Title: OPTICAL SENSOR AND METHODS FOR MEASURING MOLECULAR BINDING INTERACTIONS

Abstract: Methods and devices for the measurement of molecular binding interactions. Preferred embodiments provide real-time measurements of kinetic binding and dissociation of molecules including binding and dissociation of protein molecules with other protein molecules and with other molecules. In preferred embodiments ligands are immobilized within pores of a porous silicon interaction region produced in a silicon substrate, after which analytes suspended in a fluid are flowed over the porous silicon region. Binding reactions occur when analyte molecules diffuse closely enough to the ligands to become bound. Preferably the binding and subsequent dissociation reactions are observed utilizing a white light source and thin film interference techniques with spectrometers arranged to detect changes in indices of refraction in the region where the binding and dissociation reactions occur. In preferred embodiments both ligands and analytes are delivered by computer controlled robotic fluid flow control techniques to the porous silicon interaction regions through microfluidic flow channels.
OPTICAL SENSOR AND METHODS FOR MEASURING MOLECULAR BINDING INTERACTIONS

This application claims the benefit of provisional patent application Serial No. 60/399,524 filed 7/30/02 and is a continuation in part of Serial No. 10/616251 filed July 8, 2003. This invention relates to optical sensors and in particular to optical biosensors.

BACKGROUND OF THE INVENTION

The prior art includes a wide variety of optical sensors. An optical biosensor is an optical sensor that incorporates a biological sensing element. In recent years optical biosensors have become widely used for sensitive molecular binding measurements.

*Surface Plasmon Resonance*

An optical biosensor technique that has gained increasing importance over the last decade is the surface plasmon resonance (SPR) technique. This technique involves the measurement of light reflected into a narrow range of angles from a front side of a very thin metal film producing changes in an evanescent wave that penetrates the metal film. Ligands and analytes are located in the region of the evanescent wave on the backside of the metal film. Binding and disassociation actions between the ligands and analytes can be measured by monitoring the reflected light in real time. These SPR sensors are typically very expensive. As a result, the technique is impractical for many applications.

*Resonant Mirror*

Another optical biosensor is known as a resonant mirror system, also relies on changes in a penetrating evanescent wave. This system is similar to SPR and, like it, binding reactions between receptors and analytes in a region extremely close to the back side of a special mirror (referred to as a resonant mirror) can be analyzed by examining light reflected when a laser beam directed at the mirror is repeatedly swept through an arc of specific angles. Like SPR sensors, resonant mirror systems are expensive and impractical for many applications.
Thin Films

It is well known that monochromatic light from a point source reflected from both surfaces of a film only a few wavelengths thick produces interference fringes and that white light reflected from a point source produces spectral patterns that depend on the direction of the incident light and the index of refraction of film material. (See "Optics" by Eugene Hecht and Alfred Zajac, pg. 295-309, Addison-Wesley, 1979.)

U.S. Patent No. 6,248,539 (incorporated herein by reference) discloses an optical resonance technique that utilizes a very thin porous silicon layer within which binding reactions between ligands and analytes take place. The binding and disassociation affects the index of refraction within the thin porous silicon layer. Light reflected from the thin film produces interference patterns that can be monitored with a CCD detector array. The extent of binding can be determined from change in the spectral pattern.

Kinetic Binding Measurements

Kinetic binding measurements involve the measurement of rates of association (molecular binding) and disassociation. Analyte molecules are introduced to ligand molecules producing binding and dissociation interactions between the analyte molecules and the ligand molecules. Binding occurs at a characteristic rate \([A][B]k_{on}\) that depends on the strength of the binding interaction \(k_{on}\) and the ligand topologies, as well as the concentrations \([A]\) and \([B]\) of the analyte molecules A and ligand molecules B, respectively. Binding events are usually followed by a disassociation event, occurring at a characteristic rate \(k_{off}\) that also depends on the strength of the binding interaction. Measurements of rate constants \(k_{on}\) and \(k_{off}\) for specific molecular interactions are important for understanding detailed structures and functions of protein molecules. In addition to the optical biosensors discussed above, scientists perform kinetic binding measurements using other separations methods on solid surfaces combined with expensive detection methods (such as capillary liquid chromatography/mass spectrometry) or solution-phase assays. These methods suffer from disadvantages of cost, the need for expertise, imprecision and other factors.
Separations-Based Measurements

More recently, optical biosensors have been used as an alternative to conventional separations-based instrumentation and other methods. Most separations-based techniques have typically included 1) liquid chromatography, flow-through techniques involving immobilization of capture molecules on packed beads that allow for the separation of target molecules from a solution and subsequent elution under different chemical or other conditions to enable detection; 2) electrophoresis, a separations technique in which molecules are detected based on their charge-to-mass ratio; and 3) immunoassays, separations based on the immune response of antigens to antibodies. These separations methods involve a variety of detection techniques, including ultraviolet absorbance, fluorescence and even mass spectrometry. The format also lends itself to measure of concentration and for non-quantitative on/off detection assays.

What is needed is a device and method for efficiently making molecular binding measurements, including kinetic molecular binding measurements as well as concentration and non-quantitative on/off detection assays. In addition, such techniques and instrumentation should be capable of analyzing multiple samples in spatially distinct locations while keeping the locations accessible to microfluidic systems and each other, if necessary. Moreover, biosensors generally must meet needs relating to the sensitivity of detection to enable detection at very low sample concentrations, resolution of the molecules detected, speed and throughput of analysis to enable systematic consideration of multiple variables, and the overall cost of analysis. Typically, the choice of biomolecular sensors has involved severe trade-offs among the above factors. In order to optimize the efficacy and productivity of biomolecular analysis, there is a need for methodology and instrumentation to reduce the severity of the trade-off among the above factors. The present invention fulfills those needs and provides further related advantages.

SUMMARY OF THE INVENTION

This invention provides methods and devices for the measurement of molecular binding interactions. Preferred embodiments provide real-time measurements of kinetic binding and dissociation of molecules including binding and dissociation of protein molecules with other protein molecules and with other molecules. In preferred embodiments ligands are immobilized
within pores of a porous silicon interaction region produced within a crystalline silicon substrate and analytes are diluted in a fluid (buffer) and flowed over the porous silicon region. Binding reactions occur after analyte molecules diffuse closely enough to the ligands to become bound. Preferably the binding and subsequent disassociation reactions are observed utilizing a white light source and thin film interference techniques with spectrometers arranged to detect changes in indices of refraction in the region where the binding and disassociation reactions occur. In preferred embodiments both ligands and analytes are delivered by computer controlled robotic fluid flow control techniques to the porous silicon interaction regions through microfluidic flow channels. In a prototype unit designed as tested by applicants, four interaction regions are provided each with its own fluid delivery system and spectrometer so that up to four binding measurements can be made simultaneously. A special kinetic binding measurement model is provided to calculate apparent changes in the optical path difference (OPD) of each of the interaction regions from spectral patterns produced by spectrometers. In preferred embodiments these apparent changes in OPD are used to determine binding and disassociation rates.

In preferred embodiments novel techniques are used to immobilize the ligands in the porous silicon regions. Linker molecules are utilized to link the ligands to specially treated surfaces within the pores of the porous silicon. Preferred linker molecules includes a polyethylene glycol molecule specially assembled to link to the specially treated walls of the pores. These linker molecules in turn link to a variety of biomolecules, which function as ligands in the binding reactions with analytes of interest. Preferred embodiments of the present invention are capable of measuring surface concentrations of proteins at precision levels of 1 picogram per square millimeter.

**BRIEF DESCRIPTION OF THE DRAWINGS**

FIG. 1 is a drawing of a preferred optical biosensor unit according to the present invention.

FIG. 2 is a drawing showing flow channels and observation regions of a disposable fluidics cartridge.

FIG. 2A. is a prospective drawing of the FIG. 2 cartridge.
FIG. 3 is a cartoon drawing showing some of the features a preferred features of the present invention.

FIG. 4 is a graph showing variations in optical path difference of an interaction region with various molecule containing fluids occupying the interaction region.

FIG. 5 is a drawing showing a technique for avoiding diffusion between sample and buffer.

FIG. 6 is a drawing describing a technique for monitoring changes in optical path difference in an interaction region.

FIGS. 6A&B drawings are showing optical features of a preferred embodiment.

FIG. 7 is drawing showing magnified features of a porous silicon interaction region.

FIG. 8 is a drawing showing sample flow over a porous silicon interaction region.

FIG. 9 is a drawing showing techniques for linking a ligand to the walls of the pores in a porous silicon region.

FIG. 10 demonstrates binding and disassociation between a ligand and an analyte.

FIG. 11 demonstrates analyte concentrate vs. time in an observation region.

FIG. 12 shows graphs representing bound molecules as a function of time for the FIG. 11 situation.

FIG. 13 shows the major steps of a computer program for calculating binding parameters.

FIG. 14 is the same as FIG. 12 with noise simulated.

FIG. 15 demonstrates a technique for measuring binding reactions where optical path changes occur just above a porous silicon region.

FIGS. 16-21 are graphs explaining features of a mathematic model supporting embodiments of the present invention.

FIG. 22 is a computational flow chart for calculating OPD.

FIG. 23 is a schematic illustration of a preferred embodiment of the invention.

FIG. 24 is an illustration of a feature of a preferred embodiment.

FIGS. 25 – 28 demonstrate optical concepts important to embodiments of the present invention.
FIGS. 29 and 29A, B and C show a test set-up and test results to demonstrate features of the present invention.

FIGS. 30A & 30B are scanning electron microscope top view images of porous silicon suitable for use in the invention.

FIGS. 31A and 31B show features of an embodiment of the present invention.

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

*Observing Small Things with Long Wavelength Light*

For an understanding of the present invention the reader should keep in mind the sizes of various elements involved in the present invention. It is important to understand that, with this device, applicants are monitoring real time interactions of molecules such as proteins having dimensions as small as a few nanometers with visible light having wavelengths in the range of about 400 nm to 700 nm. These molecules are much too small to be imaged with light in these wavelengths; however, actions of these molecules can be determined because the speed of light is affected by their presence or absence in an interaction region. A light beam reflects from a top surface and a bottom surface of a thin porous silicon region to produce two reflected beams that interfere with each other. The interference produces spectral patterns that are a function of a phase delay of one of the beams relative to the other. This delay represents an apparent optical path difference and is referred to as an OPD. This OPD between the reference beam and the beam passing through the molecule containing solution can be monitored. Changes in the concentration of molecules within the interaction region produce apparent changes in the OPD. These apparent changes in OPD thus provide a measure of the concentration of the molecules in the solution.

*The Optical Biosensor*

FIG.1 is a prospective drawing showing some of the features of an optical biosensor 13 that uses a four channel fluidics cartridge for monitoring binding reactions. This unit includes robotic equipment 62, four spectrometers 71 A, B, C and D, light source 222, sample trays 55, buffer fluid tank 60A and waste tank 60B, sample pump 56 and buffer pump 58, sample injection port 66, control box 73 and pneumatic controls, firmware and software necessary for automated real-time measurements. In this unit a small (1.7 inch x 2.3 inch) disposable cartridge 42 shown in
FIGS. 2 and 2A provides four interaction regions at which molecular binding interactions can be optically observed. The disposable cartridge is inserted into fluidics enclosure 45 at location 47. Light from point light sources reflects from the top and bottom surfaces of each of each of the interaction regions and produces spectral interference patterns which are monitored in order to gather information regarding molecular binding interactions.

Fabrication Of Porous Silicon

In preferred embodiments these binding interactions occur in porous silicon regions of cartridge 42. The porous silicon regions are high surface area regions consisting of nanometer size pores in a crystalline silicon substrate. The pores are produced by an anodic electrochemical etch of bulk crystalline silicon. The starting material for porous silicon, for preferred embodiment, is a heavily doped crystalline silicon wafer, commercially available for semiconductor manufacturing purposes. Typical wafer specifications for porous silicon fabrication include p++-type boron doped silicon (0.6 – 1.0 mΩ-cm resistivity), <100> crystal orientation. The wafer is immersed in an ethanolic hydrofluoric acid solution (HF:ethanol, 3(v):1(v)) and a constant electric current is applied to the silicon wafer using a platinum electrode. The silicon atoms at the silicon/electrolyte interface are polarized, and are subject to attack by the fluoride ions in solution. Silicon atoms are released in the form of silicon hexafluoride. Porous silicon tends to etch as a distribution of long cylindrical nanotubes or pores 90 as shown in FIG. 7. Adjusting the current density and the etching time controls the distribution of pore diameters and the depth of the pores. Typical pore features for this invention are pore diameter distributions of 80 to 120 nanometers and pore depths of 1000 to 3000 nanometers. The depth of the pores is very uniform. This high uniformity of the etching process provides the two optically flat interfaces; the top surface 208 of the porous silicon, and the interface 210 between the bottom of the porous silicon region and the non-porous, or bulk, silicon. Additional details relating to this process are contained in U.S. Patent 6,248,539 that has been incorporated herein by reference.

For use in the present invention forty four porous silicon regions having dimensions of 2 mm x 11 mm are etched into a 100 mm silicon wafer. The wafer is then diced up into forty four individual die having dimensions of 10 mm x 13 mm, each referred to as a porous silicon die part 43. Flow channels about 2 mm wide are produced across the top of the porous silicon regions 202 with a machined plastic window 207 which is attached with epoxy to the silicon die 43. A
transparent plastic window 207 forms the top of the flow channels. Four flow channels 20A, 20B, 20C and 20D are thus created on each die part 43 and is incorporated into a plastic fluidics cartridge 42 containing elaborate microfluidic channels and pinch valves, all as shown in FIG. 2 and FIG 2A. Molecular interactions that occur in the porous silicon regions 202 at the bottom of the flow channels are observable through the transparent plastic window 207. We will refer in this specification to these regions of molecular interaction as interaction regions in some places and as observation regions in some cases.

FIG. 2 shows the four observation regions 20A, B, C, and D and flow channels for delivering sample fluids and buffer fluids to the four observation regions and for exhausting waste fluids. The fluidics cartridge includes 12 pneumatically controlled pinch valves 1-12. FIG. 2A is a prospective view of cartridge 42. The cartridge comprises the female portions of small tubing couplings 44. In this particular cartridge only five of the couplings are utilized as shown at 46, 48, 50, 52, and 54; the rest are blanks. In this embodiment, couplings 46-54 are automatically connected to mating sample, waste and buffer fluid channels in parts of the biosensor unit when the cartridge is inserted into its operating position in enclosure 45. These fluid channels include three waste channels connected to female coupling parts 54, 50 and 48, a sample channel in flow communication with coupling part 46 and a buffer flow channel in flow communication with coupling part 52. As shown in FIG. 3 the unit includes a one-half liter buffer tank 60 containing buffer solution and a first fluid pump 58, called the buffer pump, with valves 58A, 58B and 58C providing controlled buffer fluid flow at any flow rate between 1 to 100 microliters per minute. A preferred pump is a positive displacement piston pump available from Sapphire Engineering a division of Scivex Inc., with offices in Waltham, MA. Buffer flow from this pump enters the cartridge at location 52. The unit also includes a second fluid pump 56, called the sample pump, which like pump 58 is a positive displacement pump for providing both sample and buffer fluid flow into the fluidics cartridge at sample port 46. This pump 56 comprises valves 56A, 56B and 56C.

**Fluid Flow**
FIGS. 2, 3, 4 and 5 can be referred to in order to understand some of the typical automated steps for introducing both ligand and analyte into the observation regions (for example observation region 20A shown in FIG. 2). As explained above observation regions 20A, B, C and D include flow channels with the porous silicon regions forming the bottom of the flow channels. The observation regions each provides an optically observable region for immobilizing particular ligands which in turn bind to particular analytes which diffuse into and out of the porous silicon regions from a buffer solution flowing over the porous silicon regions. The objective of many experiments is to monitor this binding action and also in many cases a subsequent disassociation of the analyte from the ligand.

Portions of cartridge 42 may be flushed using buffer pump 58. Buffer solution can be pulled by pump 58 from tank 60 by closing valves 58B and C and opening valve 58A. The solution can then be pumped into cartridge 42 through port 52 to flush regions of the cartridge. Regions to be flushed are chosen by opening or closing various combinations of pinch valves 1-12 as shown in FIG. 2. Other portions of the cartridge can be flushed using sample pump 56. To do this, as shown in FIG. 3, computer controls are used to position robotic arm 62 so that sample needle 64 is inserted firmly into injection port 66 which is connected by tubing 68 to cartridge sample port 46. Similarly as above, pump 56 can pump buffer solution through flexible tubing 70, needle 64 and tubing 68 into sample port 46. As above, regions to be flushed are selected by appropriate combination of open and closed pinch valves 1-12 of cartridge 42. A preferred automated robotic liquid handling system is Gilson Model 223 available from Gibson, Inc. with offices in Middleton, WI.

Ligands and analytes may be flowed through observation regions 20A, B, C and D using sample pump 56 with computer controlled robotic arm 62. Ligands and analytes are located in sample vials in pre-selected locations as shown at 55 in FIG. 1. A few of these vials are also shown in FIG. 3 at 55A. A sample such as a ligand or an analyte is drawn from one of the vials 55A into needle 64 by closing valve 56C and 56B and opening valve 56C. Needle 64 is then moved by robotic arm 62 to port 66 and the sample is injected into cartridge 42 through port 46. Preferably, needle 64 is loaded with air bubbles on both sides of a useful slug of sample as shown at 72 in FIG. 5. This prevents diffusion in the needle and flow channels of sample and
buffer. A portion of the sample along with the air bubbles and some buffer is disposed as waste by appropriate valve control using valves 1-12 in cartridge 42.

**Kinetic Molecular Binding Measurements**

In preferred applications of the present invention protein molecules diluted in a buffer fluid are delivered to observation region 20A, B, C and D in order to set the initial conditions for kinetic binding measurements. The protein molecules bind to the pore walls at selected surface concentrations (pg/mm²) via special linker molecules. These protein molecules then function as ligands in a binding interaction to be monitored. Then, analyte molecules are delivered to the region in time sequences in order to provide real-time, kinetic binding measurements. Disposable microfluidics cartridge 42, displayed in FIG. 2, is a key component of fluid delivery subsystem. As described above, cartridge 42 contains microfluidic channels 74, approximately 25 – 75 microns wide, and pinch valves 1-12 to provide flow control. Silicon die 43, containing four observation regions 20A, B, C and D is incorporated in cartridge 42. An optical window 207 covers four observation regions and forms the top of four flow channels through the observation region. There is space of about 50 microns between the top of the porous silicon and the bottom of the window. Valves 1-12 along with pumps 56 and 58 are utilized as described above and are computer controlled to provide buffer solution, ligands, and analyte flow through the observation regions 20A, B, C, and D in order to perform desired binding analysis. Temperature equilibration regions 76 and 78 provide heat transfer for each upstream flow path in order that buffer, ligand and analyte fluid samples are delivered at a precisely controlled temperature.

FIGS. 6A and 6B show the integration of the optical and fluid delivery systems. The disposable fluidics cartridge 42 is thermally mounted on thermal block 82 in order to provide thermal control of both thermal equilibration regions 76 and 78 and the observation regions 20A, B, C, and D. A Peltier thermoelectric device 84 and a thermocouple temperature monitor 86 provide active temperature control of thermal block 82. Each of the four observation regions incorporates a separate optical measurement subsystem, as shown in FIGS. 6A and 6B. Four point white light sources are produced by white light lamp 222. Light from the lamp is collected into a single optical fiber and this fiber feeds the light into four separate optical fibers 236, A, B,
C, and D shown in FIGS. 6A and B. Light reflected from the four observation regions is collected in optical fibers 240 A, B, C and D as shown in FIGS. 6A and 6B and delivered by the fibers to spectrometers 71 A, B, C and D as shown in FIG. 1. As shown in FIG. 6C for each of the four optical systems (A B C and D), a lens 241 collimated the light from input fiber 236 and directs it at a slight angle to its respective observation region. Reflected light from the region is focused by the same lens into output fiber 240 which carries the reflected light to the respective spectrometer 71 (A B C or D).

For measurement of kinetic binding reactions, the concentration of analyte molecules \([A]_o\) in the observation regions (such as observation region 20A) should preferably remain as constant as feasible throughout the observation region during the measurement. This experimental condition is preferably achieved by (1) providing a continuous flow rate of analyte molecules through flow channel 61 directly above porous silicon region 202 or 150 and (2) allowing the basic diffusion mechanism to transport the analyte molecules into and out of the pores 90. FIG. 8 shows the basic geometry of the fluid flow in flow channel 61 above the porous silicon. The ideal flow sequence involved in a kinetic binding measurement features a blunt fluid interface, at time \(t = t_o\), between the buffer and analyte/buffer solutions directly upstream of observation region 20A. The analyte/buffer solution is located to the left of the \(t = t_o\) interface profile as shown in FIG. 8 and the buffer solution is located to the right of the \(t = t_o\) interface profile. Before \(t = t_o\), the buffer solution fills the pores 90 of observation region 20A, thus setting the baseline optical path differences of region 20A. At time \(t = t_o\), the flow system starts the flow of analyte/buffer solution via operation of the piston pump 56. FIG. 8 shows the parabolic fluid interface profiles between analyte/buffer and buffer solutions for successive times \(t = t_1\) through \(t = t_5\) that are a direct result of the parabolic-shaped fluid velocity profiles and the boundary condition that the velocity profiles terminate at zero velocity at the top and bottom walls of flow channel 61. Fluid flow prevents any significant quantity of the analyte/buffer solution to directly reach the surface of porous silicon observation region 20A, however, the parabolic fluid interface becomes infinitesimally closer to the surface of the region as time progresses. The basic diffusion mechanism enables the transport of analyte and buffer molecules across the fluid flow lines and into the porous silicon observation region. For some rough simplified calculations, to estimate the time for analytes to diffuse down into the pores 90, we will refer to this distance between the
bottom of the flow region and the mid region of the porous silicon interaction region 111 as a distance $\Delta x$. The average time $\tau$ that diffusion will transport an analyte molecule a distance $\Delta x$ is roughly estimated by:

$$\tau = (\Delta x)^2/D$$  \hspace{1cm} \text{Eq. (47)}

where $D$ [in units of $(\text{cm})^2/\text{sec}$] is the diffusion constant for a particular molecule. Diffusion constants for large biomolecules are typically in the $D = 2$ to $5 \times 10^{-7}$ cm$^2$/sec range. The design of flow channel 61 as shown in FIG. 8 provides a flow channel with a top to bottom width $w$ of about 36 $\mu$m and the average flow velocities in the range of 1 to 5 cm/sec. The analyte/buffer solution should be introduced, into the flow channel 61 quite close (such as 3-5 mm) to the porous silicon observation region. For example, an analyte molecule flowed to a location that is 6 $\mu$m on the average from ligand molecules immobilized within pores in the porous region of porous silicon die part 43, will diffuse to the ligands in a time $\tau$ of about $(6 \mu m)^2/(5 \times 10^{-7}$ cm$^2$/sec) = 0.7 sec. The average kinetic binding time constants are approximately 30 - 90 seconds or larger, so the diffusion time roughly calculated according to equation (47) will have negligible effect on the measurement of these binding constants.

**Example Demonstrating Chemical Features of Preferred Embodiments**

In addition to providing the key component for the optical measurement subsystem, the porous section observation regions 20A, B, C and D also serve as three-dimensional scaffolds to immobilize specific molecules. The regions provide a very large surface area in the form of cylindrical walls of pores 90. Ligand molecules are attached, or bound, to the pore walls 90 by the use of specific linker molecules. The linker molecules are attached to the pore walls by the use of surface chemistry, and the ligand molecules are then attached to the linker molecules.

FIGS. 9A-9F show a specific set of molecular interactions involved in an example of an application of the present invention. FIGS. 9A and 9B show steps a) and b) of a preferred method for immobilizing ligand protein molecules to the walls of pores 90. Steps a) and b) preferably are performed in a laboratory independent of the device shown in FIG. 1 and steps 9C-9F take place within the FIG. 1 device. The immobilization procedure is given here:
a) Hydrosilation of Porous Silicon Surface

The walls 102 of pores 90 of freshly etched porous silicon consists of hydride (Si-H) terminated silicon atoms as shown at 500 in FIG. 9A. The first step (step a) involves the hydrosilation of the hydride terminated porous silicon surface to produce a carboxylic acid functionalized (RCOOH) surface as shown at 502 in FIG. 9A. The preferred hydrosilation method involves exposing the hydride-terminated surface 500 to undecylenic acid 501 for two hours at an elevated temperature of 120 to 130 degrees Celsius.

b) Link Amino-dPEG₄ t-butyl ester to carboxylated Terminated Porous Silicon Surface

Amino-dPEG₄ t-butyl ester (NH₂-dPEG₄-t-butyl ester) is a commercially available linker molecule (Quanta Biodesign Ltd. with offices in Powell, Ohio) that consists of a polyethylene glycol molecule 104 (called PEG) with an amine (NH₂) group 503 attached to one end and a tert-butyloxycarbonyl (t-boc) group 106 attached to the other end of the PEG molecule 104, all as shown in FIG. 9B. The PEG molecule 104 consists of a plurality of PEG monomers, defined as (-CH₂-CH₂-O-)ₙ. The preferred length of the PEG molecule 104 is four PEG monomers; equivalent to a total length of about 19.2 angstroms (1.92 nm). The t-boc group 106 acts as a non-reactive cap that serves as a protecting group for the carboxylic acid on the molecule. It is not removed until an acid deprotection step that occurs within cartridge 42 after it is mounted in the FIG. 1 device. The NH₂-dPEG₄-t-butyl ester compound is dissolved in methylene chloride and the carboxylated terminated porous silicon die 43 is placed in a flask containing the NH₂-dPEG₄-t-butyl ester-methylene chloride solution. N,N'-dicyclohexylcarbodiimide (DCC) shown at 505 is added to the NH₂-dPEG₄-t-butyl ester-methylene chloride solution. DCC is used to facilitate the amide bond formation between the carboxylic acid terminated porous silicon surface 504 and the NH₂-dePEG₄-t-butyl ester compound. For twelve hours under an inert atmosphere, such as nitrogen, the reaction enables the amine terminated end 503 of the NH₂-dePEG₄-t-butyl ester compound to attach to the carboxylic acid terminated walls pores. The preferred method involves the linking of NH₂-dePEG₄-t-butyl ester molecules to the entire surface area of the pores 90 in the porous silicon observation regions 202. After this step, the porous silicon die 43 is incorporated in the microfluidics cartridge 42 as shown in FIGS. 2 and 2A and cartridge 42 is installed in the FIG. 1 optical biosensor device.

c) Create Reactive Carboxylic Acid Terminated Surface in Microfluidic Cartridge
The microfluidics cartridge 42 now containing the NH₂-dPEG₄-t-butyl ester prepared silicon die 43 is placed in FIG. 1 device for the remaining steps. Trifluoroacetic acid is flowed through a flow channel 61 (such as 20A). The acid diffuses into the pores 90; this removes the t-boc group 106, leaving a reactive carboxylic acid group (COOH) as shown at 506 in FIG. 9C. A solution of 1-(3-dimethylaminopropyl-3-ethylcarbodiimide) (EDC) molecules 110 and sulfo-N-hydroxysuccinimide (sulfo-NHS) ester molecules 112 is then flowed through flow channel 61 (as shown in FIG. 8). The advantage of adding sulfo-NHS to EDC reactions is that they are highly efficient and create stable intermediates that will eventually react with the amine of interest. EDC reacts with the carboxylate group on the deprotected NH₂-dPEG₄-t-butyl ester, creating an active O-aclylisourea leaving group. Forming a sulfo-NHS ester intermediate by reacting the hydroxyl group on the sulfo-NHS with the O-aclylisourea extends the half-life of the activated carboxylate to hours from seconds. The resulting surface is a NHS reactive binding site available for protein type conjugation via primary amines.

d) Immobilize Ligand Molecules to NHS Surface
In this preferred embodiment, the NHS modified surface will attach to free amine (R-NH₂) groups 120 located on the amino acid lysine which is one of many amino acids that comprise a protein molecules 122. Lysine, has a free amine group 120 that will attach to the surface via amide bond. The molecules designated as 122 in FIG. 9D will be treated as ligands in the following discussion concerning kinetic binding measurements. Preferably, the surface concentration of ligand molecules 122 as shown in FIG. 10 is low enough to allow ample space between receptor molecules. The space enables analyte molecules 124 to interact, or bind with ligand molecules 122 without any residual interaction with neighboring ligand molecules 122. The surface concentration of ligand molecules 122 is controlled by providing a low concentration of ligand molecules 122 in the buffer solution flowing through flow channel 61, and by measuring the optical path difference in real-time in order to provide information regarding the time to terminate the ligand molecule 122 immobilization process. After the ligand molecules 122 are immobilized, the remaining reactive binding sites 506 are capped, or rendered unreactive, by flowing a concentration of a small molecule such as ethanolamine or Tris to block any reactive NHS groups, so that binding of analyte molecules 124 will only occur with ligand molecules.
e) Binding Step
The chemistry associated with the actual binding step is demonstrated cartoon-like in FIG. 9E. Analyte molecules 124 diffusing down from continuous flow are attracted to ligands 122 as indicated at 126 in FIG. 9E and is bound as shown at 127.

f) Disassociation Step
For many binding reactions the binding is weak and temporary and after the analyte flow has been replaced with buffer flow the analyte molecules will disassociate from the ligand molecules. The amount of time necessary to remove analyte molecules completely from the surface depends on the binding strength of the biomolecular interaction between the ligand and the analyte. Ligand/analyte pairs that have a weak interaction can disassociate from each other very quickly and a buffer rinse may remove all the analyte present during a five-minute rinse step. A strong ligand/analyte interaction can disassociate at a very slow rate and by introducing a buffer step only a few analyte molecules are rinsed off during a five-minute rinse step.

g) Regeneration Step
The disassociation step can be and often is accelerated by a regeneration step in which a weak acid solution is flowed over the observation region. The weak acid decreases the pH of the solution and protonates the binding site between the ligand and analyte thus removing the analyte from the ligand. The regeneration step is always followed by a buffer rinse of the surface to bring the solution within the observation region back to a neutral pH.

Optical Path Differences

FIG. 4 is a graph providing a qualitative description of changes in optical path differences that may be measured using the equipment and techniques described above. Specifically this chart corresponds to Steps c-g with reference to FIGS. 9C – 9F as described in the proceeding section. The first two steps (a and b) are performed separately from the FIG. 1 device. When cartridge 42 is installed in unit 13 and buffer flow is initiated the measured optical path difference OPD would appear as shown at 600 in FIG. 4.
Additions of Trifluoroacetic acid (TFA) to remove the protective t-boc group 106 as shown in FIG. 9C will increase the index of refraction in the observation region and show up as an increase in the apparent OPD as shown at 602 but once the flow of buffer removes the TFA from the observation region, the OPD will decrease as shown at 604. The attachment of ligands, explained in step d and FIG. 9D appears as a gradual increase in the OPD (as shown at 606) as the ligands are covalently attached. When a sufficient quantity of ligands has been immobilized to the surface via the linker molecules the flow of ligands is stopped and replaced by a buffer flow resulting in a slight decrease in the OPD 608 as unattached ligand molecules flow out of the observation region with the buffer flow. The most important steps of the process then begin with the addition of the analyte as shown in FIG. 9E and as the analytes become bound to the ligands the measured OPD will increase as indicated at 610 in FIG. 4. The rate of increase and the equilibrium condition of the reaction are both important parameters with respect to a very large number of binding reactions that can be monitored with the present invention. Typically, after sufficient time has passed for the OPD to approach equilibrium as shown in FIG. 4, the analyte flow is replaced with buffer flow and the disassociation rate is monitored as shown at 612. After sufficient data has been collected to determine the disassociation rate, the unit can be ‘regenerated’ as described in the previous section with a weak acid solution with the effect shown at 614 in FIG. 4. Then restoration of the buffer flow restores the observation region to the condition shown at 606 as shown at 616. The unit is then ready for another experiment.

**Ligand – Analyte Binding Experiments For Device Demonstration**

The embodiment of the present invention shown in FIG. 1 may be used to test binding reactions of a very large number of molecules covering a wide range of reaction rates. Applicants have provided below four examples of ligand – analyte combinations that may be used to test the performance of this embodiment and to assure that it is functioning properly.

**Weak Interaction – DNSA/CAII**
For a weak interaction providing kinetics and equilibrium data, a good test is to use 5-dimethylamino-1-naphthalene-sulfonamide (DNSA) as the ligand and carbonic anhydrase isozyme II (CAII) as the analyte. Both proteins are available from Sigma Chemical with offices in St. Louis, MO.

**Fast On Rate, Moderate Off Rate (GFP/mAb)**

For a fast on rate and a moderate off rate, a good test set would be to use green fluorescent protein (GFP) as the ligand and monoclonal antibody (mAb) as the analyte. Both of these molecules are also available from Sigma Chemical.

**Moderate On Rate, Slow Off Rate (DNA/DNA)**

A good test for proteins with a moderate on rate and a slow off rate is to use DNA for both ligand and analyte. Reaction rates of these molecules are very well known. These molecules can be obtained from Sigma-Genosys, offices in The Woodlands, TX.

**Sensitivity of Analyte Assay (Anti-IgH/Human IgG)**

To determine the effectiveness of the device at checking the sensitivity of the analyte assay a good ligand analyte combination is Anti Immunoglobulin G (Anti-IgG) for the ligand and Human Immunoglobulin G (Human IgG) for the analyte. Both can be purchased from Pierce Chemical, with offices in Rockford, IL.

**TSH, Anti-TSH**

Another ligand-analyte example is the Human Thyroid Stimulating Hormone (TSH) and the anti-TSH antibody. This example is described in detail in a subsequent reactor of this specification.

**Software Control and Analysis**

The preferred embodiment shown in FIG. 1 includes a software control and analysis subsystem that automatically controls the timing sequence of fluid delivery of ligand and analyte molecules, monitors and/or records spectral patterns versus optical wavelength, computes optical path
difference (OPD) measurements from the spectral patterns, and stores in a personal computer the OPD data as a function time. This data represents kinetic binding data. Further analysis software calculates binding rate constants, \( k_{\text{on}} \) and \( k_{\text{off}} \), from groups of measured kinetic binding data. This software is based on a kinetic binding measurement model described below.

**Mathematical Model**

FIG. 6 is a sketch showing interferometric features of the present invention which will be referred to in order to explain some of the concepts on which this invention is based. (Some of these concepts are also explained at pages 295-309 in Optics by Eugene Hecht and Alfred Zajac, Addison Wesley.) Light beam (wavelength \( \lambda \)) from point source 222 is incident on a porous silicon interaction volume 202 in silicon substrate 204 at incident angle \( \theta_i \). The amplitude of electric field \( E_0(\lambda) \) of beam 212 is split at the first interface 208 at the top of porous silicon region 202 into two beams 214 and 216. The second beam 216 travels the path \( \overline{AB} \), is partially reflected at the second interface 210 at the bottom of region 202, and travels the path \( \overline{BC} \) to point C. The first beam 214 travels the path \( \overline{AD} \) and recombines as a linear superposition with the second 216 along the constant phase wavefront \( \overline{DC} \) 232. The optical path difference (OPD) of the interferometer is defined as

\[
\text{OPD} = n, (ps) \left[ \frac{\overline{AB}}{\lambda} + \frac{\overline{BC}}{\lambda} \right] - n, (buffer) \left[ \frac{\overline{AD}}{\lambda} \right] \tag{1}
\]

The corresponding optical phase difference associated with the OPD is given by

\[
\delta = \frac{4\pi l}{\lambda} \left( n,^2 (ps) - n,^2 (buffer) \sin^2 \theta_i \right)^{1/2} + \delta_o \tag{2}
\]

where \( \delta_o \) is a phase shift that occurs upon reflection of the second beam 216 at the second interface 210. The combined reflected beam 214 and 216 are subject to constructive or destructive interference that depends on the optical phase difference \( \delta \). (As described below, white light is used in preferred embodiments, which is equivalent to a very large number of overlapping monochromatic beams.) Total constructive interference of beams 214 and 216 occurs when
\[ \delta = 2\pi m \]  

where \( m \) is an integer. Thus, the interaction volume 202 functions as a porous silicon interferometer. The OPD can be expressed as

\[ OPD = 2L(n_s^2(ps) - n_r^2(buffer))\sin^2 \theta \frac{\sqrt{2}}{2 \pi} + \frac{\delta \lambda}{2\pi} \]  

(4)

The key optical features of the porous silicon interferometer are 1) the optical quality, partially reflective interfaces 208 and 210, and 2) the high degree of parallelism between the interfaces. The optical quality of the porous silicon optical interferometer 200 is determined primarily by the relatively small pore diameters (80 – 120 nm) compared to the wavelengths \( \lambda \) of the incident light (450 – 900 nm). The high degree of parallelism between interfaces 208 and 210 occurs as a natural spatial uniformity in the depth \( L \) of porous silicon interaction volume 202, as a result of the etching process.

**Optical Detector**

FIGS. 6A, 6B, and 6C display a preferred optical measurement layout. White light (450 – 900 nm) from a tungsten halogen lamp (preferably Ocean Optics Model LS-LL-1, shown at 222 in FIG. 1) is used to generate a simultaneous plurality of monochromatic light beams. The white light from lamp 222 is directed via a first fiber optic to an optical manifold where the light is divided into four optical fibers 236. One of these fibers is shown in FIG. 6C. Light from these four optical fibers is directed by lens 241 through optical window 207 as shown in FIG. 6A on to incident on the porous silicon interaction volume 202 at angle of incidence \( \theta_i \) as shown in FIG. 15A. For each of the four beams, light reflected from the interfaces 208 and 210 is directed back through lens 241 and through a second 400 micron diameter fiber optic 240 as shown in FIG. 6C to spectrometer 71 (preferably Tech5Helma Model MMS-1). FIG. 16 is a graphical representation of a mathematical model for a typical interference pattern 246 produced by the porous silicon interferometer that is measured as a function of light intensity versus optical wavelength \( \lambda \) by a linear photodiode array (preferably Hamamatsu Model 3904) incorporated at the optical output of the spectrometer. The interference pattern is unique for a given optical path difference. In preferred embodiments a change in the refractive index \( n_s(ps) \) of the porous silicon interaction volume 202 results in a change in the optical path difference that is measured as a
change of the entire interference pattern 243 versus wavelength \( \lambda \), as displayed in FIG. 16. It is assumed, in preferred embodiments that the optical path length corresponding to path \( \overline{AD} \) remains constant, thus acting as the reference path of the optical interferometer.

The model for the porous silicon interaction volume 202, displayed in FIG. 15 and consists of a plurality of cylindrical pores, or holes, 90 with pore diameter \( d \) and pore depth \( L \). The actual interaction region 202 consists of a distribution of pore diameters centered around an average pore diameter \( d \). The typical full width half maximum of the pore diameter distribution is approximately \( d/4 \). However, the actual pore depth distribution is tightly centered around the average depth \( L \) with the full width half maximum of the pore depth distribution approximately equal to the pore radius \( d/2 \). At the start of each experiment, the pores 90 are typically filled with buffer solution with index of refraction \( n_i(\text{buffer}) \).

The complex index of refraction \( n(ps) = n_r(ps) + in_i(ps) \) of the interaction volume 202 includes real and imaginary components. The imaginary component \( n_i(ps) \) is related to absorption of light and the real component \( n_r(ps) \) is related to changes in the speed of light, in the porous silicon interaction volume 202. The preferred embodiment of the optical biosensor exploits the measurement of changes in the real part \( n_r(ps) \) of the index of refraction of the interaction volume 202, which is modeled, using the effective medium approximation, as a volumetric average of the real part of the index of refraction \( n_r(\text{silicon}) \) of the bulk silicon and the real part of the index of refraction \( n_r(\text{med}) \) of the material, or medium, filling the pores 50,

\[
 n_r(ps) = (1 - P)n_r(\text{silicon}) + Pn_r(\text{med}) \quad \text{Eq. (5)}
\]

The porosity \( P \) is defined as the volume of the pores 90 divided by the total volume of the interaction volume 202. The pore diameter \( d \), pore depth \( L \), and porosity \( P \) are achieved by control of the porous silicon etching parameters including etching current density, etching time, hydrofluoric acid concentration, and conductivity of the bulk silicon. Typical porosities \( P = 0.80 - 0.95 \) are used for protein binding measurements. If we use parameters \( n_r(\text{silicon}) = 3.7 \), \( n_r(\text{med}) = n_r(\text{buffer}) = 1.33 \), and \( P = 0.80 \), then equation (5) gives \( n_r(ps) = 1.804 \).
In the preferred embodiment, the invention is used to measure the surface concentration of a monolayer 93 of molecules (ligands and analytes) that are attached to the cylindrical walls of pores 90. We will sometimes in this analysis refer to this monolayer of molecules as a monolayer of proteins. The index of refraction \( n_r(\text{med}) \) of pores 90 changes slightly due to attachment, via linker chemistry, of ligand molecules B to the walls of pores 90. The index of refraction \( n_r(\text{med}) \) of pores 90 also changes slightly due to the binding of analyte molecules 124 to the ligand molecules 122 attached to the walls of pores 90. The change in the index of refraction \( n_r(\text{med}) \) of pores 90 results in a change in the index of refraction \( n_r(\text{ps}) \) of the PS interaction volume as described by equation (5). The index of refraction \( n_r(\text{med}) \) of the medium filling the pores is modeled, using the effective medium approximation, as a volumetric average of the index of refraction \( n_r(\text{buffer}) \) of the buffer solution and the index of refraction \( n_r(\text{protein}) \) of the protein monolayer 93 on the walls of pores 90,

\[
n_r(\text{med}) = \frac{V_{\text{buffer}}}{V_{\text{med}}} n_r(\text{buffer}) + \frac{V_{\text{prot}}}{V_{\text{med}}} n_r(\text{protein}). \tag{6}
\]

where \( V_{\text{med}} = \frac{\pi d^2 L}{4} = V_{\text{buffer}} + V_{\text{prot}} \) is the total volume of a single pore 90.

The volume of the protein monolayer layer 93, displayed in FIG. 4, is modeled as

\[
V_{\text{prot}} = \left[ \frac{\pi d^2 L}{4} - \frac{\pi (d - 2 \rho)^2 L}{4} \right] F. \tag{7}
\]

where \( \rho \) is the thickness of the protein monolayer 93. The variable \( F \) \((0 < F < 1)\) accounts for the fractional surface coverage of the protein monolayer 93. Also, the model assumes that the volumetric coverage of the bottom of pore 90 is negligible compared to the volumetric coverage of the cylindrical pore wall. The volume of the buffer is then

\[
V_{\text{buffer}} = V_{\text{med}} - V_{\text{prot}} = \frac{\pi d^2 L}{4} - \left[ \frac{\pi d^2 L}{4} - \frac{\pi (d - 2 \rho)^2 L}{4} \right] F. \tag{8}
\]
Inserting equations (6) through (8) into equation (5) gives

\[ n_r(ps) = (1 - P)n_r(silicon) + Pn_r(buffer) + P \frac{4 \rho}{d} \left( 1 - \rho \frac{d}{d} \right) \Delta n_r F \]  

Eq. (9)

where \( \Delta n_r = n_r(protein) - n_r(buffer) \). The typical index of refraction for a 50,000 to 150,000 Dalton protein is \( n_r(protein) = 1.42 \). For a typical protein monolayer thickness \( \rho \) and pore diameter \( d \), we can approximate \( 1 - \rho \frac{d}{d} = 1 \). If we use parameters \( n_r(silicon) = 3.7 \), \( n_r(buffer) = 1.33 \), and \( P = 0.80 \), \( d = 100 \text{ nm} \), then equation (9) gives

\[ n_r(ps) = 1.804 + \left( 0.00288 \text{ nm}^{-1} \right) F \rho \]  

Eq. (10)

FIG. 17A displays \( n_r(ps) \) versus fractional surface coverage \( F \) for 150,000 Dalton protein molecules (\( \rho = 8 \text{ nm} \)).

The invention measures changes in OPD, given by equation (4), due to changes in the index of refraction \( n_r(ps) \) of the interaction volume 202. Combining equation (9) with equation (4) gives

\[ OPD = 2L \left[ (1 - P)n_r(silicon) + Pn_r(buffer) + P \frac{4 \Delta n_r}{d} \left( 1 - \rho \frac{d}{d} \right) F \rho \right]^2 - n_r^2(buffer) \sin^2 \theta_i \]  

\[ \frac{\delta \lambda}{2\pi} \]  

Eq. (11)

The fractional surface coverage \( F \) is related to the surface concentration (dimensions pg/mm\(^2\)) of proteins on the pore walls. A protein of mass \( M \) is modeled as a cylinder with diameter \( \rho \) and height \( \rho \), given by

\[ \rho = \rho_0 \left( \frac{M}{M_0} \right)^{\frac{1}{5}} \]  

Eq. (12)

where \( \rho_0 = 8 \text{ nm} \) and \( M_0 = 150,000 \) Daltons. Equation (12), plotted in FIG. 17B, shows that for the diameters of the majority of proteins examined in kinetic binding experiments (typically 30,000 to 150,000 Daltons) are in the \( \rho = 5 - 8 \text{ nm} \) range.
FIG. 18 displays a model for the surface coverage of ligands 122 on the walls of pores 90. The surface concentration of proteins ligands is given by

\[ \sigma = \frac{M}{Ax^2} \text{ (units pg/mm}^2) \]  

Eq. (13)

where M is the molecular weight of the protein (Daltons or g/mol), and \( A = 6.022 \times 10^{23} \) (molecules/mol) is Avogadro’s number. Although the proteins 122 are distributed somewhat randomly on the pore walls, the average distance between each protein molecules is x. The model assumes that the proteins 122 are arranged in a regular grid pattern, as displayed in FIG. 18. The fractional surface coverage F is then given by

\[ F = \left( \frac{\rho}{x} \right)^2, \]  

Eq. (14)

defined so that \( F = 1 \) when \( \rho = x \). By combining equations (9), (12) - (14), we can relate the OPD to the surface concentration density \( \sigma \) (units pg/mm\(^2\)) as

\[ \text{OPD} = 2L \left[ \left( 1 - P \right) n_{\text{silicon}} + P_{n_{\text{buffer}}} + P \frac{4\Delta n}{d} \left( 1 - \frac{\rho}{x} \right) \frac{\rho_{\text{buffer}}}{M} \sigma \right]^2 - n_{\text{buffer}}^2 \sin^2 \theta \right]^{\frac{1}{2}} + \frac{\delta_{\lambda}}{2\pi} \]  

Eq. (15)

For the preferred operational parameters listed previously, equation (15) gives

\[ \text{OPD} = 2L \left[ \left( 1.804 + \left( \frac{5.92E - 6 \text{mm}^2}{pg} \right) \sigma \right)^2 - 1.769 \sin^2 \theta \right]^{\frac{1}{2}} + \frac{\delta_{\lambda}}{2\pi}. \]  

Eq. (16)

The resolution of the optical measurement is a key feature of the invention. The present prototype has a 1 part per million resolution in the measurement of OPD, defined as the root mean squared (rms) variation in the baseline OPD divided by the measured OPD. A typical OPD is approximately 6000 nanometers, so the resolution of the device is approximately \( \Delta \text{OPD} = (10^{-6})(6000 \text{ nanometers}) = 0.006 \text{ nanometers} \) or 6 picometers. The high degree of resolution is provided by two key factors, 1) the use of very high optical signal averaging to increase the signal-to-noise ratio (SNR) of the measured interference fringe patterns, and 2) the use of novel computational fringe fitting algorithms that most accurately computes the OPD from the interference fringe patterns 246.
The optical signal averaging is accomplished by the use of a very deep well linear photodiode array (Hamamatsu 3904; 256 pixels, 156 million photoelectrons full well capacity) for the linear detector in the spectrometer. In addition, very fast frame rate acquisition methods are used that currently record one hundred frames of interference fringe data every second and sum the one hundred frames pixel-by-pixel to provide an interference fringe pattern versus wavelength every second with a very high SNR. For example, each pixel value in the very high SNR interference fringe pattern represents approximately \(156 \text{ million photoelectrons}/2(100) = 8 \times 10^9\) electrons. The primary noise source for this measurement is photoelectron shot noise; the rms value for this noise is the square root of the signal, \(\sqrt{8 \times 10^9 \text{ electrons}} = 9 \times 10^4 \text{ electrons}\). The SNR of the fringe pattern is then \(8 \times 10^9\) electrons/\(9 \times 10^4\) electrons = 90,000.

**Correlation Method**

The preferred embodiment uses a special correlation method for calculation of OPD from the measured interference fringe patterns, as described here. The model for the measured interference fringe pattern is given by

\[
I(\lambda) = I_0(\lambda)\left[1 - M \cos\left(\frac{2\pi \text{OPD}}{\lambda}\right)\right]
\]

**Eq. (17)**

where \(M\) is the modulation index and

\[
I_0(\lambda) = \frac{1}{\sqrt{2\pi\sigma}}\exp\left(-\frac{(\lambda - \lambda_0)^2}{2\beta^2}\right)
\]

**Eq. (18)**

is a normalized Gaussian envelope function. The actual envelope function is determined by the spectral bandwidth of the light source, spectrometer, and linear photodiode array, as well as the wavelength dependent reflection properties of the interaction volume 202. FIG. 16 shows equations (17) and (18) (246 and 248) with operational parameters \(\text{OPD} = 7216\) nm, \(\lambda_0 = 660\) nm, \(\beta = 100\) nm, and \(M = 0.2\). The measured interference fringe pattern is correlated to a test fringe pattern

\[
I_r(X; \lambda) = I_0(\lambda)\left[1 - M \cos\left(\frac{2\pi X}{\lambda}\right)\right]
\]

**Eq. (19)**

where \(X\) is a varying test optical thickness, using the correlation integral
\[ C(X) = \frac{1}{M} \int_{\lambda_{\infty}}^{\lambda_{\min}} d\lambda \left[ I_r(X; \lambda) - I_{\infty}(\lambda) \right] \left[ I_r(\lambda) - I_{\infty}(\lambda) \right] \]  
Eq. (20)

FIG. 19 shows the correlation integral \( C(X) \) versus \( X \) for the model of a typical interference fringe pattern 246 given by equation (17). The OPD is calculated from the equation (20) as the value of \( X \) corresponding to the peak 258 of \( C(X) \). This value of \( X \) is precisely determined by locating the zero crossing of the first derivative of \( C(X) \) with respect to \( X \), or \( C'(X) \).

The exact procedure for the acquisition of the interference fringe patterns and calculation of the OPD is given here:

1) Acquire reference pattern – FIG. 20 displays a typical reference pattern 260 versus optical wavelength that is acquired from the invention. This pattern is acquired by replacing the interaction volume 202 with a non-porous silicon chip in order to accurately record the envelope optical response function (i.e. without interference fringes), modeled by equation (18), of the light source, spectrometer, and linear photodiode array.

The data \( \{I[i] \text{ RawRef}[i]\} (i = 1 = 0, N\lambda) \) in FIG. 20 represents a summation of multiple frames of pixel data in order to provide greater signal-to-noise by signal averaging the shot noise of the incident photons. The reference data displayed in FIG. 20 is acquired once and is stored in a look-up table for use in the calculation of the OPD.

2) Acquire interference fringe pattern – FIG. 21 displays a typical interference fringe pattern versus optical wavelength 262 that is acquired from the interaction volume 202. Each data point in FIG. 21 represents a summation of a plurality of frames, typically one hundred, of pixel data in order to provide greater a signal-to-noise by signal averaging the shot noise of the incident photons. The data \( \{I[i] \text{ RawSig}[i]\} (i = 0, N\lambda) \) displayed in FIG. 21 is a summation of one hundred frames, summed together, every second. The value \( N\lambda = 256 \) is the number of pixels in the photodiode detector array.
3) Normalize interference fringe pattern and reference pattern – The acquired data is normalized as such:

\[ \text{Sig}[i] = \left( \sum_{j=0}^{\text{Nlambda}} \Delta \lambda_{[j]} \text{RawSig}_{[j]} \right)^{-1} \text{RawSig}_{[i]} \]  
Eq. (21)

and

\[ \text{Ref}[i] = \left( \sum_{j=0}^{\text{Nlambda}} \Delta \lambda_{[j]} \text{RawRef}_{[j]} \right)^{-1} \text{RawRef}_{[i]} \]  
Eq. (22)

4) Calculate correlation function - The correlation function given in equation (20) is calculated using the experimental data

\[ I_v(\lambda) - I_w(\lambda) = \text{Sig}[i] - \text{Ref}[i] \]  
Eq. (23)

to give

\[ C(X[j]) = -\sum_{j=0}^{\text{Nlambda}} \Delta \lambda_{[j]} [\text{Sig}[i] - \text{Ref}[i] \text{Ref}[i] \cos \left( \frac{2\pi X[j]}{\lambda_{[j]}} \right) \]  
Eq. (24)

where the value \( \Delta \lambda_{[j]} = \lambda_{[j]} - \lambda_{[j-1]} \) and \( N_{\text{transform}} < j < N_{\text{transform}} \). The preferred calculation method determines the approximate optical path length \( X[j_{\text{max}}] = \text{OPD}_{\text{approx}} \) by using a simple numerical search for the maximum value \( C(X[j_{\text{max}}]) = \text{max value} \) in the range \( \frac{N_{\text{transform}}}{3} < j_{\text{max}} < \frac{2N_{\text{transform}}}{3} \). The method then uses an interpolation method to find the true peak \( X_{\text{ph}} = \text{OPD} \) in the neighborhood of the first determination \( X[j_{\text{max}}] = \text{OPD}_{\text{approx}} \). This method iterates to find the zero of the first derivative of the correlation function

\[ F(X) = \frac{1}{2\pi} \frac{dC(X)}{dX} = -\sum_{j=0}^{\text{Nlambda}} \frac{\Delta \lambda_{[j]} \text{Sig}[i] - \text{Ref}[i] \text{Ref}[i] \sin \left( \frac{2\pi X}{\lambda_{[j]}} \right) }{\lambda_{[j]}} \]  
Eq. (25)

using the Newton-Raphson method. This method provides a sequence of values \( \{X_n\}; (n = 0, 1, 2, 3,...) \) that provide successively more accurate approximations to the root \( F(X_n) = 0 \), using the formula
\[ X_n = X_{n-1} + \Delta X_n = X_{n-1} + F(X_n) \star \left[ \frac{X_n - X_{n-1}}{F(X_{n-1}) - F(X_n)} \right] \]  
Eq. (26)

and the initial starting points \( X_1 = X\left[ j_{\text{max}} \right] \), \( X_0 = X\left[ j_{\text{max}} \right] - dX \), \( F(X_0) = F(X\left[ j_{\text{max}} \right] - dX) \), and \( F(X_1) = F(X\left[ j_{\text{max}} \right]) \). The initial value \( dX \) is chosen so that the value \( X\left[ j_{\text{max}} \right] - dX \) is close to the peak of the correlation function, typically \( dX = \frac{X\left[ j_{\text{max}} \right]}{1000} \). The iteration procedure continues until a desired level of resolution is reached; the higher the level of resolution, the more iterations are required to reach this resolution. However, the stochastic noise in the signal and reference data will ultimately limit the convergence process. We have found that the limit

\[ |F(X_n)| < C(X\left[ j_{\text{max}} \right]) \times 10^{-9} \]  
Eq. (27)

provides adequate resolution. This limit is reached in approximately \( n = 5 - 10 \) iterations with relatively smooth functions such as a typical \( F(X) \). FIG. 22 shows a computational flow chart for determining the OPD from the interference fringe data.

Alternate embodiments for the fringe-fitting algorithm include the cosine transform method and the Fourier transform method. These methods calculate the derivative of the cosine transform, or the derivative of the Fourier transform, of the normalized data given in equations (21) and (22), and then locate the zero crossing of the cosine transform, or the Fourier transform, using the Newton-Raphson method.

**Dependence of Instrument Resolution on Interferometer Length and Modulation Index**

The resolution in the calculation of the OPD from the measured fringe pattern 246 is related to the both the OPD and the modulation index \( M \) of the fringe pattern. The resolution becomes smaller, or better, as both the OPD increases and the modulation index \( M \) increases, as described here. If we add a stochastic noise term to the model, equation 17 is given by

\[ I_r(\lambda) = I_o(\lambda) - M(2\pi\text{OPD}/\lambda) + N(\lambda) \]  
Eq. (28)
and N(λ) is the noise on the spectral fringe pattern. The noise is primarily a combination of photoelectron shot noise and electronic readout noise. The correlation integral C(X) has a well defined peak at the value of $X_{pk} \approx OT$. Equation 28 is combined with equations (17) and (20) to give

$$C(X) = M \int d\lambda I_0^2(\lambda) \cos(2\pi X / \lambda) \cos(2\pi OPD / \lambda)$$

$$- \int d\lambda I_0(\lambda) \cos(2\pi X / \lambda) N(\lambda)$$

Eq. (29)

To find the peak where $X_{pk} \approx OPD$, we look for the value of X where the derivative of C(X) is equal to zero.

$$\frac{dC(X)}{dX} \bigg|_{X = X_{pk}} = 0 = -M \int d\lambda I_0^2(\lambda) \frac{2\pi}{\lambda} \sin \left( \frac{2\pi X_{pk}}{\lambda} \right) \cos \left( \frac{2\pi OPD}{\lambda} \right)$$

$$+ \int d\lambda I_0(\lambda) \frac{2\pi}{\lambda} \sin \left( \frac{2\pi X_{pk}}{\lambda} \right) N(\lambda)$$

Eq. (30)

By using the trigonometric relationship $\sin \alpha \cos \beta = \frac{1}{2} \left[ \sin(\alpha + \beta) + \sin(\alpha - \beta) \right]$, equation 30 can be expressed as

$$M \int d\lambda I_0^2(\lambda) \frac{2\pi}{\lambda} \frac{1}{2} \left\{ \sin \left( \frac{2\pi}{\lambda} \right) (X_{pk} + OPD) \right\} + \sin \left( \frac{2\pi}{\lambda} \right) (X_{pk} - OPD)$$

$$= \int d\lambda I_0(\lambda) \frac{2\pi}{\lambda} \sin \left( \frac{2\pi X}{\lambda} \right) N(\lambda)$$

Eq. (31)

The peak of the correlation function is at $X_{pk} \approx OPD$; so $\sin \left( \frac{2\pi}{\lambda} \right) (X_{pk} - OPD) = \frac{2\pi}{\lambda} (X_{pk} - OPD)$. Equation 31 can then be written as
\[ X_{ph} = \text{OPD} + \frac{\int d\lambda \frac{I_n(\lambda)}{\lambda} N(\lambda) \sin \left( \frac{2\pi X_{ph}}{\lambda^2} \right)}{\pi M \int d\lambda \frac{I_n^2(\lambda)}{\lambda^2}} \]

or

\[ X_{ph} = \text{OPD} + \varepsilon_1 + \varepsilon_2. \]

Eq. (32)

The second term

\[ \varepsilon_2 = -\frac{\int d\lambda \frac{I_n(\lambda)}{\lambda} \sin \left[ \frac{2\pi}{\lambda^2} (X_{ph} + \text{OPD}) \right]}{2\pi \int d\lambda \frac{I_n(\lambda)}{\lambda^2}} \]

Eq. (34)

is quite small because the term \( \sin \left[ \frac{2\pi}{\lambda^2} (X_{ph} + \text{OPD}) \right] \) oscillates rapidly between -1 and +1 and the integral will average to nearly zero. More importantly, this term does not depend on the measurement noise at all, so it will be constant during the kinetic binding curve measurement and will not affect the measurement data since this data is derived from differences of the OPD during the total measurement time.

The magnitude and sign of the first term

\[ \varepsilon_1 = \frac{\int d\lambda \frac{I_n(\lambda)}{\lambda} N(\lambda) \sin \left( \frac{2\pi X_{ph}}{\lambda^2} \right)}{\pi M \int d\lambda \frac{I_n^2(\lambda)}{\lambda^2}} \]

Eq. (35)

will vary from measurement to measurement as the noise \( N(\lambda) \) varies randomly.

The resolution of the measurement device can be measured by acquiring a number of independent measurements of the OPD \( X_i \) (\( i = 1, \ldots, p \)) while keeping the OPD constant. The resolution is defined as
\[ \Delta r_{\text{lim}} = \sqrt{\frac{\langle \Delta X \rangle^2}{\langle X \rangle}} \]  

Eq. (36)

where \[ \langle X \rangle = \frac{1}{p} \sum_{i=1}^{p} X_i = \text{OPD} + \varepsilon_2 \] is the average value of the measurements, and

\[ \langle \Delta X \rangle^2 = \frac{1}{p} \sum_{i=1}^{p} (X_i - \langle X \rangle)^2 = \frac{1}{p} \sum_{i=1}^{p} [\varepsilon_i(\lambda)]^2 = \langle \varepsilon^2 \rangle \]  

Eq. (37)

is the variance of the measurements. The resolution is then calculated by combining equations (35) – (38)

\[ \Delta r_{\text{lim}} = \frac{1}{\pi \text{MOPD}} \left[ \int_{-\infty}^{\infty} d\lambda \frac{I_{\text{ro}}(\lambda)}{\lambda^2} \right]^{-1} \sqrt{\left[ \int_{-\infty}^{\infty} d\lambda \frac{I_{\text{ro}}(\lambda)}{\lambda} N(\lambda) \sin \left( \frac{2\pi \text{OPD}}{\lambda} \right) \right]^2} \]  

Eq. (38)

The integrals in equation (38) are physically realized as sums over the pixels in the photodiode array of the spectrometer. The square of equation (38) can then be expressed as

\[ (\Delta r_{\text{lim}})^2 = \left( \frac{1}{\pi \text{MOPD}} \right)^2 \left[ \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{ro}}(\lambda_i)}{\lambda_i^2} \right]^{-2} \left[ \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{ro}}(\lambda_i)}{\lambda_i} N_j(\lambda_i) \sin \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \right]^2 \]  

Eq. (39)

where \[ R \] is the number of pixels in the photodiode array. The expectation value in equation (39) can also be turned into a sum as shown in equation (37).

\[ (\Delta r_{\text{lim}})^2 = \left( \frac{1}{\pi \text{MOPD}} \right)^2 \left[ \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{ro}}(\lambda_i)}{\lambda_i^2} \right]^{-2} \frac{1}{p} \sum_{j=1}^{p} \left[ \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{ro}}(\lambda_i)}{\lambda_i} N_j(\lambda_i) \sin \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \right]^2 \]  

Eq. (40)

The three sums in equation 40 can be manipulated to give
\[
(\Delta r_{\text{lim}})^2 = \frac{1}{(\pi \text{MOPD})^2} \left[ \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{r}}^2(\lambda_i)}{\lambda_i^2} \right]^{-2} \frac{1}{P} \sum_{p=1}^{P} \left\{ \sum_{i=1}^{R} \left( \Delta \lambda \frac{I_{\text{r}}(\lambda_i)}{\lambda_i} \right) N_j(\lambda_i) \sin \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \right\}^2
\]

\[+
\sum_{m=1}^{R} \sum_{n=1}^{R} \Delta \lambda^2 \frac{I_{\text{r}}(\lambda_m)}{\lambda_m} \frac{I_{\text{r}}(\lambda_n)}{\lambda_n} N_j(\lambda_m) N_j(\lambda_n) \sin \left( \frac{2\pi \text{OPD}}{\lambda_m} \right) \sin \left( \frac{2\pi \text{OPD}}{\lambda_n} \right) \right\} \]

where the second sum includes all terms except when \(m = n\). The primary noise source for the optical biosensor is the shot noise of the photoelectrons incident in the pixels of the linear detector. In this case, the photoelectrons incident on different pixels are uncorrelated and the second sum in equation (41) averages to zero. The shot noise at each pixel is given by Poisson statistics as

\[
\left\langle N^2(\lambda_i) \Delta \lambda^2 \right\rangle = \sum_{j=1}^{R} N_j^2(\lambda_i) \Delta \lambda^2 = I_{\text{r}}(\lambda_i) \left[ 1 - M \cos \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \right] \Delta \lambda . \tag{42}
\]

Combining equations (41) and (42) gives

\[
(\Delta r_{\text{lim}})^2 = \left( \frac{1}{(\pi \text{MOPD})} \right)^2 \left[ \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{r}}^2(\lambda_i)}{\lambda_i^2} \right]^{-2} \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{r}}^3(\lambda_i)}{\lambda_i^2} \left[ 1 - M \cos \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \right] \sin \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \sin^2 \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \]  

Eq. (43)

Finally, the resolution can be expressed as a function of both the OPD and the modulation index \(M\) as

\[
\Delta r_{\text{lim}} = \frac{1}{\text{OPD}} \left[ \frac{A}{M^2} - \frac{B}{M} \right]^{1/2} \tag{44}
\]

with constants \(A\) and \(B\) given by

\[
A = \frac{1}{\pi^2} \left[ \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{r}}^2(\lambda_i)}{\lambda_i^2} \right]^{-2} \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{r}}^3(\lambda_i)}{\lambda_i^2} \sin^2 \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \]  

Eq. (45)

and

\[
B = \frac{1}{\pi^2} \left[ \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{r}}^2(\lambda_i)}{\lambda_i^2} \right]^{-2} \sum_{i=1}^{R} \Delta \lambda \frac{I_{\text{r}}^3(\lambda_i)}{\lambda_i^2} \cos \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) \sin^2 \left( \frac{2\pi \text{OPD}}{\lambda_i} \right) . \tag{46}
\]
From equations (44) – (46), the resolution becomes smaller, or better, as the optical thickness OPD becomes larger. In addition, the resolution becomes smaller, or better, as the modulation index M becomes larger.

The observed modulation index is related to the diameter d of pores 90 in the interaction volume 202. Smaller pore diameters provide a higher modulation index due to less wavefront distortion of the incident optical beam. The pore diameters, however, need to be large enough to provide space for the molecular interactions to occur, and for unimpeded diffusion of the analyte molecules in and out of the PS interaction volume. In addition, the OPD is linearly related to the depth L of the interaction volume 202, so larger depths L can provide better resolution.

The modulation index M can effectively distinguish between the realm in which larger pore diameters optimizes kinetic binding assays and another realm of smaller pore diameters that is optimal for on/off capture assays because of the better resolution. The mass transport effect can be larger for the on/off capture assays because this technique is not concerned with the temporal dynamics of the binding process. The capture assays are concerned only with the presence or absence of binding.

**Kinetic Binding Measurement Model**

The basic kinetic binding model, displayed in FIG. 10, assumes that a finite collection of ligand molecules 122, at concentration $[B]_0$ (units pg/mm$^2$), are immobilized, or spatially fixed, on the wall of pores 90 of the porous silicon interaction volume 202. This model assumes as shown in FIGS. 10 and 11 that at time $t = 0$, a concentration $[A]_0$ (units M or mol/L) of analyte molecules 124 in buffer solution, are flowed at velocity $v$ through flow channel 61 and are transported into interaction volume 202 by the diffusion process. The total number of analyte molecules 124, and the velocity $v$, are both large enough so that the concentration $[A]_0$ of unbound analyte molecules 124 remains constant in interaction volume 202 during the binding measurement time. The analyte molecules 124 bind, or associate, with the ligand molecules 122, at a characteristic rate $[A]k_{on}$ (units sec$^{-1}$), to form bound, immobilized molecules AB 127. The bound molecules AB 127 also unbind, or disassociate, at characteristic rate $k_{off}$ (units sec$^{-1}$) into the mobile analyte molecules 124 and the immobilized receptor molecules 122. At the time $t = t_{stop}$, the
concentration of analyte molecules 124 is abruptly reduced to zero by the researcher so that only buffer solution is flowing through flow channel 61. The bound molecules AB 127 dissociate at characteristic rate $k_{off}$ (units sec$^{-1}$), and the resulting unbound analyte molecules 124 diffuse out of interaction volume 202 into flow channel 61, and are flowed to the waste outlet port 48, 50, or 54.

The differential rate equations that describe the binding and unbinding process are given by:

$$\frac{d[AB]}{dt} = k_{on}[A][B] - k_{off}[AB]$$

$$[B] = [B]_0 - [AB]$$

$$\frac{d[B]_0}{dt} = 0$$

Eqs. (49)

with boundary conditions

$$[A](t) = 0 \text{ and } [AB](t) = 0 \text{ for } t < 0$$

(the initiation time period)

$$[A](t) = [A]_0 \text{ for } 0 < t < t_{stop} \text{ (the association time period)}$$

Eqs. (50)

$$[A](t) = 0 \text{ for } t > t_o \text{ (the dissociation time period).}$$

The boundary conditions for the analyte molecules A given by equations 41 are displayed in FIG. 11.

An important constraint to note is that the concentration of available receptor molecules 122 $[B](t)$ is initially set by the experimenter at $[B](t) = [B]_0$ at time $t = 0$, but decreases as the concentration of bound molecules $[AB](t)$ increases. The concentration of available analyte molecules 124 is controlled to be constant at $[A](t) = [A]_0$ during the association time period $0 < t < t_o$ 130 due to the continual flow of new analyte molecules 124 to the interaction volume. Also, the concentration of available analyte molecules 124 is controlled by the researcher to be constant at $[A](t) = 0$ for the initiation time period $t < 0$ 128, and the dissociation time period
$t > t_{\text{step}} = 132$ due to a continual flow of buffer solution (i.e. zero concentration of analyte molecules 126) during this time periods.

The set of equations (49) are combined as

$$\frac{d[AB](t)}{dt} = k_{\text{on}}[A](t)[B] - [AB](t) - k_{\text{off}}[AB](t)$$

Eq. (51)

Equation 51 is solved as

$$[AB](t) = 0 \quad t < 0$$

$$[AB](t) = \frac{[B] \left[ 1 - \exp \left( -\frac{1 + \frac{[A]}{K_D} k_{\text{off}}}{1 + \frac{[A]}{K_D}} \right) \right]}{1 + \frac{K_D}{[A]}}$$

0 < t < t_0

Eq. (52)

$$[AB](t) = \frac{[AB](t_0) \exp(-k_{\text{off}}t)}{1 + \frac{K_D}{[A]}}$$

$\quad t > t_0$

where $K_D = k_{\text{off}} / k_{\text{on}}$ (units M). $(K_D)^{-1}$ is called the affinity and is indicative of the strength of interaction between analyte molecules A and ligand molecules B. FIG. 12 displays equations 52 $\frac{[AB](t)}{[B]}$ versus time t for three different concentrations $[A]_0$: $[A]_0 = 5K_D$, $[A]_0 = K_D$, and $[A]_0 = K_D/5$. There are several important features of equation 52. The concentration $[AB](t)$ of bound molecules AB reaches equilibrium

$$[AB]_e = \frac{[B]_0}{1 + \frac{K_D}{[A]}}$$

Eq. (53)

during the association time period in a time scale $\tau_{\text{assoc}} = \left[ \frac{[A]_0}{K_D} \right]^{-1}$, and decreases to zero during the dissociation time period in a time scale $\tau_{\text{dissoc}} = k_{\text{off}}^{-1}$ during the dissociation time period. The parameter $K_D$ sets the scale of the equilibrium concentration $[AB]_e$ of the bound molecules AB. If the experimenter sets the concentration of analyte molecules $[A]_0 = K_D$, then the equilibrium concentration $[AB]_e = [B]_0/2$ where $[B]_0$, the concentration of the receptor molecules B, is a parameter that the experimenter also initially sets. For higher concentrations
\([A]_0 \approx 10K_D\), the equilibrium concentration of bound molecules AB saturates to \([AB]_{eq} = [B]_0\). For lower concentrations \([A]_0 < 0.5 \ K_D\), the equilibrium concentration decreases as \([AB]_{eq} \approx ([A]_0/K_D)[B]_0\).

**Example of a Kinetic Binding Measurement**

This section demonstrates a typical kinetic binding experiment of a typical protein-protein interaction. The ligand molecule 122 is a monoclonal antibody-Anti TSH (thyroid stimulating hormone), with a 150 kDa molar mass and two binding sites per ligand molecule 122. The analyte molecule 124 is a TSH protein, with a 28 kDa molar mass. The experimentally derived kinetic binding data for this interaction are \(k_{on} = 2 \times 10^3 \ (M^{-1} \ s^{-1})\), \(k_{off} = 2 \times 10^{-3} \ (s^{-1})\), and \(K_D = 10 \ nM\). These proteins can be used to perform tests on the FIG. 1 device to confirm that the FIG. 1 device produces results consistent with the known binding rates.

A typical binding experiment attempts to determine the values of \(k_{on}\), \(k_{off}\), and \(K_D\), by measuring the binding data of the type displayed in FIG. 12 for one ligand concentration \([B]_0\) and the several (e.g. three to ten) different analyte concentration \([A]_0\) such as three different concentrations (136, 140 and 142) as shown in FIG.12. The approximate range that \([A]_0\) is varied is typically from \([A]_0 = 0.1 \ K_D\) to \([A]_0 = 10 \ K_D\). The concentrations \([A]_0\) as well as the actual timescale t of the binding experiments, should be measured with care because these values are used in the analysis of the binding curve data to calculate the final values of \(k_{on}\), \(k_{off}\), and \(K_P\). The analysis assumes that the value of \([B]_0\) is held constant over the entire series of binding experiments. The preferred device shown in FIG. 1 can perform four measurements simultaneously.

FIGS. 12 and 14 displays simulated results of a kinetic binding experiment for anti-TSH/TSH system based on Equation 52. They are the same except that FIG. 14 includes simulated noise. The parameters of the porous silicon interaction volume are \(L = 2000 \ nm\), \(d = 120 \ nm\), \(P = 0.80\). The simulated device noise is 1 part per million of the measured optical thickness. The surface concentration of the TSH-antibody was set at \(\Gamma = 0.1\). Equation (4) shows that the initial OPD for this experiment is approximately \(OPD = 2(2000 \ nm)(1.804) = 7216 \ nanometers, \ or \ nm\). Preparation of the pores with ligand molecules (\(\Gamma = 0.1\)) results in a change in OPD by \(\Delta OPD = \)
2(2000 nm)(0.0115)(0.1) = 4.6 nm. Ligands are immobilized in the pores 90 using the feature of the Fig. 1 device which permits an operator to monitor the immobilization process in interaction region 202 so the experimenter can stop the ligand molecule 122 coverage when the OPD increases from OPD = 7216 nm to OPD = 7216 nm + 4.6 nm = 7220.6 nm. The TSH molecules are introduced to the interaction volume 202 at three different concentrations, [A]₀ = 25 nM, [A]₀ = 5 nM, and [A]₀ = 1 nM (144, 146 and 148, respectively). For each experiment, after a 5 minute binding, or association, time period, the concentration of TSH molecules is switched to [A]₀ = 0, and the dissociation time period is measured for another 5 minutes.

If we measure the concentration of receptor molecules [B]₀ and the concentration of bound molecules [AB](t) in OPD units (nm), then the maximum, or saturation, value of the bound molecules,

\[ [AB]_{\text{max}} = \left( \frac{2M_A}{M_B} \right) [B], \]

Eq. (54)

where \( M_A = 28 \text{ kDa} \), \( M_B \text{ KDa} \), and the factor of 2 accounts for two binding sites per analyte molecule for this particular interaction. This gives \( [AB]_{\text{max}} = 1.7 \text{ nm} \).

Alternate Embodiments

Alternate Embodiment for Porous Silicon Optical Interferometer

Equation 1 shows that the porous silicon optical interferometer measures the optical path difference (OPD) between the optical path \( n_r(ps)(AB + BC) \) and the optical path \( n_r(buffer)(AD) \). The preferred embodiment utilizes the optical path \( n_r(ps)(AB + BC) \) as the signal path and the optical path \( n_r(buffer)(AD) \) as the reference path and assumes that the reference path does not change during the measurement period. Fig. 15B shows an alternate embodiment of the porous silicon interferometer that utilizes the interferometer path \( n_r(buffer)(AD) \) as the signal path and the interferometer path \( n_r(ps)(AB + BC) \) as the reference path. This embodiment incorporates a substantial amount of the operational features discussed above. However, the path length \( AD \) 30 is given by
\[
\overline{AD} = \frac{2L_n (\text{buffer}) \sin^2 \theta_i}{n_r (ps) \left[1 - \left(\frac{n_r (\text{buffer})}{n_r (ps)} \sin^2 \theta_i\right)^2\right]}, \quad \text{Eq. (56)}
\]

For \( \theta_i = 10 \) degrees, equation (56) gives \( \overline{AD} = 0.0499L \); thus a porous silicon depth \( L = 4000nm \) gives \( \overline{AD} = 180nm \). For this embodiment, protein receptor molecules immobilized in the top interaction volume 150 interact with analyte molecules flowing through flow channel 61 and diffusing into top interaction volume 150. The optical path difference defined by equation (4) changes due to binding interactions of analyte molecules with receptor molecules and the optical path difference changes are measured in the same manner as described for the preferred embodiment. The major difference between this embodiment and the preferred embodiment the optical path length corresponding to path \( \overline{AB + BC} \) remains constant, thus acting as the reference path of the optical interferometer. The reference path is realized by fabricating the porous silicon volume 152 so that the index of refraction \( n_r (ps) \) remains constant. The preferred method for the fabrication of the porous silicon reference volume 152 involve the etching of very small pore diameters 90, on the order of 5 nm, so that large protein molecules cannot diffuse into the pores 90. Another fabrication method involves the filling of the pores 50 with a polymer so that neither proteins nor buffer solution will enter the pores 50. Another fabrication method involves the use of a thin film non-porous volume 152 that acts as the reference path. This alternate embodiment enables the immobilization of receptor molecules in a cellular membrane that comprises the interaction volume 150. Measurement of analyte molecules interacting with the receptor molecules in the cellular membrane permits the study of protein interactions in a more natural environment.

**Alternate Embodiments for Low Cost, High Throughput Porous Silicon Optical Interferometers**

The preferred embodiment described above; including the white light source, input fiber, output fibers, spectrometers, and linear photodiode arrays; is moderately expensive per measurement channel, and becomes prohibitively expensive for a biosensor instrument with over four measurement channels. An alternate embodiment displayed in FIG. 23 and FIG. 24, provides a
relatively inexpensive apparatus and method to permit the simultaneous real-time measurement of interference fringe patterns from approximately four to one hundred or more porous silicon interaction regions. FIG. 23 and 24 show this embodiment for eight measurement channels. White light delivered via fiber-optic 300 is directed to eight separate regions 318 on porous silicon die 308 by cylindrical lens 304 and a row 302 of eight circular apertures. Each of the eight porous silicon regions 318 can incorporate a separate fluid flow channel and separate ligand molecule attachment, for example. A single analyte containing solution is then flowed over the eight channels in a serial fashion, thus producing a separate change in the OPD of each region 318. The reflected white light 311 from each of the eight regions 318 is directed via beam splitter 306 to a spectrometer 310 (Santa Barbara Instruments Group SGS Spectrograph, for example). The reflected light 311 is split into light intensity versus optical wavelength by the spectrograph 310 by focusing the reflected light 311 via lens 312 onto an 18 micron x 2 millimeter slit 313, and then directing the light onto diffraction grating 314 and second lens to produce eight separate images 322 (as shown in FIG. 24) of the eight separate interference fringe patterns on a two-dimensional charge-coupled device (CCD) array 316 (Santa Barbara Instrument Group ST-7E camera with 765 x 510 pixel CCD array, for example). Each of the eight images 322 of the fringe patterns spans approximately 50 rows by 765 columns of the CCD array 316. The eight images 322 of the separate interference fringe patterns are recorded in real-time in a computer and each image 322 is summed pixel-by-pixel in the row dimension to provide signal averaging. The OPD versus time of each porous silicon region 318 is calculated using the computational methods previously described. This method can be extended to approximately one hundred measurement channels by incorporating a row 302 of one hundred apertures, thus providing one hundred separate images 322 of the interference fringe patterns of one hundred separate porous silicon regions 318. Each image 322 spans 5 rows by 765 columns of the CCD array 316. Additional measurement channels can also be added by sequentially measuring the eight channels 318 and then scanning the entire assembly to another row of eight channels 318.

A second alternate embodiment for the optical layout involves the use of a novel micro-interferometer, displayed in FIG. 25 and FIG. 26. Monochromatic light 325 (wavelength $\lambda$), from a laser diode, for example, is directed through a circularly symmetric dual index of
refraction region 328 that comprises an outer index of refraction region 326 and an inner index of
refraction region 330. This produces a circularly symmetric phase pattern 332 in the light beam
325 with the phase $\phi_1$ of the inner portion of the beam lagging or advancing the phase $\phi_2$ of the
outer part of the beam, depending on the relative difference of the index of refractions $n_1$ and $n_2$.
Lens 334 focuses the phase pattern onto plane 336, thus producing a circularly symmetric
intensity pattern that is related to the phase difference $\phi_1 - \phi_2$.

The mathematical solution for this micro-interferometer is described here. The electric field of
the initial light wave 325 is described by

$$U(\rho, \psi) = A \exp(j\phi_1) \quad 0 < \rho < a$$
$$U(\rho, \psi) = A \exp(j\phi_2) \quad a < \rho < b$$
$$U(\rho, \psi) = 0 \quad \rho > b$$  \hspace{1cm} \text{Eq. (60)}

In equation (60), $a$ is the radius of inner region 330, $b$ is the radius of outer region 326, and $j$
denotes the imaginary axis. The electric field pattern at image plane 336 is given in the
Fraunhofer approximation as

$$U_{\text{image}}(r, \theta) = (j\lambda f)^{-1} \exp\left(\frac{jkr^2}{2f}\right) \int U(\rho, \psi) \exp\left(-\frac{jkr\rho}{f}\right) \cos(\theta - \psi) \rho d\rho d\psi \quad \text{Eq. (61)}$$

where $f$ is the focal length of lens 334, and $k = 2\pi \lambda$. Equation (61) can be solved as

$$U_{\text{image}}(r, \theta) = \left(\frac{k\lambda}{jf}\right) \exp\left(\frac{jkr^2}{2f}\right) \left(\frac{kra}{f}\right)^{\frac{1}{2}} a^2 \left(\exp[j\phi_1] - \exp[j\phi_2]\right) J_0\left(\frac{kra}{f}\right) + b^2 \exp[j\phi_2] \left(\frac{krb}{f}\right)^{\frac{1}{2}} J_0\left(\frac{krb}{f}\right) \quad \text{Eq. (62)}$$

The intensity pattern at image plane 336 is given by the square of modulus of the electric field
given in equation (62)
\[ I_{image}(r, \theta) = |U_{image}(r, \theta)|^2 = \left( \frac{kAb^2}{f} \right)^2 \left( 4 \sin^2 \left( \frac{\Delta \phi}{2} \right) \right) \left( \frac{a/b}{f} \right)^2 \left( \frac{kra}{f} \right)^2 J_1^2 \left( \frac{kra}{f} \right) - \left( \frac{a/b}{f} \right)^2 \left( \frac{krb}{f} \right)^2 J_1 \left( \frac{krb}{f} \right) \left( \frac{kra}{f} \right) + \left( \frac{krb}{f} \right)^2 J_1^2 \left( \frac{krb}{f} \right) \] 

Eq. (63)

**FIG. 27** displays equation (63) plotted for three different relative phases \( \Delta \phi = \phi_1 - \phi_2 \). These intensity patterns repeat themselves every time the relative phase increases or decreases by a factor of \( 2\pi \). The contrast of the intensity modulation maximizes when the areas of inner region 330 and outer region 326 are equal, or when \( b = a\sqrt{2} \).

**FIG. 28** displays a preferred embodiment for the actual micro-interferometer used to measure the change in the OPD of a porous silicon interaction region 354. Infrared light 347 from laser diode 346 (\( \lambda = 1.55 \) microns) is collimated by lens 348 and directed through a silicon wafer 350. The silicon wafer is transparent to the infrared light at this wavelength. Porous silicon region 354 is etched as a cylindrical region with radius \( a \) in silicon wafer 350. The cylindrically symmetric light beam with radius \( b \) passes through both the porous silicon region 354 and an outer index region 356 that is comprises of bulk silicon, thus acting as the unchanging reference path of the micro-interferometer. The light 347 then is focused by lens 358 onto a detector 360 that measures the intensity pattern of light 347. Index of refraction changes in porous silicon region 354 are measured as changes in the intensity pattern as given by equation 63 and **FIG. 27**. Detector 360 can be a single element detector that measures the integrated intensity pattern (i.e. light power), a linear photodiode array that spatially measures the intensity pattern, or an areal photodiode array that spatially measures the intensity pattern. Computational methods are applied to calculate the phase difference \( \Delta \phi \) from the measured intensity patterns. **FIGS. 29 A, B and C** display experimental data from a micro-interferometer built and tested by the applicants.

A cost efficient high-throughput biosensor can be fabricated using an array of micro-interferometers (32 x 32 measurement channels, for example). Different ligand molecules are attached to each measurement channel, and an analyte containing solution is flowed over all of the measurement channels that provide simultaneous real-time measurements of the OPD changes in each measurement channel.
Alternate Embodiment of Porous Silicon Optical Interferometer as a Gaseous Chemical Detector

Another embodiment of the porous silicon interferometer involves highly sensitive measurements of gaseous chemical species, such as G-type nerve agents or volatile organic chemicals (VOCs), for example. The modifications of the above-described embodiment primarily involve modifications of the pore etching parameters, modifications of the chemical preparation of the pores 50, and the modification to a gaseous delivery subsystem. For example, typical gaseous chemical molecules are much smaller than large protein molecules, so the diameters and depths of pores 50, for this embodiment, are in the 5 – 15 nm and 10 – 50 micron range, respectively. As an example of alternate chemical preparation steps, the G-type nerve agents feature a phosphate (R-PO₄²⁻) molecular backbone complex and a phosphorous fluorine (P-F) molecular complex. The P-F bond can be cleaved with the use of a copper catalyst with hydrofluoric acid released as a by-product. The hydrofluoric acid further etches the porous structure, thereby resulting in a measurable change in the OPD. These gaseous embodiments can be very useful for detection of hazardous substances and could be useful in searches for biological weapons and for detection of their use.

VARIATIONS

Pores of a sample-receiving interaction zone that are of a porous material typically have nominal pore diameter distributions of about 150 nanometer (nm) ± 50 nm, and pore depths of about 2000 to 10,000 nm, although the pores may be somewhat irregular in shape. The nominal pore diameters may be from about 2 nm to about 2000 nm. Pore diameters from about 10 nm to about 200 nm are preferred for visible light, e.g., white light, pore diameters from about 2 nm to about 50 nm are preferred for ultraviolet light, and pore diameters from about 100 nm to about 2000 nm are preferred for infrared light. In some embodiments, a random distribution of 50-100 nm diameter cylindrical pores, which serve as sample-receiving interaction zones, are formed in the sample plate material by a chemical etching process for purposes of performing kinetic binding measurements. Greater porosity may be preferable for on/off and other capture assays that do not require kinetic binding measurements.
When a sample-receiving interaction zone is fabricated from a porous material such as porous silicon, the porous sample-receiving interaction zone typically has a depth or thickness from about 0.5 μm to about 30 μm. Thicknesses from about 1 μm to about 10 μm are preferred for visible light, e.g., white light, thicknesses from about 0.5 μm to about 5 μm are preferred for ultraviolet light, and thicknesses from about 5 μm to about 30 μm are preferred for infrared light.

A sample plate may be constructed of any suitable material(s) capable of producing interference upon exposure to electromagnetic radiation. Preferably, the sample plate material is a material capable of being formed into a porous material. Sample plate materials include, but are not limited to, silicon, silicon alloys, germanium, aluminum, aluminum oxide, stainless steel, glass, and combinations thereof. Silicon and silicon alloys are preferred sample plate materials. Silicon and silicon alloy materials include p-doped silicon, n-doped silicon, and intrinsic (undoped) silicon. In other embodiments, silicon materials having up to about 10% by weight germanium therein can be used. Further sample plate materials and dopants are described in U.S. Patent No. 6,248,539 B1. The sample plate can include different layers of varying density and material composition.

FIGS. 30A-30C show scanning electron microscope views of porous silicon suitable for use in various embodiments. FIG. 30A shows a scanning electron micrograph image of the top surface of p++-type porous silicon etched at about 330 mA/cm². FIG. 30B shows a scanning electron micrograph image of the top surface of p++-type porous silicon etched at about 600 mA/cm². A cross-sectional region of porous silicon that has been etched to form a portion of a sample receiving interaction zone is shown in FIG. 30C. Specifically, this illustration shows a scanning electron microscope cross-sectional image of p++-type porous silicon etched at about 330 mA/cm². The pore depth is about 5 μm in this illustrative embodiment. As previously described, these pores serve as interferometric cavities and were formed using an etching process.
More specifically, porous silicon is a high surface area network of silicon nano-crystallites. Porous silicon can be produced by an anodic electrochemical etch of bulk crystalline silicon. Porous silicon tends to etch as a distribution of long nano-tubes or pores. The distribution of pore diameters and the depth of the pores is very controllable by adjusting the current density and the etching time. For example, an initial silicon material may be a heavily doped crystalline silicon wafer, e.g., commercially available wafers used for semiconductor manufacturing purposes. Typical wafer specifications include $p^{++}$-type silicon ($0.6 - 1.0 \ \Omega\cdot\text{cm}$ resistivity) with about 100 crystal orientation. In one process, the appropriate silicon wafer is immersed in an ethanolic hydrogen fluoride solution (HF:ethanol, 1:1). A constant electric current is applied to the silicon wafer using a platinum electrode. The silicon atoms at the silicon/electrolyte interface become polarized, making them susceptible to attack by the fluoride ions in solution. Silicon is released in the form of silicon hexafluoride and hydrogen gas is evolved in this process.

Techniques for selectively etching porous silicon are known in the art and include selectively illuminating the silicon wafer during the etching process. Depending on the dopant type of silicon used, light incident on the wafer during etching inhibits the etching process. A simple light mask of an array of 1 mm diameter opaque spots, for example, will produce an array of 1 mm diameter porous silicon areas surrounded by non-porous silicon. This selective etching can be accomplished without the use of photo-mask technology. Sample material will tend to coat both the porous and non-porous areas. However, the greatly enhanced surface area of the porous silicon will lead to much higher index changes for the porous silicon areas.

In embodiments that employ combinations of visible and non-visible electromagnetic radiation, an appropriate detector is selected based on the wavelengths of incident light, e.g. a multi-spectral camera. For example, a single Photoconductor on Active Pixel™ (POAP) detector may be used. See, e.g., U.S. Patent Nos. 5,528,043; 5,886,353; 5,998,794; and 6,163,030. Alternatively, multiple detectors may be used, e.g., each detecting a different range of wavelengths of incident light.
In certain embodiments, the apparatus of the invention includes a mass spectrometer that is appropriately interfaced with the sample plate to permit mass analysis of molecules in a sample-receiving interaction zone. In particular, when immobilized molecules or ligands capture an analyte, mass analysis of the captured analyte often can assist in characterizing and identifying the analyte. The combination of the interferometric techniques of the invention with mass spectrometry offers a powerful tool for the sensitive, rapid and accurate analysis and characterization of chemical and molecular interactions, e.g., ligand fishing, identification and quantification, and multiplex diagnostic assays. In particular, when the sample-receiving interaction zones are porous silicon and the apparatus includes a mass spectrometer, the apparatus and associated techniques are known as Poroferometry-MS™.

Proof of Principle Test Set-Up and Test Data

FIGS 29 and 29A, B and C show a test set-up and results related to preferred embodiments of the present invention. Here, as shown in FIG. 29 a HeNe laser beam is collimated and directed through a cube beam splitter 400 to stationary mirror 402 having a small 2 mm square hole in the center. A portion of the light is reflected from mirror 402 and an approximately equal portion is reflected from moving mirror 404. The combined reflected beam is focused by lens 406 on to CCD camera 408 producing an airy disc like pattern. FIG. 29A is a copy of the pattern when the reflected beams are out of phase and FIG. 29B is a copy of the pattern when the beams are in phase. FIG. 29C are graphs through the center of the pattern for in-phase, out of phase and in between. These data show the extreme sensitivity of this set-up. We are dealing with wavelengths of a few microns to fractions of a micron so that one-half wave (i.e., the difference between in phase and out of phase) is in the range of a few hundred nanometers. A preferred wavelength for this application is 1.5 microns. Applicants have demonstrated at least 10 percent transmission through about 100-micron thickness of doped silicon. In preferred embodiments the porous silicon replaces the moving mirror and the light reflects from the bottom of the porous region. A mirror with a small hole may be used for the stationary mirror (as in the demonstration) or in some cases the top surface of the silicon may provide the first reflection. Molecular interactions take place in the pores of the porous silicon region and those interaction
are monitored by observing changes in the interference patterns like those shown in FIGS 29A and B.

As shown in FIG. 31A, a mass spectrometer 900 may be integral with an interferometric measurement apparatus 902 and adapted to be in vacuum communication with a sample plate 904 so that mass analysis can occur directly from the sample plate 904 without intervening processing required. For example, as shown in FIG. 31A, a second source of electromagnetic radiation 906, e.g., a laser, directly strikes a sample-receiving interaction zone (not shown) with electromagnetic radiation 908 within an ion source region 910 (region within upper horizontal and right-hand side vertical dotted lines and corresponding lower horizontal and left-hand side vertical solid lines) to desorb and ionize any molecule(s) within the sample-receiving interaction zone. The desorbed ions 912 then can be directly introduced into the mass spectrometer 900 to be mass analyzed. It should be understood that depending upon the particular application and design of the apparatus, an ion source region according to the invention may be independent of the mass spectrometer, e.g., an ion source chamber as shown in FIG. 31A, or may be a region within the mass spectrometer.

In an alternative embodiment shown in FIG. 31B, a mass spectrometer 900' is separate from, but associated with, an interferometric measurement apparatus 902'. In this embodiment, the sample-receiving interaction zones (not shown) of a sample plate 904' undergo interferometric analysis within the interferometric measurement apparatus 902' then the sample plate 904' is transported via the appropriate transportation mechanism(s) or devices (not shown), e.g., a probe or mechanical arm particularly designed to hold a sample plate, into the mass spectrometer 900'. To increase throughput, the mass spectrometer typically is kept under vacuum so that when the sample plate 904' is transported along the horizontal, arrowed dotted line in FIG. 31B, the sample plate 904' passes through suitable valves, seal(s), and/or lock(s) 914 to maintain an appropriate vacuum in the mass spectrometer 900'. After the sample plate 904' is within the mass spectrometer 900' and an appropriate reduced pressure is achieved, a second source of electromagnetic radiation 906' strikes a sample-receiving interaction zone (not shown) with
electromagnetic radiation 90° to desorb and ionize any molecule(s) within the sample-receiving interaction zone to permit their mass analysis.

Other designs for associating a mass spectrometer with an interferometric measurement apparatus of the invention would be known by a skilled artisan. For example, if maintaining a vacuum in the mass spectrometer and/or an ion source region is not essential, then a sample plate can be transported or placed in a mass spectrometer and/or an ion source region at atmospheric pressure. Subsequently, a reduced pressure can be established in the mass spectrometer and/or ion source region to permit ionization and/or desorption and mass analysis to occur. As will be appreciated by skilled artisans, there are numerous techniques for moving sample plates within a mass spectrometer and for conducting the mass analysis. All of these techniques and their associated apparatus and structure are included within the scope of this invention.

For example, suitable mass spectrometers include, but are not limited to, a magnetic sector mass spectrometer, a Fourier transform ion cyclotron resonance (FTICR) mass spectrometer, a quadrupole (rods or ion trap) mass spectrometer, a time of flight (TOF) mass spectrometer, a matrix-assisted laser desorption ionization (MALDI) mass spectrometer, and combinations thereof, e.g., a MALDI-TOF mass spectrometer.

If the mass spectrometer uses MALDI, a captured analyte typically is contacted with an appropriate MALDI matrix. The MALDI matrix may be applied to a sample-receiving interaction zone subsequent to interferometric analysis. For example, a matrix applicator, e.g., an "ink-jet"-type of applicator, can be associated with a sample plate and deliver an appropriate amount of the MALDI matrix to the sample-receiving interaction zones to be mass analyzed. MALDI matrix materials are known to skilled artisans and include, but are not limited to, derivatives of cinnamic acid such as α-cyano-4-hydroxycinnamic acid and sinapinic acid.

All of the above apparatus and devices may be operated manually in a step-wise fashion. Full automation, however, is preferred. As appreciated by a skilled artisan, automation preferably
includes a microprocessor and/or computer, which controls various aspects of the apparatus and methods of the invention. For example, an interferometric measurement apparatus also may include one or more auxiliary controllers such as any suitable microprocessor based programmable logic controller, personal computer controller, or the like for process control. A suitable auxiliary controller includes features such as programmability, reliability, flexibility, and durability.

The auxiliary controller typically includes various input/output ports used to provide connections to regulate various structure and components of the interferometric measurement apparatus, including, but not limited to, the source of electromagnetic radiation; a microfluidics system including its components; and a mass spectrometer including its components. An auxiliary controller may assist in the collection, characterization, analysis, and display of information and data from the detector or any other component of an apparatus of the invention where information of interest may be generated. The auxiliary controller also may control the movement and/or alignment of various structure(s) such as the len(s), beam splitter(s), dispersion element(s), detector(s), sample plate(s); valve(s), seal(s) and/or lock(s); as well as control the environmental conditions within the apparatus, such as temperature and pressure. The auxiliary controller also includes sufficient memory to store process recipes for desired application. Of course, the type of controller used depends upon the particular application.

Each of the patent documents and scientific publications disclosed hereinabove is incorporated by reference herein.

While the present invention is described in terms of preferred embodiments, the reader should understand that these are merely examples and that many other embodiments are changes to the above embodiments will be obvious to persons skilled in this art. Although preferred embodiments utilize visible light, readers should understand that light at other wavelengths such as ultraviolet light and infrared light could be utilized in other embodiments of the present invention, and the term “light” as used in the claims includes electromagnetic radiation at any
wavelength unless otherwise limited. For example, the size, shape and number of pores in the porous silicon regions could vary greatly depending on the particular application of the present invention. In most cases the number of pores in each region will be far more than 1000. The porosity of the regions may vary greatly with the application. In preferred embodiments Applicants have chosen porosity values of the porous silicon region to produce an index of refraction for the water-filled porous silicon region of $n = 1.8$ as compared to an $n = 3.7$ for silicon and $n = 1.3$ for the water. However, in many cases many other porosity values could be utilized. Many and various chemistries can be utilized in the porous silicon reaction chambers other than the ones specifically disclosed. The porous silicon regions can utilized to act as alternate capture mechanisms. For example, rows of reaction chambers can be created with a different chemistry in each row. With such a setup, it is possible to create interaction zones with a first chemistry that permits separation of certain kinds of molecules from a larger "soup" of molecules. Then a capture mechanism can be used that more selectively binds with molecules of interest with higher resolution than would otherwise be measurable in the presence of a higher abundance of molecules. Also various optical detection methods can be used other than the ones specifically described. For example, it is known that Raman spectroscopy is of considerably value in determining molecular structure and chemical analysis. Therefore, Raman spectroscopy techniques can be adapted for use with the porous silicon observation regions and micro fluidic sample control techniques of present invention. Quad cell detection is an additional optical detection technique that could be utilized to detect changes in molecular activity in the observation regions described in the specification. In addition, other optical observation techniques may be adaptable for use in connection with the present invention. In some cases it may be desirable to utilize mass spectrometry detection techniques along with the optical detection techniques described herein to more precisely define molecular components and their activity. Therefore, the scope of the invention should be determined by the claims and their legal equivalents.
We claim:

1. An optical sensor for monitoring molecular binding interactions said sensor comprising:
   A) at least one porous silicon region comprising more than 1,000 pores, each pore having
      a nominal width and a nominal depth at least 10 times larger than said nominal width
      with the depth of each pore being approximately equal to the depth of at least most
      of the other pores in said porous silicon region, said porous silicon region defining a
      top surface and a bottom surface, said bottom surface being parallel or
      approximately parallel to said top surface;
   B) at least one buffer-sample fluid flow channel located above said at least one porous
      silicon region providing a fluid flow passage across said porous silicon region;
   C) at least one light source for illuminating said at least one porous silicon region;
   D) at least one spectral monitor for monitoring light reflected from said top surface and
      said bottom surface of said at least one porous silicon region;
   E) a fluid flow control system for producing controlled flow of buffer solutions, ligand
      containing solution and analyte containing solutions through said at least one fluid
      flow channel; and
   F) a computer processor programmed with a computer program for making molecular
      binding measurements based on changes in spectral interference patterns monitored
      by at least one spectral monitor while analytes bind with and disassociate from
      ligands attached to surfaces of said pores.

2. The optical sensor as in Claim 1 wherein said at least one porous silicon region is a
   plurality of porous silicon regions, said at least one buffer-sample fluid flow channel is a
   plurality of fluid flow channels, said at least one light source is a plurality of light sources and
   said at least one spectral monitor is a plurality of spectral monitors.

3. The optical sensor as in Claim 2 wherein said plurality of porous silicon regions is at least
   four porous silicon regions.
4. The optical sensor as in Claim 1 wherein said molecular binding measurements are kinetic molecular binding measurements.

5. The optical sensor as in Claim 1 wherein said at least one spectral monitor is at least one spectrometer.

6. The optical sensor as in Claim 1 wherein said at least one spectral monitor comprises at least one photo diode array.

7. The optical sensor as in Claim 1 wherein said porous silicon region is located on a silicon substrate.

8. The optical sensor as in Claim 7 wherein said silicon substrate is p++-type silicon with a <100> crystalline configuration.

9. The optical sensor as in Claim 7 wherein said porous silicon region is incorporated into a fluidics cartridge comprising fluid flow channels and a plurality of flow control valves, said fluid flow channels being in flow communication with said at least one buffer-sample fluid flow channel.

10. The optical sensor as in Claim 9 wherein said valves are pneumatically operated pinch valves.

11. The optical sensor as in Claim 10 wherein said pinch valves are computer controlled.

12. The optical sensor as in Claim 1 wherein said nominal widths of said pores are within the range of about 80 to 120 nanometers and said nominal depths of said pores are within a range of about 1000 to 3000 nanometers.

13. The optical sensor as in Claim 9 and also comprising a fluidics enclosure in which said fluidics cartridge is removably installed.
14. The optical sensor as in Claim 13 and also comprising robotic equipment for injecting ligand containing samples and analyte-containing samples into said fluidics enclosure.

15. The optical sensor as in Claim 1 and also comprising sample trays, at least one buffer fluid tank, at least one waste tank, a sample pump, a buffer pump and pneumatic controls, firmware and software for automated real-time measurement of kinetic binding reactions.

16. The optical sensor as in Claim 14 and also comprising sample trays, at least one buffer fluid tank, at least one waste tank, a sample pump, a buffer pump and pneumatic controls, firmware and software for automated real-time measurement of kinetic binding reactions.

17. The optical sensor as in Claim 1 wherein said at least one light source comprises a white light source or an approximately white light source.

18. The optical sensor as in Claim 1 wherein said at least one light source comprises a narrowband light source.

19. The optical sensor as in Claim 1 wherein said at least one light source comprises and ultraviolet light source.

20. The optical sensor as in Claim 1 wherein said at least one light source comprises an infrared light source.

21. The optical sensor as in Claim 1 wherein said pores comprise carboxylic acid functionalized surfaces.

22. The optical sensor as in Claim 21 and also comprised linker molecules attached to said carboxylic acid functionalized surfaces.

23. The optical sensor as in Claim 22 wherein said linker molecules comprise PEG molecules.
24. The sensor as in Claim 23 wherein most of said PEG molecules comprise four monomers.

25. The sensor as in Claim 23 wherein most of said PEG molecules have a total length of about 19.2 Angstroms.

26. The optical sensor as in Claim 1 wherein said computer program comprises algorithms for calculating changes in apparent optical path differences based on said changes in said spectral interference patterns.

27. The optical sensor as in Claim 1 wherein said at least one spectral monitor comprises a quad cell.

28. The optical sensor as in Claim 1 wherein said at least one of said at least one spectral monitor is configured to monitor Raman scattering.

29. The optical sensor as in Claim 1 wherein said nominal width of said pores in said porous silicon region is chosen to produce a modulation index for optimizing optical resolution.

30. The optical sensor as in Claim 1 wherein said nominal width of said pores in said porous silicon region is chosen to produce a modulation index for optimizing kinetic binding assays.

31. A method for measuring molecular binding interactions utilizing an optical sensor having:
   A) at least one porous silicon region comprising more than 1,000 pores, each pore having a nominal width and a nominal depth at least 10 times larger than said nominal width with the depth of each pore being approximately equal to the depth of at least most of the other pores in said porous silicon region, said porous silicon region defining a top surface and a bottom surface, said bottom surface being parallel or approximately parallel to said top surface;
   B) at least one buffer-sample fluid flow channel located above said at least one porous silicon region providing a fluid flow passage across said porous silicon region;
C) at least one light source for illuminating said at least one porous silicon region;
D) at least one spectral monitor for monitoring light reflected from said top surface and said bottom surface of said at least one porous silicon region;
E) a fluid flow control system for producing controlled flow of buffer solutions, ligand containing solution and analyte containing solutions through said at least one fluid flow channel; and
F) a computer processor programmed with a computer program for making kinetic binding measurement based on changes in spectral interference patterns monitored by said at least one spectral monitor while analytes bind with and disassociate from ligands attached to surfaces of said pores;

said method comprising:

A) Immobilizing ligand molecules within said pores;
B) Causing a solution containing analyte molecules to flow across said porous silicon region to permit analyte molecules to diffuse close to and become bound at least temporarily by said ligand molecules;
C) Illuminating at least a portion of said porous silicon region so as to produce reflections from said bottom surface and said top surface; and
D) Monitor changes in spectral patterns produced by light reflected from said top and bottom surfaces in order to obtain information concerning binding reactions between said ligand and said analyte.

32. The method as in Claim 27 and further comprising a step following Step B of causing a buffer solution to flow across said porous silicon region wherein analytes that have become bound to ligands during step B become disassociated from said ligands.

33. The method as in Claim 28 and further comprising the step of monitoring changes in spectral patterns produced by light reflected from said top and bottom surfaces in order to obtain information concerning disassociation reactions between said ligand and said analyte.
34. The method as in Claim 28 and further comprising the steps of:
   A) acquiring a reference pattern;
   B) acquiring a spectral interference pattern;
   C) normalizing said reference pattern and said spectral interference pattern;
   D) calculating a first derivative of a correlation function using said normalized spectral
      interference pattern and said normalized reference pattern;
   E) calculating a zero crossing of said first derivative of said correlation function; and
   F) recording said zero crossing as an optical path difference.

35. The method as in Claim 30 wherein said zero crossing is calculated using a Newton-
Raphson method.

36. The method as of Claim 27 wherein a region above and adjacent to said at least one porous
    silicon region provides a reference optical path length for producing interference effects.

37. The method as of Claim 27 wherein said porous silicon region provides a reference optical
    path length for producing interference effects.

38. An optical sensor for monitoring molecular binding interactions said sensor comprising:
   A) at least one porous silicon region comprising more than 1,000 pores, each pore having
      a nominal width and a nominal depth at least 10 times larger than said nominal width
      with the depth of each pore being approximately equal to the depth of at least most of
      the other pores in said porous silicon region, said porous silicon region defining a top
      surface and a bottom surface, said bottom surface being parallel or approximately
      parallel to said top surface;
   B) at least one buffer-sample fluid flow channel located above said at least one porous
      silicon region providing a fluid flow passage across said porous silicon region;
   C) at least one light source for illuminating said at least one porous silicon region;
   D) at least one spectral monitor for monitoring light reflected from said top surface and
      said bottom surface of said at least one porous silicon region;
E) a fluid flow control system for producing controlled flow of buffer solutions, ligand containing solution and analyte containing solutions through said at least one fluid flow channel; and
F) a processor means programmed with a computer program for making kinetic molecular binding measurements based on changes in spectral interference patterns monitored by at least one spectral monitor while analytes bind with and disassociate from ligands attached to surfaces of said pores.

39. The sensor as in Claim 34 wherein said processor means includes a graph forming means for producing a graph of OPD vs time during periods of ligand-analyte association and ligand-analyte disassociation.

40. The sensor as in Claim 34 wherein said processor means includes a computer program for determining values of rate constants $k_{on}$ and $k_{off}$.

41. An optical sensor for monitoring molecular binding interactions said sensor comprising:
   A) at least one porous silicon region, said porous silicon region defining a top surface and a bottom surface, said bottom surface being parallel or approximately parallel to said top surface;
   B) at least one buffer-sample fluid flow channel located above said at least one porous silicon region providing a fluid flow passage across said porous silicon region;
   C) at least one light source for illuminating said at least one porous silicon region;
   D) at least one spectral monitor for monitoring light reflected from said top surface and said bottom surface of said at least one porous silicon region;
   E) a fluid flow control system for producing controlled flow of buffer solutions, ligand containing solution and analyte containing solutions through said at least one fluid flow channel; and
   F) a computer processor programmed with a computer program for making molecular binding measurements based on changes in spectral interference patterns monitored by at least one spectral monitor while analytes bind with and disassociate from ligands attached to surfaces of said pores.
42. An optical sensor for monitoring molecular binding interactions said sensor comprising:
   A) at least one porous silicon region comprising more than 1,000 pores, each pore having a nominal width and a nominal depth at least 10 times larger than said nominal width with the depth of each pore being approximately equal to the depth of at least most of the other pores in said porous silicon region, said porous silicon region defining a top surface and a bottom surface, said bottom surface being parallel or approximately parallel to said top surface;
   B) at least one buffer-sample fluid flow channel located above said at least one porous silicon region providing a fluid flow passage across said porous silicon region;
   C) at least one light source for illuminating said at least one porous silicon region;
   D) at least one spectral monitor for monitoring light reflected from said top surface and said bottom surface of said at least one porous silicon region;
   E) a fluid flow control system for producing controlled flow of buffer solutions, ligand containing solution and analyte containing solutions through said at least one fluid flow channel; and
   F) a computer processor programmed with a computer program for making molecular concentration measurements based on changes in spectral interference patterns monitored by at least one spectral monitor while analytes bind with and disassociate from ligands attached to surfaces of said pores.

43. The optical sensor as in Claim 1 wherein said at least one porous silicon region is a plurality of porous silicon regions with more than one of said plurality of porous silicon regions having ligands immobilized within them that are different from ligands immobilized in other porous silicon regions.

44. The optical sensor as in Claim 1 and further comprising a mass spectrometer.

45. An optical sensor comprising:
   A) a light source adapted to project electromagnetic radiation along a first path;
B) a sample plate positioned along the first path and defining a plurality of sample-receiving interaction zones adapted to generate a plurality of individual interference intensity patterns; and

C) a detector positioned to detect the plurality of individual interference intensity patterns and correlate each individual interference intensity pattern of the plurality of individual interference intensity patterns with a corresponding sample-receiving interaction zone.

46. The optical sensor of claim 45 comprising a dispersion element positioned and adapted to spatially separate the wavelengths corresponding to each individual interference intensity pattern.

47. The optical sensor of claim 45 comprising a first lens positioned along the first path between the source of electromagnetic radiation and the sample plate.

48. The optical sensor of claim 45 comprising a beam splitter positioned along the first path between the source of electromagnetic radiation and the sample plate, wherein the beam splitter is adapted to transmit electromagnetic radiation along the first path and a second path.

49. The optical sensor of claim 45 further comprising a second lens positioned along the second path between the beam splitter and the dispersion element.

50. The optical sensor of claim 45 wherein the light is white light.

51. The optical sensor of claim 45 wherein the light comprises visible and non-visible light.

52. The optical sensor of claim 45 wherein the dispersion element comprises a diffraction grating.

53. The optical sensor of claim 45 wherein the detector is adapted to receive a two-dimensional array of sample-receiving interaction zone position and wavelength.
54. The optical sensor of claim 45 wherein the detector comprises a charge coupled device.

55. The optical sensor of claim 45 comprising a sample plate holder, wherein the sample plate holder is adapted to position the sample plate in the first path.

56. The optical sensor of claim 45 wherein the sample plate comprises a semiconductor material.

57. The optical sensor of claim 59 wherein the semiconductor material is silicon.

58. The optical sensor of claim 45 wherein the sample plate defines at least 64 sample-receiving interaction zones.

59. The optical sensor of claim 45 comprising an analyte disposed in at least one sample-receiving interaction zone.

60. The optical sensor of claim 45 wherein a plurality of the sample-receiving interaction zones are substantially cylindrical.

61. The optical sensor of claim 45 comprising a mass spectrometer, wherein the mass spectrometer is interfaced with the sample plate.

62. An optical sensor comprising:
   A) a light source is adapted to project white light along a first optical path;
   B) a first lens adapted to transmit white light along the first optical path to a sample plate comprising porous silicon, wherein the sample plate defines a plurality of sample-receiving interaction zones adapted to generate a plurality of individual interference intensity patterns;
   C) a beam splitter positioned along the first optical path, wherein the beam splitter is adapted to transmit white light along the first optical path and a second optical path;
   D) a second lens positioned along the second optical path;
E) a dispersion element positioned along the second optical path and comprising a diffraction grating, wherein the diffraction grating is adapted to spatially separate the wavelengths corresponding to each individual interference intensity pattern; and
F) a charge-coupled device in optical communication with the diffraction grating, wherein the charge-coupled device is adapted to receive a two-dimensional array of sample-receiving interaction zone position and wavelength, and correlate each individual interference intensity pattern of the plurality of individual interference intensity patterns with a corresponding sample-receiving interaction zone.

63. An optical sensor comprising:
means for generating a plurality of individual interference intensity patterns; and
means for correlating each individual interference intensity pattern of the plurality of individual interference intensity patterns with a corresponding sample-receiving interaction zone.

64. A method of analyzing data from an optical sensor, the method comprising the steps of:
A) generating a plurality of individual interference intensity patterns, each interference intensity pattern corresponding to a sample-receiving interaction zone; and
B) correlating each individual interference intensity pattern of the plurality of individual interference intensity patterns to a corresponding sample-receiving interaction zone.

65. The method of claim 64 wherein generating a composite interference pattern comprises the steps of:
A) projecting light along a first path incident on a plurality of sample-receiving interaction zones; and
B) transmitting light as a plurality of individual interference intensity patterns.

66. The method of claim 64 comprising separating spatially the the light according to wavelengths to produce each individual interference intensity pattern.
67. The method of claim 66 wherein correlating each individual interference intensity pattern comprises detecting each of the individual interference intensity patterns of the plurality of individual interference intensity patterns during the same time interval.

68. The method of claim 66 wherein correlating each individual interference intensity pattern comprises detecting a two-dimensional array of sample-receiving interaction zone position and wavelength.

69. The method of claim 64 comprising the step of providing a sample plate having a plurality of sample-receiving interaction zones, wherein a plurality of the plurality of sample-receiving interaction zones comprise an immobilized target.

70. The method of claim 69 comprising mass analyzing a captured analyte, wherein the captured analyte is associated with an immobilized target.

71. The method of claim 70 wherein mass analyzing comprises desorbing and ionizing the captured analyte with a source of electromagnetic radiation while under a vacuum within a mass spectrometer.

72. The method of claim 64 comprising the step of comparing the individual interference intensity pattern of a first sample-receiving interaction zone and the individual interference intensity pattern of the first sample-receiving interaction zone after the first sample-receiving interaction zone was exposed to a sample.

73. The method of claim 64 wherein the plurality of individual interference intensity patterns comprises at least 8 individual interference intensity patterns.

74. The method of claim 64 wherein the light comprises visible light and non-visible light.
$W = 36 \, \mu m$

$\Delta x = 6 \, \mu m$

FIG. 8
FIG. 9A Step a:

\[
\text{Si-H} + \text{undecylenic acid} \xrightarrow{2\text{hrs} 120-130^\circ\text{C}} \text{Product}
\]

FIG. 9B Step b:

\[
\text{Si-CHO} + \text{Amino-dPEG}_4 \text{-butyl ester} \xrightarrow{\text{Stir overnight in CH}_2\text{Cl}_2} \text{Product}
\]

FIG. 9C Step c:

\[
\text{Si-NH} \xrightarrow{\text{TFA deprotection}} \text{Product}
\]
FIG. 9F Step f.
**Kinetic Binding Experiment**
- Acquires experimental data of fringe patterns versus time for kinetic binding of analyte molecules to receptor molecules attached to pore walls

**Optical Interferometer Model**
- Calculates optical thickness OT of porous silicon interaction volume versus time from measured fringe patterns versus time

**Index of Refraction Model**
- Calibrates change in protein surface concentration on pore walls versus time from change of optical thickness OT versus time

**Kinetic Binding Model**
- Calculates $K_D$, $K_m$, and $k_{off}$ from calibrated experimental data

**Mass Transport Model**
- Calculates effects of mass transport on the kinetic binding rate equations

**Fig. 13**

**Fig. 16**
Acquire fringe pattern 
\{\lambda[i], \text{Sig}[i]\} 
\quad (i=0,N\lambda) 

Acquire reference pattern 
\{\lambda[i], \text{Sig}[i]\} 
\quad (i=0,N\lambda) 

Calculate the correlation function \(C(X[j])\) for discrete values of \(X[j]\) around the peak of \(C(X[j])\) 

Search value \(X[j_{\text{max}}]\) such that \(C(X[j_{\text{max}}]) = \text{maxvalue}\) 

Find the zero crossing \(F(X_{opt}) = 0\) using the Newton-Raphson root-finding method 

Record \(X_{opt} = \text{OT}\) (optical thickness)