(54) Title: HIGH-THROUGHPUT AND HIGHLY MULTIPLEXED IMAGING WITH PROGRAMMABLE NUCLEIC ACID
PROBES

(57) Abstract: The present invention
provides, inter alia, methods and composi-
tions for imaging, at high spatial resolu-
tion, targets of interest.

FIG. 1
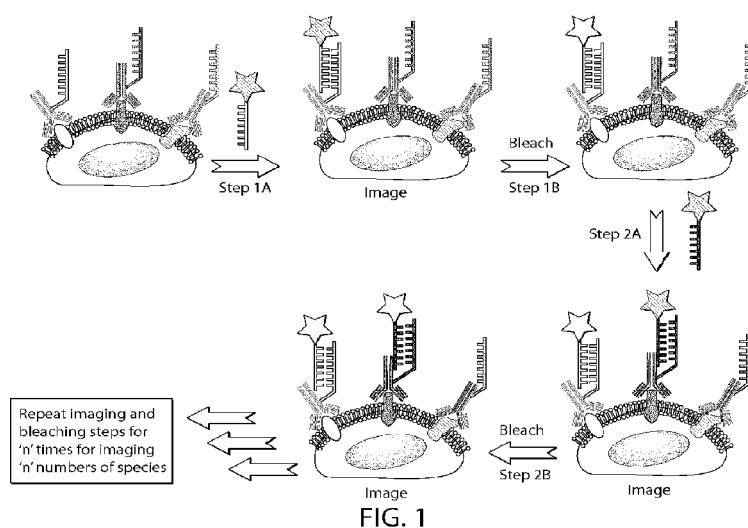
— *with sequence listing part of description (Rule 5.2(a))*

HIGH-THROUGHPUT AND HIGHLY MULTIPLEXED IMAGING WITH PROGRAMMABLE NUCLEIC ACID PROBES

RELATED APPLICATIONS

5   This application claims the benefit of U.S. Provisional Application No. 61/951,461 filed on March 11, 2014, the entire contents of which are incorporated by reference herein.

FIELD OF THE INVENTION

The invention relates generally to the field of detection and quantification of analytes

10   (*e.g.*, targets).

BACKGROUND OF THE INVENTION

Fluorescence microscopy is a powerful tool for exploring molecules in, for example, a biological system. However, the number of distinct species that can be distinguishably and

15   simultaneously visualized (*i.e.* the multiplexing power) is limited by the spectral overlap between the fluorophores.

SUMMARY OF THE INVENTION

The present invention provides, *inter alia*, methods and compositions for detecting,

20   imaging and/or quantitating targets (*e.g.*, biomolecules) of interest. Some of the methods provided herein involve (1) contacting a sample to be analyzed (*e.g.*, a sample suspected of containing one or more targets of interest) with moieties that bind specifically to the targets (each moiety being a binding partner of a given target), wherein each moiety is conjugated to a nucleic acid (referred to herein as a docking strand) and wherein binding partners of

25   different specificity are conjugated to different docking strands, (2) optionally removing unbound binding partners, (3) contacting the sample with labeled (*e.g.*, fluorescently labeled) nucleic acids having a nucleotide sequence that is complementary to and thus specific for one docking strand (such labeled nucleic acids referred to herein as labeled imager strands), (4) optionally removing unbound imager strands, (5) imaging the sample in whole or in part to

30   detect the location and number of bound imager strands, (6) extinguishing signal from the labeled imager strand from the sample (*e.g.*, by bleaching, including photobleaching), and (7) repeating steps (3)-(6) each time with an imager strand having a unique nucleotide sequence relative to all other imager strands used in the method.

Imager strands may be identically labeled, including identically fluorescently labeled. In other embodiments, imager strands having an identical sequence may be identically labeled. The first approach may be more convenient as it requires a single excitation wavelength and detector.

5   In this manner, it is possible to detect, image and/or quantitate two or more targets in a sample, regardless of their location in the sample, including regardless of whether their location in the sample is so close together to be indistinguishable if signal from the two or more targets was observed simultaneously. Thus, the distance between two or more targets may be below the resolution distance of the imaging system used to detect the targets, and

10   still using the methods provided herein it would be possible to distinguish the two or more targets from each other, thereby facilitating a more accurate and robust detection and quantitation of such targets. In some instances, the resolution distance may be about 50 nm, as an example.

It is to be understood that the "target content" of a sample may be known or

15   suspected, or unknown and unsuspected, prior to performing the method. The binding partners contacting the sample may bind to the sample, or they may not, depending on whether the target is present or absent (e.g., when the target is present, the binding partner may bind to the sample). The imager strands contacting the sample may bind to the sample, or they may not, depending on whether the target is present or absent (e.g., when the target is

20   present, the imager strand may bind a corresponding docking strand bound to the target). "Binding to the sample" means that the binding partner or the imager strand is bound to its respective target or docking strand.

The binding partners may be protein in nature, such as antibodies or antibody fragments. In the context of a binding partner that is an antibody or antibody fragment, the

25   docking strands may be conjugated thereto at a constant region. The binding partner may be an antibody such as a monoclonal antibody, or it may be an antigen-binding antibody fragment such as an antigen-binding fragment from a monoclonal antibody. In some embodiments, the binding partner is a receptor.

The binding partner may be linked to the docking strand through an intermediate

30   linker. In some embodiments, an intermediate linker comprises biotin and/or streptavidin.

The imager strands may be fluorescently labeled (i.e., they are conjugated to a fluorophore). Fluorophores conjugated to imager strands of different nucleotide sequence may be identical to each other, or they may have an emission profile that overlaps or that

doesn't overlap with that of other fluorophores. The fluorescently labeled imager strand may comprise at least one fluorophore.

In some instances, fluorescently labeled imager nucleic acids such as imager strands may comprise 1, 2, 3, or more fluorophores.

The sample may be a cell, a population of cells, or a cell lysate from a cell or a population of cells. The target may be a protein.

It will therefore be appreciated that the invention provides a method for detecting analytes by binding analytes to their respective binding partners and sequentially determining the presence of such binding partners, by repeatedly binding, detecting and extinguishing (e.g., bleaching, such as photobleaching) imager strands, that optionally are identically labeled (e.g., identically fluorescently labeled).

Accordingly, the disclosure provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each target-specific binding partner is linked to a docking strand, and wherein target-specific binding partners of different specificity are linked to different docking strands, (2) optionally removing unbound target-specific binding partners, (3) contacting the sample with labeled imager strands having a nucleotide sequence that is complementary to a docking strand, (4) optionally removing unbound labeled imager strands, (5) imaging the sample to detect location and number of bound labeled imager strands, (6) extinguishing signal from the bound labeled imager strand, and (7) repeating steps (3)-(6), each time with a labeled imager strand having a unique nucleotide sequence relative to all other labeled imager strands.

In some embodiments, the sample is contacted with more than one target-specific binding partner in step (1).

In some embodiments, the target-specific binding partner is an antibody or an antibody fragment.

In some embodiments, the labeled imager strands are labeled identically. In some embodiments, the labeled imager strands each comprise a distinct label. In some embodiments, the labeled imager strands are fluorescently labeled imager strands.

In some embodiments, the one or more targets are proteins. In some embodiments, the sample is a cell, a cell lysate or a tissue lysate.

In some embodiments, the sample is imaged in step (5) using confocal or epi-fluorescence microscopy.

In some embodiments, extinguishing signal in step (6) comprises photobleaching.

The disclosure further provides a composition comprising a sample bound to more than one target-recognition moieties such as target-specific binding partners, each target-recognition moiety bound to a docking nucleic acid such as a docking strand, and at least one docking nucleic acid stably bound to a labeled imager nucleic acid such as an imager strand.

5   The disclosure further provides a composition comprising a sample bound to more than one target-specific binding partners, each binding partner bound to a docking strand, and at least one docking strand stably bound to a labeled imager strand.

The disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-recognition moieties

10   such as target-specific binding partners, wherein each target-recognition moiety is linked to a docking nucleic acid such as a docking strand, and wherein target-recognition moieties of different specificity are linked to different docking nucleic acids, (2) optionally removing unbound target-recognition moieties, (3) contacting the sample with labeled imager nucleic acids such as imager strands having a nucleotide sequence that is complementary to a

15   docking nucleic acid, (4) optionally removing unbound labeled imager nucleic acids, (5) imaging the sample to detect location and number of bound labeled imager nucleic acids, (6) removing the bound labeled imager nucleic acids from the docking nucleic acids by altering temperature and/or buffer condition, and (7) repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager

20   nucleic acids. The imager nucleic acid dissociates from the docking nucleic acid spontaneously under such conditions.

The disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each target-specific binding partner is linked to a docking nucleic acid, and

25   wherein target-specific binding partners of different specificity are linked to different docking nucleic acids, (2) optionally removing unbound target-specific binding partners, (3) contacting the sample with labeled imager nucleic acids having a nucleotide sequence that is complementary to a docking nucleic acid, (4) optionally removing unbound labeled imager nucleic acids, (5) imaging the sample to detect location and number of bound labeled imager

30   nucleic acids, (6) removing the bound labeled imager nucleic acids from the docking nucleic acids by altering temperature and/or buffer condition, and (7) repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids. The imager nucleic acid dissociates from the docking nucleic acid spontaneously under such conditions.

In some embodiments, the labeled imager nucleic acids are removed from the docking nucleic acids by decreasing salt concentration, addition of a denaturant, or increasing temperature. In some embodiments, the salt is Mg++. In some embodiments, the denaturant is formamide, urea or DMSO.

5   The disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-recognition moieties such as target-specific binding partners, wherein each target-recognition moiety is linked to a docking nucleic acid such as a docking strand, and wherein target-recognition moieties of different specificity are linked to different docking nucleic acids, (2) optionally removing

10   unbound target-recognition moieties, (3) contacting the sample with labeled imager nucleic acids such as imager strands having a nucleotide sequence that is complementary to a docking nucleic acid, (4) optionally removing unbound labeled imager nucleic acids, (5) imaging the sample to detect location and number of bound labeled imager nucleic acids, (6) removing the bound labeled imager nucleic acids from the docking nucleic acids, and (7)

15   repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

        The disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each target-specific binding partner is linked to a docking nucleic acid, and

20   wherein target-specific binding partners of different specificity are linked to different docking nucleic acids, (2) optionally removing unbound target-specific binding partners, (3) contacting the sample with labeled imager nucleic acids having a nucleotide sequence that is complementary to a docking nucleic acid, (4) optionally removing unbound labeled imager nucleic acids, (5) imaging the sample to detect location and number of bound labeled imager

25   nucleic acids, (6) removing the bound labeled imager nucleic acids from the docking nucleic acids, and (7) repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

        In some embodiments, in step (6) the labeled imager nucleic acids are not removed from the docking nucleic acids by strand displacement in the presence of a competing nucleic

30   acid.

        In some embodiments, in step (6) the labeled imager nucleic acids are removed from the docking nucleic acids by chemically, photochemically, or enzymatically cleaving, modifying or degrading the labeled imager nucleic acids.

In some embodiments, when the labeled imager nucleic acid is bound to its respective docking nucleic acid, there is no single-stranded region on the imager nucleic acid or the docking nucleic acid. In some embodiments, the docking nucleic acid does not have a toehold sequence. In some embodiments, the imager nucleic acid does not have a toehold sequence.

In some embodiments, the labeled imager nucleic acid is not self-quenching.

The disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-recognition moieties such as target-specific binding partners, wherein each target-recognition moiety is linked to a docking nucleic acid such as a docking strand, and wherein target-recognition moieties of different specificity are linked to different docking nucleic acids, (2) optionally removing unbound target-recognition moieties, (3) contacting the sample with labeled imager nucleic acids such as imager strands having a nucleotide sequence that is complementary to a docking nucleic acid, (4) optionally removing unbound labeled imager nucleic acids, (5) imaging the sample to detect location and number of bound labeled imager nucleic acids, (6) inactivating the bound labeled imager nucleic acids, by removing or modifying their signal-emitting moieties without removing the imager nucleic acid in its entirety, and (7) repeating steps (3)-(6), each time with a labeled imager nucleic acids having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

The disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each target-specific binding partner is linked to a docking nucleic acid, and wherein target-specific binding partners of different specificity are linked to different docking nucleic acids, (2) optionally removing unbound target-specific binding partners, (3) contacting the sample with labeled imager nucleic acids having a nucleotide sequence that is complementary to a docking nucleic acid, (4) optionally removing unbound labeled imager nucleic acids, (5) imaging the sample to detect location and number of bound labeled imager nucleic acids, (6) inactivating the bound labeled imager nucleic acids, by removing or modifying their signal-emitting moieties without removing the imager nucleic acid in its entirety, and (7) repeating steps (3)-(6), each time with a labeled imager nucleic acids having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

Various embodiments apply equally to the afore-mentioned methods. These embodiments are as follows:

In some embodiments, the sample is contacted with more than one target-specific binding partner in step (1). In some embodiments, the target-specific binding partner is an antibody or an antibody fragment. In some embodiments, the target-specific binding partner is a natural or engineered ligand, a small molecule, an aptamer, a peptide or an oligonucleotide.

In some embodiments, the labeled imager nucleic acids are labeled identically. In some embodiments, the labeled imager nucleic acids each comprise a distinct label. In some embodiments, the labeled imager nucleic acids are fluorescently labeled imager nucleic acids.

In some embodiments, the one or more targets are proteins. In some embodiments, the sample is a cell, a cell lysate or a tissue lysate.

In some embodiments, the sample is imaged in step (5) using confocal or epi-fluorescence microscopy.

In some embodiments, the unbound docking nucleic acid is partially double-stranded. In some embodiments, the unbound imager nucleic acid is partially double-stranded.

In some embodiments, the imager nucleic acid is a molecular beacon or comprises a hairpin secondary structure. In some embodiments, the imager nucleic acid is a molecular beacon or comprises a hairpin secondary structure that is self-quenching. In some embodiments, the imager nucleic acid is a hemiduplex. In some embodiments, the hemiduplex is self-quenching. In some embodiments, the imager nucleic acid is bound to multiple signal-emitting moieties through a dendrimeric structure or a polymeric structure. The imager nucleic acid may be linear or branched.

In some embodiments, the docking nucleic acid comprises a hairpin secondary structure.

These and other embodiments will be described in greater detail herein.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a schematic of one embodiment of a high-throughput and intrinsically scalable multiplexed imaging approach provided in this disclosure. Cells are imaged after probe hybridization and then photobleached before a subsequent round of imaging.

FIG. 2 is a schematic of one embodiment of a high-throughput and intrinsically scalable multiplexed imaging approach based on buffer exchange using solutions with slight denaturation characteristics, such as decreased salt concentration, increased formamide concentration, or higher temperature.

FIG. 3 is a schematic of one embodiment of inactivation of the imager strand by removing the imager strand using the methods provided in this disclosure.

FIG. 4 is a schematic of one embodiment of inactivation of the imager strand by inactivating the fluorophore without removing the nucleic acid portion of the imager strand.

FIG. 5 is a schematic of one embodiment of a molecular beacon-like self-quenching imager strand.

FIG. 6 is a schematic of one embodiment of a hemi-duplex self-quenching imager strand.

FIG. 7 is a schematic of one embodiment of a non-single-stranded docking strand.

FIG. 8 is a schematic of one embodiment of an imager strand that recruits multiple copies of the signal-emitting moieties to the docking strand.

FIG. 9 is a schematic of one embodiment of a non-single-stranded imager strand.

FIG. 10 is a graph showing the predicted dissociation constants of 10 different oligonucleotides with the respective reverse-complementary strands at 3 different conditions. Sequence a1: 5'-CATCTAAAGCC-3' (SEQ ID NO: 1); Sequence a2: 5'-GAATTTCCTCG-3' (SEQ ID NO: 2); Sequence a3: 5'-GTTTAATTGCG-3' (SEQ ID NO: 3); Sequence a4: 5'-ACAATTCTTCG-3' (SEQ ID NO: 4); Sequence a5: 5'-TTTCTTGCTTC-3' (SEQ ID NO: 5); Sequence a6: 5'-GCATTGTTACT-3' (SEQ ID NO: 6); Sequence a7: 5'-ATATACAAGCG-3' (SEQ ID NO: 7); Sequence a8: 5'-GCTGTCTATTG-3' (SEQ ID NO: 8); Sequence a9: 5'-TCTTTATGCTG-3' (SEQ ID NO: 9); Sequence a10: 5'-CAATCTCATCC-3' (SEQ ID NO: 10).

DESCRIPTION OF THE INVENTION

The invention provides, *inter alia*, compositions and methods for multiplexed fluorescence imaging, for example, in a cellular environment using nucleic acid-based imaging probes (*e.g.*, DNA-based imaging probes). Methods provided herein are based, in part, on the programmability of nucleic acid docking strands and imager strands. That is, for example, docking strands and imager strands can be designed such that they bind to each other under certain conditions for a certain period of time. This programmability permits stable binding of imager strands to docking strands, as provided herein. Generally, the methods provided herein are directed to identifying one or more target(s) (*e.g.*, biomolecule(s) such as a protein or nucleic acid) in a particular sample (*e.g.*, biological sample). In some instances, whether or not one or more target(s) is present in sample is unknown. Thus, methods of the present disclosure may be used to determine the presence or

absence of one or more target(s) in a sample suspected of containing the target(s). In any one of the aspects and embodiments provided herein, a sample may contain or may be suspected of containing one or more target(s).

Thus, the invention provides methods for performing high-throughput and highly multiplexed imaging and analyte/target detection based on programmable nucleic acid (*e.g.*, DNA) probes. These methods rely on a sequential imaging approach employing orthogonal imager strands that can stably attach to a complementary docking strand immobilized on binding partners, such as antibodies (FIG. 1). After hybridization and imaging with an imager strand, an extinguishing step (such as a photobleaching step) is performed to eliminate and/or reduce fluorescence from the hybridized (bound) imager strands.

In another embodiment, the methods utilize weaker binding between docking and imaging strands in order to remove signal. For example, the hybridization conditions may be changed such that the melting point of the duplex that is formed between the docking or imager strands is slightly above room temperature (*e.g.*, 25 °C) or the imaging temperature. The labeling step (i.e., the step at which the imager strands are bound to their respective docking strands) and the imaging step are performed as described above. As an example, after the first target is imaged, the sample is subjected to a denaturing condition. The denaturing condition may be provided in a buffer exchange step using a solution with for example lower salt concentration, presence of or increase in the concentration of a denaturant such as formamide, or increased temperature (FIG. 2). The sample may be alternatively or additionally exposed to an increased temperature. The aforementioned increases or decreases are relative to the conditions existing at the labeling step (i.e., when the imager strand is bound to the docking strand). In the case of the buffer exchange, the sample may be washed, the buffer exchange may be repeated, the sample may be washed again, and then the next imager strand may be added to the sample.

For multiplexing, different reservoirs of orthogonal imager strands are sequentially applied after every step of, for example, photobleaching or other method for extinguishing signal or imager strand inactivation or removal to the same sample in order to potentially image an infinite number of targets. Unlike traditional imaging approaches, where multiplexing is limited by spectral overlap between color channels, the methods provided herein are only limited by the number of possible orthogonal nucleotide sequences (of the docking strands or alternatively the imager strands). As a larger number of orthogonal nucleotide sequences can be readily designed, this approach has intrinsically scalable multiplexing capability just by using a single fluorophore. This method can be readily

integrated with standard microscopy setups (*e.g.*, confocal or epi-fluorescence microscopes), allowing high throughput analysis of the sample.

The methods have applicability in, for example, high-throughput screening assays such as drug screening assays. This imaging approach allows analysis of large populations of cells (~ 1,000-10,000) or tissue samples in an ultra-multiplexed format while imaging using standard confocal or epi-fluorescence microscope. Screening large numbers of targets such as proteins from the same sample in a high-throughput manner will provide information about new drugs or modifiers while providing cellular heterogeneity information. The large scale screening of tissue samples with high-throughput and ultra-multiplexed imaging capabilities will be useful in pathology analysis, for example, in a hospital or other service provider setting.

Methods provided herein can also be used to identify the absolute quantity of a single target (*e.g.*, such as, for example, a particular protein), or the quantity of a single target relative to one or more other targets.

Further, methods provided herein may be used to identify the location of a target within a sample or relative to other targets in the sample.

This disclosure therefore provides a method comprising (1) contacting a sample simultaneously with a plurality of sequence-labeled target-recognition moieties, (2) introducing imager nucleic acids such as imager strands recognizing, through sequence complementarity, a subset of docking nucleic acids such as docking strands in the sequence-labeled target-recognition moieties, (3) removing or inactivating the imager nucleic acids or extinguishing signal from the imager nucleic acids, and (4) repeating step (2) and optionally step (3) at least once in order to image and detect one or more additional docking nucleic acids.

The method may optionally comprise labeling a plurality of target-recognition moieties with docking nucleic acids such as docking strands to form sequence-labeled target-recognition moieties.

This disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each target-specific binding partner is linked to a docking strand, and wherein target-specific binding partners of different specificity are linked to different docking strands, (2) optionally removing unbound target-specific binding partners, (3) contacting the sample with labeled imager strands having a nucleotide sequence that is complementary to a docking strand, (4) optionally removing unbound labeled imager strands, (5) imaging the

sample to detect location and number of bound labeled imager strands, (6) extinguishing signal from the bound labeled imager strand, and (7) repeating steps (3)-(6), each time with a labeled imager strand having a unique nucleotide sequence relative to all other labeled imager strands.

5   Steps (3)–(6) may be repeated once or multiple times. For example, steps (3)-(6) may be repeated 1-10 times or more. In some embodiments, steps (3)-(6) are repeated 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 times.

This disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-recognition moieties
10   such as target-specific binding partners, wherein each target-recognition moiety is linked to a docking nucleic acid, and wherein target-recognition moieties of different specificity are linked to different docking nucleic acids, (2) optionally removing unbound target-recognition moieties, (3) contacting the sample with labeled imager nucleic acids such as imager strands having a nucleotide sequence that is complementary to a docking nucleic acid, (4) optionally
15   removing unbound labeled imager nucleic acids, (5) imaging the sample to detect location and number of bound labeled imager nucleic acids, (6) removing the bound labeled imager nucleic acids from the docking nucleic acids, and (7) repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

20   Steps (3)–(6) may be repeated once or multiple times. For example, steps (3)-(6) may be repeated 1-10 times or more. In some embodiments, steps (3)-(6) are repeated 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 times.

This disclosure further provides a method comprising (1) contacting a sample being tested for the presence of one or more targets with one or more target-recognition moieties
25   such as target-specific binding partners, wherein each target-recognition moieties is linked to a docking nucleic acid such as a docking strand, and wherein target-recognition moieties of different specificity are linked to different docking nucleic acids, (2) optionally removing unbound target-recognition moieties, (3) contacting the sample with labeled imager nucleic acids such as imager strands having a nucleotide sequence that is complementary to a
30   docking nucleic acid, (4) optionally removing unbound labeled imager nucleic acids, (5) imaging the sample to detect location and number of bound labeled imager nucleic acids, (6) inactivating the bound labeled imager nucleic acids, by removing or modifying their signal-emitting moieties without removing the imager nucleic acid in its entirety, and (7) repeating

steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

Steps (3)–(6) may be repeated once or multiple times. For example, steps (3)-(6) may be repeated 1-10 times or more. In some embodiments, steps (3)-(6) are repeated 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 times.

In some embodiments, the methods provided herein include a step of removing an imager nucleic acid such as an imager strand that is bound to a docking nucleic acids such as a docking strand, using a method other than strand displacement.

In some embodiments, the methods provided herein include a step of removing an imager nucleic acid such as an imager strand that is bound to a docking nucleic acid such as a docking strand, wherein the imager nucleic acid emits signal (i.e., such signal is not quenched) prior to binding to the docking nucleic acid.

In some embodiments, the methods provided herein include a step of removing an imager nucleic acid such as an imager strand that is bound to a docking nucleic acid such as a docking strand, wherein the imager nucleic acid is removed using a nucleic acid that does not comprise a quencher.

In each of the foregoing methods, the docking nucleic acid including the docking strand may be a single-stranded docking nucleic acid or docking strand, or it may be a double-stranded docking nucleic acid or docking strand, or it may be a partially double-stranded docking nucleic acid or docking strand (e.g., containing a single-stranded and a double-stranded region).

In some embodiments, where a plurality of target-recognition moieties, including a plurality of binding partners, are used, the plurality may be contacted with the sample, and thus with targets of interest, simultaneously. The target-recognition moieties such as the binding partners need not be contacted with the sample sequentially, although they can be.

These various methods facilitate high throughput imaging with spinning disk confocal microscopy. It is estimated that a one color whole cell 3D imaging process would take on average about 30 seconds. The method allows for imaging of large areas (e.g., up to mm scale) with compatible 10X or 20X objective. An imaging depth of about 30-50 microns may be achieved. The methods provided herein have been used to stain actin, Ki-67, clathrin, cytokeratin, among others (data not shown).

Binding partners

The methods employ binding partners conjugated to nucleic acids (e.g., docking nucleic acids such as docking strands). These may be referred to herein as binding partner-nucleic acid conjugates ("BP-NA conjugates"). They may also be referred to as sequence-labeled target-recognition moieties. As used herein, "binding partner-nucleic acid conjugate," or "BP-NA conjugate," refers to a molecule linked (e.g., through an N-Hydroxysuccinimide (NHS) linker) to a single-stranded nucleic acid (e.g., DNA) docking strand.

The binding partner of the conjugate may be any moiety (e.g., antibody or aptamer) that has an affinity for (e.g., binds to) a target, such as a biomolecule (e.g., protein or nucleic acid), of interest. In some embodiments, the binding partner is a protein. BP-NA-conjugates that comprise a protein (or peptide) linked to a docking strand may be referred to herein as "protein-nucleic acid conjugates," or "protein-NA conjugates." Examples of proteins for use in the conjugates of the invention include, without limitation, antibodies (e.g., monoclonal antibodies), antigen-binding antibody fragments (e.g., Fab fragments), receptors, peptides and peptide aptamers. Other binding partners may be used in accordance with the invention. For example, binding partners that bind to targets through electrostatic (e.g., electrostatic particles), hydrophobic or magnetic (e.g., magnetic particles) interactions are contemplated herein.

As used herein, "antibody" includes full-length antibodies and any antigen binding fragment (e.g., "antigen-binding portion") or single chain thereof. The term "antibody" includes, without limitation, a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, or an antigen binding portion thereof. Antibodies may be polyclonal or monoclonal; xenogeneic, allogeneic, or syngeneic; or modified forms thereof (e.g., humanized, chimeric).

As used herein, "antigen-binding portion" of an antibody, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen. The antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Examples of binding fragments encompassed within the term "antigen-binding portion" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the V_H, V_L, C_L and C_{H1} domains; (ii) a F(ab')2 fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and C_{H1} domains; (iv) a Fv fragment consisting of the V_H and V_L domains of a single arm of an antibody, (v) a dAb fragment (Ward *et al.*, *Nature* 341:544 546, 1989), which

consists of a V_H domain; and (vi) an isolated complementarity determining region (CDR) or
(vii) a combination of two or more isolated CDRs, which may optionally be joined by a
synthetic linker. Furthermore, although the two domains of the Fv fragment, V_H and V_L, are
coded for by separate genes, they can be joined, using recombinant methods, by a synthetic

5   linker that enables them to be made as a single protein chain in which the V_H and V_L regions
pair to form monovalent molecules (known as single chain Fv (scFv); *see, e.g.*, Bird *et al.*
Science 242:423 426, 1988; and Huston *et al. Proc. Natl. Acad. Sci. USA* 85:5879-5883,
1988). Such single chain antibodies are also encompassed within the term "antigen-binding
portion" of an antibody. These antibody fragments are obtained using conventional

10   techniques known to those with skill in the art, and the fragments are screened for utility in
the same manner as are intact antibodies.

       As used herein, "receptors" refer to cellular-derived molecules (*e.g.*, proteins) that
bind to ligands such as, for example, peptides or small molecules (*e.g.*, low molecular weight
(<900 Daltons) organic or inorganic compounds).

15   As used herein, "peptide aptamer" refers to a molecule with a variable peptide
sequence inserted into a constant scaffold protein (*see, e.g.*, Baines IC, *et al. Drug Discov.*
Today 11:334–341, 2006).

       In some embodiments, the molecule of the BP-NA conjugate is a nucleic acid such as,
for example, a nucleic acid aptamer. As used herein, "nucleic acid aptamer" refers to a small

20   RNA or DNA molecules that can form secondary and tertiary structures capable of
specifically binding proteins or other cellular targets (*see, e.g.*, Ni X, *et al. Curr Med Chem.*
18(27): 4206–4214, 2011). Thus, in some embodiments, the BP-NA conjugate may be an
aptamer-nucleic acid conjugate.

       Some embodiments of the invention use target-recognition moieties to identify and

25   label targets. Target-recognition moieties are agents that specifically recognize targets of
interest in the sample. Examples of target-recognition moieties include binding partners such
as those recited herein. Target-recognition moieties include antibodies, antibody fragments
and antibody derivatives such as single-chain antibodies, single-chain Fv domains, Fab
domains, nanobodies, and the like, peptides, aptamers, and oligonucleotides (*e.g.*, to detect

30   nucleic acids of interest in procedures such as fluorescence in situ hybridization, or FISH).

Docking nucleic acids such as docking strands

       Certain embodiments of the invention may refer to docking nucleic acids. Docking
nucleic acids include docking strands as described herein. Docking nucleic acids are linear

nucleic acids capable of binding to a nucleic acid having a complementary sequence (such as an imager nucleic acid). A docking nucleic acid may be comprised of or may consist of DNA, RNA, or nucleic acid-like structures with other phosphate-sugar backbones (*e.g.* 2'-O-methyl RNA, 2'-fluoral RNA, LNA, XNA) or backbones comprising non-phosphate-sugar

5   moieties (*e.g.*, peptide nucleic acid and morpholino). The nucleobases may include naturally occurring nucleobases such as adenine, thymine, guanine, cytosine, inosine, and their derivatives, as well as non-naturally occurring nucleobases such as isoC, isoG, dP and dZ. A docking nucleic acid, when not bound to its complementary imager nucleic acid, may be single-stranded without stable secondary structure. Alternatively, the docking nucleic acid

10   may comprise secondary structure such as a hairpin loop (FIG. 7, top). A docking nucleic acid may be part of a multi-strand complex (FIG. 7, bottom).

As used herein, a "docking strand" refers to a single-stranded nucleic acid (*e.g.*, DNA) capable of stably binding to its complementary imager strands. Stable binding may be a result of the length of the docking strand (and conversely the imager strand) or it may be the

15   result of the particular conditions under which hybridization occurs (*e.g.*, salt concentration, temperature, etc.). In some embodiments, a docking strand is about 20 to about 60, or more, nucleotides in length. A docking strand may be capable of binding to one or more identical imager strands (of identical sequence and identically labeled).

20   ***Imager nucleic acids such as imager strands***

Certain embodiments of the invention may refer to imager nucleic acids. Imager nucleic acids include imager strands as described herein. Imager nucleic acids are nucleic acids that can (1) interact with a docking nucleic acid via sequence-specific complementarity and (2) recruit a signal-emitting moiety or multiple copies of signal-emitting moieties by

25   covalent or non-covalent interactions. The imager nucleic acids may be linear or branched as described herein. One imager nucleic acid may recruit multiple copies of the signal-emitting moiety via a polymeric (FIG. 8, top) or dendrimeric structure (FIG. 8, bottom). For example, a polymeric or dendrimeric structure can be synthesized chemically using methods such as those discussed in Nazemi A. *et al. Chemistry of Bioconjugates: Synthesis, Characterization,*

30   *and Biomedical Applications*, Published Online: 13 Feb. 2014) and references provided therein. Alternatively, the polymeric or dendrimeric structure can be formed by DNA hybridization as shown, for example, in Dirks R. *et al. Proc. Nat. Acad. Sci. U.S.A.*, 2004;1010(43):15275-78; and in Um S.H. *et al. Nat. Protocols* 2006;1:995-1000, each of which is incorporated by reference herein.

An imager nucleic acid may be comprised of or may consist of DNA, RNA, or nucleic acid-like structures with other phosphate-sugar backbones (*e.g.* 2'-O-methyl RNA, 2'-fluoral RNA, LNA, XNA) or backbones comprising non-phosphate-sugar moieties (*e.g.*, peptide nucleic acid and morpholino). The nucleobases may include naturally occurring nucleobases such as adenine, thymine, guanine, cytosine, inosine, and their derivatives, as well as non-naturally occurring nucleobases such as isoC, isoG, dP and dZ.

In some embodiments, an imager nucleic acid is about 30 to about 60 nucleotides, or more, in length, including 30, 35, 40, 45, 50, 55 or 60 nucleotides in length. In some embodiments, an imager nucleic acid is 30 to 40, 30 to 50, 40 to 50, 40 to 60, or 50 to 60 nucleotides in length.

An imager nucleic acid, when not bound to its complementary docking nucleic acid, may be single-stranded without stable secondary structure. Alternatively, the imager nucleic acid may comprise secondary structure such as a hairpin loop (FIG. 9, top). An imager nucleic acid may be part of a multi-strand complex (FIG. 9, bottom).

In some embodiments, the imager strand can be self-quenching, intending that the unbound imager nucleic acid may carry a quencher moiety that is in close proximity with the signal-emitting moiety such as a fluorophore. To achieve this, the imager nucleic acid can be designed to adopt either a molecular beacon-like structure (FIG. 5) or a hemiduplex structure (FIG. 6).

This self-quenching variation can be used to reduce background and/or avoid the washing step. Additionally or alternatively, the binding and imaging buffer may contain additives routinely used in FISH, Northern Blotting and Southern Blotting (*e.g.*, negatively charged polymers such as dextran sulfate and heparin) to reduce non-specific binding.

A "signal-emitting moiety," as used herein, is a moiety that, under certain conditions, emits detectable signal, such as photon, radiation, positron, electromagnetic wave, and magnetic-nuclear resonance.

As used herein, an "imager strand" is a single-stranded nucleic acid (*e.g.*, DNA) that is about 30 to about 60 nucleotides, or more, in length. An imager strand of the invention is complementary to a docking strand and stably binds to the docking strand. Stable binding intends that the imager and docking strands remained bound to each other for the length of the assay, or for at least 30 minutes, or for at least for 60 minutes, or for at least for 2 hours, or more. Such binding may or may not be reversible or irreversible.

In some embodiments, a docking nucleic acid is considered stably bound to an imager nucleic acid such as an imager strand if the nucleic acids remain bound to each other for (or

for at least) 30, 35, 40, 45, 50, 55 or 60 minutes (min). In some embodiments, a docking nucleic acid is considered stably bound to an imager nucleic acid if the nucleic acids remain bound to each other for (or for at least) 30 to 60 min, 30 to 120 min, 40 to 60 min, 40 to 120 min, or 60 to 120 min. Such binding may or may not be reversible, or may or may not be

5   irreversible.

As used herein, "binding" refers to an association between at least two molecules due to, for example, electrostatic, hydrophobic, ionic and/or hydrogen-bond interactions, optionally under physiological conditions.

Two nucleic acids, or nucleic acid domains, are "complementary" to one another if

10   they base-pair, or bind, with each other to form a double-stranded nucleic acid molecule via Watson-Crick interactions.

In some embodiments, nucleic acids of the invention such as the docking nucleic acids and the imager nucleic acids bind to each other with "perfect complementary," which refers to 100% complementary (e.g., 5' – ATTCGC – 3' is perfectly complementary to 5'

15   GCGAAT – 3').

Imager strands of the invention may be labeled with a detectable label (*e.g.*, a fluorescent label, and thus are considered "fluorescently labeled"). For example, in some embodiments, an imager strand may comprise at least one (*i.e.*, one or more) fluorophore. Examples of fluorophores for use in accordance with the invention include, without

20   limitation, xanthene derivatives (*e.g.*, fluorescein, rhodamine, Oregon green, eosin and Texas red), cyanine derivatives (*e.g.*, cyanine, indocarbocyanine, oxacarbocyanine, thiacarbocyanine and merocyanine), naphthalene derivatives (*e.g.*, dansyl and prodan derivatives), coumarin derivatives, oxadiazole derivatives (*e.g.*, pyridyloxazole, nitrobenzoxadiazole and benzoxadiazole), pyrene derivatives (*e.g.*, cascade blue), oxazine

25   derivatives (*e.g.*, Nile red, Nile blue, cresyl violet and oxazine 170), acridine derivatives (*e.g.*, proflavin, acridine orange and acridine yellow), arylmethine derivatives (*e.g.*, auramine, crystal violet and malachite green), and tetrapyrrole derivatives (*e.g.*, porphin, phthalocyanine and bilirubin).

Imager nucleic acids including imager strands may be covalently labeled with a

30   detectable label such as those recited herein or known in the art. In some instances, imager nucleic acids including imager strands may comprise 2, 3, 4, or more detectable labels such as fluorophores.

Orthogonal imager nucleic acids including imager strands may comprise a distinct label (*e.g.*, a red fluorophore, a blue fluorophore, or a green fluorophore), or they may all comprise the same label (*e.g.*, red fluorophores) even if they differ in nucleotide sequence.

5   *Sequence-labeled target recognition moieties such as binding partner and docking strand conjugates*

The BP-NA conjugates (*e.g.*, protein-nucleic acid conjugates) of the invention may, in some embodiments, comprise an intermediate linker that links (*e.g.*, covalently or non-covalently) the binding partner to a docking strand. The intermediate linker may comprise

10   biotin and/or streptavidin. For example, in some embodiments, an antibody and a docking strand may each be biotinylated (*i.e.*, linked to at least one biotin molecule) and linked to each other through biotin binding to an intermediate streptavidin molecule. Other intermediate linkers may be used in accordance with the invention. In some embodiments, such as those where the molecule is a nucleic acid, an intermediate linker may not be

15   required. For example, the docking strand of a BP-NA conjugate may be an extension (*e.g.*, 5' or 3' extension) of a nucleic acid molecule such as, for example, a nucleic acid aptamer. Similar approaches may be used to generate sequence-labeled target recognition moieties as provided herein.

Pluralities of BP-NA conjugates (*e.g.*, protein-nucleic acid conjugates) and imager

20   strands are provided herein. A plurality may be a population of the same species or distinct species. A plurality of BP-NA conjugates of the same species may comprise conjugates that all bind to the same target (*e.g.*, biomolecule) (*e.g.*, the same epitope or region/domain). Conversely, a plurality of BP-NA conjugates of distinct species may comprise conjugates, or subsets of conjugates, each conjugate or subset of conjugates binding to a distinct epitope on

25   the same target or to a distinct target. A plurality of imager strands of the same species may comprise imager strands with the same nucleotide sequence and the same fluorescent label (*e.g.*, Cy2, Cy3 or Cy4). Conversely, a plurality of imager strands of distinct species may comprise imager strands with distinct nucleotide sequences (*e.g.*, DNA sequences) and distinct fluorescent labels (*e.g.*, Cy2, Cy3 or Cy4) or with distinct nucleotide sequences and

30   the same fluorescent (*e.g.*, all Cy2). The number of distinct species in a given plurality of BP-NA conjugates is limited by the number of binding partners (*e.g.*, antibodies) and the number of docking strands of different nucleotide sequence (and thus complementary imager strands). In some embodiments, a plurality of BP-NA conjugates (*e.g.*, protein-nucleic acid conjugates) comprises at least 10, 50, 100, 500, 1000, 2000, 3000, 4000, 5000, 10^4, 50000,

10^5, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11} BP-NA conjugates. Likewise, in some embodiments, a plurality of fluorescently labeled imager strands comprises at least 10, 50, 100, 500, 1000, 2000, 3000, 4000, 5000, 10^4, 50000, 10^5, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11} fluorescently labeled imager strands. In some embodiments, a plurality may contain 1 to about 200 or

5   more distinct species of BP-NA conjugates and/or imager strands. For example, a plurality may contain at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200 or more distinct species. In some embodiments, a plurality may contain less than about 5 to about 200 distinct species of BP-NA conjugates and/or imager strands. For example, a plurality may contain less than 5, 6, 7, 8, 9, 10, 15, 20,

10   25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175 or 200 distinct species. These embodiments apply to sequence-labeled target recognition moieties as provided herein.

Signal or imager nucleic acid inactivation

15   To achieve imager nucleic acid inactivation in some of the methods provided herein, the imager nucleic acids, including the imager strands, may be removed from the target-recognition moieties, including the binding partners, (FIG. 3) by means such as but not limited to increasing temperature; decreasing the concentration of counter-ions (*e.g.*, free Mg++); introducing or increasing the concentration of denaturants (*e.g.* formamide, urea,

20   DMSO, and the like); and chemically, photochemically or enzymatically cleaving, modifying or degrading the imager strand, or any combination thereof.

To achieve imager nucleic acid inactivation in some of the methods provided herein, the imager nucleic acids, including the imager strands, may be inactivated by removing and/or modifying the signal-emitting moiety without removing the entirety of the nucleic acid

25   portion of the imager nucleic acid from the docking strands. (FIG. 4.)

As an example, the removal of the imager nucleic acid may be facilitated by cleaving the imager strand into multiple parts. In some embodiments, the imager nucleic acid comprises a chemically cleavable moiety that can be cleaved by introduction of the chemical compound that acts upon such cleavable moiety. Examples of such chemically cleavable

30   moieties include but are not limited to allyl groups, which can be cleaved by certain Pd-based reagents (Ju J. *et al., Proc Natl Acad Sci U S A.* 2006 Dec 26;103(52):19635-40, incorporated by reference herein); azido groups, which can be cleaved by certain phosphorous-based reagents such as TCEP (Guo J *et al. Proc Natl Acad Sci U S A.* 2008 Jul 8;105(27):9145-50, incorporated by reference herein); bridging phosphorothiolates, which can be cleaved by

silver-based reagents (Mag M. *et al. Nucleic Acids Res.* 1991 Apr 11;19(7):1437-41, incorporated by reference herein); disulfide bonds, which can be cleaved by reducing agents such as DTT and TCEP; and ribose, which can be cleaved by a variety of nucleophiles such as hydroxide and imidazole.

5   In some embodiments, the imager nucleic acid comprises a photocleavable linker that can be cleaved photochemically (*e.g.*, by UV exposure). In some embodiments, the imager nucleic acid contains a moiety that can be cleaved by an enzyme. Examples of such enzymatically cleavable moieties include but are not limited to ribonucleotides, which can be cleaved by a variety of RNases; deoxyuridines, which can be cleaved by enzyme

10   combinations such as USER (New England Biolabs); and restriction sites, which can be cleaved by sequence-specific nicking enzymes or restriction enzymes. In some embodiments, the restriction enzyme may cleave both the imager nucleic acid and the docking nucleic acid. In still other embodiments, the removal of the imager nucleic acid may be facilitated by modifying the imager nucleic acid into a form that binds the docking nucleic

15   acid to form a duplex with decreased stability (or lower melting temperature).

As an example, the imager nucleic acid comprises azobenzene, which can be photoisomerized, wherein different isomers affect the binding strength of the imager nucleic acid to the docking nucleic acid differently (Asanuma H. *et al. Angew Chem Int Ed Engl.* 2001 Jul 16;40(14):2671-2673, incorporated by reference herein). In some embodiments, the

20   imager nucleic acid comprises a deoxyuridine, in which the uracil group may be cleaved by uracil-DNA glycosylase. After the uracil is removed the binding strength of the imager strand is weakened.

Alternatively, the removal of the signal-emitting moiety can be achieved by cleaving a linker between the imager nucleic acid and the signal-emitting moiety, if such a linker

25   exists. Chemistries described in herein can be used for this purpose as well.

The inactivation of the signal-emitting moiety can be achieved by chemically or photochemically modifying the signal-emitting moiety. For example, when the signal-emitting moiety is a fluorophore, it can be bleached by chemical agents (such as for example hydrogen peroxide, Gerdes M. *et al. Proc Natl Acad Sci U S A.* 2013 Jul 16;110(29):11982-

30   87, incorporated by reference herein) or photobleached (*e.g.*, using soft multiwavelength excitation as described in Schubert W. *et al. Nat. Biotech.* 2006;24:1270-78, incorporated by reference herein).

As will be understood in the art, "photobleaching" refers to the photochemical alteration of a dye or a fluorophore molecule such that it is unable to fluoresce. This is

caused by cleavage of covalent bonds or non-specific reactions between the fluorophore and surrounding molecules. Loss of activity caused by photobleaching can be controlled, in some embodiments, by reducing the intensity or time-span of light exposure, by increasing the concentration of fluorophores, by reducing the frequency and thus the photon energy of the

5   input light, or by employing more robust fluorophores that are less prone to bleaching (*e.g.* Alexa Fluors or DyLight Fluors). *See, e.g.*, Ghauharali R. *et al. Journal of Microscopy* 2001;198: 88-100; and Eggeling C. *et al. Analytical Chemistry* 1998;70:2651-59.

Thus, photobleaching may be used to remove, modify or in some instance extinguish signal from a signal-emitting moiety. Photobleaching may be performed by exposing

10   fluorophores to a wavelength of light of suitable wavelength, energy and duration to permanently and irreversibly extinguish the ability of the fluorophore to emit further signal. Photobleaching techniques are known in the art.

It was also found that, unlike antibodies that are generally able to bind their targets at a wide range of temperature below the physiological temperature (*i.e.*, 0 °C to 37 °C) and can

15   tolerate mild variation in salt concentration (*i.e.*, monovalent cation concentration from 10 mM to 1 M; divalent cation from 0 to 10 mM), the affinity of short nucleic acid hybridization is dependent on temperature and salt concentration. For example, the predicted dissociation constant (using the parameter sets outlined in reference PMID 15139820) between ssDNA 5'-CATCTAAAGCC-3' and its reverse-complementary strand 5'-GGCTTTAGATG-3' is ~90

20   pM at 23°C with 500 mM [Na+] and 10 mM [Mg++] concentration. In other words, in this condition the binding is very strong. The predicted dissociation constant of this pair of ssDNA is as high as ~500 nM at 37°C with 150 mM [Na+] and 0 mM [Mg++]. In other words, in this condition the binding is fairly weak. The dissociation constants of these two conditions varies by nearly 4 orders of magnitude even though most antibodies are expected

25   to bind their target strongly in both conditions. Similar trends are observed for other DNA sequences (FIG. 10). As a further example, the imaging condition can be 23°C with 500 mM [Na+] and 10 mM [Mg++], and the dye-inactivating condition can be 37°C with 150 mM [Na+] and 0 mM [Mg++].

In some embodiments, the sample being analyzed is cultured cells, tissue sections, or

30   other samples from living organisms.

In some embodiments, the sample is dissociated cells that are immobilized to a solid surface (*e.g.* glass slide or cover slip), including individually immobilized. For example, the sample may be cells in blood. For example, the sample may contain cancer cells circulating

in the blood (also known as circulating tumor cells, or CTCs). The sample may be cells grown in suspension. The sample may be cells disseminated from a solid tissue.

Sample

5   A "sample" may comprise cells (or a cell), tissue, or bodily fluid such as blood (serum and/or plasma), urine, semen, lymphatic fluid, cerebrospinal fluid or amniotic fluid. A sample may be obtained from (or derived from) any source including, without limitation, humans, animals, bacteria, viruses, microbes and plants. In some embodiments, a sample is a cell lysate or a tissue lysate. A sample may also contain mixtures of material from one source

10   or different sources. A sample may be a spatial area or volume (*e.g.*, a grid on an array, or a well in a plate or dish). A sample, in some embodiments, includes target(s), BP-NA conjugate(s) and imager strand(s). The cells may be disseminated (or dissociated) cells.

Target

15   A "target" is any moiety that one wishes to observe or quantitate and for which a binding partner exists. A target, in some embodiments, may be non-naturally occurring. The target, in some embodiments, may be a biomolecule. As used herein, a "biomolecule" is any molecule that is produced by a living organism, including large macromolecules such as proteins, polysaccharides, lipids and nucleic acids (*e.g.*, DNA and RNA such as mRNA), as

20   well as small molecules such as primary metabolites, secondary metabolites, and natural products. Examples of biomolecules include, without limitation, DNA, RNA, cDNA, or the DNA product of RNA subjected to reverse transcription, A23187 (Calcimycin, Calcium Ionophore), Abamectine, Abietic acid, Acetic acid, Acetylcholine, Actin, Actinomycin D, Adenosine, Adenosine diphosphate (ADP), Adenosine monophosphate (AMP), Adenosine

25   triphosphate (ATP), Adenylate cyclase, Adonitol, Adrenaline, epinephrine, Adrenocorticotropic hormone (ACTH), Aequorin, Aflatoxin, Agar, Alamethicin, Alanine, Albumins, Aldosterone, Aleurone, Alpha-amanitin, Allantoin, Allethrin, α-Amanatin, Amino acid, Amylase, Anabolic steroid, Anethole, Angiotensinogen, Anisomycin, Antidiuretic hormone (ADH), Arabinose, Arginine, Ascomycin, Ascorbic acid (vitamin C), Asparagine,

30   Aspartic acid, Asymmetric dimethylarginine, Atrial-natriuretic peptide (ANP), Auxin, Avidin, Azadirachtin A – C35H44O16, Bacteriocin, Beauvericin, Bicuculline, Bilirubin, Biopolymer, Biotin (Vitamin H), Brefeldin A, Brassinolide, Brucine, Cadaverine, Caffeine, Calciferol (Vitamin D), Calcitonin, Calmodulin, Calmodulin, Calreticulin, Camphor - (C10H16O), Cannabinol, Capsaicin, Carbohydrase, Carbohydrate, Carnitine, Carrageenan,

Casein, Caspase, Cellulase, Cellulose - (C6H10O5), Cerulenin, Cetrimonium bromide

(Cetrimide) - C19H42BrN, Chelerythrine, Chromomycin A3, Chaparonin, Chitin, α-

Chloralose, Chlorophyll, Cholecystokinin (CCK), Cholesterol, Choline, Chondroitin sulfate,

Cinnamaldehyde, Citral, Citric acid, Citrinin, Citronellal, Citronellol, Citrulline, Cobalamin

5   (vitamin B12), Coenzyme, Coenzyme Q, Colchicine, Collagen, Coniine, Corticosteroid,

Corticosterone, Corticotropin-releasing hormone (CRH), Cortisol, Creatine, Creatine kinase,

Crystallin, α-Cyclodextrin, Cyclodextrin glycosyltransferase, Cyclopamine, Cyclopiazonic

acid, Cysteine, Cystine, Cytidine, Cytochalasin, Cytochalasin E, Cytochrome, Cytochrome C,

Cytochrome c oxidase, Cytochrome c peroxidase, Cytokine, Cytosine – C4H5N3O,

10   Deoxycholic acid, DON (DeoxyNivalenol), Deoxyribofuranose, Deoxyribose, Deoxyribose

nucleic acid (DNA), Dextran, Dextrin, DNA, Dopamine, Enzyme, Ephedrine, Epinephrine –

C9H13NO3, Erucic acid – CH3(CH2)7CH=CH(CH2)11COOH, Erythritol, Erythropoietin

(EPO), Estradiol, Eugenol, Fatty acid, Fibrin, Fibronectin, Folic acid (Vitamin M), Follicle

stimulating hormone (FSH), Formaldehyde, Formic acid, Formnoci, Fructose, Fumonisin B1,

15   Gamma globulin, Galactose, Gamma globulin, Gamma-aminobutyric acid, Gamma-

butyrolactone, Gamma-hydroxybutyrate (GHB), Gastrin, Gelatin, Geraniol, Globulin,

Glucagon, Glucosamine, Glucose – C6H12O6, Glucose oxidase, Gluten, Glutamic acid,

Glutamine, Glutathione, Gluten, Glycerin (glycerol), Glycine, Glycogen, Glycolic acid,

Glycoprotein, Gonadotropin-releasing hormone (GnRH), Granzyme, Green fluorescent

20   protein, Growth hormone, Growth hormone-releasing hormone (GHRH), GTPase, Guanine,

Guanosine, Guanosine triphosphate (+GTP), Haptoglobin, Hematoxylin, Heme, Hemerythrin,

Hemocyanin, Hemoglobin, Hemoprotein, Heparan sulfate, High density lipoprotein, HDL,

Histamine, Histidine, Histone, Histone methyltransferase, HLA antigen, Homocysteine,

Hormone, human chorionic gonadotropin (hCG), Human growth hormone, Hyaluronate,

25   Hyaluronidase, Hydrogen peroxide, 5-Hydroxymethylcytosine, Hydroxyproline, 5-

Hydroxytryptamine, Indigo dye, Indole, Inosine, Inositol, Insulin, Insulin-like growth factor,

Integral membrane protein, Integrase, Integrin, Intein, Interferon, Inulin, Ionomycin, Ionone,

Isoleucine, Iron-sulfur cluster, K252a, K252b, KT5720, KT5823, Keratin, Kinase, Lactase,

Lactic acid, Lactose, Lanolin, Lauric acid, Leptin, Leptomycin B, Leucine, Lignin,

30   Limonene, Linalool, Linoleic acid, Linolenic acid, Lipase, Lipid, Lipid anchored protein,

Lipoamide, Lipoprotein, Low density lipoprotein, LDL, Luteinizing hormone (LH),

Lycopene, Lysine, Lysozyme, Malic acid, Maltose, Melatonin, Membrane protein,

Metalloprotein, Metallothionein, Methionine, Mimosine, Mithramycin A, Mitomycin C,

Monomer, Mycophenolic acid, Myoglobin, Myosin, Natural phenols, Nucleic Acid,

Ochratoxin A, Oestrogens, Oligopeptide, Oligomycin, Orcin, Orexin, Ornithine, Oxalic acid,

Oxidase, Oxytocin, p53, PABA, Paclitaxel, Palmitic acid, Pantothenic acid (vitamin B5),

parathyroid hormone (PTH), Paraprotein, Pardaxin, Parthenolide, Patulin, Paxilline, Penicillic

acid, Penicillin, Penitrem A, Peptidase, Pepsin, Peptide, Perimycin, Peripheral membrane

5   protein, Perosamine, Phenethylamine, Phenylalanine, Phosphagen, phosphatase,

Phospholipid, Phenylalanine, Phytic acid, Plant hormones, Polypeptide, Polyphenols,

Polysaccharides, Porphyrin, Prion, Progesterone, Prolactin (PRL), Proline, Propionic acid,

Protamine, Protease, Protein, Proteinoid, Putrescine, Pyrethrin, Pyridoxine or pyridoxamine

(Vitamin B6), Pyrrolysine, Pyruvic acid, Quinone, Radicicol, Raffinose, Renin, Retinene,

10   Retinol (Vitamin A), Rhodopsin (visual purple), Riboflavin (vitamin B2), Ribofuranose,

Ribose, Ribozyme, Ricin, RNA - Ribonucleic acid, RuBisCO, Safrole, Salicylaldehyde,

Salicylic acid, Salvinorin-A – C23H28O8, Saponin, Secretin, Selenocysteine,

Selenomethionine, Selenoprotein, Serine, Serine kinase, Serotonin, Skatole, Signal

recognition particle, Somatostatin, Sorbic acid, Squalene, Staurosporin, Stearic acid,

15   Sterigmatocystin, Sterol, Strychnine, Sucrose (sugar), Sugars (in general), superoxide, T2

Toxin, Tannic acid, Tannin, Tartaric acid, Taurine, Tetrodotoxin, Thaumatin, Topoisomerase,

Tyrosine kinase, Taurine, Testosterone, Tetrahydrocannabinol (THC), Tetrodotoxin,

Thapsigargin, Thaumatin, Thiamine (vitamin B1) – C12H17ClN4OS•HCl, Threonine,

Thrombopoietin, Thymidine, Thymine, Triacsin C, Thyroid-stimulating hormone (TSH),

20   Thyrotropin-releasing hormone (TRH), Thyroxine (T4), Tocopherol (Vitamin E),

Topoisomerase, Triiodothyronine (T3), Transmembrane receptor, Trichostatin A, Trophic

hormone, Trypsin, Tryptophan, Tubulin, Tunicamycin, Tyrosine, Ubiquitin, Uracil, Urea,

Urease, Uric acid – C5H4N4O3, Uridine, Valine, Valinomycin, Vanabins, Vasopressin,

Verruculogen, Vitamins (in general), Vitamin A (retinol), Vitamin B, Vitamin B1 (thiamine),

25   Vitamin B2 (riboflavin), Vitamin B3 (niacin or nicotinic acid), Vitamin B4 (adenine),

Vitamin B5 (pantothenic acid), Vitamin B6 (pyridoxine or pyridoxamine), Vitamin B12

(cobalamin), Vitamin C (ascorbic acid), Vitamin D (calciferol), Vitamin E (tocopherol),

Vitamin F, Vitamin H (biotin), Vitamin K (naphthoquinone), Vitamin M (folic acid),

Wortmannin and Xylose.

30   In some embodiments, a target may be a protein target such as, for example, proteins

of a cellular environment (*e.g.*, intracellular or membrane proteins). Examples of proteins

include, without limitation, fibrous proteins such as cytoskeletal proteins (*e.g.*, actin, arp2/3,

coronin, dystrophin, FtsZ, keratin, myosin, nebulin, spectrin, tau, titin, tropomyosin, tubulin

and collagen) and extracellular matrix proteins (*e.g.*, collagen, elastin, f-spondin, pikachurin,

and fibronectin); globular proteins such as plasma proteins (*e.g.*, serum amyloid P component and serum albumin), coagulation factors (*e.g.*, complement proteins,C1-inhibitor and C3-convertase, Factor VIII, Factor XIII, fibrin, Protein C, Protein S, Protein Z, Protein Z-related protease inhibitor, thrombin, Von Willebrand Factor) and acute phase proteins such as C-

5   reactive protein; hemoproteins; cell adhesion proteins (*e.g.*, cadherin, ependymin, integrin, Ncam and selectin); transmembrane transport proteins (*e.g.*, CFTR, glycophorin D and scramblase) such as ion channels (*e.g.*, ligand-gated ion channels such nicotinic acetylcholine receptors and GABAa receptors, and voltage-gated ion channels such as potassium, calcium and sodium channels), synport/antiport proteins (*e.g.*, glucose transporter); hormones and

10   growth factors (*e.g.*, epidermal growth factor (EGF), fibroblast growth factor (FGF), vascular endothelial growth factor (VEGF), peptide hormones such as insulin, insulin-like growth factor and oxytocin, and steroid hormones such as androgens, estrogens and progesterones); receptors such as transmembrane receptors (*e.g.*, G-protein-coupled receptor, rhodopsin) and intracellular receptors (*e.g.*, estrogen receptor); DNA-binding proteins (*e.g.*, histones,

15   protamines, CI protein); transcription regulators (*e.g.*, c-myc, FOXP2, FOXP3, MyoD and P53); immune system proteins (*e.g.*, immunoglobulins, major histocompatibility antigens and T cell receptors); nutrient storage/transport proteins (*e.g.*, ferritin); chaperone proteins; and enzymes.

In some embodiments, a target may be a nucleic acid target such as, for example,

20   nucleic acids of a cellular environment. As used herein with respect to targets, docking strands, and imager strands, a "nucleic acid" refers to a polymeric form of nucleotides of any length, such as deoxyribonucleotides or ribonucleotides, or analogs thereof. For example, a nucleic acid may be a DNA, RNA or the DNA product of RNA subjected to reverse transcription. Non-limiting examples of nucleic acids include coding or non-coding regions

25   of a gene or gene fragment, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant nucleic acids, branched nucleic acids, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. Other examples of nucleic acids include, without limitation, cDNA, aptamers, peptide nucleic acids ("PNA"), 2'-5' DNA

30   (a synthetic material with a shortened backbone that has a base-spacing that matches the A conformation of DNA; 2'-5' DNA will not normally hybridize with DNA in the B form, but it will hybridize readily with RNA), locked nucleic acids ("LNA"), and nucleic acids with modified backbones (*e.g.*, base- or sugar-modified forms of naturally-occurring nucleic acids). A nucleic acid may comprise modified nucleotides, such as methylated nucleotides

and nucleotide analogs ("analogous" forms of purines and pyrimidines are well known in the art). If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. A nucleic acid may be a single-stranded, double-stranded, partially single-stranded, or partially double-stranded DNA or RNA.

5   In some embodiments, a nucleic acid (*e.g.*, a nucleic acid target) is naturally-occurring. As used herein, a "naturally occurring" refers to a nucleic acid that is present in organisms or viruses that exist in nature in the absence of human intervention. In some embodiments, a nucleic acid naturally occurs in an organism or virus. In some embodiments, a nucleic acid is genomic DNA, messenger RNA, ribosomal RNA, micro-RNA, pre-micro-

10   RNA, pro-micro-RNA, viral DNA, viral RNA or piwi-RNA. In some embodiments, a nucleic acid target is not a synthetic DNA nanostructure (*e.g.*, two-dimensional (2-D) or three-dimensional (3-D) DNA nanostructure that comprises two or more nucleic acids hybridized to each other by Watson-Crick interactions to form the 2-D or 3-D nanostructure).

          The nucleic acid docking strands and imager strands described herein can be any one

15   of the nucleic acids described above (*e.g.*, DNA, RNA, modified nucleic acids, nucleic acid analogues, naturally-occurring nucleic acids, synthetic nucleic acids).

Compositions

          Provided herein are compositions that comprise at least one or at least two (*e.g.*, a

20   plurality) BP-NA conjugate(s) (*e.g.*, protein-nucleic acid conjugate(s)) of the invention. The BP-NA conjugates may be bound to a target of interest (*e.g.*, biomolecule) and/or stable bound to a complementary fluorescently labeled imager strand. A composition may comprise a plurality of the same species or distinct species of BP-NA conjugates. In some embodiments, a composition may comprise at least 10, 50, 100, 500, 1000, 2000, 3000, 4000,

25   5000, 10^4, 50000, 10^5, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11} BP-NA conjugates. In some embodiments, a composition may comprise at least 10, 50, 100, 500, 1000, 2000, 3000, 4000, 5000, 10^4, 50000, 10^5, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11} complementary fluorescently labeled imager strands. In some embodiments, a composition may contain 1 to about 200 or more distinct species of BP-NA conjugates and/or imager strands. For example, a composition

30   may contain at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200 or more distinct species. In some embodiments, a composition may contain less than about 5 to about 200 distinct species of BP-NA conjugates and/or imager strands. For example, a composition may contain less than 5, 6, 7, 8, 9, 10, 15,

20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175 or 200 distinct species.

It should be understood that the number of complementary fluorescently labeled imager strands imager stands in a composition may be less than, equal to or greater than the

5   number of BP-NA conjugates in the composition.

Kits

The invention further provides kits comprising one or more components of the invention. The kits may comprise, for example, a BP-NA conjugate and/or a fluorescently

10   labeled imager strands. The kits may also comprise components for producing a BP-NA conjugate or for labeling an imager strand. For example, the kits may comprise a binding partner (*e.g.*, antibody), docking strands and intermediate linkers such as, for example, biotin and streptavidin molecules, and/or imager strands. The kits can be used for any purpose apparent to those of skill in the art, including, those described above.

15   The kits may include other reagents as well, for example, buffers for performing hybridization reactions. The kit may also include instructions for using the components of the kit, and/or for making and/or using the BP-NA conjugates and/or labeled imager strands.

Applications

20   The BP-NA conjugates (*e.g.*, protein-nucleic acid conjugates or antibody-nucleic acid conjugates) of the invention can be used, *inter alia*, in any assay in which existing target detection technologies are used.

Typically assays include detection assays including diagnostic assays, prognostic assays, patient monitoring assays, screening assays, bio-warfare assays, forensic analysis

25   assays, prenatal genomic diagnostic assays and the like. The assay may be an *in vitro* assay or an *in vivo* assay. The present invention provides the advantage that many different targets can be analyzed at one time from a single sample using the methods of the invention, even where such targets are spatially not resolvable (and thus spatially indistinct) using prior art imaging methods. This allows, for example, for several diagnostic tests to be performed on

30   one sample.

The BP-NA conjugates can also be used to simply observe an area or region.

The methods of the invention may be applied to the analysis of samples obtained or derived from a patient so as to determine whether a diseased cell type is present in the sample and/or to stage the disease. For example, a blood sample can be assayed according to any of

the methods described herein to determine the presence and/or quantity of markers of a cancerous cell type in the sample, thereby diagnosing or staging the cancer.

Alternatively, the methods described herein can be used to diagnose pathogen infections, for example infections by intracellular bacteria and viruses, by determining the presence and/or quantity of markers of bacterium or virus, respectively, in the sample. Thus, the targets detected using the compositions and methods of the invention may be either patient markers (such as a cancer marker) or markers of infection with a foreign agent, such as bacterial or viral markers.

The quantitative imaging methods of the invention may be used, for example, to quantify targets (e.g., target biomolecules) whose abundance is indicative of a biological state or disease condition (e.g., blood markers that are upregulated or down-regulated as a result of a disease state).

Further, the compositions and methods of the invention may be used to provide prognostic information that assists in determining a course of treatment for a patient. For example, the amount of a particular marker for a tumor can be accurately quantified from even a small sample from a patient. For certain diseases like breast cancer, overexpression of certain proteins, such as Her2-neu, indicate a more aggressive course of treatment will be needed.

The methods of the present invention may also be used for determining the effect of a perturbation, including chemical compounds, mutations, temperature changes, growth hormones, growth factors, disease, or a change in culture conditions, on various targets, thereby identifying targets whose presence, absence or levels are indicative of a particular biological states. In some embodiments, the present invention is used to elucidate and discover components and pathways of disease states. For example, the comparison of quantities of targets present in a disease tissue with "normal" tissue allows the elucidation of important targets involved in the disease, thereby identifying targets for the discovery/screening of new drug candidates that can be used to treat disease.

The sample being analyzed may be a biological sample, such as blood, sputum, lymph, mucous, stool, urine and the like. The sample may be an environmental sample such as a water sample, an air sample, a food sample and the like. The assay may be carried out with one or more components of the binding reaction immobilized. Thus, the targets or the BP-NA conjugates may be immobilized. The assay may be carried out with one or more components of the binding reaction non-immobilized. The assays may involve detection of a number of targets in a sample, essentially at the same time, in view of the multiplexing

potential offered by the BP-NA conjugates and fluorescently labeled imager strands of the invention. As an example, an assay may be used to detect a particular cell type (*e.g.*, based on a specific cell surface receptor) and a particular genetic mutation in that particular cell type. In this way, an end user may be able to determine how many cells of a particular type

5   carry the mutation of interest, as an example.

Various embodiments

This disclosure provides a variety of embodiments including but not limited to the following numbered embodiments:

10   1.   A method comprising

(1) contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each target-specific binding partner is linked to a docking strand, and wherein target-specific binding partners of different specificity are linked to different docking strands,

15   (2) optionally removing unbound target-specific binding partners,

(3) contacting the sample with labeled imager strands having a nucleotide sequence that is complementary to a docking strand,

(4) optionally removing unbound labeled imager strands,

(5) imaging the sample to detect location and number of bound labeled imager

20   strands,

(6) extinguishing signal from the bound labeled imager strand, and

(7) repeating steps (3)-(6), each time with a labeled imager strand having a unique nucleotide sequence relative to all other labeled imager strands.

2.   The method of embodiment 1, wherein the sample is contacted with more than one

25   target-specific binding partner in step (1).

3.   The method of embodiment 1 or 2, wherein the target-specific binding partner is an antibody or an antibody fragment.

4.   The method of any one of embodiments 1-3, wherein the labeled imager strands are labeled identically.

30   5.   The method of any one of embodiments 1-3, wherein the labeled imager strands each comprise a distinct label.

6.   The method of any one of embodiments 1-5, wherein the labeled imager strands are fluorescently labeled imager strands.

7.   The method of any one of embodiments 1-6, wherein the one or more targets are proteins.

8.   The method of any one of embodiments 1-7, wherein the sample is a cell, a cell lysate or a tissue lysate.

9.   The method of any one of embodiments 1-8, wherein the sample is imaged in step (5) using confocal or epi-fluorescence microscopy.

10.   The method of any one of embodiments 1-9, wherein extinguishing signal in step (6) comprises photobleaching.

11.   A composition comprising

a sample bound to more than one target-specific binding partners, each binding partner bound to a docking strand, and

at least one docking strand stably bound to a labeled imager strand.

12.   A method comprising

(1) contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each target-specific binding partner is linked to a docking nucleic acid, and wherein target-specific binding partners of different specificity are linked to different docking nucleic acids,

(2) optionally removing unbound target-specific binding partners,

(3) contacting the sample with labeled imager nucleic acids having a nucleotide sequence that is complementary to a docking nucleic acid,

(4) optionally removing unbound labeled imager nucleic acids,

(5) imaging the sample to detect location and number of bound labeled imager nucleic acids,

(6) removing the bound labeled imager nucleic acids from the docking nucleic acids, and

(7) repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

13.   The method of embodiment 12, wherein the sample is contacted with more than one target-specific binding partner in step (1).

14.   The method of embodiment 12 or 13, wherein the target-specific binding partner is an antibody or an antibody fragment.

15.   The method of embodiment 12 or 13, wherein the target-specific binding partner is a natural or engineered ligand, a small molecule, an aptamer, a peptide or an oligonucleotide.

16.   The method of any one of embodiments 12-15, wherein the labeled imager nucleic acids are labeled identically.

17.   The method of any one of embodiments 12-15, wherein the labeled imager nucleic acids each comprise a distinct label.

18.   The method of any one of embodiments 12-17, wherein the labeled imager nucleic acids are fluorescently labeled imager nucleic acids.

19.   The method of any one of embodiments 12-18, wherein the one or more targets are proteins.

20.   The method of any one of embodiments 12-19, wherein the sample is a cell, a cell lysate or a tissue lysate.

21.   The method of any one of embodiments 12-20, wherein the sample is imaged in step (5) using confocal or epi-fluorescence microscopy.

22.   The method of any one of embodiments 12-21, wherein the labeled imager nucleic acids are removed from the docking nucleic acids by decreasing salt concentration, addition of a denaturant, or increasing temperature.

23.   The method of embodiment 22, wherein the salt is Mg++.

24.   The method of embodiment 22, wherein the denaturant is formamide, urea or DMSO.

25.   The method of any one of embodiments 12-21, wherein the labeled imager nucleic acids are not removed from the docking nucleic acids by strand displacement in the presence of a competing nucleic acid.

26.   The method of any one of embodiments 12-21, wherein the labeled imager nucleic acids are removed from the docking nucleic acids by chemically, photochemically, or enzymatically cleaving, modifying or degrading the labeled imager nucleic acids.

27.   The method of any one of embodiments 12-21, wherein, when the labeled imager nucleic acid is bound to its respective docking nucleic acid, there is no single-stranded region on the imager nucleic acid or the docking nucleic acid.

28.   The method of any one of embodiments 12-21, wherein the labeled imager nucleic acid is not self-quenching.

29.   The method of any one of embodiments 12-28, wherein the unbound docking nucleic acid is partially double-stranded.

30.   The method of any one of embodiments 12-28, wherein the unbound imager nucleic acid is partially double-stranded.

31.   The method of any one of embodiments 12-28, wherein the imager nucleic acid is a molecular beacon or comprises a hairpin secondary structure.

32.   The method of any one of embodiments 12-27 and 29-31, wherein the imager nucleic acid is a molecular beacon or comprises a hairpin secondary structure that is self-quenching.

33.   The method of any one of embodiments 12-28, wherein the imager nucleic acid is a hemiduplex.

34.   The method of embodiment 33, wherein the hemiduplex is self-quenching.

35.   The method of any one of embodiments 12-34, wherein the docking nucleic acid comprises a hairpin secondary structure.

36.   The method of any one of embodiments 12-35, wherein the imager nucleic acid is bound to multiple signal-emitting moieties through a dendrimeric structure or a polymeric structure.

34.   A method comprising

(1) contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each target-specific binding partner is linked to a docking nucleic acid, and wherein target-specific binding partners of different specificity are linked to different docking nucleic acids,

(2) optionally removing unbound target-specific binding partners,

(3) contacting the sample with labeled imager nucleic acids having a nucleotide sequence that is complementary to a docking nucleic acid,

(4) optionally removing unbound labeled imager nucleic acids,

(5) imaging the sample to detect location and number of bound labeled imager nucleic acids,

(6) inactivating the bound labeled imager nucleic acids, by removing or modifying their signal-emitting moieties without removing the imager nucleic acid in its entirety, and

(7) repeating steps (3)-(6), each time with a labeled imager nucleic acids having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

35.   The method of embodiment 34, wherein the sample is contacted with more than one target-specific binding partner in step (1).

36.   The method of embodiment 34 or 35, wherein the target-specific binding partner is an antibody or an antibody fragment.

37.   The method of embodiment 34 or 35, wherein the target-specific binding partner is a natural or engineered ligand, a small molecule, an aptamer, a peptide or an oligonucleotide.

38.   The method of any one of embodiments 34-37, wherein the labeled imager nucleic acids are labeled identically.

39.   The method of any one of embodiments 34-37, wherein the labeled imager nucleic acids each comprise a distinct label.

40.   The method of any one of embodiments 34-39, wherein the labeled imager nucleic acids are fluorescently labeled imager nucleic acids.

41.   The method of any one of embodiments 34-40, wherein the one or more targets are proteins.

42.   The method of any one of claims 34-41, wherein the sample is a cell, a cell lysate or a tissue lysate.

43.   The method of any one of embodiments 34-42, wherein the sample is imaged in step (5) using confocal or epi-fluorescence microscopy.

44.   The method of any one of embodiments 34-43, wherein the unbound docking nucleic acid is partially double-stranded.

45.   The method of any one of embodiments 34-43, wherein the unbound imager nucleic acid is partially double-stranded.

46.   The method of any one of embodiments 34-45, wherein the imager nucleic acid is a molecular beacon or comprises a hairpin secondary structure.

47.   The method of any one of embodiments 34-45, wherein the imager nucleic acid is a molecular beacon or comprises a hairpin secondary structure that is self-quenching.

48.   The method of any one of embodiments 34-45, wherein the imager nucleic acid is a hemiduplex.

49.   The method of embodiment 48, wherein the hemiduplex is self-quenching.

50.   The method of any one of embodiments 34-49, wherein the docking nucleic acid comprises a hairpin secondary structure.

51.   The method of any one of embodiments 34-50, wherein the imager nucleic acid is bound to multiple signal-emitting moieties through a dendrimeric structure or a polymeric structure.

EQUIVALENTS

While several inventive embodiments have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the function and/or obtaining the results and/or one or more of the advantages described herein, and each of such variations and/or modifications is deemed to be within the scope of the inventive embodiments described herein. More generally, those skilled in the art will readily appreciate that all parameters, dimensions, materials, and

configurations described herein are meant to be exemplary and that the actual parameters, dimensions, materials, and/or configurations will depend upon the specific application or applications for which the inventive teachings is/are used. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific inventive embodiments described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents thereto, inventive embodiments may be practiced otherwise than as specifically described and claimed. Inventive embodiments of the present disclosure are directed to each individual feature, system, article, material, kit, and/or method described herein. In addition, any combination of two or more such features, systems, articles, materials, kits, and/or methods, if such features, systems, articles, materials, kits, and/or methods are not mutually inconsistent, is included within the inventive scope of the present disclosure.

All definitions, as defined and used herein, should be understood to control over dictionary definitions, definitions in documents incorporated by reference, and/or ordinary meanings of the defined terms.

All references, patents and patent applications disclosed herein are incorporated by reference with respect to the subject matter for which each is cited, which in some cases may encompass the entirety of the document.

The indefinite articles "a" and "an," as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean "at least one."

The phrase "and/or," as used herein in the specification and in the claims, should be understood to mean "either or both" of the elements so conjoined, *i.e.*, elements that are conjunctively present in some cases and disjunctively present in other cases. Multiple elements listed with "and/or" should be construed in the same fashion, *i.e.*, "one or more" of the elements so conjoined. Other elements may optionally be present other than the elements specifically identified by the "and/or" clause, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, a reference to "A and/or B", when used in conjunction with open-ended language such as "comprising" can refer, in one embodiment, to A only (optionally including elements other than B); in another embodiment, to B only (optionally including elements other than A); in yet another embodiment, to both A and B (optionally including other elements); etc.

As used herein in the specification and in the claims, "or" should be understood to have the same meaning as "and/or" as defined above. For example, when separating items in

a list, "or" or "and/or" shall be interpreted as being inclusive, *i.e.*, the inclusion of at least one, but also including more than one, of a number or list of elements, and, optionally, additional unlisted items. Only terms clearly indicated to the contrary, such as "only one of" or "exactly one of," or, when used in the claims, "consisting of," will refer to the inclusion of

5   exactly one element of a number or list of elements. In general, the term "or" as used herein shall only be interpreted as indicating exclusive alternatives (*i.e.* "one or the other but not both") when preceded by terms of exclusivity, such as "either," "one of," "only one of," or "exactly one of." "Consisting essentially of," when used in the claims, shall have its ordinary meaning as used in the field of patent law.

10   As used herein in the specification and in the claims, the phrase "at least one," in reference to a list of one or more elements, should be understood to mean at least one element selected from any one or more of the elements in the list of elements, but not necessarily including at least one of each and every element specifically listed within the list of elements and not excluding any combinations of elements in the list of elements. This definition also

15   allows that elements may optionally be present other than the elements specifically identified within the list of elements to which the phrase "at least one" refers, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, "at least one of A and B" (or, equivalently, "at least one of A or B," or, equivalently "at least one of A and/or B") can refer, in one embodiment, to at least one, optionally including more than one,

20   A, with no B present (and optionally including elements other than B); in another embodiment, to at least one, optionally including more than one, B, with no A present (and optionally including elements other than A); in yet another embodiment, to at least one, optionally including more than one, A, and at least one, optionally including more than one, B (and optionally including other elements); etc.

25   It should also be understood that, unless clearly indicated to the contrary, in any methods claimed herein that include more than one step or act, the order of the steps or acts of the method is not necessarily limited to the order in which the steps or acts of the method are recited.

         In the claims, as well as in the specification above, all transitional phrases such as

30   "comprising," "including," "carrying," "having," "containing," "involving," "holding," "composed of," and the like are to be understood to be open-ended, *i.e.*, to mean including but not limited to. Only the transitional phrases "consisting of" and "consisting essentially of" shall be closed or semi-closed transitional phrases, respectively, as set forth in the United States Patent Office Manual of Patent Examining Procedures, Section 2111.03.

What is claimed is:

1.   A method comprising

(1)   contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each of the target-specific binding partners is linked to a docking nucleic acid, and wherein target-specific binding partners of different specificity are linked to different docking nucleic acids,

(2)   optionally removing unbound target-specific binding partners,

(3)   contacting the sample with labeled imager nucleic acids having a nucleotide sequence that is complementary to a docking nucleic acid,

(4)   optionally removing unbound labeled imager nucleic acids,

(5)   imaging the sample to detect location and number of bound labeled imager nucleic acids,

(6)   removing the bound labeled imager nucleic acids from the docking nucleic acids by enzymatically cleaving, modifying or degrading the labeled imager nucleic acids, and

(7)   repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

2.   The method of claim 1, wherein

(a)   the labeled imager nucleic acids are removed by enzymatically cleaving the labeled imager nucleic acids with (i) at least one nicking enzyme or restriction enzyme, (ii) RNase, (iii) nucleic acid glycosylase, optionally a uracil-DNA glycosylase, or (iv) an enzyme that cleaves at one or more deoxyuridine base, optionally wherein the enzyme is a USER enzyme; and/or

(b)   the labeled imager nucleic acids comprise a photocleavable moiety that is cleaved by UV exposure.

3.   The method of claim 1, wherein removing the labeled imager nucleic acids comprises:

(a)   enzymatic cleavage and photochemical modification; or

(b)   enzymatic cleavage and chemical modification/degradation.

4.   A method comprising

(1)   contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each of the target-specific binding partners is linked to a docking nucleic acid, and wherein target-specific binding partners of different specificity are linked to different docking nucleic acids,

(2)   optionally removing unbound target-specific binding partners,

(3)   contacting the sample with labeled imager nucleic acids having a nucleotide sequence that is complementary to a docking nucleic acid,

(4)   optionally removing unbound labeled imager nucleic acids,

(5)   imaging the sample to detect location and number of bound labeled imager nucleic acids,

(6)   removing the bound labeled imager nucleic acids from the docking nucleic acids by altering temperature and/or buffer condition, and

(7)   repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

5.   The method of claim 4, wherein the labeled imager nucleic acids are removed from the docking nucleic acids by decreasing salt concentration, addition of a denaturant, or increasing temperature.

6.   The method of claim 5, wherein the salt comprises Mg++.

7.   The method of claim 5, wherein the denaturant is formamide, urea or DMSO.

8.   A method comprising

(1)   contacting a sample being tested for the presence of one or more targets with one or more target-specific binding partners, wherein each of the target-specific binding partners is linked to a docking nucleic acid, and wherein target-specific binding partners of different specificity are linked to different docking nucleic acids,

(2)   optionally removing unbound target-specific binding partners,

(3)   contacting the sample with labeled imager nucleic acids having a nucleotide sequence that is complementary to a docking nucleic acid and a signal-emitting moiety linked via a chemically or photochemically cleavable linker,

(4)   optionally removing unbound labeled imager nucleic acids,

(5)   imaging the sample to detect location and number of bound labeled imager nucleic acids,

(6)   inactivating the bound labeled imager nucleic acids, by removing or modifying their signal-emitting moieties without removing the bound imager nucleic acids in their entireties, by chemically or photochemically cleaving the linker between the imager nucleic acid and the signal-emitting moiety, and

(7)   repeating steps (3)-(6), each time with a labeled imager nucleic acid having a unique nucleotide sequence relative to all other labeled imager nucleic acids.

9.   The method of claim 8, wherein step (6) comprises cleaving the chemically cleavable linker between the imager nucleic acid and the signal-emitting moiety by introduction of a cleaving agent.

10.   The method of claim 9, wherein the chemically cleavable linker comprises disulfide bonds, and the cleaving agent is a reducing agent, optionally the reducing agent being Dithiothreitol (DTT) or tris(2-carboxyethyl)phosphine (TCEP).

11.   The method of any one of claims 8-10, wherein (6) comprises cleaving the photocleavable linker between the imager nucleic acid and the signal-emitting moiety by UV exposure.

12.   The method of any one of claims 1-11, wherein the labeled imager nucleic acids are labeled identically.

13.   The method of any one of claims 1-11, wherein the labeled imager nucleic acids comprise a distinct label.

14.   The method of any one of claims 1-13, wherein the labeled imager nucleic acids are fluorescently labeled imager nucleic acids.

15.   The method of any one of claims 1-14, wherein the one or more targets are proteins and/or the sample is a cell or tissue sample, a cell lysate, a tissue lysate, or a bodily fluid.

16.   The method of any one of claims 1-15, wherein in step (5) the sample is imaged using confocal or epifluorescence microscopy.

17.   The method of any one of claims 1-16, wherein in step (1) the sample is contacted with more than one target-specific binding partner.

18.   The method of any one of claims 1-17, wherein the target-specific binding partner is an antibody or an antibody fragment.

19.   The method of any one of claims 1-18, wherein the target-specific binding partner is a natural or engineered ligand, a small molecule, an aptamer, a peptide or an oligonucleotide.

20.   A kit when used for testing for the presence of one or more targets with one or more target-specific binding partners comprising:

(1)   one or more target-specific binding partners, wherein each of the target-specific binding partners is linked to a docking nucleic acid, and wherein target-specific binding partners of different specificity are linked to different docking nucleic acids;

(2)   labeled imager nucleic acids that comprise a signal-emitting moiety and bind to a docking nucleic acid, wherein the kit comprises at least two unique imager nucleic acid compositions;

wherein, the kit further comprises an agent for enzymatically cleaving, modifying, or degrading the labeled imager nucleic acids, or an agent for chemically cleaving a cleavable linker between the imager nucleic acids and the signal moiety; and

(3)   optionally one or more buffers.

21.   The method or kit of any one of claims 1-20, wherein the imager and docking nucleic acids remain bound to each other for at least 30, 35, 40, 45, 50, 55, or 60 minutes or at least 2 hours.

22.   The method or kit of any one of claims 1-20, wherein the imager and docking nucleic acids remain bound to each other for at least 30 to 60 minutes, 30 to 120 minutes, 40 to 60 minutes, 40 to 120 minutes, or 60 to 120 minutes.
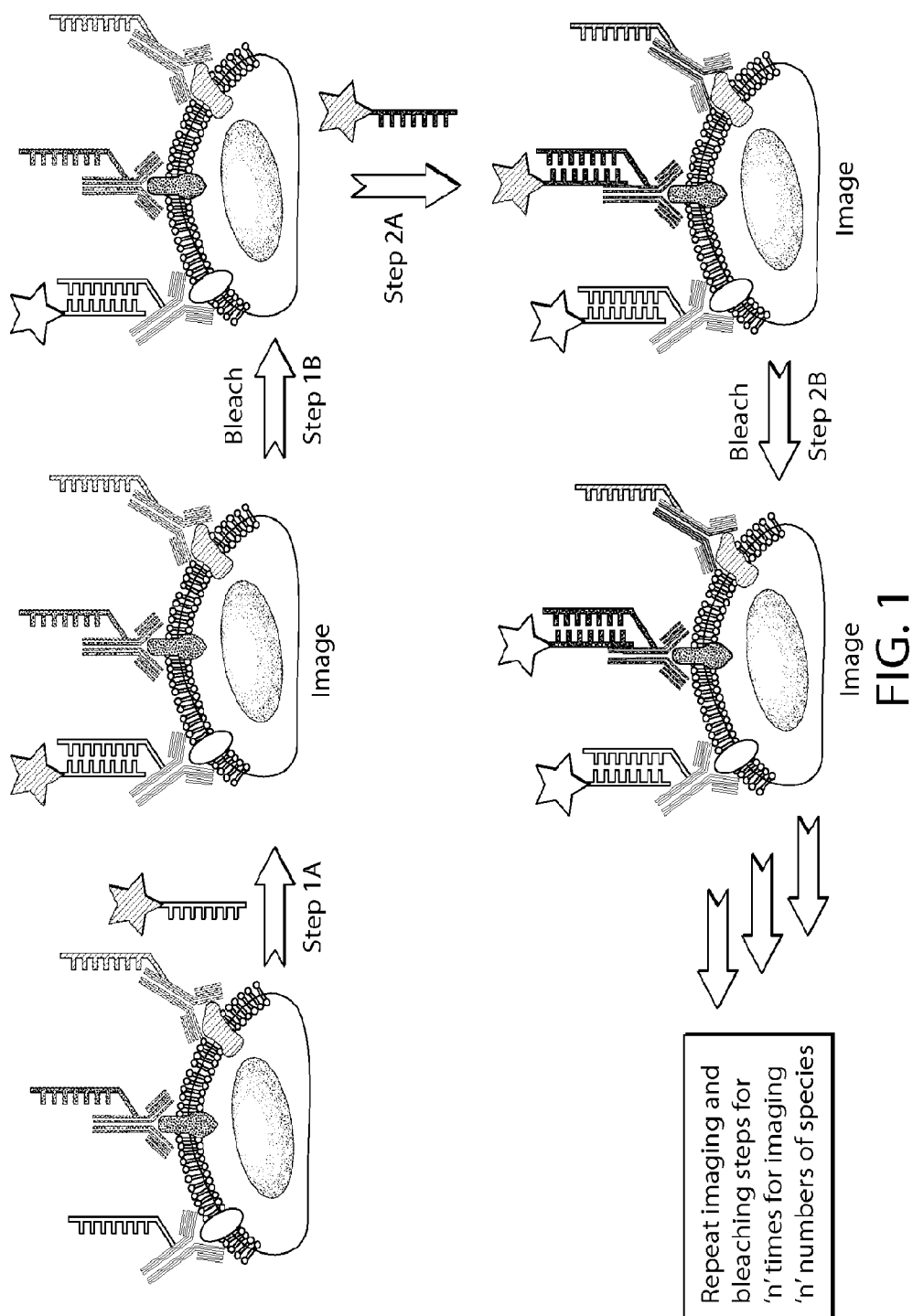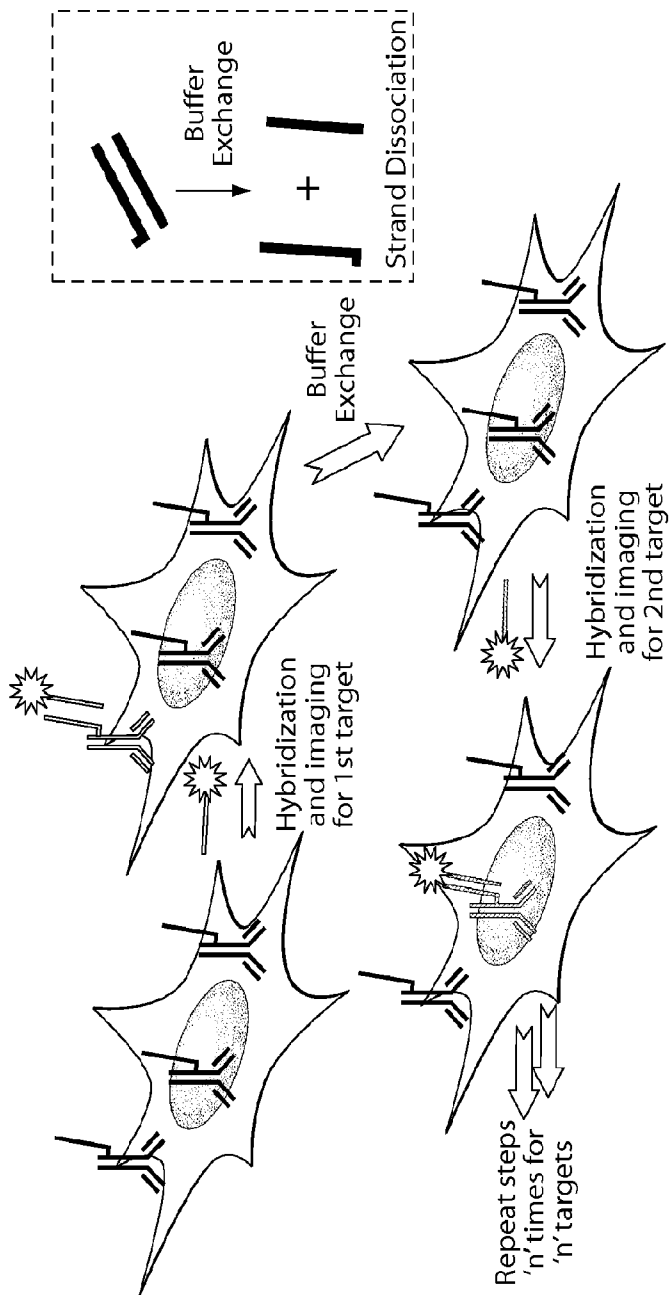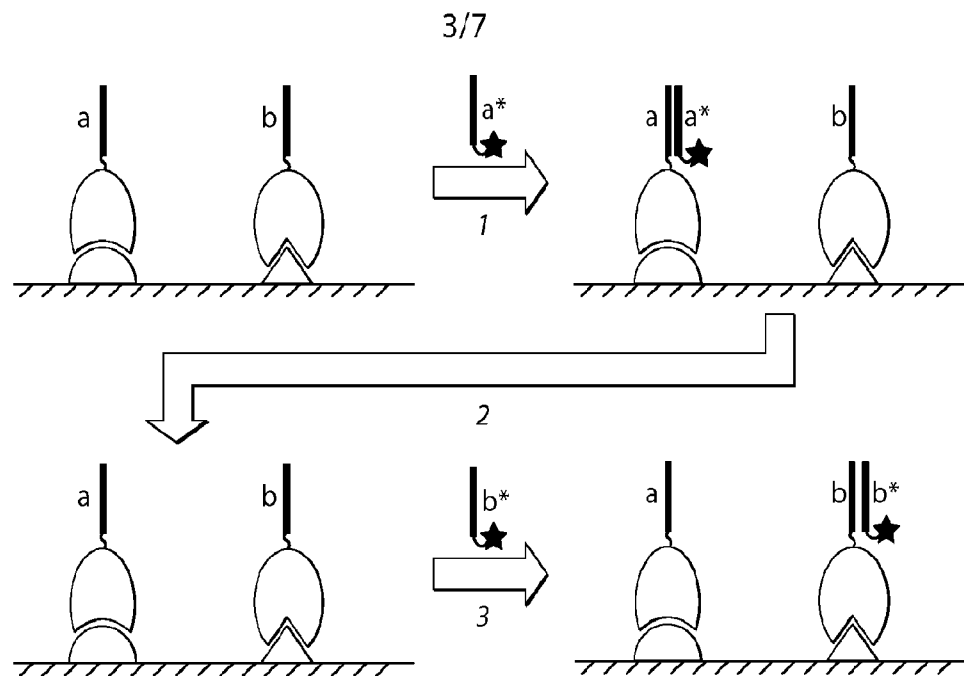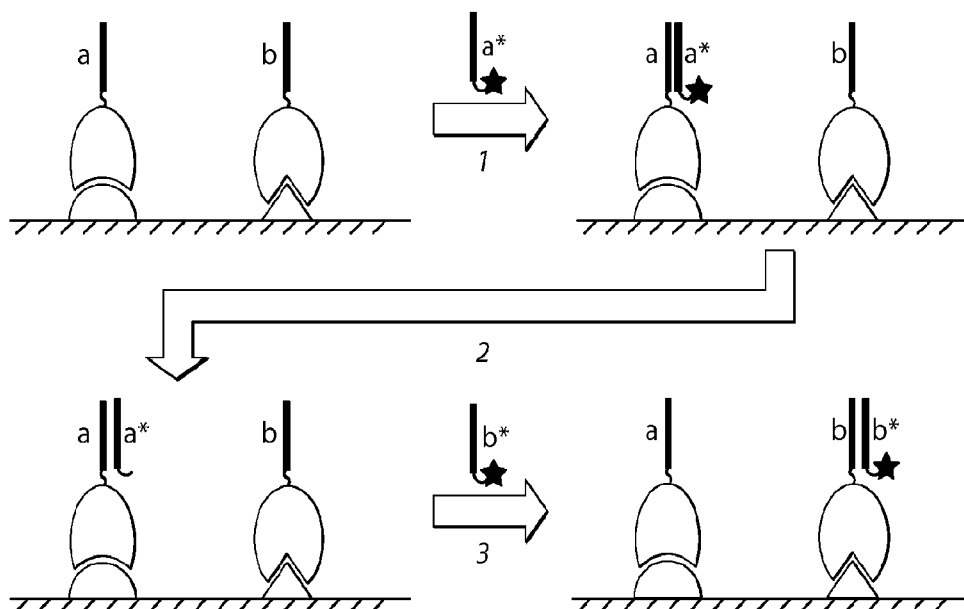
FIG. 1

2/7
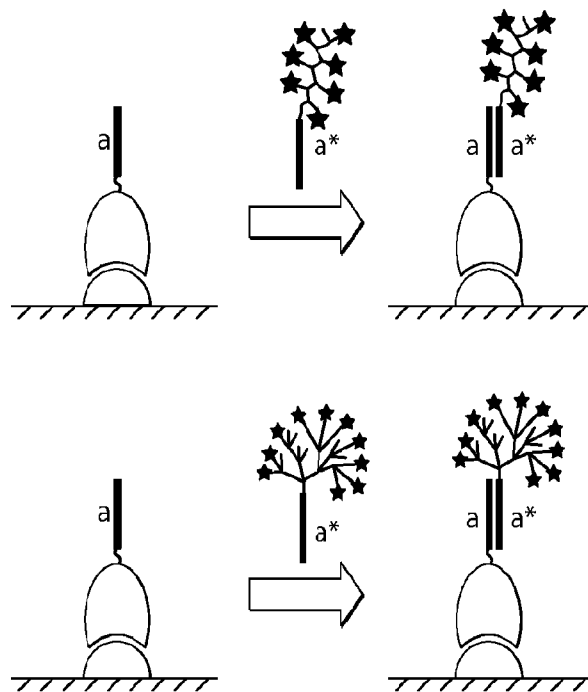

FIG. 2

3/7

FIG. 3

FIG. 4

FIG. 5

FIG. 6

5/7
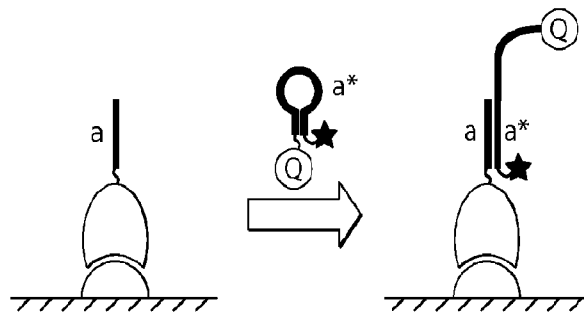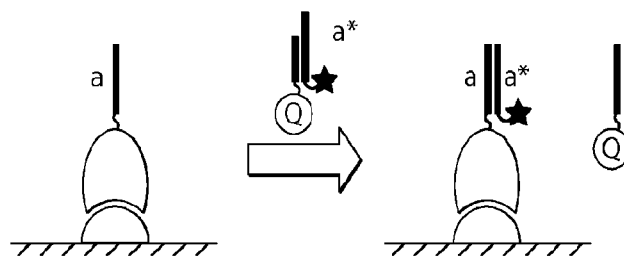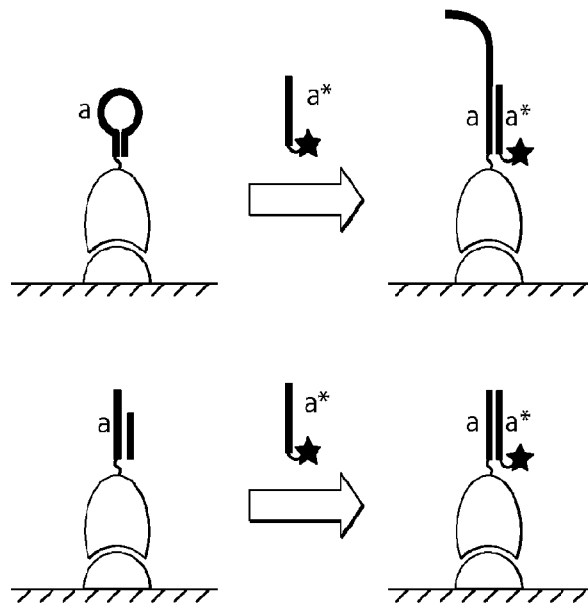
FIG. 7

FIG. 8
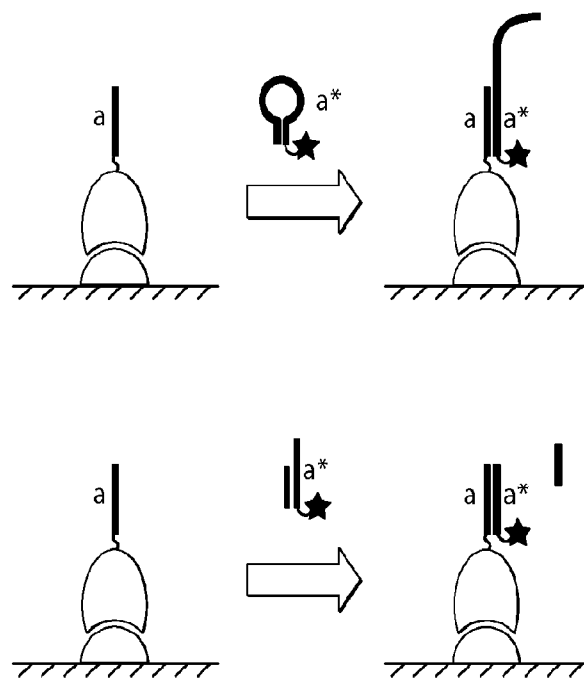
FIG. 9

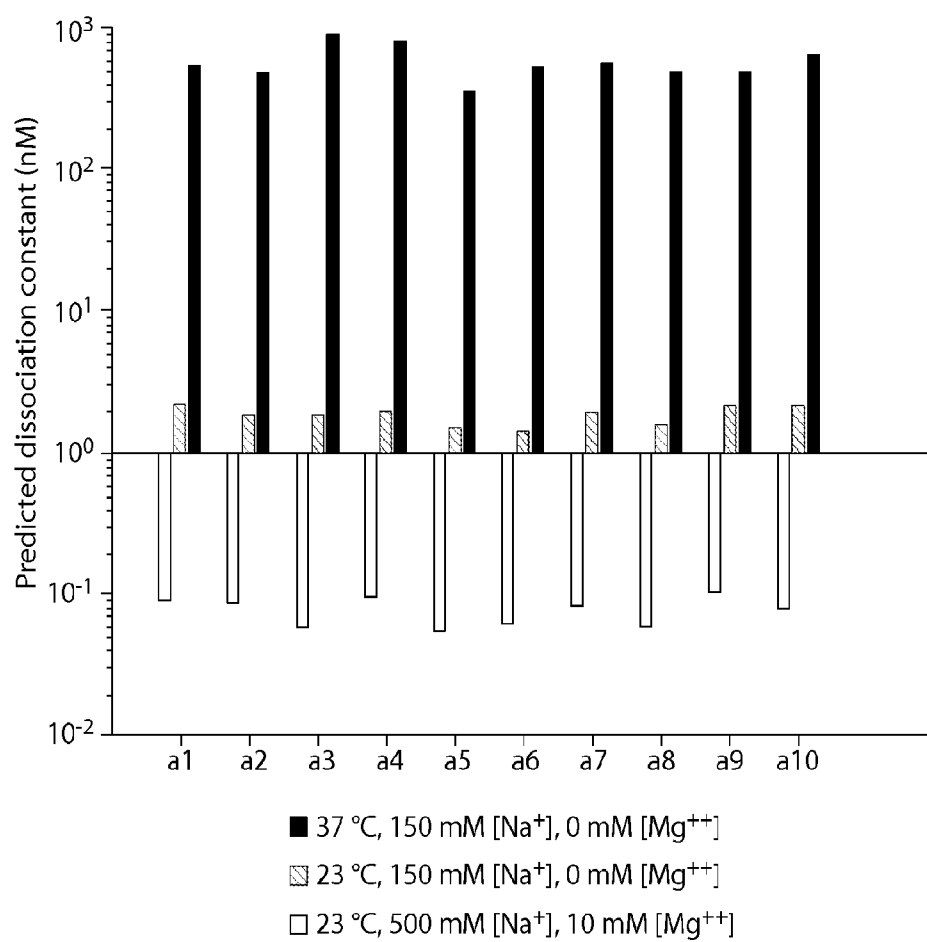FIG. 10

SEQUENCE LISTING

<110> President and Fellows of Harvard College

<120> HIGH-THROUGHPUT AND HIGHLY MULTIPLEXED IMAGING WITH PROGRAMMABLE
       NUCLEIC ACID PROBES

<130> HO498.70501WOOO

<140> TBD
<141> 2015-03-11

<150> US 61/951,461
<151> 2014-03-11

<160> 10

<170> PatentIn version 3.5

<210> 1
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 1
catctaaagc c   11

<210> 2
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 2
gaatttcctc g   11

<210> 3
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 3
gtttaattgc g   11

<210> 4
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 4
acaattcttc g   11

<210> 5

```
<211>  11
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  5
tttcttgctt c                                                              11


<210>  6
<211>  11
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  6
gcattgttac t                                                              11


<210>  7
<211>  11
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  7
atatacaagc g                                                              11


<210>  8
<211>  11
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  8
gctgtctatt g                                                              11


<210>  9
<211>  11
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  9
tctttatgct g                                                              11


<210>  10
<211>  11
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic Polynucleotide

<400>  10
```

caatctcatc c