa ggtgtgtac cctgtggatg atcatcactt taagggtgatc 300
ctgcccatacg gcacactggt aatcgacggg gttacgcggg acaagctgaa ctatccgga 360
cggccgtatcg aaggcatcgccgtgtccgac ggccaaaaaga tcactaccac agggaccctg 420
tggAACGCGCA acaaaaattatcgacgacgctgtatcgatcccgactaa 468
```

```
SEQ ID NO: 445 moltype = AA length = 155
FEATURE Location/Qualifiers
REGION
1..155
note = synthetic
source
1..155
mol_type = protein
organism = synthetic construct
SEQUENCE: 445
MKHHHHHHVFTLDDFVGDW QTAAYNLQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDDHHFKVII LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER LIDPD 155
```

```
SEQ ID NO: 446 moltype = DNA length = 468
FEATURE Location/Qualifiers
misc_feature
1..468
note = synthetic
source
1..468
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 446
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacctt ggaccaagtcc ttgaacagg gaggtgtgtc cagtttgcgt 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattt tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaaag aggtgtttaa ggtgtgtac cctgtggatg atcatcactt taagggtgatc 300
ctgcccatacg gcacactggt aatcgacggg gttacgcggg acaagctgaa ctatccgga 360
cggccgtatcg aaggcatcgccgtgtccgac ggccaaaaaga tcactaccac agggaccctg 420
tggAACGCGCA acaaaaattatcgacgacgctgtatcgatcccgactaa 468
```

```
SEQ ID NO: 447 moltype = AA length = 155
FEATURE Location/Qualifiers
REGION
1..155
note = synthetic
source
1..155
mol_type = protein
organism = synthetic construct
SEQUENCE: 447
MKHHHHHHVFTLDDFVGDW QTAAYNLQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDDHHFKVII LPYGTLVIDG VTPNKLNYFG 120
RPYEGIAVFD GKKITTTGTL WNGNKIIDER LITDD 155
```

```
SEQ ID NO: 448 moltype = DNA length = 468
FEATURE Location/Qualifiers
misc_feature
1..468
note = synthetic
source
1..468
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 448
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cctacaacctt ggaccaagtcc ttgaacagg gaggtgtgtc cagtttgcgt 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattt tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaaag aggtgtttaa ggtgtgtac cctgtggatg atcatcactt taagggtgatc 300
ctgcccatacg gcacactggt aatcgacggg gttacgcggg acaagctgaa ctatccgga 360
cggccgtatcg aaggcatcgccgtgtccgac ggccaaaaaga tcactaccac agggaccctg 420
tggAACGCGCA acaaaaattatcgacgacgctgtatcgatcccgactaa 468
```

```
SEQ ID NO: 449 moltype = AA length = 155
FEATURE Location/Qualifiers
REGION
1..155
note = synthetic
source
1..155
mol_type = protein
organism = synthetic construct
SEQUENCE: 449
MKHHHHHHVFTLDDFVGDW QTAAYNLQV LEQGGVSSL QNLAVSVTPI MRIVRSGENA 60
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LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPYGTLVIDG VTPNKLNYFG 120  
HPYEGIAVFD GEKITTTGTL WNGNKIIDER LITPD 155

SEQ ID NO: 450 moltype = DNA length = 468  
FEATURE Location/Qualifiers  
misc\_feature 1..468  
note = synthetic  
source 1..468  
mol\_type = other DNA  
organism = synthetic construct  
  
SEQUENCE: 450  
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60  
cagacagccg cctacaacct ggaccaagtc cttgaacagg gaggtgtgtc cagttgtcg 120  
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaatgcc 180  
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaataatgcc 240  
cagatcgaa aggtgtttaa ggtgtgtac cctgtggatgc atcatcacca taagggtatc 300  
ctgcccattatg gcacactgggt aatcgacggg gttacgcggaa acaagctgaa ctatttcgga 360  
caccctgtatg aaggcatcgc cgtgttcgac ggcgagaaga tcactaccac agggaccctg 420  
tggAACGGCA aaaaaattat cgacgacgccc ctgatcgatc ccgactaa 468

SEQ ID NO: 451 moltype = AA length = 155  
FEATURE Location/Qualifiers  
REGION 1..155  
note = synthetic  
source 1..155  
mol\_type = protein  
organism = synthetic construct  
  
SEQUENCE: 451  
MKHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSLQ QNLAVSVTPI MRIVRSGENA 60  
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPYGTLVIDG VTPNKLNYFG 120  
HPYEGIAVFD GEKITTTGTL WNGNKIIDER LIDPD 155

SEQ ID NO: 452 moltype = DNA length = 468  
FEATURE Location/Qualifiers  
misc\_feature 1..468  
note = synthetic  
source 1..468  
mol\_type = other DNA  
organism = synthetic construct  
  
SEQUENCE: 452  
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60  
cagacagccg cctacaacct ggaccaagtc cttgaacagg gaggtgtgtc cagttgtcg 120  
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaatgcc 180  
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaataatgcc 240  
cagatcgaa aggtgtttaa ggtgtgtac cctgtggatgc atcatcacca taagggtatc 300  
ctgcccattatg gcacactgggt aatcgacggg gttacgcggaa acaagctgaa ctatttcgga 360  
caccctgtatg aaggcatcgc cgtgttcgac ggcgagaaga tcactaccac agggaccctg 420  
tggAACGGCA aaaaaattat cgacgacgccc ctgatcgatc atgactaa 468

SEQ ID NO: 453 moltype = AA length = 155  
FEATURE Location/Qualifiers  
REGION 1..155  
note = synthetic  
source 1..155  
mol\_type = protein  
organism = synthetic construct  
  
SEQUENCE: 453  
MKHHHHHHVF TLDDFVGDWE QTAAYNLDQV LEQGGVSSLQ QNLAVSVTPI MRIVRSGENA 60  
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPYGTLVIDG VTPNKLNYFG 120  
HPYEGIAVFD GEKITTTGTL WNGNKIIDER LIDDD 155

SEQ ID NO: 454 moltype = DNA length = 468  
FEATURE Location/Qualifiers  
misc\_feature 1..468  
note = synthetic  
source 1..468  
mol\_type = other DNA  
organism = synthetic construct  
  
SEQUENCE: 454  
atgaaacatc accatcacca tcatgtttc acactcgacg atttcgttgg ggactggaa 60  
cagacagccg cctacaacct ggaccaagtc cttgaacagg gaggtgtgtc cagttgtcg 120  
cagaatctcg ccgtgtccgt aactccgatc atgaggatttgc tccggagccg tgaaaatgcc 180  
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaataatgcc 240  
cagatcgaa aggtgtttaa ggtgtgtac cctgtggatgc atcatcacca taagggtatc 300  
ctgcccattatg gcacactgggt aatcgacggg gttacgcggaa acaagctgaa ctatttcgga 360  
caccctgtatg aaggcatcgc cgtgttcgac ggcgagaaga tcactaccac agggaccctg 420

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tggAACGGCA ACAAAATTAT CGACGAGCGC CTGATCGATC CCGACTAA          468
SEQ ID NO: 455 moltype = AA length = 155
FEATURE Location/Qualifiers
REGION 1..155
note = synthetic
source 1..155
mol_type = protein
organism = synthetic construct
SEQUENCE: 455
MKHHHHHHDF TLDDFVGDWE QTAAYNLQV LEQGGVSSLQ NLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPIGTLVIDG VTPNKLNYFG 120
HPYEGIAVFD GEKITTGTL WNGNKIIDER LIDPD 155

SEQ ID NO: 456 moltype = DNA length = 468
FEATURE Location/Qualifiers
misc_feature 1..468
note = synthetic
source 1..468
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 456
atgaaacatc accatcacca tcatgtttc acactcgacg atttcgttgg ggactggaa 60
cagacacgccc cttacaacct ggaccaagtcc ttgaacagg gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattt tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtgttgc atcatcattt taaggtgtac 300
ctgccccatcg gcacactgggt aatcgacggg gagacgcggc acaagctgaa ctattccgaa 360
caccctgtatcg aaggcatcgcc cgatgtcgac ggcgagaaga tcaactaccac agggaccctg 420
tggAACGGCA ACAAAATTAT CGACGAGCGC CTGATCGATC CCGACTAA          468

SEQ ID NO: 457 moltype = AA length = 155
FEATURE Location/Qualifiers
REGION 1..155
note = synthetic
source 1..155
mol_type = protein
organism = synthetic construct
SEQUENCE: 457
MKHHHHHHHF TLDDFVGDWE QTAAYNLQV LEQGGVSSLQ NLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPIGTLVIDG ETPNKLNYFG 120
HPYEGIAVFD GEKITTGTL WNGNKIIDER LIDPD 155

SEQ ID NO: 458 moltype = DNA length = 468
FEATURE Location/Qualifiers
misc_feature 1..468
note = synthetic
source 1..468
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 458
atgaaacatc accatcacca tcatgtttc acactcgacg atttcgttgg ggactggaa 60
cagacacgccc cttacaacct ggaccaagtcc ttgaacagg gaggtgtgtc cagttgtcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggattt tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgccga ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtgttgc atcatcattt taaggtgtac 300
ctgccccatcg gcacactgggt aatcgacggg gttacgcggc acaagctgaa ctattccgaa 360
caccctgtatcg aaggcatcgcc cgatgtcgac ggcgagaaga tcaactaccac agggaccctg 420
tggAACGGCA ACAAAATTAT CGACGAGCGC CTGATCGATC CCGACTAA          468

SEQ ID NO: 459 moltype = AA length = 155
FEATURE Location/Qualifiers
REGION 1..155
note = synthetic
source 1..155
mol_type = protein
organism = synthetic construct
SEQUENCE: 459
MKHHHHHHHF TLDDFVGDWE QTAAYNLQV LEQGGVSSLQ NLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVYY PVDHHFKVI LPIGTLVIDG VTPNKLNYFG 120
HPYEGIADFD GEKITTGTL WNGNKIIDER LIDPD 155

SEQ ID NO: 460 moltype = DNA length = 468
FEATURE Location/Qualifiers
misc_feature 1..468
note = synthetic

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source          1..468
               mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 460
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cttacaacctt ggaccaagtgc cttaaacagg gagggtgttc cagtttgcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatgg tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgca ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtggatg atcatcactt taagggtgatc 300
ctgcccattcg gcacactggta aatcgacggg gagaacgcggc acaagctgaa ctatattcgga 360
caccctatcg aaggcatcgc cgatattcgatc ggcgagaaga tcactaccac agggacacctg 420
tggAACGGCA aaaaaattat ccacgagcgc ctgatcgatc ccgactaa 468

SEQ ID NO: 461      moltype = AA  length = 155
FEATURE           Location/Qualifiers
REGION            1..155
note = synthetic
source             1..155
mol_type = protein
organism = synthetic construct

SEQUENCE: 461
MKHHHHHHHVF TLDDDFVGDWE QTAAYNLQDV LEQGGVSSLQ NLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDDHHFKVII LPIGTLVIDG ETPNKLNYFG 120
HPYEGIADFD GEKITTTGTL WNGNKKIIDER LIDPD 155

SEQ ID NO: 462      moltype = DNA  length = 327
FEATURE           Location/Qualifiers
misc_feature       1..327
note = synthetic
source              1..327
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 462
atgaaacatc accatcacca tcatgtcttc acactcgacg atttcgttgg ggactggaa 60
cagacagccg cttacaacctt ggaccaagtgc cttaaacagg gagggtgttc cagtttgcg 120
cagaatctcg ccgtgtccgt aactccgatc atgaggatgg tccggagccg tgaaaatgcc 180
ctgaagatcg acatccatgt catcatcccg tatgaagggtc tgagcgcgca ccaaattggcc 240
cagatcgaag aggtgtttaa ggtgtgtac cctgtggatg atcatcactt taagggtgatc 300
ctgcccattcg gcacactggta aatcgac 327

SEQ ID NO: 463      moltype = AA  length = 109
FEATURE           Location/Qualifiers
REGION            1..109
note = synthetic
source             1..109
mol_type = protein
organism = synthetic construct

SEQUENCE: 463
MKHHHHHHHVF TLDDDFVGDWE QTAAYNLQDV LEQGGVSSLQ NLAVSVTPI MRIVRSGENA 60
LKIDIHVIIP YEGLSADQMA QIEEVFKVVY PVDDHHFKVII LPYGTLVIDG 109

SEQ ID NO: 464      moltype = AA  length = 11
FEATURE           Location/Qualifiers
REGION            1..11
note = synthetic
source             1..11
mol_type = protein
organism = synthetic construct

SEQUENCE: 464
VSGWRLFKKI S 11

SEQ ID NO: 465      moltype = AA  length = 10
FEATURE           Location/Qualifiers
REGION            1..10
note = synthetic
source             1..10
mol_type = protein
organism = synthetic construct

SEQUENCE: 465
VSGWRLFKKI 10

SEQ ID NO: 466      moltype = AA  length = 15
FEATURE           Location/Qualifiers
REGION            1..15
note = synthetic
source             1..15

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SEQUENCE: 466 WNGNKIIDER LITPD	mol_type = protein organism = synthetic construct	
		15
SEQ ID NO: 467 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic	
source	1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 467 KKITTTGTLW NGR		13
SEQ ID NO: 468 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = synthetic	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 468 RPYEGIAVFD GK		12
SEQ ID NO: 469 FEATURE REGION	moltype = AA length = 24 Location/Qualifiers 1..24 note = synthetic	
source	1..24 mol_type = protein organism = synthetic construct	
SEQUENCE: 469 GKMLFRVTI W KVSVSGWRLF KKIS		24
SEQ ID NO: 470 FEATURE REGION	moltype = AA length = 22 Location/Qualifiers 1..22 note = synthetic	
source	1..22 mol_type = protein organism = synthetic construct	
SEQUENCE: 470 GKMLFRVTI W KVSGWRLF KK		22
SEQ ID NO: 471 FEATURE REGION	moltype = AA length = 26 Location/Qualifiers 1..26 note = synthetic	
source	1..26 mol_type = protein organism = synthetic construct	
SEQUENCE: 471 GSMKFRVTIN SWKVSGWR LFKKIS		26
SEQ ID NO: 472 FEATURE REGION	moltype = AA length = 24 Location/Qualifiers 1..24 note = synthetic	
source	1..24 mol_type = protein organism = synthetic construct	
SEQUENCE: 472 GSMKFRVTIN SWKVSGWRLF KKIS		24
SEQ ID NO: 473 FEATURE REGION	moltype = AA length = 26 Location/Qualifiers 1..26 note = synthetic	
source	1..26 mol_type = protein organism = synthetic construct	
SEQUENCE: 473 GSMKFRVTIN SWKNVTGYRL FKKISN		26
SEQ ID NO: 474	moltype = AA length = 24	

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FEATURE	Location/Qualifiers
REGION	1..24
source	note = synthetic
	1..24
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 474	
GSMKFRVTIN SWKVTGYRLF EKIS	24
SEQ ID NO: 475	moltype = AA length = 24
FEATURE	Location/Qualifiers
REGION	1..24
source	note = synthetic
	1..24
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 475	
GSMKFRVTIW KVSVSGWRLF KKIS	24
SEQ ID NO: 476	moltype = AA length = 22
FEATURE	Location/Qualifiers
REGION	1..22
source	note = synthetic
	1..22
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 476	
GSMKFRVTIW KVSGWRLF KK	22
SEQ ID NO: 477	moltype = AA length = 26
FEATURE	Location/Qualifiers
REGION	1..26
source	note = synthetic
	1..26
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 477	
GRMLFRVTIN SWKVSVSGWR LFKKIS	26
SEQ ID NO: 478	moltype = AA length = 24
FEATURE	Location/Qualifiers
REGION	1..24
source	note = synthetic
	1..24
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 478	
GRMLFRVTIN SWKVSVSGWRLF KKIS	24
SEQ ID NO: 479	moltype = AA length = 24
FEATURE	Location/Qualifiers
REGION	1..24
source	note = synthetic
	1..24
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 479	
GRMLFRVTIW KVSVSGWRLF KKIS	24
SEQ ID NO: 480	moltype = AA length = 22
FEATURE	Location/Qualifiers
REGION	1..22
source	note = synthetic
	1..22
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 480	
GRMLFRVTIW KVSGWRLF KK	22
SEQ ID NO: 481	moltype = AA length = 24
FEATURE	Location/Qualifiers
REGION	1..24
source	note = synthetic
	1..24
	mol_type = protein
	organism = synthetic construct

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SEQUENCE: 481
GSMLFRVTIN SVSVSGWRLF KKIS                                24

SEQ ID NO: 482      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
source            note = synthetic
                  1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 482
GSMLFKVTIN SVSGWRLFKK IS                                    22

SEQ ID NO: 483      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
source            note = synthetic
                  1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 483
GSMLFQVTIN SVSGWRLFKK IS                                    22

SEQ ID NO: 484      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
source            note = synthetic
                  1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 484
GSMLFEVTIN SVSGWRLFKK IS                                    22

SEQ ID NO: 485      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
source            note = synthetic
                  1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 485
GSMLFNVTIN SVSGWRLFKK IS                                    22

SEQ ID NO: 486      moltype = AA  length = 21
FEATURE          Location/Qualifiers
REGION           1..21
source            note = synthetic
                  1..21
mol_type = protein
organism = synthetic construct

SEQUENCE: 486
GRPYEGIAVF DGKKITTTGT L                                     21

SEQ ID NO: 487      moltype = AA  length = 24
FEATURE          Location/Qualifiers
REGION           1..24
source            note = synthetic
                  1..24
mol_type = protein
organism = synthetic construct

SEQUENCE: 487
GSMKFRVTIN SWKVTGYRLF EKES                                 24

SEQ ID NO: 488      moltype = AA  length = 24
FEATURE          Location/Qualifiers
REGION           1..24
source            note = synthetic
                  1..24
mol_type = protein
organism = synthetic construct

SEQUENCE: 488
GSMKFRVTIN SWKVEGYRLF EKIS                                 24

SEQ ID NO: 489      moltype = AA  length = 24
FEATURE          Location/Qualifiers
REGION           1..24

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source          note = synthetic
               1..24
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 489
KIKTTTGTLL NGNKKIIDERL ITPD                                24

SEQ ID NO: 490      moltype = AA  length = 26
FEATURE          Location/Qualifiers
REGION           1..26
note = synthetic
source          1..26
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 490
WNNGNKIIDERL LITPDGSMMLF RVTINS                            26

SEQ ID NO: 491      moltype = AA  length = 13
FEATURE          Location/Qualifiers
REGION           1..13
note = synthetic
source          1..13
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 491
GKMLFRVTIQ KWK                                         13

SEQ ID NO: 492      moltype = AA  length = 13
FEATURE          Location/Qualifiers
REGION           1..13
note = synthetic
source          1..13
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 492
GKMLFRVTIG KWK                                         13

SEQ ID NO: 493      moltype = AA  length = 13
FEATURE          Location/Qualifiers
REGION           1..13
note = synthetic
source          1..13
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 493
GKMLFRVTIG RWK                                         13

SEQ ID NO: 494      moltype = AA  length = 13
FEATURE          Location/Qualifiers
REGION           1..13
note = synthetic
source          1..13
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 494
GKMLFRVTIG NWK                                         13

SEQ ID NO: 495      moltype = AA  length = 13
FEATURE          Location/Qualifiers
REGION           1..13
note = synthetic
source          1..13
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 495
GKMLFRVTIQ NWK                                         13

SEQ ID NO: 496      moltype = AA  length = 13
FEATURE          Location/Qualifiers
REGION           1..13
note = synthetic
source          1..13
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 496
GKMLFRVTID KWK                                         13

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SEQ ID NO: 497	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 497	
GKMLFRVTIE KWK	13
SEQ ID NO: 498	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 498	
EKMLFRVTIE SWK	13
SEQ ID NO: 499	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 499	
EKLLFRVTIE SWK	13
SEQ ID NO: 500	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 500	
EKLLFRVTIE SYK	13
SEQ ID NO: 501	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 501	
GKMLFRVTIE RWK	13
SEQ ID NO: 502	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 502	
GKMLFRVTID RWK	13
SEQ ID NO: 503	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 503	
DKMLFRVTIQ KWK	13
SEQ ID NO: 504	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13

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	mol_type = protein organism = synthetic construct	
SEQUENCE: 504 DKMLFRVTIG KWK		13
SEQ ID NO: 505 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic	
source	1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 505 DKMLFRVTIG RWK		13
SEQ ID NO: 506 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic	
source	1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 506 DKMLFRVTIG NWK		13
SEQ ID NO: 507 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic	
source	1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 507 DKMLFRVTIQ NWK		13
SEQ ID NO: 508 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic	
source	1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 508 DKMLFRVTID KWK		13
SEQ ID NO: 509 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic	
source	1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 509 DKMLFRVTIE KWK		13
SEQ ID NO: 510 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic	
source	1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 510 DKMLFRVTIE RWK		13
SEQ ID NO: 511 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic	
source	1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 511 DKMLFRVTID RWK		13
SEQ ID NO: 512	moltype = AA length = 35	

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FEATURE	Location/Qualifiers
REGION	1..35
source	note = synthetic 1..35 mol_type = protein organism = synthetic construct
SEQUENCE: 512	
RPYEGIAVFD GKKITVTGTL WNGNKIIDER LITPD	35
SEQ ID NO: 513	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 513	
EKMLFRVTIQ KWK	13
SEQ ID NO: 514	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 514	
EKMLFRVTIG KWK	13
SEQ ID NO: 515	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 515	
EKMLFRVTIG RWK	13
SEQ ID NO: 516	moltype = AA length = 22
FEATURE	Location/Qualifiers
REGION	1..22
source	note = synthetic 1..22 mol_type = protein organism = synthetic construct
SEQUENCE: 516	
DKMLFTVTIQ KVSGWRLFKK IS	22
SEQ ID NO: 517	moltype = AA length = 22
FEATURE	Location/Qualifiers
REGION	1..22
source	note = synthetic 1..22 mol_type = protein organism = synthetic construct
SEQUENCE: 517	
DKLLFTVTIE KVSGWRLFKK IS	22
SEQ ID NO: 518	moltype = AA length = 24
FEATURE	Location/Qualifiers
REGION	1..24
source	note = synthetic 1..24 mol_type = protein organism = synthetic construct
SEQUENCE: 518	
DKLLFTVTIE KWKVSGWRLF KKIS	24
SEQ ID NO: 519	moltype = AA length = 24
FEATURE	Location/Qualifiers
REGION	1..24
source	note = synthetic 1..24 mol_type = protein organism = synthetic construct

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SEQUENCE: 519
DKLLFTVTIE KYKVSGWRLF KKIS                                24

SEQ ID NO: 520      moltype = AA  length = 26
FEATURE          Location/Qualifiers
REGION           1..26
note = synthetic
source            1..26
mol_type = protein
organism = synthetic construct

SEQUENCE: 520
DKLLFTVTIE KYKVSVSGWR LFKKIS                                26

SEQ ID NO: 521      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
note = synthetic
source            1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 521
KMMLFRVTIQ KVSGWRLFKK IS                                    22

SEQ ID NO: 522      moltype = AA  length = 26
FEATURE          Location/Qualifiers
REGION           1..26
note = synthetic
source            1..26
mol_type = protein
organism = synthetic construct

SEQUENCE: 522
KMMLFRVTIQ KWGVSVSGWR LFKKIS                                26

SEQ ID NO: 523      moltype = AA  length = 24
FEATURE          Location/Qualifiers
REGION           1..24
note = synthetic
source            1..24
mol_type = protein
organism = synthetic construct

SEQUENCE: 523
KMMLFRVTIQ KWGVSGWRLF KKIS                                24

SEQ ID NO: 524      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
note = synthetic
source            1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 524
DKLLFTVTIG KVSGWRLFKK IS                                    22

SEQ ID NO: 525      moltype = AA  length = 24
FEATURE          Location/Qualifiers
REGION           1..24
note = synthetic
source            1..24
mol_type = protein
organism = synthetic construct

SEQUENCE: 525
DKLLFTVTIG KYKVSGWRLF KKIS                                24

SEQ ID NO: 526      moltype = AA  length = 26
FEATURE          Location/Qualifiers
REGION           1..26
note = synthetic
source            1..26
mol_type = protein
organism = synthetic construct

SEQUENCE: 526
DKLLFTVTIG KYKVSVSGWR LFKKIS                                26

SEQ ID NO: 527      moltype = AA  length = 26
FEATURE          Location/Qualifiers
REGION           1..26

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source          note = synthetic
               1..26
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 527
DKLLFTVTIG KWKVSVSGWR LFKKIS                                26

SEQ ID NO: 528      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
note = synthetic
source          1..22
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 528
DKLLFVTIQT KVSGWRLFKK IS                                    22

SEQ ID NO: 529      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
note = synthetic
source          1..22
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 529
KKMLFTVTIQT KVSGWRLFKK IS                                  22

SEQ ID NO: 530      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
note = synthetic
source          1..22
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 530
KKLLFRVTIQT KVSGWRLFKK IS                                  22

SEQ ID NO: 531      moltype = AA  length = 21
FEATURE          Location/Qualifiers
REGION           1..21
note = synthetic
source          1..21
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 531
DKLLFTVTIE KVSGWRLFKK I                                    21

SEQ ID NO: 532      moltype = AA  length = 25
FEATURE          Location/Qualifiers
REGION           1..25
note = synthetic
source          1..25
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 532
DKLLFTVTIE KYKVSVSGWR LFKKI                                25

SEQ ID NO: 533      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
note = synthetic
source          1..22
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 533
DRLLFTVTIE RVSGWRLFKK IS                                 22

SEQ ID NO: 534      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
note = synthetic
source          1..22
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 534
EKLLFTVTIE KVSGWRLFKK IS                                 22

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SEQ ID NO: 535      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
source            note = synthetic
                 1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 535
KKLLFTVTIG KVSGWRLFKK IS                                22

SEQ ID NO: 536      moltype = AA  length = 24
FEATURE          Location/Qualifiers
REGION           1..24
source            note = synthetic
                 1..24
mol_type = protein
organism = synthetic construct

SEQUENCE: 536
GSMRFRVTIN SWRVVTGYRLF ERES                               24

SEQ ID NO: 537      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
source            note = synthetic
                 1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 537
GSMKFRVTIN SVTGYRLFEK ES                                22

SEQ ID NO: 538      moltype = AA  length = 17
FEATURE          Location/Qualifiers
REGION           1..17
source            note = synthetic
                 1..17
mol_type = protein
organism = synthetic construct

SEQUENCE: 538
KKITTTGTLW NGNKIID                                         17

SEQ ID NO: 539      moltype = AA  length = 29
FEATURE          Location/Qualifiers
REGION           1..29
source            note = synthetic
                 1..29
mol_type = protein
organism = synthetic construct

SEQUENCE: 539
ERLITPDGSM LFRVTINSVS GWRLFKKIS                           29

SEQ ID NO: 540      moltype = AA  length = 58
FEATURE          Location/Qualifiers
REGION           1..58
source            note = synthetic
                 1..58
mol_type = protein
organism = synthetic construct

SEQUENCE: 540
GRPYEGIAVD FGKKITTTGT LWNGNKIIDE RLITPDGSML FRVTINSVSG WRLFKKIS  58

SEQ ID NO: 541      moltype = AA  length = 68
FEATURE          Location/Qualifiers
REGION           1..68
source            note = synthetic
                 1..68
mol_type = protein
organism = synthetic construct

SEQUENCE: 541
GVTPNKLNYF GRPYEGIAVD FGKKITTTGT LWNGNKIIDE RLITPDGSML FRVTINSVSG 60
WRLFKKIS                                         68

SEQ ID NO: 542      moltype = AA  length = 13
FEATURE          Location/Qualifiers
REGION           1..13
source            note = synthetic

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source	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 542	
EKMLFRVTIG NWK	13
SEQ ID NO: 543	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 543	
EKMLFRVTIQ NWK	13
SEQ ID NO: 544	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 544	
EKMLFRVTID KWK	13
SEQ ID NO: 545	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 545	
EKMLFRVTIE KWK	13
SEQ ID NO: 546	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 546	
EKMLFRVTIE RWK	13
SEQ ID NO: 547	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 547	
EKMLFRVTID RWK	13
SEQ ID NO: 548	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 548	
KKMLFRVTIG KWK	13
SEQ ID NO: 549	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 549	
KKMLFRVTIG RWK	13

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SEQ ID NO: 550	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 550	
KKMLFRVTIG NWK	13
SEQ ID NO: 551	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 551	
KKMLFRVTIQ NWK	13
SEQ ID NO: 552	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 552	
KKMLFRVTID KWK	13
SEQ ID NO: 553	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 553	
KKMLFRVTIE KWK	13
SEQ ID NO: 554	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 554	
KKMLFRVTIE RWK	13
SEQ ID NO: 555	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 555	
KKMLFRVTID RWK	13
SEQ ID NO: 556	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 556	
RKMLFRVTIQ KWK	13
SEQ ID NO: 557	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein

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SEQUENCE: 557 RKMLFRVTIG KWK	organism = synthetic construct	
		13
SEQ ID NO: 558 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 558 RKMLFRVTIG RWK	organism = synthetic construct	
		13
SEQ ID NO: 559 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 559 RKMLFRVTIG NWK	organism = synthetic construct	
		13
SEQ ID NO: 560 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 560 RKMLFRVTIQ NWK	organism = synthetic construct	
		13
SEQ ID NO: 561 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 561 RKMLFRVTID KWK	organism = synthetic construct	
		13
SEQ ID NO: 562 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 562 RKMLFRVTIE KWK	organism = synthetic construct	
		13
SEQ ID NO: 563 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 563 RKMLFRVTIE RWK	organism = synthetic construct	
		13
SEQ ID NO: 564 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 564 RKMLFRVTID RWK	organism = synthetic construct	
		13
SEQ ID NO: 565 FEATURE	moltype = AA length = 13 Location/Qualifiers	

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REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 565		
EQMLFRVTIN SWK		13
SEQ ID NO: 566	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 566		
SRMLFRVTIN SWK		13
SEQ ID NO: 567	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 567		
GEMLFRVTIN SWK		13
SEQ ID NO: 568	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 568		
GKMKFRVTIN SWK		13
SEQ ID NO: 569	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 569		
GKMLFRVKIN SWK		13
SEQ ID NO: 570	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 570		
GKMLFRVRIN SWK		13
SEQ ID NO: 571	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 571		
GKMLFRVDIN SWK		13
SEQ ID NO: 572	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 572		

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GKMLFRVTID SWK	13
SEQ ID NO: 573 FEATURE REGION source SEQUENCE: 573 EKMLFKVTIQ KWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 574 FEATURE REGION source SEQUENCE: 574 EKMLFTVTIQ KWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 575 FEATURE REGION source SEQUENCE: 575 EKMLFKVTID KWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 576 FEATURE REGION source SEQUENCE: 576 EKMLFTVTID KWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 577 FEATURE REGION source SEQUENCE: 577 EKMLFKVTIG RWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 578 FEATURE REGION source SEQUENCE: 578 DKMLFKVTIQ KWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 579 FEATURE REGION source SEQUENCE: 579 DKMLFTVTIQ KWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 580 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic

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source	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 580	
DKMLFKVTID KWK	13
SEQ ID NO: 581	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 581	
DKMLFTVTID KWK	13
SEQ ID NO: 582	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 582	
GKMLFKVTE KWK	13
SEQ ID NO: 583	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 583	
GKMLFTVTIE KWK	13
SEQ ID NO: 584	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 584	
DKMLFKVTIG KWK	13
SEQ ID NO: 585	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 585	
DKMLFTVTIG KWK	13
SEQ ID NO: 586	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 586	
DKMLFKVTIG NWK	13
SEQ ID NO: 587	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 587	
DKMLFKVTIQ NWK	13

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SEQ ID NO: 588	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
SEQUENCE: 588	organism = synthetic construct
GKMLFKVTIN KWK	
	13
SEQ ID NO: 589	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
SEQUENCE: 589	organism = synthetic construct
GKMLFTVTIN KWK	
	13
SEQ ID NO: 590	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
SEQUENCE: 590	organism = synthetic construct
DKMLFKVTIE KWK	
	13
SEQ ID NO: 591	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
SEQUENCE: 591	organism = synthetic construct
DKMLFTVTIE KWK	
	13
SEQ ID NO: 592	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
SEQUENCE: 592	organism = synthetic construct
DKLLFKVTIG KWK	
	13
SEQ ID NO: 593	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
SEQUENCE: 593	organism = synthetic construct
DKMLFTVTIN KWK	
	13
SEQ ID NO: 594	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
SEQUENCE: 594	organism = synthetic construct
DKLLFTVTIQ KWK	
	13
SEQ ID NO: 595	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein

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SEQUENCE: 595 DKLLFTVTIQ KYK	organism = synthetic construct	
		13
SEQ ID NO: 596 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 596 DKLLFTVTIE KWK	organism = synthetic construct	
		13
SEQ ID NO: 597 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 597 DKLLFTVTIG KWK	organism = synthetic construct	
		13
SEQ ID NO: 598 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 598 DKLLFTVTIG KYK	organism = synthetic construct	
		13
SEQ ID NO: 599 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 599 DKLLFTVTIN KWK	organism = synthetic construct	
		13
SEQ ID NO: 600 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 600 DKLMLFRVTIN KYK	organism = synthetic construct	
		13
SEQ ID NO: 601 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11	
source	note = synthetic 1..11 mol_type = protein	
SEQUENCE: 601 GKMLFRVTIN S	organism = synthetic construct	
		11
SEQ ID NO: 602 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11	
source	note = synthetic 1..11 mol_type = protein	
SEQUENCE: 602 DKMLFTVTIQ K	organism = synthetic construct	
		11
SEQ ID NO: 603 FEATURE	moltype = AA length = 11 Location/Qualifiers	

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REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 603	
DKMLFKVTIQ K	11
SEQ ID NO: 604	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 604	
DKLLFTVTIG K	11
SEQ ID NO: 605	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 605	
DKMLFTVTIG K	11
SEQ ID NO: 606	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 606	
DKMLFTVTIE K	11
SEQ ID NO: 607	moltype = AA length = 11
FEATURE	Location/Qualifiers
REGION	1..11
source	note = synthetic
	1..11
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 607	
DKLLFTVTIE K	11
SEQ ID NO: 608	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 608	
DKMLFRVTIN SWK	13
SEQ ID NO: 609	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 609	
EKMLFRVTIN SWK	13
SEQ ID NO: 610	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 610	

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RKMLFRVTIN SWK	13
SEQ ID NO: 611 FEATURE REGION source SEQUENCE: 611 KMLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 612 FEATURE REGION source SEQUENCE: 612 HKMLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 613 FEATURE REGION source SEQUENCE: 613 GLMLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 614 FEATURE REGION source SEQUENCE: 614 GQMLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 615 FEATURE REGION source SEQUENCE: 615 GTMLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 616 FEATURE REGION source SEQUENCE: 616 GKLLFRVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 617 FEATURE REGION source SEQUENCE: 617 GKMLFKVTIN SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 618 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic

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source	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 618 GKMLFRVTIQ SWK	
	13
SEQ ID NO: 619 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic
source	1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 619 GKMLFRVTID SWK	
	13
SEQ ID NO: 620 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic
source	1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 620 GKMLFRVTIG SWK	
	13
SEQ ID NO: 621 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic
source	1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 621 GKMLFRVTIN TWK	
	13
SEQ ID NO: 622 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic
source	1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 622 GKMLFRVTIN NWK	
	13
SEQ ID NO: 623 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic
source	1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 623 GKMLFRVTIN QWK	
	13
SEQ ID NO: 624 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic
source	1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 624 GKMLFRVTIN PWK	
	13
SEQ ID NO: 625 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic
source	1..13 mol_type = protein organism = synthetic construct
SEQUENCE: 625 GKMLFRVTIN KWK	
	13

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SEQ ID NO: 626	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 626	
GKMLFRVTIN SWQ	13
SEQ ID NO: 627	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 627	
GKMLFRVTIN SWN	13
SEQ ID NO: 628	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 628	
GKMLFRVTIN SWT	13
SEQ ID NO: 629	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 629	
GKMLFRVTIN SWH	13
SEQ ID NO: 630	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 630	
GKMLFRVTIN SWP	13
SEQ ID NO: 631	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 631	
GKMLFRVTIN SWR	13
SEQ ID NO: 632	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 632	
GKMKFRVTID SWK	13
SEQ ID NO: 633	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein

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SEQUENCE: 633 GKMLFRVEIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 634 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 634 GKMLFRVQIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 635 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 635 GKMKFRVKIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 636 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 636 GKMKFRVRIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 637 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 637 GKMKFRVIEIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 638 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 638 GKMKFRVDIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 639 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 639 GKMKFRVQIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 640 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 640 GKMKFRVNIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 641 FEATURE	moltype = AA length = 13 Location/Qualifiers	

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REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 641	
GKMKFRVSIN SWK	13
SEQ ID NO: 642	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 642	
GKMLFRVNIN SWK	13
SEQ ID NO: 643	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 643	
GKMLFRVSIN SWK	13
SEQ ID NO: 644	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 644	
GKMLFRVWIN SWK	13
SEQ ID NO: 645	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 645	
GKMSFRVTIN SWK	13
SEQ ID NO: 646	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 646	
GKMWFRVTIN SWK	13
SEQ ID NO: 647	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 647	
GKMNFRVTIN SWK	13
SEQ ID NO: 648	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 648	

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GSMFLFRVTIN SYK	13
SEQ ID NO: 649 FEATURE REGION source SEQUENCE: 649 GKMLFRVTIN SYK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 650 FEATURE REGION source SEQUENCE: 650 GKMLFRVTIK SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 651 FEATURE REGION source SEQUENCE: 651 GKMLFRVTIE SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 652 FEATURE REGION source SEQUENCE: 652 GKMKFRVTIQ SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 653 FEATURE REGION source SEQUENCE: 653 GKMKFRVTIE SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 654 FEATURE REGION source SEQUENCE: 654 GKMKFRVTIK SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 655 FEATURE REGION source SEQUENCE: 655 GKMKFRVTIR SWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 656 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic

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source	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 656	
RLMLFRVTIN SWK	
	13
SEQ ID NO: 657	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 657	
RQMLFRVTIN SWK	
	13
SEQ ID NO: 658	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 658	
KLMLFRVTIN SWK	
	13
SEQ ID NO: 659	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 659	
KQMLFRVTIN SWK	
	13
SEQ ID NO: 660	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 660	
ELMLFRVTIN SWK	
	13
SEQ ID NO: 661	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 661	
DLMFLFRVTIN SWK	
	13
SEQ ID NO: 662	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 662	
DQMLFRVTIN SWK	
	13
SEQ ID NO: 663	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 663	
DKMLFRVTIN SWK	
	13

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SEQ ID NO: 664	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 664	
EKMLFRVTIN SWK	13
SEQ ID NO: 665	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 665	
RKMLFRVTIN SWK	13
SEQ ID NO: 666	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 666	
KKMLFRVTIN SWK	13
SEQ ID NO: 667	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 667	
GKMLFRVTIG SWK	13
SEQ ID NO: 668	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 668	
GKMLFRVTIN KWK	13
SEQ ID NO: 669	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 669	
GKMLFRVTIS KWK	13
SEQ ID NO: 670	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 670	
GKMLFRVTIQ KWK	13
SEQ ID NO: 671	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein

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SEQUENCE: 671 GKMLFRVTIT KWK	organism = synthetic construct	
		13
SEQ ID NO: 672 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 672 GKMLFRVTIK KWK	organism = synthetic construct	
		13
SEQ ID NO: 673 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 673 GKMLFKVTIN SWK	organism = synthetic construct	
		13
SEQ ID NO: 674 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 674 RILMLFRVTIG KWK	organism = synthetic construct	
		13
SEQ ID NO: 675 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 675 GKMLFRVTIN RWK	organism = synthetic construct	
		13
SEQ ID NO: 676 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 676 EKMLFTVTIG KWK	organism = synthetic construct	
		13
SEQ ID NO: 677 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 677 EKLLFTVTIG KWK	organism = synthetic construct	
		13
SEQ ID NO: 678 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13	
source	note = synthetic 1..13 mol_type = protein	
SEQUENCE: 678 EKMLFTVTIG RWK	organism = synthetic construct	
		13
SEQ ID NO: 679 FEATURE	moltype = AA length = 13 Location/Qualifiers	

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REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 679		
EKMLFTVTIE KWK		13
SEQ ID NO: 680	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 680		
DKMLFRVTIE SWK		13
SEQ ID NO: 681	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 681		
EKLLFRVTIG KYK		13
SEQ ID NO: 682	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 682		
DKLLFKVTIQ KWK		13
SEQ ID NO: 683	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 683		
DKLLFKVTIQ KYK		13
SEQ ID NO: 684	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 684		
DKLLFKVTIG KYK		13
SEQ ID NO: 685	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 685		
DKLLFKVTE KWK		13
SEQ ID NO: 686	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
source	note = synthetic	
	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 686		

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DKLLFKVTIE KYK	13
SEQ ID NO: 687 FEATURE REGION source SEQUENCE: 687 KKLLFRVTIQ KWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 688 FEATURE REGION source SEQUENCE: 688 DRMLFRVTIQ RWR	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 689 FEATURE REGION source SEQUENCE: 689 ERMLFRVTIG RWR	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 690 FEATURE REGION source SEQUENCE: 690 GRMLFRVTIN RWR	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 691 FEATURE REGION source SEQUENCE: 691 DRMLFRVTIE RWR	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 692 FEATURE REGION source SEQUENCE: 692 DKMLFKVTIQ KYK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 693 FEATURE REGION source SEQUENCE: 693 DKMLFRVTIN KWK	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic 1..13 mol_type = protein organism = synthetic construct
SEQ ID NO: 694 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = synthetic

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source	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 694	
DKMLFKVTIE KYK	
	13
SEQ ID NO: 695	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 695	
DKMLFKVTIN KWK	
	13
SEQ ID NO: 696	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 696	
GRMLFRVTIN SWR	
	13
SEQ ID NO: 697	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 697	
GRLLFVVVIE RYR	
	13
SEQ ID NO: 698	moltype = AA length = 12
FEATURE	Location/Qualifiers
REGION	1..12
source	note = synthetic
	1..12
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 698	
VSGWRLFRRI SC	
	12
SEQ ID NO: 699	moltype = AA length = 14
FEATURE	Location/Qualifiers
REGION	1..14
source	note = synthetic
	1..14
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 699	
GRMLFRVTIN SWRC	
	14
SEQ ID NO: 700	moltype = AA length = 14
FEATURE	Location/Qualifiers
REGION	1..14
source	note = synthetic
	1..14
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 700	
GRLLFTVTIE RYRC	
	14
SEQ ID NO: 701	moltype = AA length = 13
FEATURE	Location/Qualifiers
REGION	1..13
source	note = synthetic
	1..13
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 701	
GKLLFVVVIE KYK	
	13

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SEQ ID NO: 702      moltype = AA length = 21
FEATURE          Location/Qualifiers
REGION           1..21
note = synthetic
source            1..21
mol_type = protein
organism = synthetic construct

SEQUENCE: 702
GKLLFVTIEK VSGWRLFKKI S                               21

SEQ ID NO: 703      moltype = AA length = 170
FEATURE          Location/Qualifiers
REGION           1..170
note = synthetic
source            1..170
mol_type = protein
organism = synthetic construct

SEQUENCE: 703
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPDGS MLFRVTINSV SGWRLFKKIS 170

SEQ ID NO: 704      moltype = AA length = 170
FEATURE          Location/Qualifiers
REGION           1..170
note = synthetic
source            1..170
mol_type = protein
organism = synthetic construct

SEQUENCE: 704
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKII DERLITPDGS MLFRVTINSV TGYRLFEEIL 170

SEQ ID NO: 705      moltype = AA length = 102
FEATURE          Location/Qualifiers
REGION           1..102
note = synthetic
source            1..102
mol_type = protein
organism = synthetic construct

SEQUENCE: 705
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV ID 102

SEQ ID NO: 706      moltype = AA length = 124
FEATURE          Location/Qualifiers
REGION           1..124
note = synthetic
source            1..124
mol_type = protein
organism = synthetic construct

SEQUENCE: 706
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDG 124

SEQ ID NO: 707      moltype = AA length = 133
FEATURE          Location/Qualifiers
REGION           1..133
note = synthetic
source            1..133
mol_type = protein
organism = synthetic construct

SEQUENCE: 707
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTL 133

SEQ ID NO: 708      moltype = AA length = 148
FEATURE          Location/Qualifiers
REGION           1..148
note = synthetic
source            1..148
mol_type = protein
organism = synthetic construct

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SEQUENCE: 708
MVFTLDDFVG DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIMRIVRSG ENALKIDIHV 60
IIPYEGLSAD QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNKLN YFGRPYEGIA 120
VFDGKKITTT GTLWNGNKKII DERLITPD 148

SEQ ID NO: 709      moltype = AA length = 68
FEATURE          Location/Qualifiers
REGION           1..68
note = synthetic
source            1..68
mol_type = protein
organism = synthetic construct

SEQUENCE: 709
GVTPNKLNYF GRPYEGIAVF DGKKITTGT LWNGNKKIDE RLITPDGSML FRVTINSVSG 60
WRLFKKIS                                68

SEQ ID NO: 710      moltype = AA length = 46
FEATURE          Location/Qualifiers
REGION           1..46
note = synthetic
source            1..46
mol_type = protein
organism = synthetic construct

SEQUENCE: 710
KKITTTGTLW NGNKKIDERL ITPDGSMFLR VTINSVSGWR LFKKIS                46

SEQ ID NO: 711      moltype = AA length = 37
FEATURE          Location/Qualifiers
REGION           1..37
note = synthetic
source            1..37
mol_type = protein
organism = synthetic construct

SEQUENCE: 711
WNGNKKIDERL LITPDGSMLF RVTINSVSGW RLFKKIS                         37

SEQ ID NO: 712      moltype = AA length = 22
FEATURE          Location/Qualifiers
REGION           1..22
note = synthetic
source            1..22
mol_type = protein
organism = synthetic construct

SEQUENCE: 712
GSMLFRVTIN SVSGWRLFKK IS                                         22

SEQ ID NO: 713      moltype = AA length = 68
FEATURE          Location/Qualifiers
REGION           1..68
note = synthetic
source            1..68
mol_type = protein
organism = synthetic construct

SEQUENCE: 713
GVTPNKLNYF GRPYEGIAVF DGKKITTGT LWNGNKKIDE RLITPDGSML FRVTINSVTG 60
YRLFEEIL                                68

SEQ ID NO: 714      moltype = AA length = 46
FEATURE          Location/Qualifiers
REGION           1..46
note = synthetic
source            1..46
mol_type = protein
organism = synthetic construct

SEQUENCE: 714
KKITTTGTLW NGNKKIDERL ITPDGSMFLR VTINSVTGYR LFEEIL                 46

SEQ ID NO: 715      moltype = AA length = 37
FEATURE          Location/Qualifiers
REGION           1..37
note = synthetic
source            1..37
mol_type = protein
organism = synthetic construct

SEQUENCE: 715
WNGNKKIDERL LITPDGSMLF RVTINSVTGY RLFEEL                           37

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SEQ ID NO: 716      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
source            note = synthetic
                 1..22
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 716
GSMLMFRVTIN SVTGYRLFEE IL                                22

SEQ ID NO: 717      moltype = AA  length = 22
FEATURE          Location/Qualifiers
REGION           1..22
source            note = synthetic
                 1..22
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 717
GVTPNKLNYF GRPYEGIAVF DG                                22

SEQ ID NO: 718      moltype = AA  length = 9
FEATURE          Location/Qualifiers
REGION           1..9
source            note = synthetic
                 1..9
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 718
KIKTTTGTL                                9

SEQ ID NO: 719      moltype = AA  length = 15
FEATURE          Location/Qualifiers
REGION          1..15
source            note = synthetic
                 1..15
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 719
WNGNKIIDER LITPD                                15

SEQ ID NO: 720      moltype = AA  length = 297
FEATURE          Location/Qualifiers
REGION          1..297
source            note = synthetic
                 1..297
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 720
MAEIGTGFPF DPHYVEVLGE RMHYVVDGPR DGTPVLFLHG NPTSSYVWRN IIPHVAPTHR 60
CIAPDLIGMG KSDKPDLGYF FDDHVRFMDA FIBALGLEEV VLVIHDWGSQ LGFHWAKRNP 120
ERVKGKIAFME FIRPIPTWDE WPEFARETFO AFRTTDVGKR LIIDQNVFIE GTLPMGVVRP 180
LTEVEMDHYR EPFLNPVDRE PLWRFPNELP IAGEPANIVA LVEEYMDWLH QSPVPKLLFW 240
GTPGVLIIPPA EAARLAKSLP NCKAVDIGPG LNLLQEDNPD LIGSEIARWL STLEISG 297

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What is claimed is:

**1-68.** (canceled)

**69.** A lateral flow detection system comprising:  
an analytical membrane comprising at least one detection region and a control region, wherein the at least one detection region comprises a first target analyte binding agent immobilized to the detection region;  
a conjugate pad comprising a second target analyte binding agent; and  
a sample pad;  
wherein a liquid sample added to the sample pad will flow from the sample pad through the conjugate pad to the at least one detection region and the control region on the analytical membrane;  
wherein the first target analyte binding agent and the second target analyte binding agent form a bioluminescent analyte detection complex in the at least one detection region when a target analyte is detected in a sample  
wherein the bioluminescent analyte detection complex is capable of emitting a bioluminescent signal in the presence of a luminogenic substrate.

**70.** The system of claim **69**, wherein the first target analyte binding agent comprises a first target analyte binding element and is non-luminescent, and wherein the second target analyte binding agent comprises a second target analyte binding element and a bioluminescent polypeptide.

**71.** The system of claim **70**, wherein the bioluminescent polypeptide has at least 60% sequence identity with SEQ ID NO: 5.

**72.** The system of claim **69**, wherein the first target analyte binding agent comprises a target first analyte binding element and a polypeptide component of a bioluminescent complex, and the second target analyte binding agent comprises a second target analyte binding element and a peptide component of a bioluminescent complex, wherein the bioluminescent signal produced in the presence of the luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent, as compared to a bioluminescent signal produced by the first target analyte binding agent and the luminogenic substrate alone.

**73.** The system of claim **69**, wherein the first target analyte binding agent comprises a first target analyte binding element and a peptide component of a bioluminescent complex, and the second target analyte binding agent comprises a second target analyte binding element and a polypeptide component of a bioluminescent complex, wherein a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent, as compared to a bioluminescent signal produced by the first target analyte binding agent and the luminogenic substrate alone.

**74.** The system of claim **72**, wherein the polypeptide component of a bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 6, and wherein the peptide component of a bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 10.

**75.** The system of claim **72**, wherein the polypeptide component of a bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 12, and wherein the peptide component of a bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 14.

**76.** The system of claim **69**, wherein the conjugate pad further comprises a polypeptide component of a tripartite bioluminescent complex, wherein the first target analyte binding agent comprises a first target analyte binding element and a first peptide component of the tripartite bioluminescent complex, and the second target analyte binding agent comprises a second target analyte binding element and a second peptide component of the tripartite bioluminescent complex, wherein a bioluminescent signal produced in the presence of a luminogenic substrate is substantially increased when the first target analyte binding agent contacts the second target analyte binding agent and the polypeptide component of the tripartite bioluminescent complex, as compared to a bioluminescent signal produced by (i) the first target analyte binding agent, the second target analyte binding agent, and/or the polypeptide component and (ii) the luminogenic substrate alone.

**77.** The system of claim **76**, wherein the first peptide component of the tripartite bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 11, wherein the first peptide component of the tripartite bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 13, and wherein the polypeptide component of the tripartite bioluminescent complex has at least 60% sequence identity with SEQ ID NO: 12.

**78.** The system of claim **69**, wherein the target analyte is a target antibody.

**79.** The system of claim **78**, wherein the first target analyte binding agent comprises an element that binds non-specifically to antibodies.

**80.** The system of claim **79**, wherein the second target analyte binding agent comprises an element that binds specifically to the target antibody.

**81.** The system of claim **78**, wherein the target antibody is an antibody against a pathogen, toxin, or therapeutic biologic.

**82.** The system of claim **69**, wherein a target analyte binding element is selected from the group consisting of an antibody, a polyclonal antibody, a monoclonal antibody, a recombinant antibody, an antibody fragment, protein A, an Ig binding domain of protein A, protein G, an Ig binding domain of protein G, protein A/G, an Ig binding domain of protein A/G, protein L, a Ig binding domain of protein L, protein M, an Ig binding domain of protein M, an oligonucleotide probe, a peptide nucleic acid, a DARPin, an aptamer, an affimer, a protein domain, and a purified protein.

**83.** The system of claim **69**, further comprising a luminogenic substrate.

**84.** The system of claim **83**, wherein the luminogenic substrate is selected from coelenterazine, coelenterazine-h, coelenterazine-h-h, furimazine, and other coelenterazine analogs or derivatives.

**85.** The system of claim **84**, wherein the luminogenic substrate is applied to the system as part of a composition comprising the luminogenic substrate and a polymer selected from pullulan, trehalose, maltose, cellulose, dextran, polystyrene, poly(meth)acrylate, and a combination of any thereof.

**86.** The system of claim **85**, wherein the composition is applied to at least one of the sample pad, the conjugation pad, the at least one detection region, and the control region.

**87.** The system of claim **69**, wherein the analytical membrane comprises a plurality of detection regions with each

detection region comprising a distinct target analyte binding agent comprising distinct target analyte binding elements.

**88.** The system of claim **69**, wherein the system further comprises a device for detecting or quantifying bioluminescent signals from the analyte detection complex.

**89-133.** (canceled)

**134.** A method of detecting an analyte in a sample using the lateral flow assay system of claim **69**, the method comprising:

applying a sample to the sample pad;

facilitating flow of the sample from the sample pad to the conjugate pad, and then from the conjugate pad to the detection region and the control region on the analytical membrane;

wherein the first target analyte binding agent, the second target analyte binding agent, and the target analyte form the analyte detection complex in the at least one detection region.

**135.** The method of claim **134**, wherein the sample is selected from blood, serum, plasma, urine, stool, cerebral spinal fluid, interstitial fluid, tissue, and saliva.

**136.** The method of claim **134**, wherein the sample is selected from a water sample, a soil sample, a plant sample, a food sample, a beverage sample, an oil, and an industrial fluid sample.

**137.** The method of claim **134**, wherein detecting the target analyte in the sample comprises detecting a bioluminescent signal generated from the analyte detection complex.

**138.** The method of claim **134**, wherein the method further comprises quantifying a bioluminescent signal generated from the analyte detection complex.

**139.** The method of claim **134**, wherein the method further comprises diagnosing a subject from which the sample was obtained as having or not having a disease based on the detection of the analyte.

**140-177.** (canceled)

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