US007799554B2

(12) **United States Patent**
Mazumdar et al.

(10) **Patent No.: US 7,799,554 B2**
(45) **Date of Patent: Sep. 21, 2010**

(54) **LATERAL FLOW DEVICES**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 432 days.

(21) Appl. No.: **11/686,601**

(22) Filed: **Mar. 15, 2007**

(65) **Prior Publication Data**

US 2007/0269821 A1 Nov. 22, 2007

Related U.S. Application Data

(60) Provisional application No. 60/782,949, filed on Mar. 16, 2006, provisional application No. 60/821,043, filed on Aug. 1, 2006.

(51) **Int. Cl.**
C12M 1/00 (2006.01)
C07H 21/02 (2006.01)

(52) **U.S. Cl.** **435/283.1**; 536/23.1

(58) **Field of Classification Search** ..... None
See application file for complete search history.

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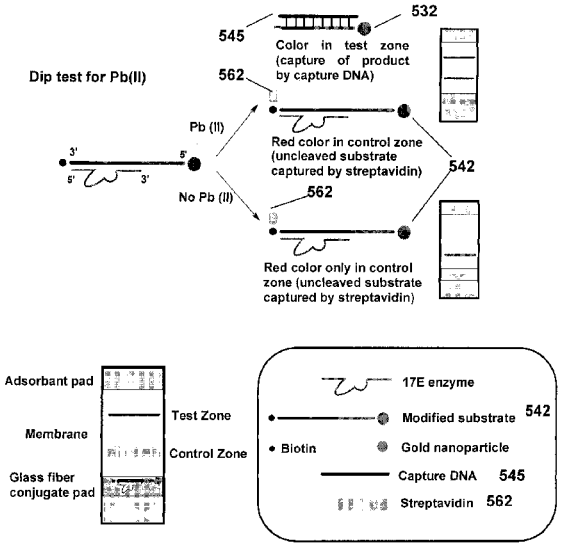
(57) **ABSTRACT**

An analytical test for an analyte comprises (a) a base, having a reaction area and a visualization area, (b) a capture species, on the base in the visualization area, comprising nucleic acid, and (c) analysis chemistry reagents, on the base in the reaction area. The analysis chemistry reagents comprise (i) a substrate comprising nucleic acid and a first label, and (ii) a reactor comprising nucleic acid. The analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising nucleic acid and the first label, and the capture species can bind the visualization species.

11 Claims, 14 Drawing Sheets



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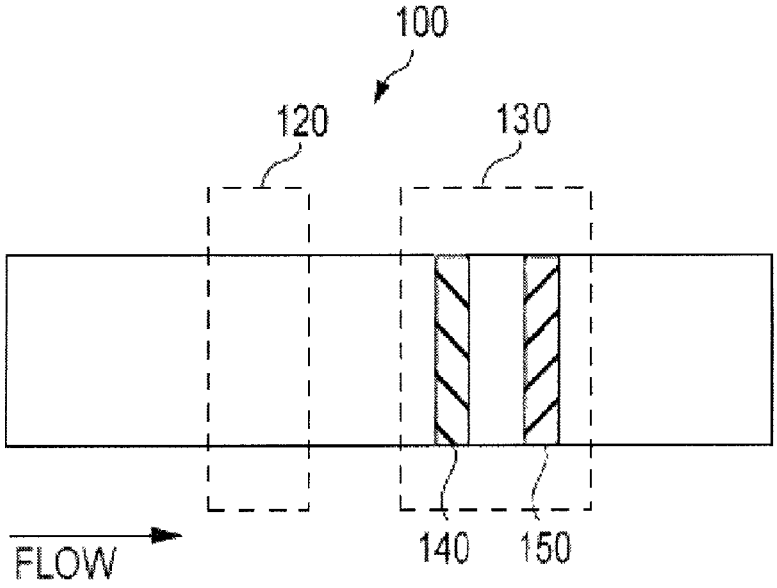


FIG. 1A

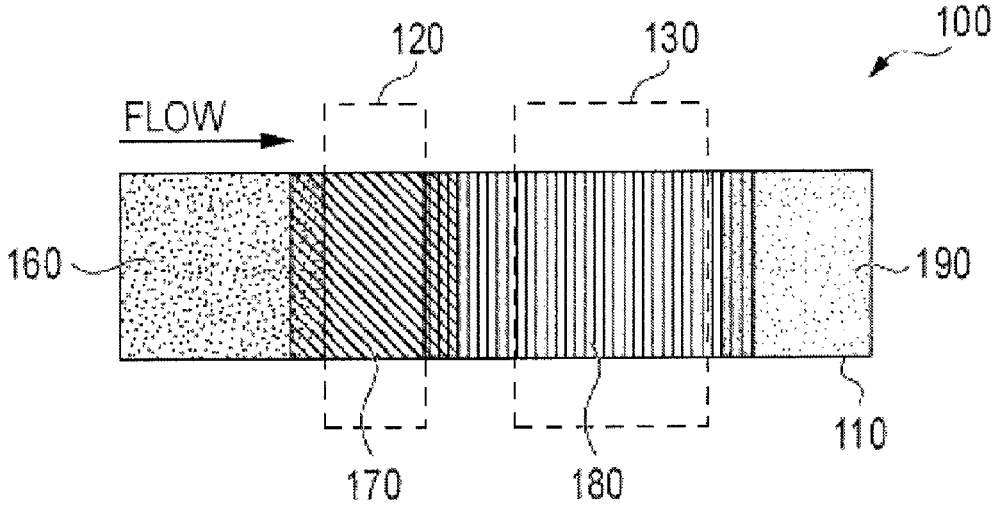


FIG. 1B

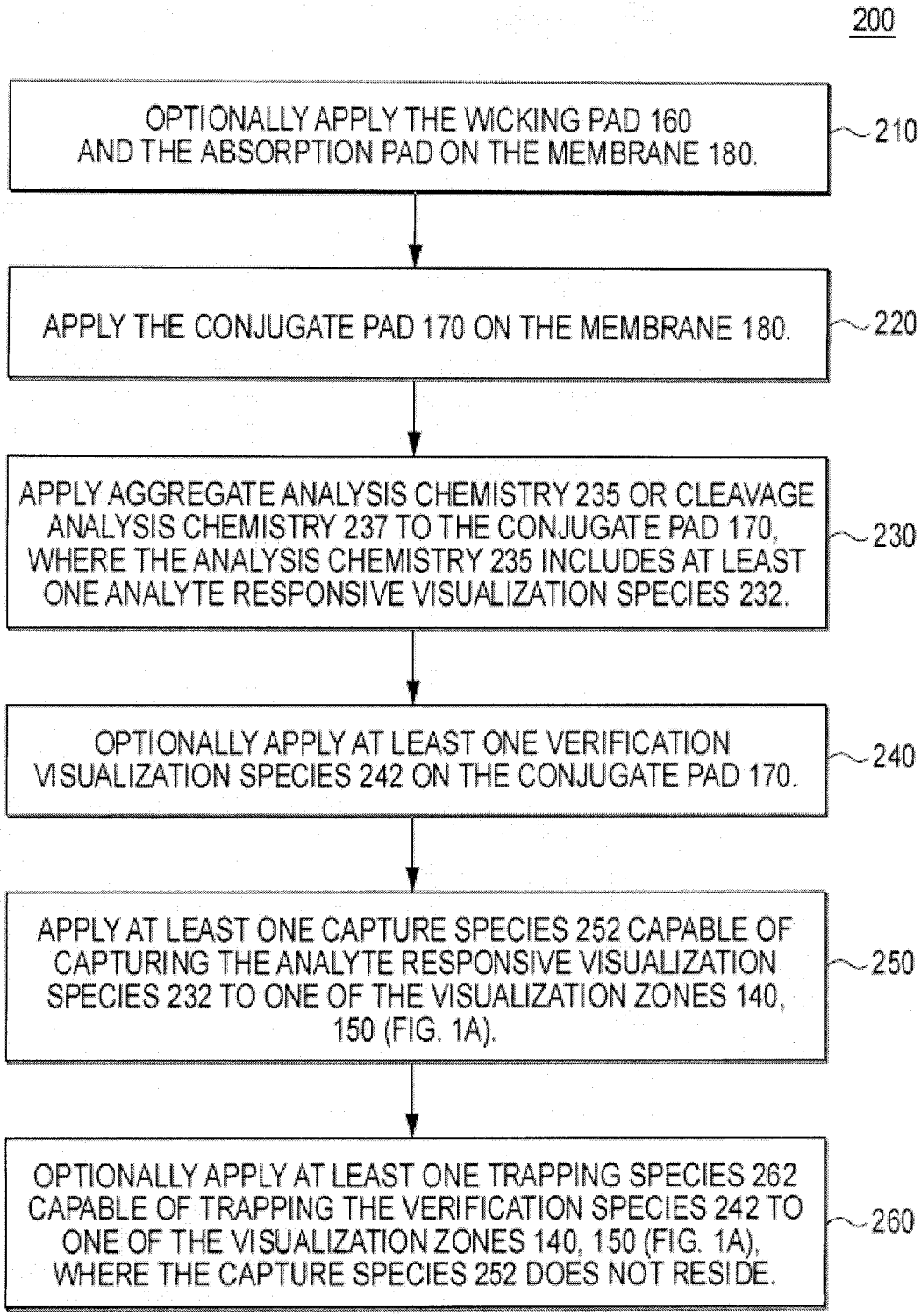

200
OPTIONALLY APPLY THE WICKING PAD 160 AND THE ABSORPTION PAD ON THE MEMBRANE 180.
210
APPLY THE CONJUGATE PAD 170 ON THE MEMBRANE 180.
220
APPLY AGGREGATE ANALYSIS CHEMISTRY 235 OR CLEAVAGE ANALYSIS CHEMISTRY 237 TO THE CONJUGATE PAD 170, WHERE THE ANALYSIS CHEMISTRY 235 INCLUDES AT LEAST ONE ANALYTE RESPONSIVE VISUALIZATION SPECIES 232.
230
OPTIONALLY APPLY AT LEAST ONE VERIFICATION VISUALIZATION SPECIES 242 ON THE CONJUGATE PAD 170.
240
APPLY AT LEAST ONE CAPTURE SPECIES 252 CAPABLE OF CAPTURING THE ANALYTE RESPONSIVE VISUALIZATION SPECIES 232 TO ONE OF THE VISUALIZATION ZONES 140, 150 (FIG. 1A).
250
OPTIONALLY APPLY AT LEAST ONE TRAPPING SPECIES 262 CAPABLE OF TRAPPING THE VERIFICATION SPECIES 242 TO ONE OF THE VISUALIZATION ZONES 140, 150 (FIG. 1A), WHERE THE CAPTURE SPECIES 252 DOES NOT RESIDE.
260

FIG. 2

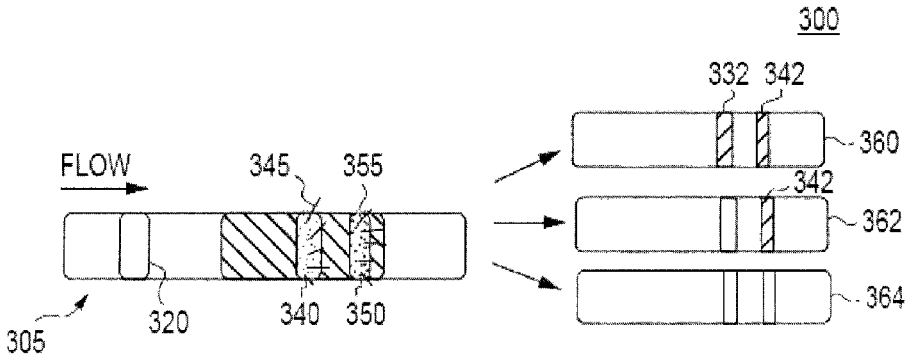

300
332
342
360
FLOW
345
355
342
362
364
320
340
350
305

FIG. 3

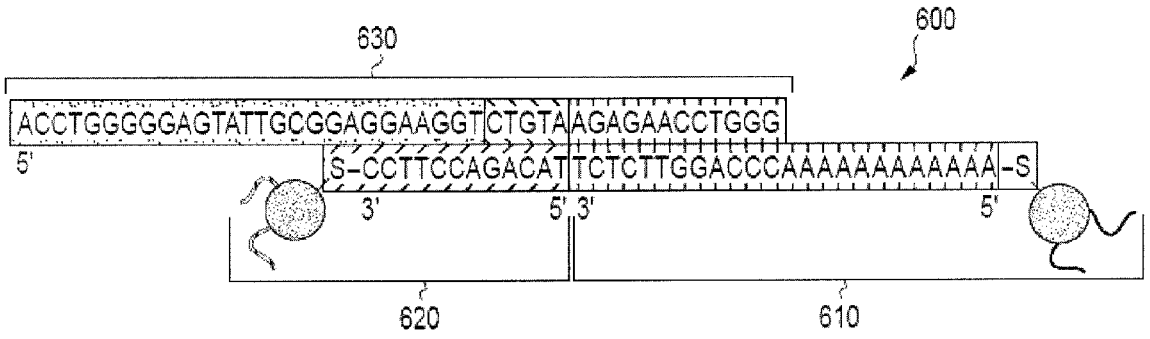

630
600
ACCTGGGGGAGTATTGCGGAGGAAGGTCTGTAAGAGAACCTGGG
5'
S-CCTTCCAGACATTCTCTTGGACCCAAAAAAAAAAAAA-S
3'
5'
3'
5'
620
610

FIG. 6

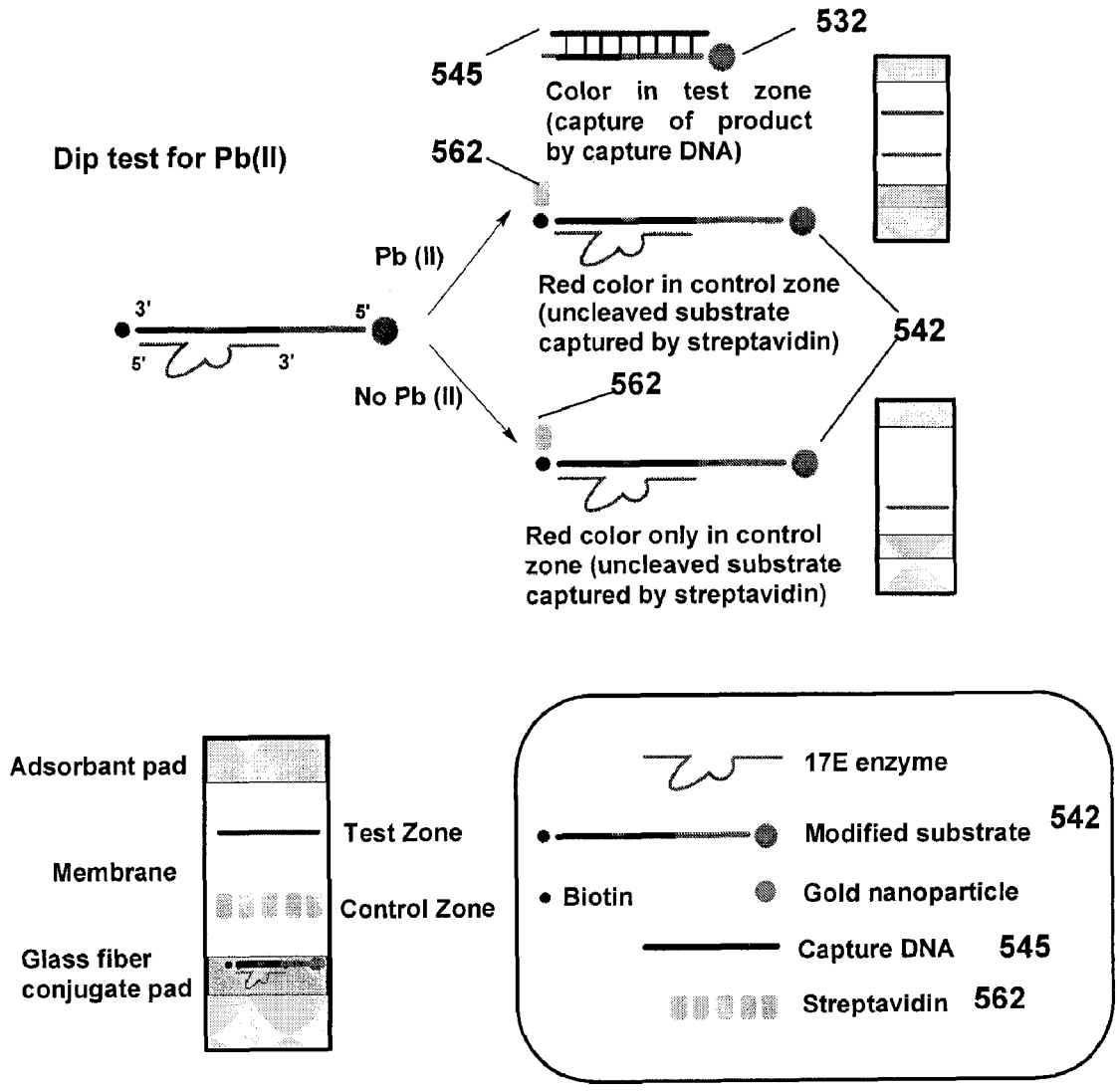

Dip test for Pb(II)
545
532
Color in test zone (capture of product by capture DNA)
562
Pb (II)
3'
5'
5'
3'
Red color in control zone (uncleaved substrate captured by streptavidin)
542
No Pb (II)
562
Red color only in control zone (uncleaved substrate captured by streptavidin)
Adsorbant pad
Test Zone
Membrane
Control Zone
Glass fiber conjugate pad
17E enzyme
Modified substrate
542
Biotin
Gold nanoparticle
Capture DNA
545
Streptavidin
562

FIG. 4

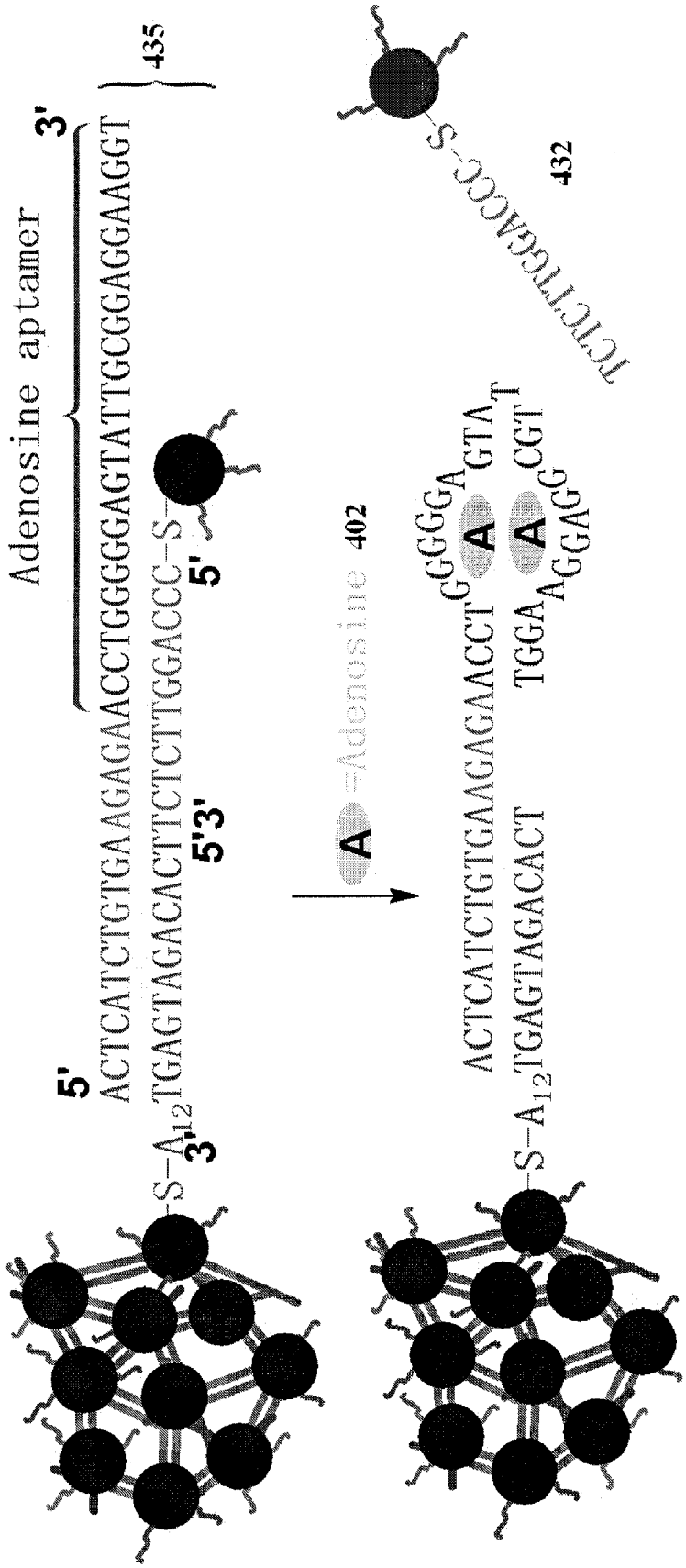

Adenosine aptamer
5'
3'
435
ACTCATCTGTGAAGAGAACCTGGGGAGTATTGCGGAGGAAGGT
5'3'
S–A12TGAGTAGACACTTCTCTTGGACCC–S–
3'
5'
A =Adenosine 402
ACTCATCTGTGAAGAGAACCT
TGGA
CGT
S–A12TGAGTAGACACT
TCTCTTGGACCC–S–
432

FIG. 5

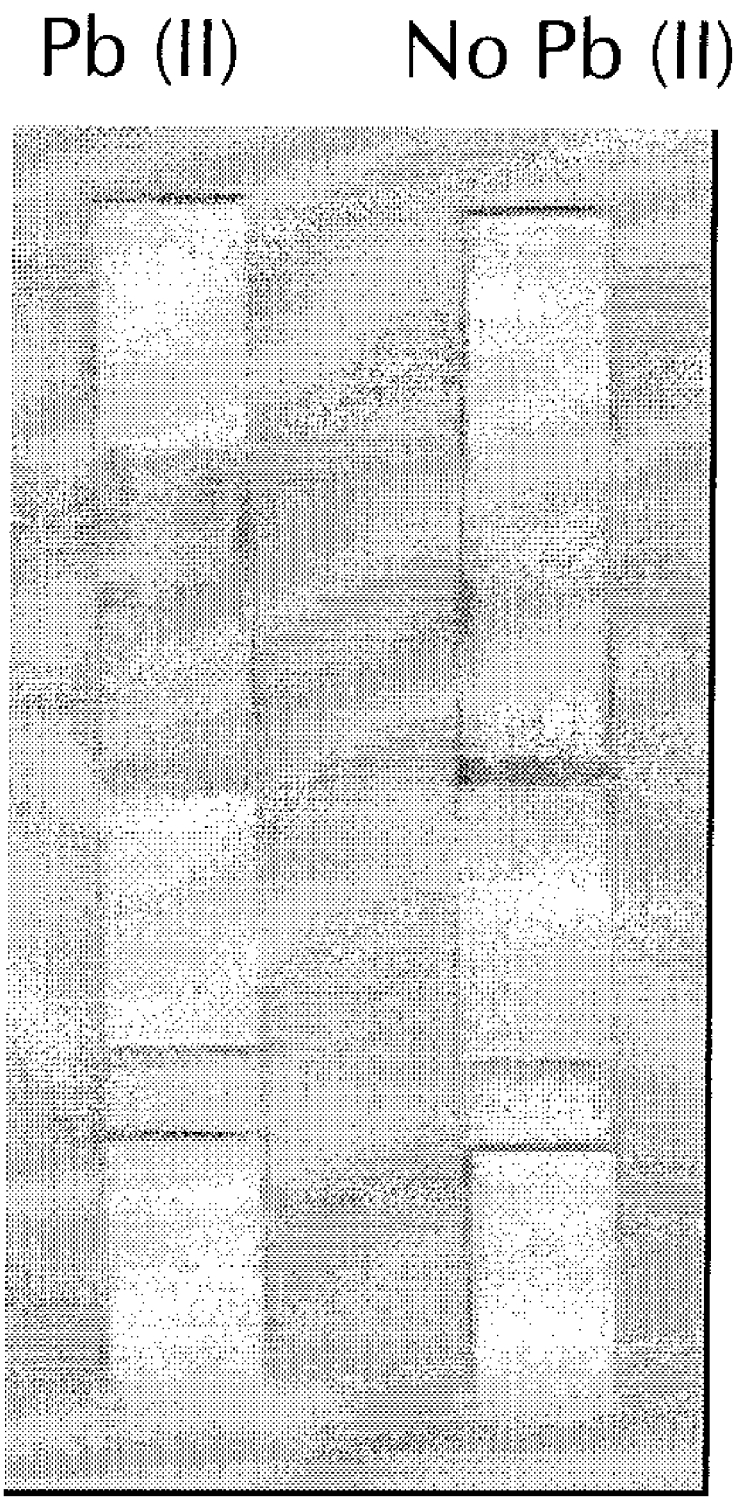


FIG. 7

FIG. 8

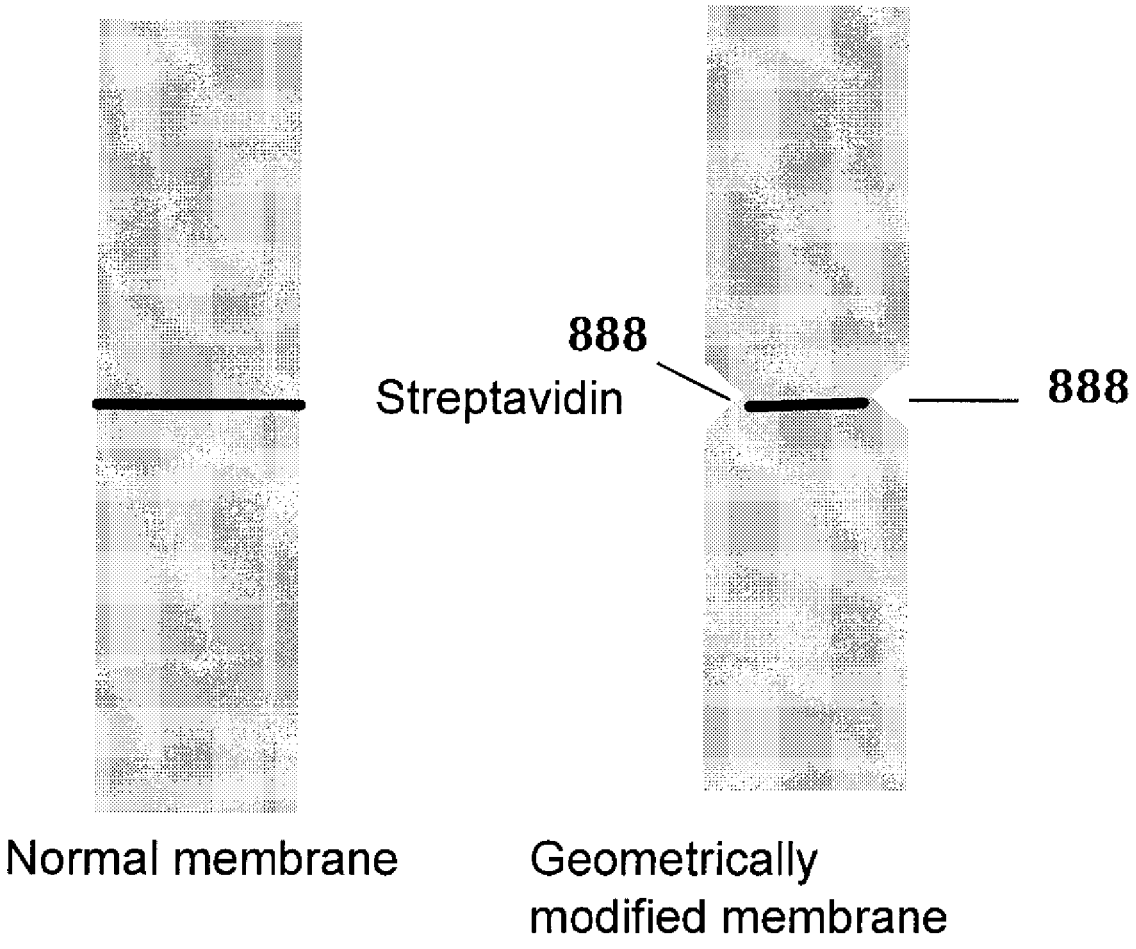

888
Streptavidin
888
Normal membrane
Geometrically
modified membrane

FIG. 9

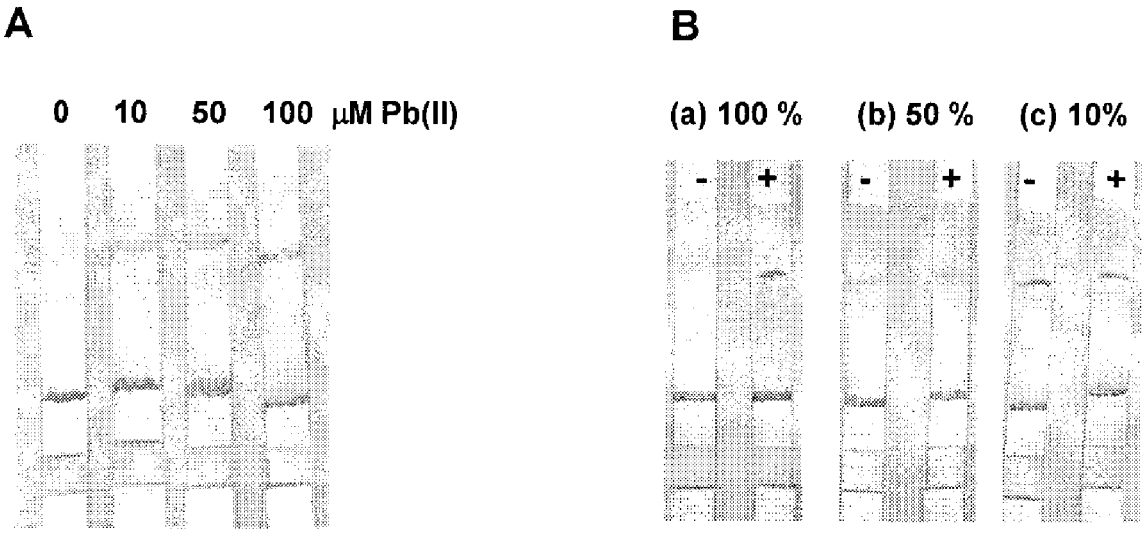


FIG. 10

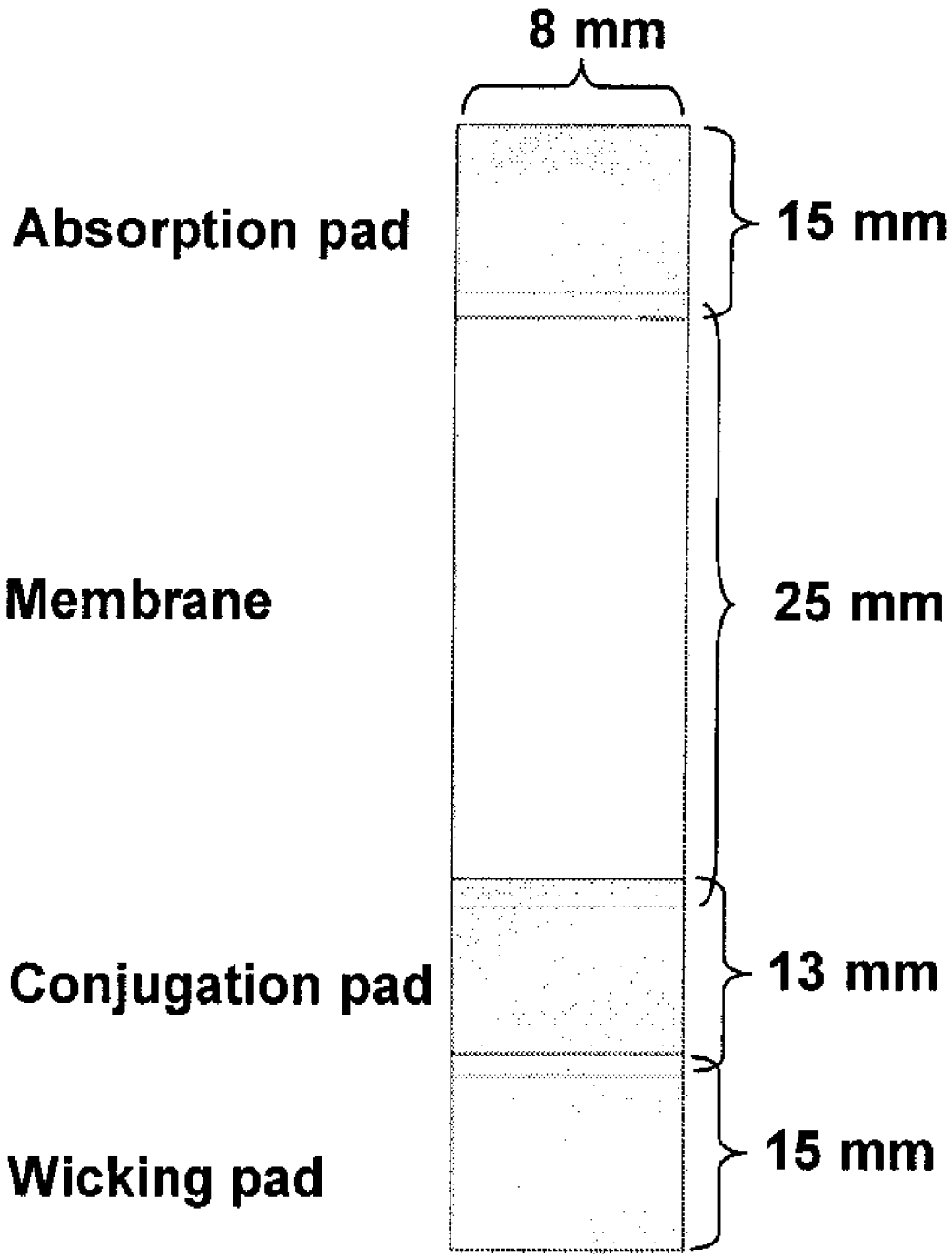

8 mm
Absorption pad
15 mm
Membrane
25 mm
Conjugation pad
13 mm
Wicking pad
15 mm

FIG. 11

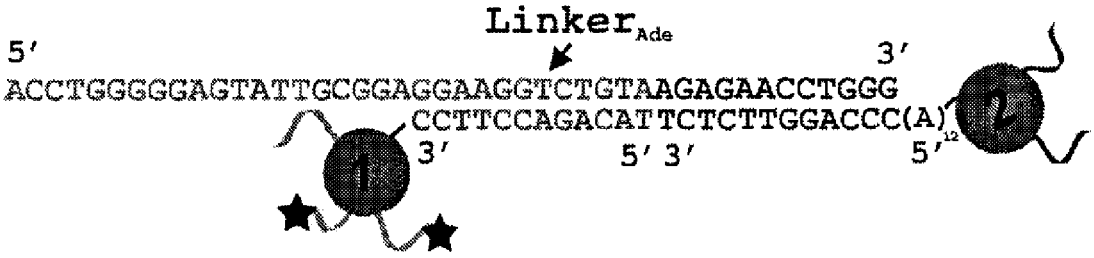

Linker Ade
5′
3′
ACCTGGGGGAGTATTGCGGAGGAAGGTCTGTAAGAGAACCTGGG
CCTTCCAGACATTCTCTTGGACCC(A)12
3′
5′ 3′
5′
1
2

FIG. 12

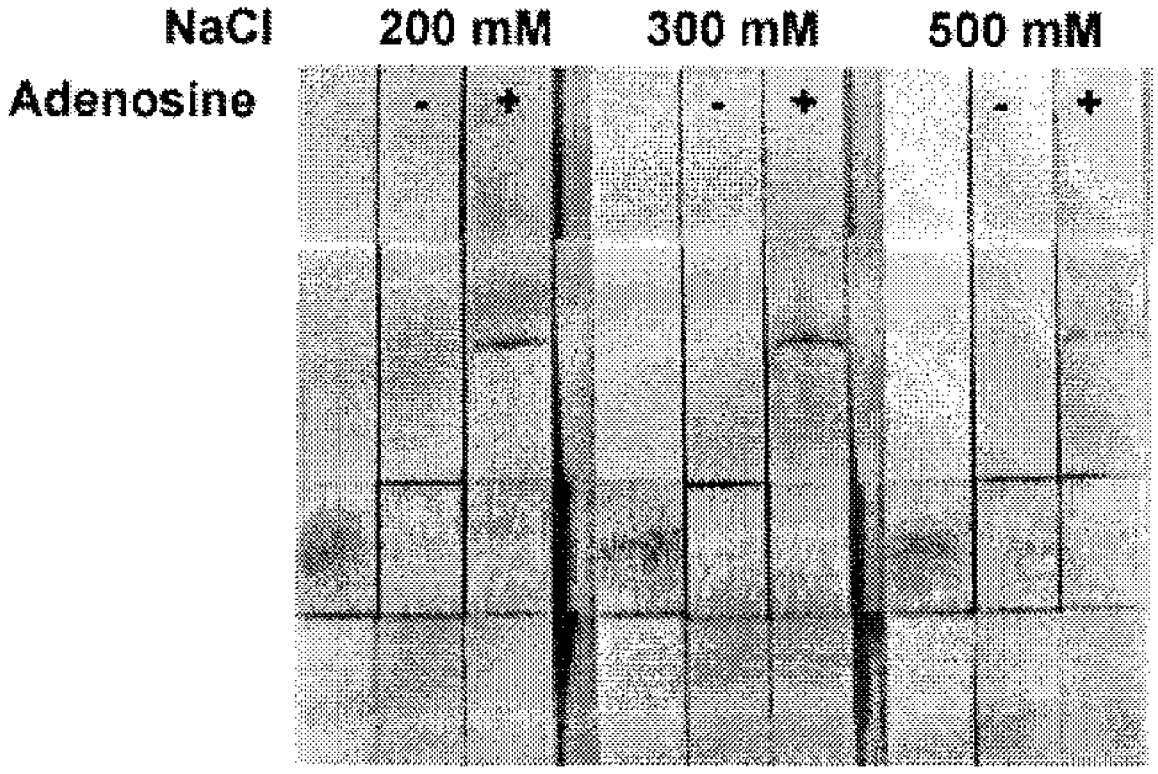


FIG. 13

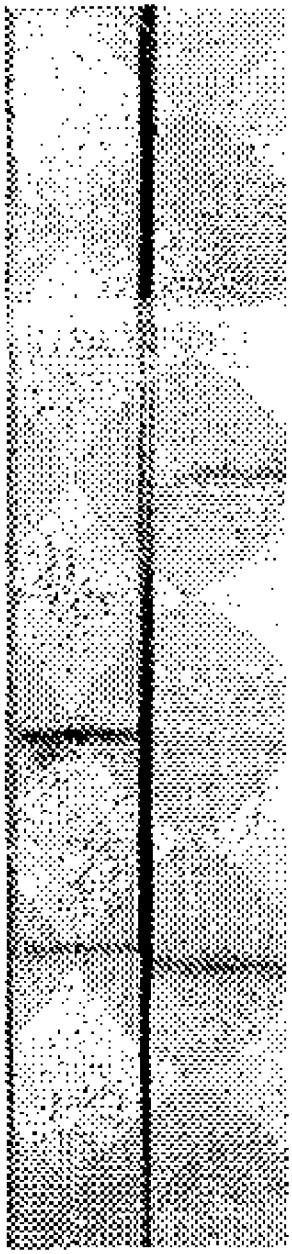


FIG. 14

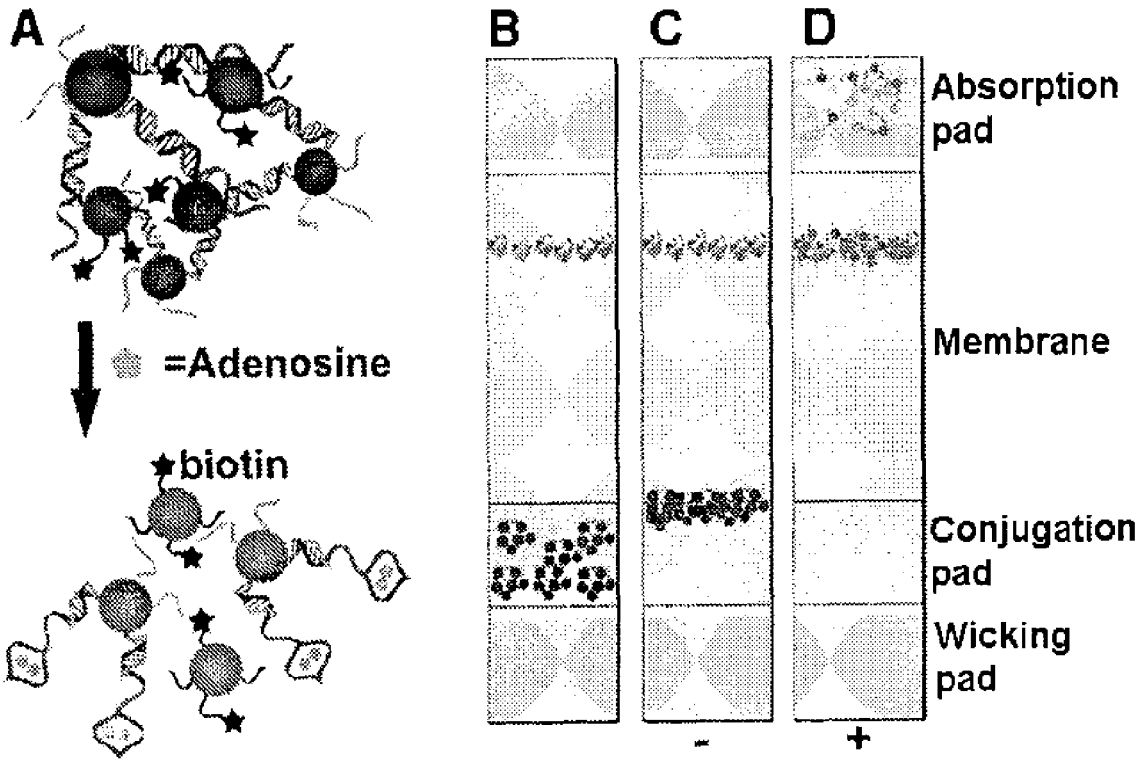
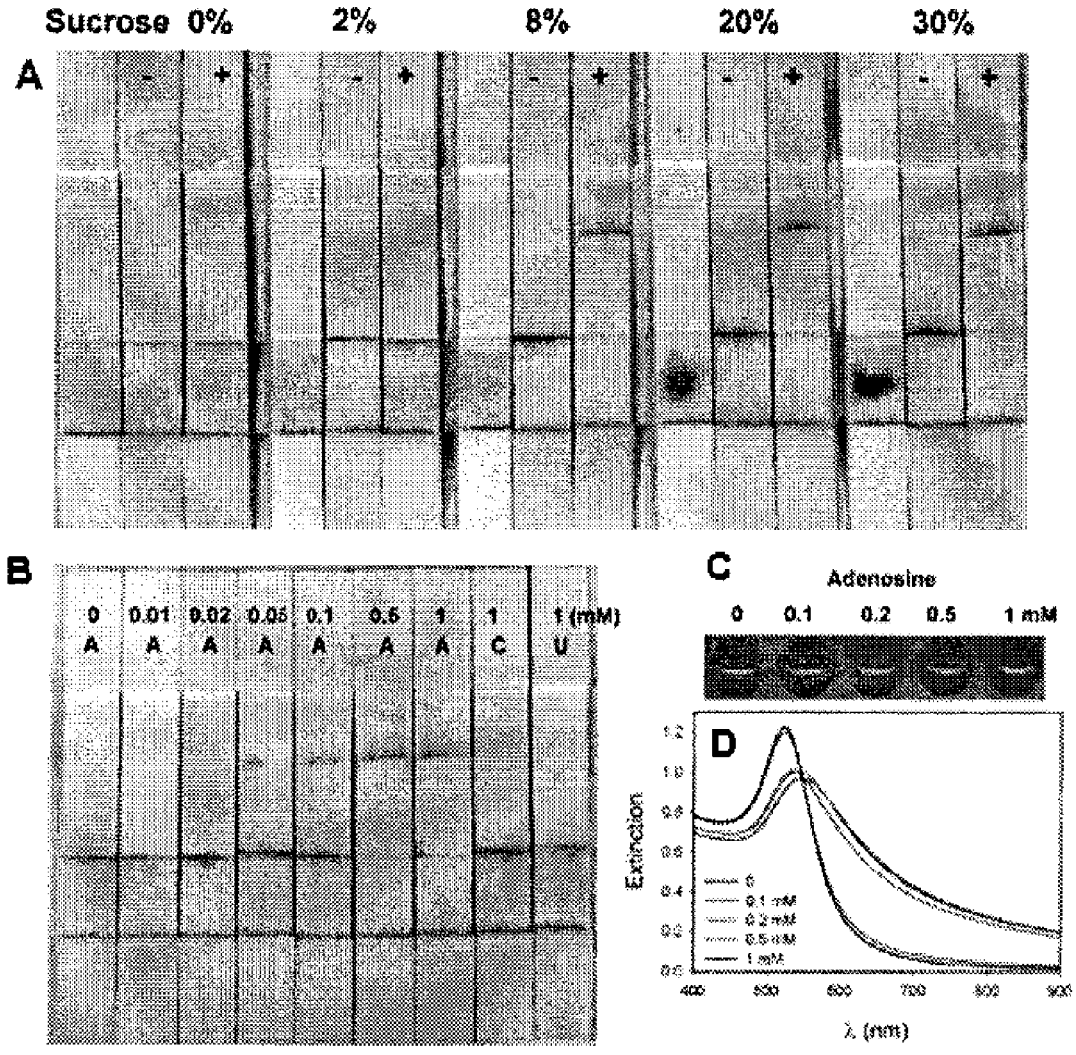

A
=Adenosine
biotin
B
C
D
Absorption pad
Membrane
Conjugation pad
Wicking pad
-
+

FIG. 15


Sucrose 0%
2%
8%
20%
30%
A
B
0 A
0.01 A
0.02 A
0.05 A
0.1 A
0.5 A
1 A
1 C
1 (mM) U
C
Adenosine
0
0.1
0.2
0.5
1 mM
D
Extinction
λ (nm)

LATERAL FLOW DEVICES

REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 60/782,949 entitled "Lateral Flow Devices" filed Mar. 16, 2006 and U.S. Provisional Application No. 60/821,043 entitled "Lateral Flow Devices" filed Aug. 1, 2006, which are incorporated by reference in their entirety.

FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

The subject matter of this application may have been funded in part under the following research grants and contracts: Contract Numbers DMR-0117792 and CTS-0120978 awarded by the National Science Foundation, Contract Number DEFG02-01ER63179 awarded by United States Department of Energy, and Contract Number DAAD19-03-1-0227 awarded by the Department of Defense. The U.S. Government may certain have rights in this invention.

BACKGROUND

The ability to determine the presence of an analyte in a sample is of significant benefit. For example, many metals and metal ions, such as lead, mercury, cadmium, chromium, and arsenic, pose significant health risks when present in drinking water supplies. To prevent the contamination of drinking and other water supplies, it is common to test industrial waste-streams before their release to the water treatment plant. Biological fluids, such as blood and those originating from body tissues, also may be tested for a variety of analytes to determine if the body has been exposed to harmful agents or if a disease state exists. There is also a need to test for other toxins, for example detection of trace amounts of anthrax in a variety of samples has recently emerged.

While many analyses are performed in solution, some have been adapted to lateral flow devices. Lateral flow devices may provide multiple advantages over solution methods, such as the ability to provide the reagents in a dry or nearly dry state. Lateral flow devices also may provide the user with a simple "all in one" kit, which has a long shelf life. However, conventional lateral flow devices are typically limited to detecting specific biological analytes.

Commonly available lateral flow devices include pregnancy test kits, which test for the presence of the hCG hormone. The analysis chemistry of these devices relies on a dye labeled antibody that binds to the hCG hormone, which is then trapped by a second antibody in a visualization zone. A disadvantage of this method is the need to isolate and synthesize an antibody specific to the analyte. Another conventional calorimetric lateral flow device detects a DNA analyte by hybridization with gold nanoparticles functionalized with complementary DNA (Glynou, K., et al., *Anal. Chem.,* 75, 4155-60 (2003)). A disadvantage of this method is that the analyte must be a bio-molecule capable of DNA hybridization.

SUMMARY

In a first aspect, the present invention is an analytical test for an analyte, comprising (a) a base, having a reaction area and a visualization area, (b) a capture species, on the base in the visualization area, comprising nucleic acid, and (c) analysis chemistry reagents, on the base in the reaction area. The analysis chemistry reagents comprise (i) a substrate comprising nucleic acid and a first label, and (ii) a reactor comprising nucleic acid. The analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising nucleic acid and the first label, and the capture species can bind the visualization species.

In a second aspect, the present invention is an analytical test for an analyte, comprising (a) a base, having a reaction area and a visualization area, (b) a capture species, on the base in the visualization area, and (c) analysis chemistry reagents, on the base in the reaction area. The analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising a first label, the capture species can bind the visualization species, and the visualization species does not comprise the analyte.

In a third aspect, the present invention is an analytical test for an analyte, comprising (a) a base, having a reaction area and a visualization area, (b) a capture species, on the base in the visualization area, and (c) analysis chemistry reagents, on the base in the reaction area. The analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising a first label, the capture species can bind the visualization species, and the capture species cannot specifically bind the analyte.

In a fourth aspect the present invention is a lateral flow device for an analytical test for an analyte, comprising (a) a base, having a reaction area and a visualization area, (b) a capture species, on the base in the visualization area, comprising nucleic acid, and (c) at least one reagent, on the base in the reaction area. The at least one reagent comprises a substrate comprising nucleic acid and a first label. The at least one reagent can react with a reactor and a sample comprising the analyte and water, to produce a visualization species comprising nucleic acid and the first label, and the capture species can bind the visualization species.

The following definitions are included to provide a clear and consistent understanding of the specification and claims.

The term "sample" is defined as a composition suspected of containing the analyte of interest that will be subjected to analysis. Typically, a sample for analysis is in liquid form, or can be converted into liquid form, and preferably the sample is an aqueous composition. A sample may be from any source, such as an industrial sample from a waste stream, or a biological sample such as blood, urine or saliva. A sample may be treated, such as by extract, dilution or filtration, or it may be a reconstituted precipitate from an industrial or biological source.

The term "analyte" is defined as one or more substances potentially present in a sample, for which the analysis tests. An analysis for an analyte determines the presence, quantity or concentration, of the analyte in the sample.

The term "analysis chemistry reagents" refers to one or more reagents, that when reacted with a sample containing an analyte, produce a visualization species. Preferably, the visualization species is produced in proportion to the amount or concentration of the analyte. Analysis chemistry reagents preferably include a reactor and a substrate. The "reactor" is at least one compound, moiety and/or material; the "substrate" is also at least one compound, moiety and/or material. When the reactor and the substrate are mixed with the analyte, they will react to produce a visualization species. As used herein, the term "produce" includes forming by chemical reaction, as well as releasing from being bound or attached to something else. Preferably, the reactor is specific for an analyte, and the substrate is specific for a reactor. Preferably, the substrate includes a label. The reactor and the substrate may be attached, for example covalently or by hydrogen bonding (hybridization).

The term "visualization species" is a compound, moiety or material that can be detected, such as a colored compound, a fluorescent compound, a magnetic material, a radioactive material, and the like. A visualization species includes a label, which is that part of the visualization species that allows for detection, for example a colored label (such as a dye or a colored particle, including semiconductor nanoparticles (quantum dots)), a fluorescent label (such as fluorescent compound), or a magnetic label (such as a magnetic particle). Preferably, the label of the visualization species originated as the label of the substrate. It is possible for the visualization species and the substrate to be the same.

The term "capture species" refers to a compound, moiety or material that will bind the visualization species. Optionally, the capture species specifically binds the visualization species. Preferably, the capture species does not substantially bind the verification species. Preferably, the capture species does not specifically bind the analyte, more preferably the capture species does substantially bind the analyte. The capture species may form part of the visualization species, for the visualization species may not be formed until after binding the capture species.

The term "verification species" means a compound, moiety or material that can be detected, such as a colored compound, a fluorescent compound, a magnetic material, a radioactive material, and the like. A verification species includes a label. The verification species is preferably different from the visualization species. Preferably, the verification species may be detected in the same manner as the visualization species.

The term "trapping species" refers to a compound, moiety or material that will bind the verification species. Optionally, the trapping species specifically binds the verification species. Preferably, the trapping species does not substantially bind the visualization species. The trapping species may form part of the verification species, for example the verification species may not be formed until after binding by the trapping species.

The term "specifically bind" means that binding between the two things is more favored binding, as compared to most other members of the same class or genus. For example, the binding between an antibody specific for an antigen, and the antigen; and hybridization between two complementary strands of DNA; are both examples of specific binding.

The term "calorimetric" is defined as an analysis where the reagent or reagents constituting the sensor system produce a color change in the presence or absence of an analyte, for example when the visualization species is colored.

The term "aptamer" refers to nucleic acid that specifically binds a target compound or moiety. The term "nucleic acid enzyme" (NAE) refers to nucleic acid that catalyses a chemical reaction (such as cleavage of a substrate) when it binds a specific cofactor (such as a divalent metal ion). Both an aptamer and a nucleic acid enzyme are examples of reactors.

The term "conformational change" refers to the process by which a nucleic acid, such as an aptamer, adopts a different secondary or tertiary structure. The term "fold" may be substituted for conformational change.

BRIEF DESCRIPTION OF THE DRAWINGS

The invention can be better understood with reference to the following drawings and description. The components in the figures are not necessarily to scale and are not intended to accurately represent molecules or their interactions, emphasis instead being placed upon illustrating the principles of the invention. In the figures, like referenced numerals designate corresponding parts throughout the different views.

FIG. **1**A represents a lateral flow device having reaction and visualization areas.

FIG. **1**B represents a lateral flow device including a membrane and wicking, conjugate, and absorption pads.

FIG. **2** represents a method of making a lateral flow device.

FIG. **3** represents an analysis using a lateral flow device.

FIG. **4** depicts a lateral flow device adapted for use with cleavage analysis chemistry.

FIG. **5** depicts a lateral flow device adapted for use with aggregate analysis chemistry. Figure discloses SEQ ID NOS 47-51, respectively, in order of appearance.

FIG. **6** represents aggregate units that aggregate to form analysis chemistry. Figure discloses SEQ ID NOS 52-53, respectively, in order of appearance.

FIG. **7** is a photograph of lateral flow devices.

FIG. **8** is a geometrically confined membrane; streptavidin is denoted as a black line.

FIG. **9** is a scanned images of lateral flow test for Pb(II), devices: (A) Tests done with different concentration of Pb(II); (B) Effect of varying the percentage of biotinylated substrate on the performance of the test.

FIG. **10** is a lateral flow device.

FIG. **11** shows DNA linkages in aptamer-assembled gold nanoparticle aggregates. Figure discloses SEQ ID NOS 52-53, respectively, in order of appearance.

FIG. **12** shows the effect of NaCl concentration during drying of the nanoparticle aggregates on the conjugation pad.

FIG. **13** shows the effect of NaCl concentration during drying of the nanoparticle aggregates on the conjugation pad.

FIG. **14** illustrates an aptamer/nanoparticle-based lateral flow device: (A) Adenosine induced disassembly of nanoparticles into red-colored dispersed nanoparticles—biotin is denoted as a black star; lateral flow devices loaded with the aggregates (on the conjugation pad) and streptavidin (on the membrane) before use (B), in a negative (C), or positive (D) test.

FIG. **15** shows a test for adenosine: (A) Performance of the test after drying with different sucrose concentrations; (B) Test of the lateral flow device with varying concentrations of nucleosides; (C) Scanned color of adenosine-dependent color change in solution phase; (D) UV-vis spectra of the solution samples in (C).

DETAILED DESCRIPTION

The present invention includes lateral flow devices that include analysis chemistry reagents, which preferably include aptamers or nucleic acid enzymes, allowing for adaptation of the device to many different analytes. Unlike conventional lateral flow devices, which rely on the analyte to bind specifically to a labeled species and travel to a visualization area where the analyte (now labeled) binds specifically to a capture species, the analysis chemistry of the present invention does not require specific binding of the analyte for binding of the visualization species by the capture species. Instead, the analyte reacts with the analysis chemistry reagents to produce a visualization species. Furthermore, the analysis chemistry reagents may be applied at any time prior to use, allowing for the manufacture of a large number of lateral flow devices, which can be used to analyze for any one of a large variety of analytes; the remaining analysis chemistry reagent or reagents that are specific for the analyte of interest can be applied to the lateral flow device just prior to sale or use, or may be added to the sample by the user.

Preferred methods of activating the release of the visualization species rely on the disaggregation of an aggregate, the cleavage of a substrate by a NAE, or a conformational change

of a nucleic acid. Because the analyte triggers the release of the visualization species, the visualization species does not depend on the analyte for its chemical nature, i.e. there is more than one visualization species that may be chosen, by selection of analysis chemistry reagents, for a given analyte. The lateral flow device may be designed to operate with only a single visualization species even for analyses of different analytes by changing analysis chemistry reagents; the device may be rapidly adapted to a different analyte by modifying the analysis chemistry reagents.

FIGS. **1**A-**1**B depict a lateral flow device **100** that includes a base **110**, a reaction area **120**, and a visualization area **130**. The visualization area **130** may include a first visualization zone **140** and optionally a second visualization zone **150**.

The base **110** may be made from any material that is compatible with the analysis chemistry and allows visualization species **135** (not shown) to travel from the reaction area **120** to the visualization area **130**. As depicted in FIG. **1**B, the base **110** may include a wicking pad **160**, a conjugate pad **170**, a membrane **180**, and an absorption pad **190** on a plastic backing (not shown). In one aspect, the membrane **180** may be present under one or more of the pads.

The reaction area **120** is where the analysis chemistry occurs (a chemical reaction between the analysis chemistry reagents and any analyte in the sample), and thus may include at least a portion of the conjugate pad **170** to provide a potential attachment site for some of the analysis chemistry reagents. The visualization area **130** is where the visualization species **135** are observed to determine the results of the analysis. In one aspect, the visualization area **130** includes at least a portion of the membrane **180**. The visualization area **130** may include one or more capture species that bind the visualization species **135** released from the reaction area **120** during the analysis. In a preferred aspect, the visualization area **130** includes at least two agents, a capture species and optionally a trapping species.

FIG. **2** represents a method **200** of making a lateral flow device, such as the lateral flow device **100** of FIG. **1**B. In **210**, the wicking pad **160** and the absorption pad **190** are optionally applied on the membrane **180**. In **220**, the conjugate pad **170** is applied on the membrane **180**. Depending on the analysis chemistry used with the device **100**, the composition of the conjugate pad **170** may be altered.

In **230**, the analysis chemistry reagents **235** that react with the analyte, to form a visualization species **232**, may be applied to the conjugate pad **170**. Optionally, in addition to the visualization species **232**, at least one verification species **242**, or reagents that will form at least one verification species, may be applied on the conjugate pad **170** in **240**.

The optional verification species **242** provides a species that is similar to the visualization species **232** that will travel from the reaction area **120** to the visualization area **130** of FIGS. **1**A-**1**B, regardless of the presence of the analyte. Thus, in one aspect, if the verification species **242** is not detected in the visualization area **130** during the analysis, the analysis has failed and the result should be discarded.

In **250**, preferably at least one capture species **252** is applied to one of the visualization zones **140**, **150** of FIG. **1**A. As depicted in FIGS. **1**A-**1**B, the visualization zones **140**, **150** may be present on the membrane **180**. Thus, if the visualization species **232** includes a gold nanoparticle functionalized with DNA (a colored species), the capture species **252** may be DNA complimentary to the DNA of the nanoparticle, which would specifically bind this visualization species. Nitrocellulose may be used as the capture species, which does not specifically bind this visualization species.

In **260**, preferably at least one trapping species **262** may be applied to one of the visualization zones **140**, **150** (FIG. **1**A), where the capture species **252** does not reside. Thus, if the first visualization zone **140** includes the trapping species **262**, then the second visualization zone **150** includes the capture species **252** and vice versa. For example, if the verification species **242** includes a gold nanoparticle functionalized with DNA and biotin, the trapping species **262** may be streptavidin, which specifically binds this verification species.

FIG. **3** represents an analysis **300** for determining the presence of an analyte **302** (not shown) with a lateral flow device, such as the device **305**. The lateral flow device **305** is depicted with a reaction area **320**, and first and second visualization zones **340**, **350**, respectively. The first visualization zone **340** is prepared with second DNA as the capture species **345**, while the second visualization zone **350** was treated with streptavidin **355** to serve as the trapping species.

The reaction area **320** is treated with analysis chemistry reagents that released gold nanoparticles functionalized with a first DNA complementary to a second DNA, in the presence of the analyte **302**. The reaction area **320** also is treated with verification species **342** in the form of gold nanoparticles functionalized with third DNA and biotin, capable of being bound by the streptavidin **355** (the trapping species) present in the second visualization zone **350**. The third DNA is not complementary to the second DNA **345** present in the first visualization zone **340**.

To begin the analysis **300**, a sample **301** (not shown) suspected of contain the analyte **302** is deposited on the reaction zone **320**. A liquid eluent, such as water including a buffer, is then applied to the left side of the device **305**. The eluent may be any liquid that does not interfere with the analysis chemistry and that has the ability to move the visualization species from the reaction area **320** to the visualization zones **340**, **350**. Preferably, the eluent is an aqueous solution. As the liquid travels through the reaction zone **320** and through the visualization zones **340**, **350**, three scenarios are possible, illustrated from the top down on the right side of FIG. **3**.

Post analysis lateral flow device **364** depicts a failed test where neither the analyte responsive species **332**, nor the verification species **342** reaches the visualization zones **340**, **350**. The failure of the verification species **342** to reach the visualization zone **350** may mean that the sample **301** was incompatible with the analysis chemistry or that the liquid eluent failed to transport the verification species **342**. In either instance, the analysis failed.

Post analysis lateral flow device **362** represents the scenario when the verification species **342** is trapped by the streptavidin **355** present in the second visualization zone **350**. The device **362** shows a color change in the second visualization zone **350** due to the arrival of the verification species **342**. Thus, the analysis is successful, but the sample lacked the analyte required to activate the analysis chemistry.

Post analysis lateral flow device **360** represents the scenario when the visualization species **332** is hybridized by the second DNA present in the first visualization zone **340** and the verification species **342** is trapped in the second visualization zone **350**. Thus, the analysis is successful and the sample included the analyte which activated the analysis chemistry to release the visualization species.

A variety of analysis chemistry, and hence analysis chemistry reagents, may be used, and may be selected based on the choice of analyte and label. For example, U.S. patent application Ser. No. 11/202,380 entitled "Aptamer-Based Colorimetric Sensor Systems" to Yi Lu et al., filed 11 Aug. 2005, describes an aptamer-based calorimetric sensor system, which produces a visualization species containing a nucleic

acid attached to a nanoparticle (which serves as the label); the analysis chemistry reagents form an aggregate, containing the visualization species and the aptamer. When the analyte is present, it specifically binds to the aptamer, preventing the aptamer from binding to the visualization species, and causing the visualization species to be released from the aggregate. Since different aptamers which specifically bind different analyte may be designed which will all form an aggregate with the same visualization species, all parts of the analytical test may be the same for different analytes, as long as the analysis chemistry reagents contain an aptamer which specifically binds the analyte of interest.

Table I below lists analytes, the aptamer or aptamers that bind with and fold in response to that analyte, and the reference or references where the sequence of each aptamer is described.

TABLE I

Analyte class	Example	Aptamer Motif Sequence (SEQ ID NO.)	Ref
Metal ions	K(I)	GGGTTAGGGTTAGGGTTAGGG (SEQ ID NO. 1)	1
	Zn(II)	AGGCGAGGUGAAAUGAGCGGUAAU AGCCU (SEQ ID NO. 2)	2
	Ni(II)	GGGAGAGGAUACUACACGUGAUAG UCAGGGAACAUGACAAACACAGGG ACUUGCGAAAAUCAGUGUUUUGCC AUUGCAUGUAGCAGAAGCUUCCG (SEQ ID NO. 3)	3
Organic dyes	Cibacron blue	GGGAGAATTCCCGCGGCAGAAGCCC ACCTGCCTTTGAACTCTATGTTATTGG GTGGGGGAAACTTAAGAAAACTACC ACCCTTCAACATTACCGCCCTTCAGCC TGCCAGCGCCCTGCAGCCCGGGAAG CTT (SEQ ID NO. 4)	4
	Malachite green	GGAUCCCGACUGGCGAGAGCCAGG UAACGAAUGGAUCC (SEQ ID NO. 5)	5
	Sulforhodamine B	CCGGCCAAGGGTGGGAGGGAGGGG GCCGG (SEQ ID NO. 6)	6
Small organic molecules	Biotin	AUGGCACCGACCAUAGGCUCGGGU UGCCAGAGGUUCCACACUUUCAUC GAAAAGCCUAUGC (SEQ ID NO. 7)	7
	Theophylline	GGCGAUACCAGCCGAAAGGCCCUU GGCAGCGUC (SEQ ID NO. 8)	8
	Adenine	GAUAGGACGAUUAUCGAAAAUCAC CAGAUUGGACCCUGGUUAACGAUC CAUU (SEQ ID NO. 9)	9
	Cocaine	GGGAGACAAGGATAAATCCTTCAATG AAGTGGGTCGACA (SEQ ID NO. 10)	10
	Dopamine	GGGAAUUCCGCGUGUGCGCCGCG GAAGAGGGAAUAUAGAGGCCAGCA CAUAGUGAGGCCCUCCUCCC (SEQ ID NO. 11)	11
Amino acids	Arginine	GGGAGCUCAGAAUAAACGCUCAAG GAGGACCGUGCACUCCUCGAACAU UUCGAGAUGAGACACGGAUCCUGC (SEQ ID NO. 12)	12
	Citrulline	GACGAGAAGGAGUGCUGGUUAUAC UAGCGGUUAGGUCACUCGUC (SEQ ID NO. 13)	13
Nucleosides & nucleotides	ATP	ACCTGGGGGAGTATTGCGGAGGAAG GT (SEQ ID NO. 14)	14
	cAMP	GGAAGAGAUGGCGACUAAAACGAC	15

TABLE I-continued

Analyte class	Example	Aptamer Motif Sequence (SEQ ID NO.)	Ref
		UUGUCGC (SEQ ID NO. 15)	
	GTP	UCUAGCAGUUCAGGUAACCACGUA AGAUACGGGUCUAGA (SEQ ID NO. 16)	16
	Guanosine	GGGAGCUCAGAAUAAACGCUCAAC CCGACAGAUCGGCAACGCCNUGUU UUCGACANGAGACACCGAUCCUGC ACCAAAGCUUCC (SEQ ID NO. 17)	17
	Adenosine	ACCTGGGGGAGTATTGCGGAGGAAG GT (SEQ ID NO. 18)	18
RNA	TAR-RNA	GCAGTCTCGTCGACACCCAGCAGCG CATGTAACTCCCATACATGTGTGTGCT GGATCCGACGCAG (SEQ ID NO. 19)	19
Biological cofactors	CoA	GGGCACGAGCGAAGGGCAUAAGCU GACGAAAGUCAGACAAGACAUGGU GCCC (SEQ ID NO. 20)	20
	NMN	GGAACCCAACUAGGCGUUUGAGGG GAUUCGGCCACGGUAACAACCCCU C (SEQ ID NO. 21)	21
	FAD	GGGCAUAAGGUAUUUAAUUCCAUA CAAGUUUACAAGAAAGAUGCA (SEQ ID NO. 22)	22
	Porphyrin	TAAACTAAATGTGGAGGGTGCGACG GGAAGAAGTTTA (SEQ ID NO. 23)	23
	Vitamin B12	CCGGUGCGCAUAACCACCUCAGUG CGAGCAA (SEQ ID NO. 24)	24
Amino-glycosides	Tobramycin	GGGAGAAUUCCGACCAGAAGCUUU GGUUGUCUUGUACGUUCACUGUU ACGAUUGUGUUAGGUUUAACUACA CUUUGCAAUCGCAUAUGUGCGUCU ACAUGGAUCCUCA (SEQ ID NO. 25)	25
Oligo-saccharides	Cellobiose	GCGGGGTTGGGCGGGTGGGTTCGC TGGGCAGGGGGCGAGTG (SEQ ID NO. 26)	26
Poly-saccharides	Sephadex	UACAGAAUGGGUUGGUAGGCAUAC CUAAUCGAGAAUGAUA (SEQ ID NO. 27)	27
Antibiotics	Viomycin	GGAGCUCAGCCUUCACUGCAAUGG GCCGCUAGGUUGAUGUGCAGUGA AGUCAGCUGAGGCCCAGGGCUGAA AGGAUCGCCCUCCUCGACUCGUGC CACCACGGUCGGAUCCAC (SEQ ID NO. 28)	28
	Streptomycin	GGAUCGCAUUUGGACUUCUGCCCA GGGGGCACCACGGUCGGAUCC (SEQ ID NO. 29)	29
	Tetracycline	GGCCUAAAACAUACCAGAUUUCGA UCUGGACAGGUGAAGAAUUCGACC ACCUAGGCCGGU (SEQ ID NO. 30)	30

TABLE I-continued

Analyte class	Example	Aptamer Motif Sequence (SEQ ID NO.)	Ref
	Vasopressin	ACGTGAATGATAGACGTATGTCGAG1 31 TGCTGTGTGCGGATGAACGT (SEQ ID NO. 31)	
Peptides	Substance P	GGGAGCUGAGAAUAAACGCUCAAG GGCAACGCGGGCACCCCGACAGGU GCAAAAACGCACCGACGCCCGGCCG AAGAAGGGGAUUCGACAUGAGGCC CGGAUCCGGC (SEQ ID NO. 32)	32
Enzymes	HIV Rev Tran- scriptase	UCCGUUUUCAGUCGGGAAAAACUG (SEQ ID NO. 33)	33
	Human thrombin	GGTTGGTGTGGTTGG (SEQ ID NO. 34)	34
Growth factors	$VEGF_{165}$	GCGGUAGGAAGAAUUGGAAGCGC (SEQ ID NO. 35)	35
Transcription factors	NE-κB	GGGAUAUCCUCGAGACAUAAGAAA CAAGAUAGAUCCUGAAACUGUUUU AAGGUUGGCCGAUCUUCUGCUCGA GAAUGCAUGAAGCGUUCCAUAUUU UU (SEQ ID NO. 36)	36
Antibodies	Human IgE	GGGGCACGTTTATCCGTCCCTCCTAG TGGCGTGCCCC (SEQ ID NO. 37)	37
Gene Regulatory factors	Elongation factor Tu	GGGGCUAUUGUGACUCAGCGGUU CGACCCCGCUUAGCUCCACCA (SEQ ID NO. 38)	38
Cell adhesion molecules	Human CD4	UGACGUCCUUAGAAUUGCGCAUUC CUCACACAGGAUCUU (SEQ ID NO. 39)	39
cells	YPEN-1 endothelial	ATACCAGCTTATTCAATTAGGCGGTG CATTGTGGTTGGTAGTATACATGAGC TTTGGTTGAGACTAGTCGCAAGATAT AGATAGTAAGTGCAATCT (SEQ ID NO. 40)	40
Viral/bacterial components	Anthrax spores Rous sarcoma virus	Sequences are not given AGGACCCUCGAGGGAGGUUGCGCA GGGU (SEQ ID NO. 42)	41 42

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Another example of analysis chemistry is described in U.S. patent application Ser. No. 10/980,856 entitled "Nucleic Acid Enzyme Light-Up Sensor Utilizing Invasive DNA" to Yi Lu et al., filed 3 Nov. 2004, describes a colorimetric sensor system which uses a nucleic acid substrate to form an aggregate, by hybridization of the substrate with nucleic acid attached to a nanoparticle. This system also produces a visualization species containing a nucleic acid attached to a nanoparticle. The analysis chemistry reagents comprise a nucleic acid enzyme, which in the presence of the analyte (for example, a metal ion) will cleave the substrate, releasing the visualization species from the aggregate. Again, nucleic acid enzymes which will cleave the same substrate, but in the presence of different analytes, may be prepared. Similarly to the system described above, all parts of the analytical test may be the same for different analytes, as long as the analysis chemistry reagents contain a nucleic acid enzyme which will cleave the substrate in the presence of the analyte of interest.

In a variation of this system, the substrate may be attached to the base in the reaction area at one end, and the other end attached to a label, such as a fluorescent compound or a particle; when the analyte of interest is present, the nucleic acid enzyme will cleave the substrate, releasing the visualization species which contains the label and a portion of the substrate. The attachment may be covalent, for example through an amine, thio or carboxyl group, or may be through physical adsorption. For a more detailed treatment of how to prepare oligonucleotide functionalized particles, See U.S. Pat. No. 6,361,944; Mirkin, et al., *Nature* (London) 1996, 382, 607-609; Storhoff, et al., *J. Am. Chem. Soc.* 1998, 20, 1959-1064; and Storhoff, et al., *Chem. Rev.* (Washington, D.C.) 1999, 99, 1849-1862. In another variation of this system, the nucleic acid enzyme, which is mostly sensitive to the presence of metal ions, can be replaced with an allosteric nucleic acid enzyme (aptazyme). In this system, nucleic acid complementary to the portion of the substrate that is present in the visualization species may be used.

Other systems are possible. For example, an analytic test for protease could use a protein which is cleaved by the protease. One end of the protein is attached to the base in the reaction area, and the other end of the protein attached to a label. In the presence of the protease, the protein would be cleaved, and a portion of the protein attached to the label would be released, as the visualization species. A capture species, such as an antibody specific for the portion of the protein, may be used.

As another example, an analytic test for an esterase may be made. Here, biotin attached to the base with an ester linkage, and having a label attached to the biotin, would be present in the reaction area. If an esterase were present in the sample, then the ester linkage would be broken, releasing the labeled biotin as the visualization species. A capture species, such as streptavidin, may be used.

The label of the visualization species and verification species allows for detection. Examples of labels include nanocrystals and quantum dots such as semiconductor nanocrystals and quantum dots, dyes, fluorophores, raman dyes, radioactive isotopes, magnetic particles and colored particles. Detection may be by any means or system which can detect the visualization and/or verifications species, including by the human eye and instrumentation such as a spectrophotometer.

The particles, which may be used as labels, include metals such as gold, silver, copper, and platinum; semiconductors, such as CdSe, CdS, and CdS or CdSe coated with ZnS; and magnetic colloidal materials, such as those described in Josephson, Lee, et al., Angewandte Chemie, International Edition (2001), 40(17), 3204-3206. Specific useful particles may include ZnS, ZnO, TiO_2, AgI, AgBr, HgI_2, PbS, PbSe, ZnTe, CdTe, In_2S_3, In_2Se_3, Cd_3P_2, Cd_3AS_2, InAs, and GaAs. A specific example is gold (Au) nanoparticles that have an average diameter of 5 to 70 nanometers (nm) or 10 to 50 nm.

FIG. **5** depicts aggregate analysis chemistry for use with the lateral flow device **100** (FIGS. **1**A-**1**B) where an aggregate composed of analysis chemistry reagents **435** disaggregates in the presence of the analyte **402**. In this manner, the disaggregated fragments of the aggregate serve as the visualization species **432** and travel from the reaction area **120** to the visualization area **130** (FIG. **1**A). Due to the physical size of the aggregates, the aggregates do not substantially travel away from the conjugate pad **170** (FIG. **1**B) until disaggregation.

FIG. **4** depicts analysis chemistry reagents **535** for use with the lateral flow device **100** (FIGS. **1**A-**1**B) where a nucleic acid substrate having a gold nanoparticle attached at the 5' end and a biotin moiety attached at the 3' end, is cleaved by a NAE that relies on the analyte as a co-factor. The substrate and the NAE, which together form the analysis chemistry reagents **535**, is on the conjugate pad **170** (for example, a glass fiber conjugate pad) (FIG. **1**B) of the device **100**; this forms the reaction area **120**. When cleaved by the NAE, the portion of the substrate functionalized to the nanoparticle becomes the visualization species **532** and travels from the reaction area **120** to the visualization area **130** (FIG. **1**A). In this example, the first visualization zone **140** contains the trapping species (streptavidin) **562**, and the second visualization zone **150** contains the capture species (DNA complementary to the portion of the substrate present in the visualization species) **545**. In this example, all species containing biotin are stopped at the first visualization zone. Therefore, if the analyte is not present, then the substrate is not cleaved and the verification species **542** is trapped at the first visualization zone and no visualization species **532** is produced. If the analyte is present, the at least some of the substrate is cleaved producing visualization species **532** which passes through the first visualization zone (since it does not contain biotin) and is captured by capture species **545** in the second visualization zone, and verification species **542** (present because an excess of the analysis chemistry reagents **535** is present) is trapped by the trapping species. Additional visualization zones containing the trapping species, streptavidin, may be included to reduce leakage of uncleaved substrate to reduce false positive results. Furthermore, the particles may be functionalized with a mix-

ture of substrate and non-substrate nucleic acid, to reduce the density of the substrate with biotin moiety.

Different shapes of the membrane, other than a rectangle, may be used to guide the flow so that the capture can be concentrated, or other beneficial effects can be generated. Shown in FIG. **8** are a normal rectangular membrane and a geometrically modified membrane. By cutting the membrane, the capture nanoparticles will be concentrated with a shorter width. The modification cuts **888** are illustrated in the figure.

The following examples are provided to illustrate one or more preferred embodiments of the invention. Numerous variations can be made to the following examples that lie within the scope of the invention.

EXAMPLES

All DNA samples were purchased from Integrated DNA Technology Inc., Coralville, Iowa. The aptamer linkers, substrates, and enzyme portions of the DNAzyme were purified by HPLC prior to use. Gold nanoparticles having an average diameter of 13 nm were prepared and functionalized with 12-mer thiol-modified DNA following literature procedures, such as those disclosed in Storhoff, J., et al., "One-pot calorimetric differentiation of polynucleotides with single base imperfections using gold particle probes," *JACS* 120: 1959-1964 (1998), for example. The average diameter of the functionalized gold nanoparticles was verified by transmission electronic microscope (JEOL 2010).

Example 1

Preparation of A Lateral Flow Device

A Millipore "Assembly Kit" (Cat#HF090AK020, Millipore, Billerica, Mass.) was used to assemble a lateral flow device. The kit contains a membrane on plastic backing (Hi-Flow Plus Cellulose Ester Membrane with capillary flow time of 90 sec/4 cm and a nominal thickness of 135 microns, HF 090 Type 60 mm×300 mm, directly cast onto a 2 mil polyester backing). The absorption pad (Sample pads (AP22) 20 mm×300 mm), conjugate pad (glass fiber conjugate pads 10 mm×300 mm), and wicking pad (adsorption pad) were assembled as shown in FIG. **1**A. The membrane was placed at the center of a plastic adhesive backing. The glass fiber conjugate pad was placed on one side of the membrane with part of the conjugate pad overlapping the membrane. Adsorbent pads were placed on each end of the adhesive strip. The 35 cm wide backing including the assembled components was then cut into 1 cm wide lateral flow devices for use. In this manner, the adsorbent pads were on each longitudinal end of the lateral flow devices.

Example 2

Preparation of Lateral Flow Device for Aggregate Based Analysis Chemistry

Ten μL of a prepared aggregate was dropped on the conjugate pad (10 mm width) of the lateral flow device of Example 1 and was allowed to dry. Four μL of 200 μM capture DNA having the sequence 3'-AGAGAAC-CTGGGTTTTTTTTTTTT-5' (SEQ ID NO: 43) was applied on the membrane portion of the device to form a capture zone. The capture DNA was complementary to the 5'-thiol-modified DNA functionalized nanoparticle described below with regard to Example 3. The device was allowed to dry at room temperature.

Example 3

Preparation of Aggregate Based Analysis Chemistry

Aggregate based analysis chemistry for application to a lateral flow device, such as the device of Example 2, was prepared by forming gold nanoparticle aggregates. FIG. **6** represents aggregate units **600** that aggregate to form the analysis chemistry. The units **600** were prepared by combining 6 nM of DNA functionalized nanoparticles **610** and 6 nM of DNA functionalized nanoparticles **620** with linker **630**. The linker **630** included an aptamer portion that folds in response to adenosine, the analyte. The functionalized nanoparticles **610**, **620** and the linker **630** were combined in an aqueous solution including 300 mM NaCl and 25 mM Tris acetate buffer, pH 8.2. The total volume of the sample was 500 μL. After combination, the mixture was stored at 4° C. for 1.5 hours as aggregates having a deep purple color formed. The mixture was centrifuged and the supernatant removed. The remaining aggregates were re-dispersed in 100 μL of an aqueous buffer solution containing 100% sucrose, 150 mM NaCl, and 25 mM Tris acetate, pH 8.2.

Example 4

Analysis and Detection of an Adenosine Analyte

A lateral flow device was prepared as described in Example 2 and equipped with the analysis chemistry from Example 3 to detect adenosine as an analyte in a sample. For detection, the device was dropped into a water solution containing either 5 mM adenosine or 5 mM uridine with various NaCl concentrations. For the samples containing adenosine, a red color was observed in the absorption pad of each device. However, no red color was observed for samples dipped in uridine. When the sample lacked NaCl, functionalized nanoparticle capture was substantially reduced. Capture was observed when either 100 or 200 mM of NaCl was added to the sample. Because capture was based on DNA hybridization, increasing the NaCl concentration increased capture. The experiment demonstrated that the lateral flow device can be used for the calorimetric detection of an analyte, such as adenosine.

Example 5

Preparation of Lateral Flow Device for Cleavage Based Analysis Chemistry

The lateral flow device was assembled as described in Example 1. Four μL of 10 mg/mL streptavidin (Promega Corp.) was applied on the membrane close to the conjugate pad of a lateral flow device. Further away from the conjugate pad, 4 μL of 1 mM capture DNA (capture-SH-mem-biotin-2) was applied on the membrane. The device was allowed to dry overnight.

FIG. **4** shows the scheme for a dip test for Pb(II). The substrate modified with gold nanoparticles is pre-hybridized with the DNA enzyme and then dried onto the conjugate pad. There are two capture areas on the membrane, called the control zone (with streptavidin) and the test zone (with DNA complementary to the 5' cleavage product, called capture DNA). When the test strip is dipped in a flow buffer the DNAzyme-gold nanoparticles are rehydrated. Any uncleaved substrate will be captured by streptavidin in the control zone, producing a red colored line. If the flow buffer contains Pb(II), cleavage reaction can occur and the 5' product of the substrate (containing the gold nanoparticles) can move fur-

ther on the membrane and be captured by a complementary DNA strand in the test zone. Thus two red bands on the membrane indicates the presence of Pb(II).

Example 6

Preparation of Cleavage Based Analysis Chemistry

Gold nanoparticles with an average diameter of 13 nm were functionalized with the chimeric substrate SH-mem-biotin-2 which has a thiol group on the 5' end and a biotin moiety on the 3' end. DNA was activated by adding tris-carboxy ethyl phosphine (TCEP) in the ratio of 1:2 (DNA: TCEP) and incubating at room temperature for 2 hours. The gold nanoparticles were functionalized by adding the activated DNA to the as prepared nanoparticles to a final DNA concentration of 3 μM (Typically 15 μL of 1 mM DNA is added to 5 mL of nanoparticles). After incubation for approximately 24 h, NaCl was added to a final concentration of 100 mM and the solution was incubated for one day.

The functionalized nanoparticles were then centrifuged at 13000 rpm for 20 minutes. The nanoparticles settled to the bottom and the supernatant containing free DNA was removed. The nanoparticles were then re-dispersed in an aqueous solution including 25 mM Tris-HCl, 100 mM NaCl, at a pH of 8.0 and the centrifugation step was repeated 2 more times. The nanoparticles were finally dispersed in a 50 mM Tris-HCl buffer solution (pH 8.0) containing 100% sucrose (weight/weight), 0.25% sodium dodecyl sulfate (weight/weight), and 100 mM NaCl to a nanoparticle concentration of ~30-50 nM (~400-600 μL total volume).

Table 1, below, provides the base sequences for the analysis chemistry reagents and the visualization area of a lateral flow device where Pb(II) (analyte), serves as the co-factor for the NAE.

Moiety	SEQ ID NO	Sequence 5'→3'
SH-mem-biotin-2	44	SSH-C6-AAGAAGAAGAAGAAGAAG CACTA T rAGGAAGAGATGTC-C6-Biotin
17E + 2-3	45	GACATCTCTTCTCCGAGCCGGTCGAAATAG TG
Capture-SH-mem-biotin-2	46	ATAGTGCTTCTTCTTCTTCTTCTT

Example 7

Analysis and Detection of a Lead Analyte: Synthesizing the Reaction Chemistry on the Device

A lateral flow device was prepared as described in Example 5 and equipped with the analysis chemistry from Example 6 to detect lead as an analyte in a sample. Eight μL of substrate functionalized gold nanoparticles and 1 μL of 1 mM enzyme 17E+2-3 in 25 mM Tris-HCl buffer, pH 8.0 was hybridized and applied on the conjugate pad. This was allowed to dry for at least 3 h. Ten μL of 4 mM Pb(II), was added on the adsorbent pad (reaction area) next to the conjugate pad. The control (no Pb(II)) was prepared by substituting the Pb(II) with water. The pad was dipped in a liquid flow buffer including 25 mM Tris-HCl (pH 8.0), 100 mM NaCl, 4% glycerol, and 0.1% SDS. After a few minutes, when the buffer had migrated completely to the top of the membrane, the pad was laid horizontally on a flat surface. Analyses were performed for multiple enzyme and lead concentrations. FIG. **7** is a photograph of the lateral flow devices tested in the presence and absence of the analyte, Pb(II).

Example 8

Analysis and Detection of a Lead Analyte: Synthesizing the Reaction Chemistry off the Device

FIG. **9***a* shows the result from an experiment carried out with different concentrations of Pb(II) in the flow buffer. In the absence of Pb(II), there is only one red line at the control zone. As the Pb(II) concentration is increased a red line of increasing intensity appears at the test zone. This test can be semi-quantitative as the ratio of intensity of color at the test zone versus intensity of color at the control zone will increase with increasing concentration of Pb(II).

The effect of using varying fractions of the biotinylated substrate to modify the gold nanoparticles was also investigated (FIG. **9***b*). Unlike in the case of the aptamer based lateral flow device, it is best to use 100% biotinylated substrate to modify the gold nanoparticles. Using a mixture of biotinylated substrate and non-biotinylated DNA leads to inefficient capture of uncleaved substrate at the streptavidin zone. Thus, as the fraction of biotinylated DNA is decreased, no difference can be seen between the Pb and no Pb case because the gold nanoparticles with uncleaved substrate can escape capture at the control zone and are non-specifically captured by DNA at the test zone.

Example 9

Analysis and Detection of a Lead Analyte: Synthesizing the Reaction Chemistry off the Device

Eight μL of substrate functionalized gold nanoparticles, 1 μL of 1 mM enzyme, and 1 μL of 500 μM Pb(II) (water used for the no Pb(II) control) was incubated in a tube at 37° C. for 10 minutes. The mixture was then applied to the conjugate pad and allowed to dry. The pad was then dipped in the flow liquid allowing the cleaved visualization species to migrate toward the visualization area of the device. In this example, the lateral flow device is simply being used to observe the reaction result, whereas the Pb(II) catalyzed cleavage reaction is performed off the device.

Example 10

Adenosine-Responsive Nanoparticle Aggregates Containing Two Kinds of DNA-Functionalized Gold Nanoparticles and an Aptamer DNA

a. Lateral Flow Device

Approximately 50% of the nanoparticles were functionalized with biotinylated thiol-modified DNA and the other 50% with thiol-modified DNA lacking the biotin group. The biotin group is denoted as a black star in FIG. **14**A. The biotin modification allows the nanoparticle to be captured by streptavidin. We chose to use 50% biotinylated DNA because 100% biotinylated DNA led to low nanoparticle aggregate yield (<20%), while 100% biotinylated DNA led to inadequate streptavidin capture (data not shown).

The Millipore Hi-Flow™ Plus Assembly Kit (Millipore Corporation, Bedford, Mass.) was used. The kit contains a Hi-Flow Plus Cellulose Ester Membrane with a nominal cap-

illary flow time of 90 seconds/4 cm and a nominal membrane thickness of 135 μm directly cast onto 2 mil polyester backing and placed on an adhesive card. The length of the membrane along the flow direction is 2.5 cm on the backing. The absorption pad and wicking pad were cut from Millipore cellulose fiber sample pads, and the conjugation pad was cut from the Millipore glass fiber conjugate pad. The absorption pad, wicking pad, and conjugation pad were attached to the adhesive card of the membrane in a way as shown in FIG. **10**. The overlap for each pad was ~2 mm, and the width was ~8 mm cut by a paper cutter.

The device included four overlapping pads placed on a backing with the overlaps being 2 mm (FIG. **14**B). The four pads are (from top to bottom): an absorption pad (15 mm), a membrane (25 mm), a conjugation pad (13 mm), and a wicking pad (15 mm). The nanoparticle aggregates were spotted on the conjugation pad while streptavidin (2 μL of 10 mg/mL) was applied on the membrane (FIG. **14**B), after which the whole device was dried overnight at room temperature before use. Nanoparticle aggregates are too large to migrate along the membrane, while dispersed nanoparticles can migrate. If the device is dipped into a solution without adenosine, the aggregates would be re-hydrated and would migrate to the bottom of the membrane where it would stop because of its large micrometer size (FIG. **14**C). In the presence of adenosine, the nanoparticles would be disassembled due to binding of adenosine by the aptamer (FIG. **14**A). The smaller dispersed nanoparticles can now migrate along the membrane and be captured by streptavidin to form a red line (FIG. **14**D).

b. Aptamer-Assembled Nanoparticle Aggregates

Gold nanoparticles (13 nm diameter) were synthesized by citrate reduction method following literature procedures. Thiol-modified DNA was activated with two equivalents of Tris(2-carboxyethyl)phosphine hydrochloride (TCEP). After mixing TCEP activated thiol-modified DNA (3 μM) and gold nanoparticles (~8 nM) at room temperature for 16 hours or longer, the solution was brought to 100 mM NaCl and 5 mM Tris acetate, pH 8.2. DNA-functionalized nanoparticles were purified by centrifugation and removal of supernatant before use. It needs to be noted that particle **1** (FIG. **11**) was functionalized with 2 kinds of 3'-thiol modified DNA with equal molar ratio. One DNA contained a biotin moiety at the 5'-end, and the other one did not contain a biotin; for functionalization, 1.5 μM of each DNA was added to the nanoparticles. Particle **2** was functionalized with only a 5'-thiol modified DNA. To prepare aggregates, 500 μL of each kind of nanoparticle was centrifuged to replace with a buffer containing 300 mM NaCl, 25 mM Tris acetate, pH 8.2 to a final total volume of 500 μL. One μL of 100 μM of the linking DNA was added and the mixture was placed at 4° C. for 6 hours. Dark purple precipitants were formed at the bottom of the tube. After very brief centrifugation, the supernatant was removed and the nanoparticle aggregates were dispersed in designated buffers (in most experiments: 8% sucrose, 200 mM NaCl, 25 mM Tris acetate, pH 8.2). In the presence of adenosine, the aptamer part (FIG. **11**, 5' to arrow) bound to adenosine and releases particle **1**. As a result, particle **1** and **2** were separated and the color of the nanoparticles turned red.

c. Apply Reagents to Lateral Flow Devices

Six μL of nanoparticle aggregates were spotted on each conjugation pad, and 2 μL of 10 mg/mL streptavidin was applied on the membrane by a 2 μL pipet to form a line. The loaded devices were stored in a drawer overnight before use.

d. Detection

Various concentrations of nucleosides were dissolved in a buffer containing 100 mM NaCl, 25 mM Tris acetate, pH 8.2. The wicking pad of each device was dipped into the solutions for ~20 seconds when the conjugation pad was fully hydrated and the liquid started to migrate on the membrane. Then the device was placed flat on a plastic surface for the flow to continue. A digital camera was used to take the pictures of the devices after ~5 minutes.

e. Effect of NaCl Concentration During Drying

Because the nanoparticle aggregates were stabilized by DNA base pairing interactions, NaCl concentration (ionic strength) played a very important role on the properties of the aggregates. The aggregates were dispersed in various concentration of NaCl: 200, 300, and 500 mM (all with 8% sucrose). The devices were tested with either no adenosine or 500 μM adenosine, and an untested device is also presented in FIG. **12** for comparison. At all the three salt concentrations, adenosine induced a red band; while no band was observed in the absence of adenosine. Five hundred mM NaCl gave the lowest band intensity, and therefore all future experiments used 200 mM NaCl.

f. Stability Studies on the Device

Preliminary studies on the stability of the devices were tested. After sitting at room temperature and unprotected conditions for a week, the devices were tested with solutions containing 0 or 500 μM adenosine (FIG. **13**). The device has retained its function because no red band was observed in the absence of adenosine (left panel, FIG. **13**), and a clear red band was observed in the presence of adenosine (right panel, FIG. **13**).

To successfully carry out the detection, the first challenge is to preserve the aptamer activity and the connections between nanoparticles in the dry state. Each aggregate contained thousands of DNA-linked nanoparticles. Directly drying the aggregates in buffer could lead to the loss of hydrogen bonds in the DNA. Sucrose is a commonly used additive to keep DNA in its native state, and the effect of sucrose on drying was first studied. Five conditions with varying sucrose concentrations were tested (FIG. **15**A). At each concentration, three devices were tested, with the first one being an unused device, the second one being a negative test (without adenosine), and the third one being a positive test (with 0.5 mM adenosine). Direct drying of aggregates on the conjugation pads deactivated the aggregates, and no red bands were observed in the presence of adenosine (FIG. **15**A, 0% sucrose). Interestingly, inclusion of 2% sucrose helped preserve the aggregates and a slight red band was observed on the membrane. With 8% sucrose, an intense red band was observed in the positive test, while no band was observed in the negative test. Instead, a dark band at the boundary between the conjugation pad and the membrane was observed. This observation supported the hypothesis that the aggregates cannot migrate along the membrane. The presence of unreacted aggregates on the boundary provides a useful control; if no such line is observed for a negative sample, the test is invalid, indicating poor re-hydration or flow of the device. Further increase of sucrose concentration up to 30% also showed intense red bands, but a slight band in the background could also be observed. Therefore, 8% sucrose during drying was chosen for further experiments. If the untested strips are compared (i.e., the first strip in each group), increasing the sucrose concentration led to a more intense color on the conjugation pads, even though the same amount of aggregates were applied to each pad. This result indicated that the nanoparticles were still in their native states; that strong individual and coupled surface plasmons still exist and that the nanoparticles had not collapsed due to drying.

Under the optimized drying conditions, the sensitivity and selectivity of the devices were tested. After drying overnight, the devices were dipped into buffers containing various

nucleoside species at different concentrations (FIG. **15**B). No red band was observed in the absence of adenosine. With increasing adenosine concentrations, more intense red bands were observed, and the detection limit was estimated to be ~20 μM. No red bands were observed with 1 mM cytidine or uridine, suggesting that the high selectivity of the aptamer had been maintained. For comparison, a solution phase reaction was carried out. Under optimized conditions, 500 μM of adenosine was needed to observe a red color (FIG. **15**C). The extinction spectra of the solution phase samples were also recorded on spectrophotometer (FIG. **15**D), and a small shift was observable with only 100 μM adenosine. This difference, however, cannot be distinguished by the naked eye. When the test results from solution phase and from lateral flow devices were compared, the flow device had at least 10-fold higher sensitivity if the naked eye was used as a detector.

While various embodiments of the invention have been described, it will be apparent to those of ordinary skill in the art that other embodiments and implementations are possible within the scope of the invention. Accordingly, the invention is not to be restricted except in light of the attached claims and their equivalents.

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What is claimed is:

1. An analytical test for an analyte, comprising:

(a) a base, having a reaction area and a visualization area,

(b) a capture species, on the base in the visualization area, comprising nucleic acid, and

(c) analysis chemistry reagents, on the base in the reaction area, comprising

(i) a substrate comprising nucleic acid and a first label, and

(ii) a reactor comprising nucleic acid,

wherein the analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising nucleic acid and the first label, and

the capture species can bind the visualization species,

wherein the reactor comprises a nucleic acid enzyme, and the substrate can be cleaved by the nucleic acid enzyme in the presence of the analyte.

2. An analytical test for an analyte, comprising:

(a) a base, having a reaction area and a visualization area,

(b) a capture species, on the base in the visualization area, comprising nucleic acid, and

(c) analysis chemistry reagents, on the base in the reaction area, comprising

(i) a substrate comprising nucleic acid and a first label, and

(ii) a reactor comprising nucleic acid,

wherein the analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising nucleic acid and the first label, and

the capture species can bind the visualization species,

wherein

the reactor comprises an aptamer,

the aptamer can bind the substrate,

the aptamer can bind the analyte, and

the aptamer cannot simultaneously bind both the analyte and the substrate.

3. The analytical test of claim **1**, wherein the reactor comprises an aptazyme.

4. An analytical test for an analyte, comprising:

(a) a base, having a reaction area and a visualization area,

(b) a capture species, on the base in the visualization area, comprising nucleic acid, and

(c) analysis chemistry reagents, on the base in the reaction area, comprising

(i) a substrate comprising nucleic acid and a first label, and

(ii) a reactor comprising nucleic acid,

wherein the analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising nucleic acid and the first label, and

the capture species can bind the visualization species,

wherein the analyte is a metal ion.

5. An analytical test for an analyte, comprising:

(a) a base, having a reaction area and a visualization area,

(b) a capture species, on the base in the visualization area, comprising nucleic acid, and

(c) analysis chemistry reagents, on the base in the reaction area, comprising

(i) a substrate comprising nucleic acid and a first label, and

(ii) a reactor comprising nucleic acid,

wherein the analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising nucleic acid and the first label, and

the capture species can bind the visualization species,

wherein the analyte is a lead ion.

6. An analytical test for an analyte, comprising:

(a) a base, having a reaction area and a visualization area,

(b) a capture species, on the base in the visualization area, comprising nucleic acid, and

(c) analysis chemistry reagents, on the base in the reaction area, comprising

(i) a substrate comprising nucleic acid and a first label, and

(ii) a reactor comprising nucleic acid,

wherein the analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising nucleic acid and the first label, and

the capture species can bind the visualization species,

(d) a trapping species, on the base in the visualization area,

wherein the analysis chemistry reagents can react with a sample comprising water, to produce a verification species comprising a second label, and

the trapping species can bind the verification species,

wherein

the reactor comprises a nucleic acid enzyme, and

the substrate can be cleaved by the nucleic acid enzyme in the presence of the analyte

the first and second labels comprise colored labels, or the first and second labels comprise fluorescent labels, and

the analyte is a metal ion.

7. An analytical test for an analyte, comprising:

(a) a base, having a reaction area and a visualization area,

(b) a capture species, on the base in the visualization area, and

(c) a trapping species, on the base in the visualization area, and

(d) analysis chemistry reagents, on the base in the reaction area,

wherein the analysis chemistry reagents can react with a sample comprising the analyte and water, to produce a visualization species comprising a first label,

the analysis chemistry reagents can react with a sample comprising water, to produce a verification species comprising a second label,

the capture species can bind the visualization species,

the trapping species can bind the verification species, and

the visualization species does not comprise the analyte.

8. The analytical test of claim **7**, wherein the capture species specifically binds the visualization species.

9. The analytical test of claim **7**, wherein the first label comprises at least one member selected from the group consisting of a colored label, a fluorescent label, a radioactive label and a magnetic label.

10. The analytical test of claim **7**, wherein the capture species specifically binds the visualization species, and the trapping species specifically binds the verification species.

11. The analytical test of claim **7**, wherein the first and second labels comprise colored labels, or the first and second labels comprise fluorescent labels.

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