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DESCRIPTION

[0001] The invention regards the field of nanotechnology and describes the utilization of electric fields for the manipulation of molecular mechanisms. In this way, a molecular machine is provided, which allows movement in response to said electrical fields.

[0002] In the past decades, several biomolecular mechanisms and machines have been demonstrated for the application in nanotechnology. However, none of them grew past the "proof of principle" phase.

[0003] Among the naturally occurring molecular machines mainly kinesin motors and microtubules were deployed, e.g., for the transport of nanoparticles (cf. prior art references 1 to 3). In so-called "in vitro motility assays" kinesin motors were fixed on lithographically patterned chip surfaces to transport microtubules through lithographically produced channel systems. Here electric manipulation was also used e.g. for the sorting of microtubules (cf. prior art reference 4).

[0004] In the past years, artificial biomolecular nanomachines were mainly produced on the basis of DNA molecules. The production of DNA machines utilizes the characteristic, sequence specific molecular interactions between DNA strands. Adequate choice of DNA sequences allows to "programmably" construct complex molecular structures from single DNA strands. A combination of relatively flexible single stranded DNA components with more rigid double stranded elements allows the construction of molecular mechanisms in which molecular components can be moved relative to each other. These include "DNA tweezers" as well as various "DNA walker" systems. An overview of such systems is given in prior art reference 5. With the recent development of the so-called "DNA origami method" it has become much easier to construct larger molecular systems (typically on the length scale of 10 - 100 nm). Recently this method was used to construct basic molecular machine elements, including several rotary joint and linear sliding structures (prior art references 6 to 9).

[0005] So far, the described molecular mechanisms have been actuated chemically or in some cases photo-chemically. In the case of chemical actuation, e.g., so-called DNA fuel strands were used to drive the movement of a mechanism through DNA strand hybridization reactions. Due to the slow kinetics of these reactions only very slow motion could be realized (prior art references 10 to 12). The same limitations apply to deoxyribozymes and DNA modifying enzymes (prior art reference 13).

[0006] Alternatively, motion of molecular mechanisms was achieved with a change of buffer conditions, e.g. by a change in pH or a change of the solution's ionic conditions. These methods come with the disadvantage that they unspecifically influence all system components and that buffer conditions are often not compatible with the chemistry of potential applications (e.g. enzymes are not functional in the specific conditions, nanoparticles can aggregate, etc.)

[0007] The aforementioned chemical methods typically require the external addition of solutions. In principle, this can be done with the help of microfluidic systems, which could allow a certain degree of automation. However, such an approach requires rather elaborate instruments and causes high material consumption.

[0008] At first glance, an attractive method for external control of nanomachines is based on photoswitchable molecules, typically derivatives of the photoswitchable molecule azobenzene (prior art references 14 to 16). Incorporation of such photoswitches into DNA double strands makes it possible to destabilize them upon light irradiation (in UV range) and stabilize them by irradiation with light of larger wavelength, and this procedure can be used to drive molecular mechanisms. The downside of this method, apart from the necessary chemical modification of the mechanisms, again is the slow and incomplete switching behavior.

[0009] Prior art reference 22 describes a biosensor including a gold platform. This biosensor allows only binary switching between an adhesive state and a non-adhesive state. No fine adjustment of the movement is possible. Prior art reference 23 describes the movement of molecular mechanisms in response to UV light.

[0010] None of the described approaches could ever demonstrate the exertion of a relevant force against an external load.

[0011] It is an object of the present invention to provide a molecular machine which allows quick reaction to control commands, which can generate high forces, and which can provide an exact movement.

[0012] The object is solved by the features of the independent claim. The dependent claims contain advantageous embodiments of the present invention.

[0013] The object is therefore solved by a molecular machine comprising a movement part and a control part. The movement part comprises several machine elements which are adapted to be moved with respect to each other. These machine parts are molecular structures, particularly nanomolecular structures. The movement part includes a first molecular element, a second molecular element and a linking element. The first molecular element and the second molecular element preferably are separate and/or independent elements. The linking element is adapted to constrain a relative movement of the first molecular element and the second molecular element while allowing a relative movement between the first molecular element and the second molecular element in at least one degree of freedom. Preferably, the first molecular element and the second molecular element can not be separated from each other and establish a moving mechanism with the linking element acting as bearing and/or joint.

[0014] In order to control the relative movement of the first molecular element and the second molecular element, the control part is configured to generate an electrical field around the movement part. Preferably, the control part includes an electrical device which applies said electrical field. The first molecular element is fixed relative to the control part such that the first molecular element is fixed relative to the electrical field generating means. Hence, even a change in the electrical field cannot cause a movement of the first molecular element. The first molecular element rather acts as a base for movement of the second molecular element. The second molecular element is therefore the only part which can be moved in response to the electrical field.

[0015] At least the second molecular element is electrically charged. The second molecular element can be an electrically charged molecule, particularly a biomolecule, or can be artificially electrically charged. In particular, an electrically charged functional group can be added to a molecular structure in order to create the electrically charged second molecular element. Due to the electrical charge, the second molecular element aligns to said electrical field. In case the electrical field is changed in orientation, the orientation of the second molecular element is also changed. This means that the control part can control fine adjustment of the second molecular element with respect to the first molecular element. The second molecular element can be transferred to and held in any orientation with respect to the first molecular element that is not prevented by the linking element. Additionally, a continuous movement of the second molecular element can be realized.

[0016] In summary, the movement part sets up the kinematics of the molecular machine, while the control part powers and controls any movement of said kinematics via electric actuation. Electric actuation solves several technical challenges that are currently faced by molecular nanomachines. In particular, electric actuation allows controlling molecular switches and mechanisms faster, with higher precision, and with less complex instrumentation compared to conventional methods. Moreover, the invention offers the solution to a central challenge of nanomanipulation (the "fat fingers" problem) since the externally controlled nanomanipulators are of the same small length scale as the manipulated nanoscale objects and molecules.

[0017] In a preferred embodiment, the control part comprises a fluidic channel. The movement part is provided

in the fluidic channel. The control part further comprises an electrical device including electrodes. The electrodes are connected to the fluidic channel. In this way, the electrical field as described above can be created. The electrical device comprises a voltage source and electrical wiring to apply the voltage to the electrodes. Preferably, the electrical device comprises two electrodes for generating the electrical field. Alternatively, the voltage source can be a three-phase voltage source such that the electrical device has three electrodes. This allows providing a rotating electrical field such that the second molecular element can be rotated in a simple way.

[0018] Preferably, the control part comprises at least two electrical devices and fluidic channels with different orientations. In this way, two independent overlaying electrical fields can be created. The fluidic channels are arranged to intersect at an intersection area and the movement part is placed at the intersection area. Therefore, a two-dimensional movement of the second molecular element can be controlled. Alternatively, the above described three-phase voltage and the three electrodes might be used for two-dimensional movement control.

[0019] Favorably, the first molecular element is fixed to the fluidic channel. This means that the first molecular element can not move in response to the electrical field. The molecular element rather is a fixed base for the movement of the second molecular element. In this way, it is ensured that only the second molecular element can be moved. Further the fixation of the first molecular element allows very fine adjustment of the second molecular element, which aligns to the electrical field while the first molecular element does not move and/or align to the electrical field.

[0020] Providing the electrical device including electrodes might cause unwanted electrochemical effects. Particularly in case the movement part is employed for synthesis purposes, electrochemical effects to the synthesized products should be avoided. Therefore, the electrical device preferably includes an isolating element for isolating the electrodes from the movement part. The isolating elements particularly comprise membranes and/or gels and/or salt bridges. This means that only selected molecules can pass through the isolating elements such that the electrodes are separated from the movement part. However, the electrical field generated by the electrical devices is not influenced or at least not significantly influenced by the isolating element. Therefore, the control of movement of the second molecular element is not affected. The isolating element preferably also reduces the volume provided for reactions. This particularly allows holding the components of a desired reaction close to the movement part such that the components can manipulated and/or moved by the molecular machine.

[0021] The linking element is favorably part of the first molecular element or the second molecular element. Particularly, the first molecular element and/or the second molecular element might comprise a functional group which is adapted to link the first molecular element and the second molecular element. In this way, the manufacturing process of the molecular machine is simplified. Additionally, the linking element can be part of at least one of two or more mechanically interlocked molecules. This is particularly preferred in a case in which the movement part comprises rotaxanes. In such structures, the first molecular element comprises a linear part and the linking element and the second molecular element comprises a ring structure. The ring structure can rotate about the linear part and the linking element avoids the ring structure slipping off the linear part.

[0022] The first molecular element and/or the second molecular element and/or the linking element preferably are biomolecules. The biomolecules are particularly electrically charged. In a further preferred embodiment, the first molecular element and/or the second molecular element and/or the linking element are made of DNA (deoxyribonucleic acid), preferably DNA-origami, and/or RNA (ribonucleic acid) and/or protein and/or artificial charged supramolecular structures.

[0023] In a preferred embodiment, the first molecular element is a platform and the second molecular element is a positioning arm. The positioning arm is fixed to the platform via the linking element. The linking element

constrains all relative movement of the first molecular element and the second molecular element except of a rotation of the second molecular element within a plane parallel to the first molecular element. Therefore, the positioning arm is preferably moved by aligning to two overlaid electrical fields. This allows adjusting the positioning arm in relation to the platform. Particularly, a full rotation of the positioning arm is possible, wherein the positioning arm can be stopped and hold in any position. Further, high forces are generated which allow manipulation of further molecules.

[0024] The first molecular element and/or the second molecular element are addressable. This means, that functional groups can be provided on the first molecular element and the second molecular element. Preferably, both, the first molecular element and the second molecular element can be addressed. Therefore, the movement part can be adapted to specific needs. This allows employing the molecular machine in various environments and/or for various purposes.

[0025] Preferably, fluctuations of the first molecular element and/or the second molecular element due to diffusion are within a tolerance of at most 10 nm, preferably at most 1 nm, particularly preferable at most 0.5 nm. Hence, a fine adjustment of the second molecular element is facilitated.

[0026] Preferably, any dimension of the first molecular element and the second molecular element is less than 1000 nm. Particularly, the above described platform is preferably made of square shape with a length of 50 to 55 nm. The positioning arm is preferably shorter than said length. Particularly, the positioning arm is adequately addressable within the overlap with the platform. Such dimensions allow manipulation of molecules with the molecular machine. Therefore, the molecular machine is a molecular nanomechanism.

[0027] In a preferred embodiment, the linking element is made from a crossed two-layer scaffold routing. A top layer is preferably rotated with respect to a bottom layer by an angle between 80° and 100°, particularly 90°. Therefore, a stable base plate is generated.

[0028] The second molecular element is particularly made from a DNA six-helix bundle. Therefore, the second molecular element can be provided as positioning arm. This positioning arm might be used as robot arm for several purposes, for example for manipulating molecular mechanisms.

[0029] On the top layer of the first molecular element, the second molecular element forming the positioning arm is preferably connected to the plate via two adjacent scaffold crossovers with 3 and 4 unpaired bases, respectively. These short single-stranded segments create a flexible joint, which allows rotational movement of the second molecular element with respect to the first molecular element. While this joint cannot turn in the same direction indefinitely without winding up, it is still sufficiently flexible to allow the arm to reach any angle on the plate. This design is preferred over other potential designs for two reasons. First, this design allows us to use a one pot folding approach for the first molecular element and second molecular element, particularly the platform with the integrated 6HB arm, which confers the benefit of fast preparation and short experimental iteration periods. Second, a joint created by a double scaffold crossover provides higher resistance against external mechanical strain. For comparison, a single staple crossover would allow rotation around a single covalent bond, but the connection to the arm would always be oriented in a duplex unzipping geometry for one specific orientation of the arm during rotation. In this configuration, the connection to the first molecular element could potentially be unzipped, leading to the dissociation of the arm. By contrast, utilization of the scaffold strand (as in this work) to create the joint ensures a stable covalent connection between base plate and arm. With a circular scaffold strand, this strategy necessarily results in two single-stranded connections between arm and plate. For angles in which one strand is exposed to forces in unzipping geometry, the second strand is oppositely oriented in shear geometry and may therefore act as a strain relief. A linearized scaffold would allow for a covalent connection with only a single connecting strand, but would still be prone to unzipping when exposed to forces antiparallel to the direction of the scaffold strand in the plate next to its crossover to the arm structure. Particularly for experiments in which the length of the lever arm is exploited to create forces

on the base plate (e.g. in the 20bp unzipping experiment, Fig. 9C and 9D), bearing forces of the same order are expected to act on the joint. In this case, a high mechanical stability of the joint is crucial and was therefore prioritized over the possibility of indefinite unidirectional rotation.

[0030] The second molecular element is preferably adapted to transport inorganic nanoparticles. Therefore, fast operations of biohybrid plasmonic systems are enabled.

[0031] A specific embodiment will be described together with the attached drawings:

Fig. 1
is a schematic view of a moving part of a molecular machine according to an embodiment of the invention.

Fig. 2
is a schematic view of a first alternative of a control part of the molecular machine according to the embodiment of the invention.

Fig. 3
is a schematic view of a second alternative of a control part of the molecular machine according to the embodiment of the invention.

Fig. 4
is a schematic view of the moving part of the molecular machine according to the embodiment of the invention, which is modified for proof of functionality.

Fig. 5
is a schematic view of montage of single images from a microscope video showing the movement of the molecular machine according to the embodiment of the invention.

Fig. 6
is a schematic view of a diagram showing movement of the molecular machine according to the embodiment of the invention.

Fig. 7
shows stochastic switching experiments. (A) For single-molecule multi-color FRET experiments, a donor fluorophore (Alexa Fluor 488) is attached to the 6HB arm and two acceptor fluorophores (ATTO 565 and ATTO 647N) to staple strand extensions on opposite sides of the plate. The pictograms on the left show hybridization of an extended staple of the arm to the staple extension of the base plate labelled with ATTO 647N. The length of the docking duplex was varied between 8 and 10 bp. A schematic 3D representation is shown on the right. (B) Fluorescence traces obtained from the three fluorophores during donor excitation of the structures containing 9 bp docking duplexes. The change between green and red fluorescence indicates switching of the arm between corresponding docking sites. The zoom-in (bottom panel) reveals short periods of free diffusion between unbinding and rebinding events during which the donor (Alexa Fluor 488 = "blue") fluorescence is dominant. (C) Average dwell times for the bound and unbound states and their dependence on duplex length. Dwell times for the bound states (high acceptor signals-ATTO 647N = "red" or ATTO 565 = "green", top panel) correspond to the times spent at the respective docking site. The dwell times for the unbound state (high donor signal-blue, bottom panel) represent the length of the traversal periods of the freely diffusing arm. (D) The average durations of the unbound states for various transitions and their dependence on duplex length. Based on start and end point of the traversal period (docking site or bound state-g or r before and after the unbound state), the unbound states can be classified as g→r and g→g or r→g and r→r traversals.

Fig. 8
shows external electric control of the robotic arm. (A) Two pointer extension designs for the robot arm and corresponding TEM images. The linear extension (left) pointer has a length of 411 nm (total length from center of rotation to tip: 436 nm). The pointer on the right has a shape complementary connection that withstands higher torque (total length of 354 nm, pivot point to tip: 332 nm). (B) Cross section and (C) top and isometric view of the cross-shaped electrophoretic sample chamber. (D) A schematic depiction of the experimental setup with four electrodes. (E) Fluorescence microscopic images of three

structures that are switched in the electric field. For the highlighted particle, movements are shown as snapshots and kymographs. The two arrows indicate the axes chosen for the kymographs. Top: Switching left and right with 1 Hz. Bottom: Switching up and down with 1 Hz. (F) Top: One clockwise turn of 1 Hz rotation. Bottom: The kymographs show multiple turns of clockwise rotation followed by multiple counter-clockwise turns, separately for x and y axis and as an overlay. Reversal of the voltage and thus of the rotation direction is indicated by a red arrowhead. (G) Kymographs (x- and γ-projection) obtained from a frequency sweep from 0 to 8 Hz and back, shown as an overlay of the kymograph along x-axis and y-axis. (H) High speed 360° clockwise and counter-clockwise rotation with 25 Hz. For each frame, the center of the pointer tip is indicated by a red cross. Reversal of the rotation direction is indicated by red arrowheads. Unlabeled scale bars: 1 µm.

Fig. 9

shows controlled hybridization and force-induced duplex dissociation. (A) Field-controlled switching of the extended robot arm between two 9bp docking positions. Left: Scheme of the setup. Right: Single molecule localization image of pointer positions acquired during electrical rotation at 1 Hz. The number of localizations is increased at angles corresponding to the two docking positions. (B) Angle plotted over time for 1, 2, and 4 Hz rotation with 110V. The arm shows pronounced lagging for two angles (highlighted by grey bands), higher frequencies result in a larger number of missed turns, indicated by the red arrowheads. (C) Unzipping of a 20 bp DNA duplex with the extended robot arm. Extensions from the platform and from the arm feature a short 8 bp strain relief domain that prevents the staple strands from being pulled out of the structure. Experiments with two example particles are shown. Without electric field, the arm is fixed at one of two docking positions on the base plate. (D) Rotation requires unzipping of the duplex, which is shown in the images (before rotation, during rotation and after rotation) and kymographs at the bottom. Particle #1 rebinds to the starting position, whereas particle #2 rebinds to the position on the opposite side.

Fig. 10

shows electrically controlled movement of molecules and nanoparticles. (A) Configuration of the robot arm with shape complementary extension for transport of the FRET donor Alexa Fluor 488 between two 9 nt docking sites with the acceptors ATTO 565 and ATTO 647N. (B) Acceptor signals for continuous donor excitation for electrical rotation at 1 Hz (top), 2 Hz (middle) and 4 Hz (bottom). (C) For application of the robot arm in switchable plasmonics, a gold nanorod (AuNR) with 25 nm length is attached to the side of the 6HB arm and 11 ATTO 565 and ATTO 655 dyes are placed on opposite halves of the platform. (D) TEM micrograph of structure with a 25 nm AuNR and fluorescence traces for continuous excitation of the dyes while the robot arm is rotated at 1 Hz, 2 Hz and 4 Hz.

Fig. 11

is a schematic overview of fixing the platform of the molecular machine according to the embodiment of the invention.

Description of the embodiment

[0032] Figure 1 is a schematic view of a movement part 2 of a molecular machine 1 according to an embodiment of the invention. In the embodiment, the movement part 2 comprises a platform 4, which corresponds to the first molecular element. On the platform 4, a position arm 5 is mounted, which corresponds to the second molecular element. A linking element 6 constrains the relative movement between platform 4 and positioning arm 5 such that the only possible relative movement is a rotation of the positioning arm 5 in a plane parallel to the platform 4. Platform 4 and positioning arm 5 are constructed with the DNA origami method. The DNA origami method is well-known in the art and is for example described in prior art references 17 to 18. The square platform 4 consists of two layers of DNA double helices. In all figures, each double helix is represented by a cylinder. The positioning arm 5 is a six helix bundle. The linking element 7 comprises two

DNA strands and connects the positioning arm 5 to the platform 4. Transmission electron microscopy micrographs can show the structure and quality of these objects.

[0033] The platform 4 and the positioning arm 5 can be built from different molecules e.g. RNA, proteins, artificial charged supramolecular structures. The positioning arm 5 might be elongated by coupling to further structures. An example for such elongation is described with respect to figure 4.

[0034] DNA molecules and thus also DNA origami structures are heavily charged biomolecules that can be electrically or electrophoretically manipulated. This fact can be exploited to achieve control and movement of molecular mechanisms.

[0035] Electric fields can be created in a simple electrophoretic or micro-electrophoretic setup. In the embodiment, a control part 3 is employed, which is shown in figures 2 and 3. Figure 2 is a schematic view of the molecular machine 1 including a control part 3 according to a first alternative, while figure 3 is a schematic view of the molecular machine including a control part 3 according to a second alternative.

[0036] As shown in figure 2, a fluidic channel 9 is provided which is contacted by platinum electrodes 11 of an electrical device 7. The movement part 2 is placed in the center of this fluidic channel 7, preferably as far away from the electrodes as possible. Isolating elements 13 might be provided in order to isolate the electrodes 13 from the movement part 2. The Isolating elements 13 preferably comprise membranes, gels or salt bridges. The isolating elements 13 do not allow transfer of selected molecules such that the electrodes are separated form the movement part 2 such that no unwanted traveling of elements from the movement part 2 to the electrodes 11 can take place. This avoids unwanted electrochemical influences of the electrodes 11.

[0037] Electric control is achieved by applying voltages to the electrodes. For that purpose, low control voltages as output channels of a DAQ board (data acquisition board) are amplified to adequate voltages by an operational amplifier. In the embodiments, the electrical device 7 applies voltages of up to 200 V.

[0038] Two-dimensional movement of the positioning arm 5 can be realized with a crossed channel geometry. This is shown in figure 3. The control part 3 comprises a first electrical device 7 and a second electrical device 8, both are identical to the above described electrical device of figure 2. The first electrical device 7 is connected to a first fluidic channel 9 and the second electrical device 9 is connected to a second fluidic channel 10, wherein the first fluidic channel 9 and second fluidic channel 10 are both identical as the above described fluidic channel of figure 2. The first fluidic channel 9 and the second fluidic channel 10 intersect at an intersection area 12 and are orientated perpendicular to each other. The movement part 2 is placed in the intersection area 12. Due to such a design, the electrical fields of the first electrical device 7 and the second electrical device 8 are superposed. Superposition of electrical fields in the fluidic channels 9, 10 allows to adjust the positioning arm 5 in arbitrary angles or to rotate it in circles relative to the platform 4.

[0039] In order to ensure that only the positioning arm 5 rotates while the platform 4 remains still, the platform 4 is fixed to at least one of the fluidic channels 9, 10 of the control part 3. In this way, the platform is fixed relative to the control part 3 which means that no movement of the platform 4 is possible in response to the electrical field.

[0040] In an alternative setup, lithographically designed microelectrodes can be used, which require much smaller voltages for manipulation. In principle, this enables the miniaturization of the whole setup and the integration e.g. on a USB-Stick.

[0041] The electrically charged positioning arm 5 aligns to the electrical fields generated via the first electrical device 7 and the second electrical device 8. In this way, an exact positioning of the positioning arm 5 can be reached. Particularly, the positioning arm 5 can be moved with a tolerance of at most 1 nm.

Proof of Functionality

[0042] Evidence for the electro-controlled movement of positioning arms 5 can be provided in several ways.

[0043] Figure 4 is a sketch of the DNA platform 4 with the positioning arm 5 that is modified with a blue donor dye 15. The platform 4 was labeled at two positions with a green first acceptor dye 16 and red second acceptor dye 17, respectively. The positioning arm 5 movement can be proven via single molecule FRET (fluorescence resonance energy transfer). Further, for better electric coupling (via the DNA-structures charge) and to enable direct optical observation an additional lever/pointer structure 14 is provided to extend the positioning arm 5 to a length of several 100 nm (in this example ~400nm).

[0044] The movement of the positioning arm can be characterized by means of single molecule fluorescence resonance energy transfer (smFRET), which demonstrates the system's positioning precision on the nanometer scale. As the blue donor dye 15, Alexa Fluor 488 is employed, as the green first acceptor dye 16, ATTO 565 is employed, and as the red second acceptor dye 17, ATTO 647N is employed. The blue donor dye 15 can excite the first acceptor dye 16 and second acceptor dye 17 via FRET if donor and acceptor are in closer proximity than the Foerster radius (~6 nm).

[0045] Figure 5 illustrates single molecule FRET traces corresponding to the sketch in figure 4. The rotation of the positioning arm 5 is externally driven at 1 Hz while the donor dye 15 on the positioning arm 5 is being excited. This results in an alternating emission of green by the first acceptor dye 16, as shown in the top diagram of figure 5, and red by the second acceptor dye 17, as shown in the middle diagram of figure 5. An overlay of both traces, which is shown in the bottom diagram of figure 5, clearly shows the periodic alternating excitation.

[0046] As shown in figure 6, the invention can provide a periodic movement of the positioning arm 5 from one position of the platform 4 to the other. This experiment also demonstrates the potential of the invention to transport and position molecules on the platform 4, which is of great importance for a wide range of applications.

[0047] An alternative way of proof of movement of the positioning arm 5 is shown in Figure 6. Figure 6 shows a montage of single images from a microscope video, which shows the electrically driven rotation of the positioning arm (exposure per frame: 50 ms, Scale bar: 500 nm). Fluorescent dyes are fixed to the tip of positioning arm 5. The origami platform 4 is located in the image center and is indicated by a cross. The particle rotates in an external field. For figure 6, fluorescent dyes have been placed on the tip of the extension of the positioning arm 5, i.e. on the additional lever/pointer structure 14. The positioning arm 5 is rotated in circles with a frequency of 1 Hz. As shown on the image series, the particle at the tip of the positioning arm is performing the desired rotational movement. This also shows the controlled movement of a nanoscale object on a length scale of 1 µm.

Industrial Application Perspectives

[0048] The key capability to position molecules precisely, fast and electrically controlled as well as the possibility to locally exert directed forces trough molecular mechanisms on the nanoscale enables a wide variety of application opportunities in nanotechnology. Below, three possible areas of application will be briefly discussed.

Single Molecule Sensing and Force Spectroscopy

[0049] Highly specific molecular interactions are responsible for a wide range of biological processes and are also the mechanism of action of pharmacological substances. For this reason, biological research has been focused on the precise biochemical and biophysical characterization of these interactions for quite some time. In biophysical research, the strength of interactions is often analyzed in single molecule experiments. Here special instruments are used to exert forces on the binding partners. This includes experiments with atomic force microscopes, optical tweezers and magnetic tweezers.

[0050] The movement part 2 of platform 4 and positioning arm 5 according to the described embodiment of the invention make it possible to apply forces to molecules in situ. That is to say, in the case of the invention, the force applying lever itself is a molecular structure. Contrary to the other methods mentioned, it is relatively simple to conjugate the molecules and binding partners that are to be characterized to the platform 4 and the positioning arm 5. The experimental setup used to create electric forces is much simpler. This enables highly parallelizable execution of force measurements of molecular interaction partners since a vast number of measuring platforms 4 can be actuated at the same time. The sensor principle can also be used for screening of molecule libraries by "barcoding" (cf. prior art reference 19) of single platforms 4.

DNA Templated Synthesis

[0051] In the past 15 years, DNA templated synthesis was established as a novel method to increase the efficiency of chemical reactions and for the sequence based production of molecule libraries. This approach exploits the highly increased local concentration of molecules that were conjugated to a DNA strand and are thereby colocalized by sequence specific base pairing on the template (cf. prior art references 20 and 21).

[0052] This principle can be transferred to reactions with electrically driven molecular mechanisms. Electrically addressable moving molecular mechanisms can bring molecules into close proximity to induce their reaction. In this way for example, the same reaction can be repeated depending on an external clocking signal or sequential reactions can be performed according to a programmable protocol. Contrary to existing "proof of principle" experiments, the possibility of repeated and highly parallelized performance of such reactions enable the production of technologically relevant amounts of substances. The invention, i.e. the development of the electrical switchable molecular machine 1, is therefore an enabling technology for the realization of genuine molecular robotic systems and molecular assembly lines.

Photonics/Plasmonics

[0053] The molecular actuators according to the invention can readily be modified with inorganic particles like e.g. metal or semiconductor particles. For instance, a change in position of the molecular mechanisms can vary the particles' orientation with respect to a polarized external field. Accordingly, the occurrence of plasmonic effects (e.g. field enhancement, energy transfer, heating effects) can be switched via electric control.

Summary

[0054] With the described invention, nanoscale objects or molecules can be controllably moved and positioned. As an embodiment and for the demonstration of the general working principle a molecular positioning arm 5 from DNA molecules was explained. The nanoscale molecular positioning arm 5 is fixated on a specifically addressable platform 4 with a flexible joint that allows rotation around the pivot point. The positioning arm 5 movement can be precisely controlled by external electric fields. The positioning arm 5 can

transport molecules, control chemical processes and exert forces on other molecules "in situ". The method exploits the intrinsic electric charge of biomolecules and can be generally applied to synthetic as well as naturally occurring biomolecular mechanisms.

Further aspects

[0055] In the molecular machine, sequence-specific switching is deliberately abandoned and electrical fields are used to move the components of a DNA machine with respect to each other. Thus many orders of magnitude in operation speed, almost perfect switching yield and the capability of computer-controlled nanoscale motion and positioning are gained.

[0056] The actuator unit of our system is comprised of a 55 × 55 nm^2 DNA origami plate (platform 4) with an integrated, 25 nm long arm (positioning arm 5) defined by a DNA six-helix bundle (6HB), allowing for a high-yield one-pot folding procedure. For the rigid DNA plate, a crossed two-layer scaffold routing is utilized, in which the top layer is rotated with respect to the bottom layer by 90°. The 6HB functioning as the robot arm is connected to the top-layer of the base plate via a flexible joint (linking element 6) created by three and four unpaired bases, respectively. Successful assembly of the structure with ≈ 90% yield was verified using transmission electron microscopy (TEM) and atomic force microscopy (AFM). Consistent with the design, AFM yields a height of 4 nm for the base plate and an additional 4 nm for the 6HB arm.

[0057] First, the diffusive motion of the arm with respect to the base plate is investigated using single-molecule multi-color Forster Resonance Energy Transfer (FRET) experiments. This is illustrated in figure 7. For these experiments, two staple strands on opposite sides of the plate were extended with an identical short docking sequence, while a staple strand on the arm was extended with the complementary sequence. Transient binding of the arm results in stochastic switching between the two docking sites, which we observed with the help of three reporter dyes - a FRET donor at the tip of the arm, and two different acceptor dyes at the docking sites (figure 7A). A typical trace of stochastically alternating FRET signals is shown in figure 7B. Upon donor excitation, a high donor (blue, solid line) fluorescence indicates a freely diffusing arm, while a high acceptor fluorescence (green, dashed line, or red, dotted line) indicates docking at the respective site. Dwell times for the three states were extracted from fluorescence traces of over 1000 robot arm platforms using a hidden Markov model (HMM) analysis. As expected, the dwell time in the bound states increases with docking duplex length (figure 7C, top panel). Interestingly, the dwell time spent in the unbound state also increases (figure 7C, bottom panel), indicating slower diffusion and/or a reduced hybridization rate for longer docking duplexes. Observed state transitions can be classified into transitions from one binding site to the other (green/red or red/green), or rebinding events to the same docking site (green/green, red/red). When the arm initially unbinds from the green docking site, it binds to either site with roughly the same transition time (figure 7D, top panel). Conversely, arms starting at the red docking site have a higher tendency to return to the same site (figure 7D, bottom panel). This bias is consistent with the expected orientation of the arm on the base plate, which is designed to point towards the red docking site. The corresponding higher effective concentration of the arm in the vicinity of the red docking site results in faster rebinding transitions. Photophysical origins of the observed changes in the FRET signal (such as fluorescent dark states or environmental quenching of the fluorophores) were excluded by performing alternating laser excitation experiments.

[0058] To facilitate direct observation of the arm's motion by diffraction-limited fluorescence microscopy, two versions of pointer structures were designed that were multiply labeled with the fluorophore ATTO 655. Version one extended the arm linearly by 411 nm (Figure 8A left). Version two extended the arm by 308 nm (Figure 8A, right) and was modularly plugged onto the robot arm using a shape-complementary connector structure, creating a more stable connection between pointer and arm to allow for better torque transmission. Both pointers are based on a rigid 6HB with a persistence length > 1 µm (25). The two designs were motivated by the differing requirements for the experiments described below. For rotational diffusion experiments in the

absence of docking sites, the linear pointer was found to interact less with the base plate than the shape-complementary pointer. However, when used to exert forces the linear pointer displayed a reduced stability and tended to break at the connection site. In the presence of docking sites, single molecule localization images of both pointers were consistent with the positions of the docks on the platform, proving that the extensions point along the axis of the short arm and that the interactions with the docking sites dominated over unspecific sticking.

[0059] In order to realize dynamic external control of the robot arm, electrical fields were applied to the system - a natural choice for the manipulation of charged biomolecules. Electrical fields have been previously used only to stretch or orient substrate-immobilized DNA duplexes but not to dynamically control the conformation of nanomechanical DNA devices. We created a cross-shaped electrophoretic chamber constituted by two perpendicular fluidic channels intersecting at the center of a microscopy cover slip, with two pairs of platinum electrodes inserted into the four buffer reservoirs (Figure 8B & C). DNA nanostructures immobilized at the center of the cross chamber experience a superposition of the fields generated by the electrode pairs. Hence, a voltage can be applied to arbitrarily control the direction that the arm points (Figure 8D).

[0060] Electrical actuation of the arms results in a movement of the pointers, which were observed with an EMCCD camera using TIRF microscopy. In Figure 8E, switching of an arm in two perpendicular directions is shown, rotation with a constant frequency of one Hertz (Figure 8F) and with variable frequency (Figure 8G), ramping from 0 to 8 Hz and back to 0 Hz. In order to characterize faster arm movements, TIRF microscopy videos with a 2 ms time resolution using a CMOS camera were recorded. An image series taken from a video in which the robot arm was rotated back and forth at f = 25 Hz is shown in Figure 8H. Kymographs displaying the projected motion of the arm's pointer along the x- and y-axis show the expected sinusoidal characteristics. In high-viscosity buffer solution containing 65% sucrose, motion of the arm was significantly slowed down.

[0061] Next, the angular positioning precision of the arm that can be achieved in the absence of docking sites by the electrical field alone is assessed. For large applied voltages (≥ 120 V in our setup) the angular standard deviation is ≈ 0.1 rad, which translates to a positioning precision of ≈ 2.5 nm on the plate.

[0062] In order to investigate the interaction of the arm with binding sites on the platform during electrical manipulation, "latching experiments" were performed with the same arrangement of docks as in Figure 7 and an identical 9 base pair (bp) docking sequence (Figure 9A). When rotated at frequencies of f = 1, 2, and 4 Hz temporary stalling of the pointer at the two angle positions that corresponded to the two docking sites were observed (Figure 9B), indicating that the arm "snaps" into the binding positions during rotation. Whereas the signal followed the external control faithfully for f = 1 Hz, occasional "skips" occurred for f = 2 Hz and 4 Hz. This behavior is caused by the statistical nature of single molecule duplex dissociation, whose frequency increases exponentially with the application of a force and, in dynamic experiments, also depends on the force rate. Apparently, the dissociation rate (~ 0.4 s-1, cf. Figure 7B) of the docking duplex is sufficiently enhanced by the electrical force to follow the 1 Hz rotation. For higher frequencies, the duplex does not always dissociate fast enough and the arm cannot follow the rotation of the electrical field. By contrast, at a slower rotation speed of f = 0.1 Hz, dynamic latching can be observed also to four different docking sites.

[0063] Next it is tested whether the robotic arm can wrest apart a 20 bp docking duplex, which is a stable structure at room temperature. While the arm is firmly locked in place in the absence of an electrical field, it can be released from the docking site by actuating the arm and rotated as shown in Figure 9C and 9D. Unzipping is expected to be most effective when the field is applied perpendicularly to the fixed arm. As the base plates are randomly oriented with respect to the sample chamber, the field is slowly rotated at a frequency of 0.2 Hz in order to guarantee each structure has sufficient time to experience a strong enough unzipping force. When switching off the field during rotation at an arbitrary phase, the arm immediately localizes to an available docking site.

[0064] At the field strengths generated in the sample chamber, field-induced melting of DNA duplexes is not expected as observed, e.g., for DNA structures immobilized on electrode surfaces. Instead, the arm acts as a lever which mechanically transduces the electrical force acting on its large charge to the docking duplex. Force-induced unzipping of DNA duplexes has been previously achieved using single molecule manipulation techniques such as AFM, optical tweezers or within nanopores. These experiments have shown that DNA unzipping requires forces on the order of 10-20 pN, which is consistent with the typical binding free energy of DNA base-pairs and their sub-nanometer spacing. A rough theoretical treatment suggests that forces that can be generated by the robot arm are on this scale. Importantly, the ability to separate stable duplexes by force facilitates the electrically controlled dissociation of the arm from one docking site and its subsequent placement at a different target position, which is then maintained also at zero field.

[0065] In order to show controlled movement of a cargo molecule attached to the arm, the three-color FRET system already employed in the stochastic switching experiments was utilized (Figure 10A). In contrast to the stochastic switching experiments, the donor fluorophore is actively transported between two 9 nucleotides (nt) long docking positions by rotating the arm with the help of the high torque extension at rotation frequencies of f = 1, 2, and 4 Hz, respectively. Alternating FRET traces (Figure 10B) with the periodicity of the externally applied field are observed. In agreement with the latching experiments (Figure 9B), higher rotation frequencies come with an increase in the number of "skips".

[0066] To demonstrate transport of inorganic nanoparticles by the robot arm, a gold nanorod (AuNR) was attached to one side of the 6HB arm, and its plasmonic interaction was probed with red (dotted line) and green (dashed line) fluorophores immobilized on the platform (Figure 10C). As shown in Figure 10D, the AuNR alternatingly modulates the fluorescence of the fluorophores during rotation of the arm at the externally prescribed frequency. Electrical manipulation enables faster operation of switchable biohybrid plasmonic systems than previously achieved with the fuel strand technique. More sophisticated systems involving multiple particles for the creation of switchable field enhancement or circular dichroism appear feasible.

[0067] In summary, an electrical actuation was introduced as a viable strategy for fast, computer-controlled operation of biohybrid nanorobotic systems, which can exert forces at the molecular scale. Compared to nanoscale manipulation methods such as scanning probe techniques, optical or magnetic tweezers, electrical control is contact-free and can be implemented with low-cost instrumentation. The robotic movements achieved are at least 5 orders of magnitude faster than previously reported for the fastest DNA motor systems and comparable to ATPase driven biohybrids. The robot arm system may be scaled up and integrated into larger hybrid systems using a combination of lithographic and self-assembly techniques. For instance, the platforms can be easily connected to form long filaments with multiple DNA robot arms or to create extended lattices. Utilization of algorithmic self-assembly will enable the creation of structures with different types of robot platforms with dedicated tasks. Lithographic patterning of the substrate will further allow the fabrication of robot arm arrays with defined platform orientations. Using nanostructured control electrodes, single robot arms could even be addressed individually and their positioning state could act as a molecular mechanical memory. Combined with appropriate pick-up and release mechanisms, it is conceivable that this technology can be also applied to DNA-templated synthesis. Electrically clocked synthesis of molecules with a large number of robot arms in parallel could then be the first step towards the realization of a genuine nanorobotic production factory.

Short description of materials and methods:

[0068] In the following, the materials and methods used in the above explained embodiments are shortly described.

Buffer solution summary

[0069]

- FB20 - Origami folding buffer 20 mM $MgCl_2$: 1xTAE + 20 mM $MgCl_2$
- NaB - Origami storage and assembly buffer: 1xTAE + 1 M NaCl
- EB - Electrophoresis buffer: 0.5xTBE + 6 mM $MgCl_2$
- EBPC - Electrophoresis buffer based photo cocktail: EB + 2 mM Trolox (UV activated for about 15 min) + 50 nM Protocatechuate 3,4-Dioxygenase (PCD) + 2.5 mM Protocatechuic acid (PCA) + 10 mM Ascorbic Acid (AA).
- StSwB - Stochastic switching buffer: 1xTE + 12.5 mM MgCl2
- StSwBPC - Stochastic switching buffer based photo cocktail: StSwB + 1 mM Trolox (UV activated for about 15 min) + 10% Glycerol + 10%(w/v) Glucose + 10%(v/v) Glucoseoxidase-Catalase solution. Adjusted from protocol in Stein et al.(42).

DNA origami preparation

[0070] The scaffold strand for DNA origami folding was provided as a 100 nM solution in ddH_2O. All basic staple strands were added in a 2-fold excess over the scaffold strand. Staple strands with special functions, i.e., staples with additional extended sequences for site-specific binding or chemical modifications (fluorophores/biotin) were supplied in 5-fold excess. The solution was adjusted to contain 1xTAE and 20 mM MgCl2. The structures were annealed in a Thermocycler (Bio-Rad Tetrad, Hercules, California, USA) that controls a temperature ramp from 70 °C to 20 °C over 12 h and successively holds the temperature at 40 °C for at least 3 hours. The unpurified samples were stored at room temperature until further use. A complete list of all oligonucleotide sequences is attached.

Structure purification

[0071] All DNA origami samples were separated from excess strands by PEG precipitation. The detailed protocol can be found in the following paragraph. Fluorescent dyes for smFRET experiments were directly folded into the origami structure as covalent modifications of staple strands. All other dyes were attached by means of an adapter strand that hybridizes to an extended staple sequence. Adapter strands were added in 2-fold excess over each binding site and incubated for 1 h, followed by an additional step of PEG precipitation.

PEG precipitation protocol

[0072] The sample was mixed thoroughly in a 1:1 ratio with precipitation buffer (1xTAE, 1 M NaCl, 11% w/v PEG8k), and centrifuged at 20°C with 20,000 rcf for 20 minutes. Afterwards the supernatant was carefully removed and the pellet resuspended in assembly buffer (1xTAE + 1 M NaCl). Magnesium was replaced by sodium to avoid potential unspecific binding. This process is repeated a second time followed by determination of the concentration with a nanophotometer (NanoPhotometer Pearl, Implen GmbH, München, Germany).

Pointer attachment

[0073] Pointer extensions were attached to the short 6HB arm of the robotic platform through incubation of 20

nM platform structure with 25 nM of the extension structure for at least 1 h at 37°C while shaking.

AFM imaging

[0074] AFM data was acquired with an Asylum Research Cypher ES (Oxford Instruments, Abingdon, UK) using Olympus BL-AC40TS-C2 (Olympus, Japan) cantilevers in AC mode. Structures were deposited on freshly cleaved mica and imaged in 1xTAE containing 12.5 mM $MgCl_2$.

TEM imaging

[0075] TEM images were acquired with a Philips CM100 100 kV TEM and an AMT 4x4 Megapixel CCD camera. For negative staining, 25 µl NaOH was added to a 2% uranyl formate solution. The staining solution was centrifuged for 5 min at 20,000 rcf to avoid stain crystals. 5 µl of Nanostructure samples were incubated on glow discharged formvar coated carbon Cu400 TEM grids provided by Science Services (München, Germany) and incubated for 30 s. Subsequently, the grid was washed with 5 µl of staining solution, incubated for 40 s with 15 µl staining solution and dried with filter paper.

Biotin-PEG slide preparation

[0076] 25 x 25 mm #1,5 cover slips (Menzel-Gläser, Braunschweig, Germany) were used. Biotin-PEG-silane MW 3,400 was acquired from Laysan Bio, Inc., Arab, USA and stored under an argon atmosphere. The procedure for PEG modification of cover slips was adapted from a protocol that was kindly provided by Matthias Schickinger (Dietz lab, TUM).

[0077] Cleaning:

1. 1. Place cover slips in a chemically inert rack inside a staining jar.
2. 2. Soak slides in 2 M NaOH for ~ 20 minutes, rinse with ddH2O.
3. 3. Heat 200 ml 2% Hellmanex II (Hellma GmbH & Co. KG, Müllheim, Germany) to ~ 100 °C and pour in staining jar. Sonicate 5 minutes.
4. 4. Rinse 3x with ddH2O, fill up with ddH_2O. Sonicate 5 minutes.
5. 5. Repeat step 4.
6. 6. Fill staining jar with ethanol (99%). Sonicate 5 minutes.
7. 7. Dry in oven at 70°C, ~ 1h.

[0078] PEG coating:

1. 1. Prepare 0.5% biotin-PEG-silane in ethanol (p.a.) -25 µl solution per slide.
2. 2. Add acetic acid (99%) to 1% final concentration.
3. 3. Place first slide on clean surface and add 25 µl of biotin-PEG-silane solution.
4. 4. Immediately place second slide on top. Repeat process until all slides are stacked.
5. 5. Incubate for 30 minutes at 70°C.
6. 6. Place stack in staining jar and sonicate in ddH_2O for 5 minutes. Rinse twice.
7. 7. Separate slides and put back in rack.
8. 8. Repeat step 6.
9. 9. Blow dry with N_2 and store in dark and dry place.

Flow chamber production

[0079] Flow chambers were assembled from three elements: a biotin-PEG functionalized cover slip, a PMMA chip and a layer of double-sided tape. The double-sided tape acts as a spacer between the coverslip and PMMA chip and defines the channel height (about 50 µm). The double-sided tape 3M 467MP (3M Company, Maplewood, Minnesota, USA) was cut with a laser cutter (Trotec Speedy 100, Trotec Laser, Marchtrenk, Austria) to achieve precise and reproducible channel geometries. The double-sided tape was attached to the center of the PMMA chip and covered with the cover slip. The cover slip was pressed onto the slide with office clamps for at least 30 minutes.

[0080] 5 mm thick PMMA plates were laser-cut into rectangular pieces of 75 x 25 mm with reservoirs that can hold 150-200 µl buffer volume each. Small indentations on the outside edge are used to fix a custom-made plug carrying 4 platinum electrodes. The electrodes are deliberately placed in large buffer reservoirs distant from the sample area to minimize detrimental effects of electrochemical processes occurring at the electrodes on the sample. The fully assembled sample during the experiment is shown in Figure S6D. A 4-pin LEMO plug connects the 4-electrode plug to the power source.

Sample preparation for electric field alignment experiments

[0081] Cutting of PMMA and tape as well as PEG functionalization was performed in advance at a larger scale (in batches of 20-30 pieces) and the components could then be stored over several weeks. Before each measurement, the fully assembled sample chambers were prepared for the experiment and discarded afterwards. Each chamber was flushed with 400 µl ddH_2O, then flushed with 20 µl NeutrAvidin (ThermoFisher Scientific, Waltham, Massachusetts, USA) solution (0.5 mg/ml in ddH2O) and incubated for 30 seconds. Afterwards, the channels were rinsed thoroughly with 600 µl ddH2O followed by 400 µl assembly buffer (1xTAE, 1 M NaCl). 20 µl origami solution (500 pM structure concentration) was supplied to the flow chamber and incubated for 10 seconds. Afterwards, the channels were thoroughly flushed with 600 µl assembly buffer followed by 600 µl electrophoresis buffer (0.5xTBE, 6 mM MgCl2). The remaining buffer was removed from all edges of the reservoirs and 400 µl of the intended imaging buffer for the specific experiment was added. All electrophoretic switching experiments except the smFRET experiments were conducted in electrophoresis buffer. For increased lifetimes in smFRET electric switching experiments, the buffer was amended by an oxygen scavenging system (0.5xTBE, 6 mM MgCl2, 2 mM Trolox UV activated for >15 min, 50 nM Protocatechuate 3,4-Dioxygenase (PCD) + 2.5 mM Protocatechuic acid (PCA) + 10 mM L-Ascorbic acid (AA), adjusted from Aitken et al. (41)). PCD, PCA, AA and Trolox were acquired from Sigma-Aldrich, St. Louis, Missouri, USA.

Voltage control

[0082] A custom written LabView program was used to generate control voltages between +3.85 V and -3.85 V on two independent output cannels of a NI PCI-6036E DAQ Board (National Instruments Corporation, Austin, Texas, USA). The control voltages were amplified linearly to ±200 V by a home built DC amplifier containing an Apex PA443 high voltage operational amplifier (Apex Microtechnology, Tucson, Arizona, USA). The current setup controls the direction and strength of the electric field on a millisecond time scale, mainly limited by the loop time of the LabView program. A faster electrical response could be realized when necessary.

Alignment strength measurements

[0083] For each measurement, the structures were first rotated clockwise and counter clockwise with 1 Hz and 120 V for several turns and then aligned in one static direction with the target voltage for at least 1000 acquisition frames. The resulting videos were analyzed with the ThunderSTORM ImageJ plugin (45). Each point spread function was localized with a 2D Gaussian fit. The whole dataset was drift corrected and spot localizations with a fit accuracy of 50 nm or worse were discarded. Well-formed particles, which were sufficiently far from any other particle for reliable localization, were picked and the event list was further processed with MATLAB. For each individual particle, the localizations obtained during the first rotations were used to fit a circle. Subsequently the angular distribution of the localizations was measured in the presence of an electric field applied at a fixed angle. For each voltage, 38-150 particles were analyzed and the mean of each dataset was plotted.

AuNR modification protocol

[0084] AuNRs were purchased from Sigma-Aldrich (München, Germany). 50 µl thiolated DNA (100 µM) was incubated with 10 mM Tris(carboxyethyl) phosphine hydrochloride (TCEP) for at least 30 min. The DNA, 50 µl sodium dodecyl sulfate (SDS), and 10 x TAE buffer were added to 1 ml AuNRs (1 nM). The pH was adjusted to 3 with HCl and incubated for 1 hour on a shaker. Subsequently, 0.5 M NaCl was added and the solution was again incubated for 3 h. Excess oligonucleotides were removed by centrifugation at 6,000 rcf for 20 min. The supernatant was removed and the pellet was dissolved in 2 ml 0.5 x TAE containing 0.03% SDS. The centrifugation procedure was repeated 4 times. DNA functionalized AuNRs were added in 5-fold excess to the DNA nanostructures and incubated over night. Unbound AuNRs were removed from the origami sample by agarose gel electrophoresis purification.

Polymerization into filaments

[0085] Polymerization of base plates was performed using a one-pot folding protocol. Two different scaffold lengths were used, which resulted in a statistical distribution of base plates with integrated robot arms and base plates that did not carry an arm. For baseplates without an arm, a p7249 scaffold was used. For base plates with an arm structure, we used a p7704 scaffold. The two folding solutions were pipetted separately and mixed in a 1:20 ratio of arm-less (p7249) and arm-forming (p7704) solution before folding. Polymerization was achieved by replacing the staples used for passivation of the edges of the bottom layer of the base plate by a set of staples that connects these two edges.

Fluorescence microscopy

a) TIRF microscopy setup for stochastic switching kinetics

[0086] Single-molecule multi-color FRET experiments were performed on a home built multi-color prism-type TIRF (total internal reflection fluorescence) setup based on an inverted microscope (TE 2000-U, Nikon, Japan) with four continuous-wave diode-pumped solid state lasers (Cobolt, Solna, Sweden) for excitation: 491 nm (Cobolt Calypso, 75 mW), 532 nm (Cobolt Samba, 100 mW), 561 nm (Cobolt Jive, 75 mW) and 647 nm (Cobolt MLD, 120 mW). The laser beams were aligned through an acousto-optical tunable filter (AOTFnC.400-

650-PV-TN, Pegasus Optik, Wallenhorst, Germany) and coupled into a single-mode fiber to allow for intensity regulation and switching between the laser lines for alternating laser excitation (ALEX (24), see also below). The sample chambers were formed by sandwiching a nesco film channel cut-out between coverslip and a surface-functionalized quartz prism with holes to insert the sample. The quartz prisms were prepared as described earlier in Schluesche et al. (47). Briefly, the prism surface was silanized (3-aminopropyltriethoxysilane, Sigma-Aldrich, St. Louis, Missouri, USA) and then incubated with a solution of 45% polyethylene glycol (mPEG-SVA, MW 5000) and 3% biotin-PEG (biotin-PEG-SVA, MW 5000, Laysan Bio Inc., Arab, Alabama, USA) in 100 mM sodium bicarbonate (pH 9.0) to achieve surface passivation.

[0087] Fluorescence from the sample was collected by a water immersion objective (CFI Plan Apo IR 60x NA 1.27 WI objective, Nikon) and separated by the dichroic mirrors 630 DCXR and 560 DCXR (AHF Analysentechnik AG, Tübingen, Germany). After selecting the different spectral regions with the respective emission filters HQ 525/50, HQ 595/50 and HQ 715/150, the fluorescence of the donor (Alexa Fluor 488) and two acceptor (ATTO 565 and ATTO 647N) fluorophores was detected on individual EMCCD cameras (Andor iXon 3, Andor Technologies, Belfast, UK).

b) Experimental procedure for stochastic switching kinetics experiments without pointer extension

[0088] The prisms were initially incubated with a streptavidin (Sigma-Aldrich, St. Louis, Missouri, USA) solution (0.3 mg/ml in PBS) for 20 minutes and washed with stochastic switching buffer (StSwB: 1xTE + 12.5 mM $MgCl_2$). The samples were diluted to 100 pM in StSwB, added to the sample chamber and immobilize on the prism surface through biotin-streptavidin-biotin linkage. Untethered structures were removed by flushing with StSwB after 2-3 min. The prism was then flushed twice with stochastic switching buffer-based photo-cocktail (StSwBPC). Finally, the prism was filled completely with StSwBPC and the holes were sealed to facilitate oxygen removal. In the case of continuous donor excitation, the videos were recorded with 11 mW 491 nm excitation and simultaneous detection on the three EMCCD cameras at 30 ms exposure for 3000 frames. For the alternating laser excitation (ALEX) experiments, the laser excitation wavelength was synchronized with the camera frame rate using the AOTF and was switched frame by frame in the sequence red-green-blue (647 nm: 3 mW, 561 nm: 5 mW and 491 nm: 11 mW). ALEX videos were recorded for 3000 frames at 30 ms exposure and simultaneous detection. The videos were analyzed with a custom-written MATLAB program (Mathworks, Massachusetts, USA). Each fluorescent spot in a movie is presumed to represent a single structure. Spots belonging to the same structure were identified on the videos of the three fluorescence detection channels and fluorescence intensity traces were extracted from them.

c) Hidden Markov model (HMM) analysis of the traces

[0089] Intensity traces for each color were individually subjected to a three-state HMM analysis. Two of the states correspond to the arm bound to either of the docking sites and are characterized by low donor fluorescence due to quenching by FRET to the acceptor at the docking site. The third state corresponds to the freely diffusing arm (unbound), characterized by high donor fluorescence in the absence of quenching by FRET.

[0090] Similarly, every trace of each of the two acceptors was individually subjected to a two-state HMM analysis, where one state corresponds to the arm bound to a particular docking site, characterized by high acceptor fluorescence due to FRET from the donor. The other state corresponds to the arm either docked to the other site or diffusing freely and is characterized by low acceptor fluorescence due to the absence of FRET. From the HMM analysis, the Viterbi path - the most likely sequence of states - was obtained for each fluorophore and for each trace. As an example, the trace from figure 7 in the top panel was replotted, whereas, in the bottom panel, the same trace is shown superimposed with the Viterbi paths of the three fluorophores in

their designated colors. The anti-correlated movement of the donor and acceptors is clearly seen with every transition in the donor Viterbi path being mirrored by a transition of either of the acceptors.

[0091] Subsequently, the dwell times of the high fluorescence states of the fluorophores were determined from the Viterbi paths. The dwell time for a high acceptor fluorescence state corresponds to the time spent by the arm in the bound state (bound to a particular docking site). The dwell time for a high donor fluorescence signal corresponds to the time spent by the arm in the unbound state, where it can diffuse between the docking sites.

d) Stochastic switching without pointer extension: Control experiments

[0092] Control experiments without docking: A control experiment for the stochastic switching experiments was performed by measuring samples where the arm lacks the extended staple strand for docking to the docking site with donor excitation. The resulting traces display an almost constant high donor fluorescence signal with hardly any switching of the fluorescence signals of the acceptors. Only a residual signal is observed in the acceptor channels, which can be accounted for by the direct-excitation of the acceptors upon donor excitation (491 nm) and crosstalk from the donor channel. This shows that, in the absence of the extended staple strand, docking of the arm does not occur. Hence, no stochastic switching of the acceptor signal is observed as the arm's rotational diffusion is much faster than the acquisition rate of the EMCCD cameras used in the setup (-30 fps).

[0093] ALEX experiments with docking: For samples with an extended staple strand on the arm for docking (docking duplex lengths 8-10 bp), videos were recorded with alternating laser excitation (ALEX), where the lasers were alternated every frame (frame time ~33ms) in the sequence red-green-blue (647 nm laser-561 nm laser-491 nm laser) and with simultaneous detection on all three EMCCD cameras. An exemplary trace of an ALEX experiment with a 9 bp docking duplex arm structure shows that initially all fluorophores were present and active. At $t \approx 275$ s, the donor Alexa Fluor 488 bleaches. This was accompanied by a drop in total intensity (grey) to zero implying that the signal in the acceptor channels was solely due to FRET from the donor. Furthermore, upon 561 nm excitation (direct excitation of ATTO 565), there is clearly no FRET between the two acceptors. This is expected since the distance between the acceptors (~ 43 nm) is beyond the working range of FRET. The residual signal in the ATTO 647N channel after 561 nm excitation is attributed to the spectral crosstalk from ATTO 565 and a small amount of direct excitation of ATTO 647N by the 561 nm laser. Upon excitation with the 647 nm laser, only fluorescence from ATTO 647N is observed. The trace in figure S3B bottom panel shows that the ATTO 647N fluorophore is active throughout the experiment and does not bleach for the entire duration of the -300 s long movie. The ALEX experiment thus demonstrates that the stochastic switching of the signals of the three fluorophores is only seen upon donor excitation, with all intensities dropping to zero when the donor bleaches. Since direct excitation of the acceptors shows that they were active for the entire duration of the experiment, a contribution of fluorophore photophysics to the stochastic switching of the signals can be ruled out.

e) TIRF microscopy of structures with pointer extension

[0094] All experiments involving electric field alignment were performed on a home built, objective type TIRF microscope based on an Olympus IX71 (Olympus, Japan). Three laser light sources with wavelengths 642 nm (Toptica iBeam smart, diode laser, 150 mW, Gräfelfing, Germany), 532 nm (Oxxius 532-50, diode-pumped solid state laser, 50 mW, Lannion, France), and 488 nm (Toptica iPulse, diode laser, 20 mW) are aligned in parallel, widened by a factor of 8.3 and focused on the back focal plane of a 100x oil immersion objective (UAPON 100xO TIRF objective, NA 1.49 oil, Olympus, Japan). The filter cube was configured with a ZT532/640RPC dichroic mirror and a ZET532/640 (Chroma Technology, Olching, Germany) emission filter. Except for the high-speed imaging experiments, the detected image is split into two emission channels, which

are projected on two separate halves of the CCD chip of an Andor iXon 897 EMCCD camera (Andor Technologies, Belfast, UK). For this purpose, a Hamamatsu W-viewer (Hamamatsu Photonics, Japan) with the two filters (BrightLine HC 582/75 and ET Bandpass 700/75) and two dichroic mirrors (Beam splitter 630 DCXR and Beam Splitter Q 630 SPXR) was mounted on the left IX71 camera port (all from AHF analysentechnik AG, Tübingen, Germany). Structures with a multiply labeled extension were observed with 642 nm excitation and a laser power of 1-4 mW, depending on the desired observation time and SNR. For electric switching of the FRET signal, 7 mW of 488 nm excitation was used. Structures functionalized with AuNRs were excited with 1 mW at 642 nm and 1.7 mW at 532 nm. High-speed videos were recorded with an Andor Neo sCMOS camera (Andor Technologies, Belfast, UK) mounted to the right camera port of the Olympus IX71 body. In these measurements, the sample was excited with 50 mW at 642nm.

cadnano designs

[0095] DNA origami structures were designed using cadnano. For the creation of 3D graphics, a set of MATLAB tools was used to convert the JSON file generated in cadnano into a PDB file that can be further used in UCSF Chimera. JSON files are available upon request from the authors.

Supplementary Text

Comparison of the two pointer designs

[0096] In this work, two different approaches were utilized to create pointer extension structures for the central 6HB arm integrated with the platform. These extensions serve two purposes. First, they facilitate the observation of the robot arm's motion with diffraction limited light microscopy methods. Second, they act as highly charged levers that allow the application of larger forces to the central arm unit.

[0097] *Stability*: The linear pointer extension is attached to the tip of the arm. While this rather straightforward approach allows an extension by over 400 nm using the common p7249 scaffold, the low number of possible staple connections between the two origami structures did not seem to withstand the high bending forces that are associated with the transmission of torque to the arm. By contrast, the shape complementary pointer with its more bulky connector structure has a roughly 100 nm shorter range but connects to the arm with a larger number of staples, which are also spread over a larger area. This design appeared to be more stable against torque induced breakage.

[0098] *Interactions with the plate/substrate*: The two pointer designs significantly differed in their unspecific interactions with the origami base plate. While the linear extension showed relatively little interactions, the shape complementary pointer displayed two pronounced bias angles during rotational diffusion, or when actuated with low field strength. These undesired bias angles complicate the analysis of the movements.

[0099] *Super-resolution imaging and defective devices*: To compare the two pointer designs in terms of free rotational diffusion, a combination of localization microscopy and DNA-PAINT super-resolution microscopy was used. Three corners of the base plate were labeled with transient binding sites for DNA PAINT. For each image, videos were recorded with 1-2 mW at 642 nm excitation and 25 ms exposure. About 1000 frames with 25 ms exposure time were analyzed (spot detection, localization via Gaussian fitting, drift correction) with the ThunderSTORM ImageJ plugin. To reduce potential, unspecific sticking effects promoted by divalent ions, assembly buffer for imaging was used (1xTAE, 1 M NaCl). Subsequently, PAINT imaging buffer (1xTAE, 1 M NaCl, 0.05% TWEEN20, 5nM imager strands) was added and a DNA-PAINT video was recorded (7000 frames,

250 ms exposure, 50mW 642 nm excitation). The linear pointer has a slight bias to point in one direction perpendicular to the helix axis of the top layer of the origami plate, whereas the shape complementary pointer has two much stronger bias points on opposite sides of the plate along this direction.

[0100] Apart from a large fraction of correctly assembled structures, super-resolution images showed mainly two types of apparently damaged or misassembled structures. For type 1, the particle shows localizations also within a filled circle, instead of a ring-like pattern. This localization pattern suggests that the tip of the pointer is not restricted to the X-Y plane as designed but moves in the entire hemisphere above the base plate. It is assumed that the entire structure is misfolded or the connection between arm and pointer extension is defective. Type 2 is characterized by a ring without bias angles. Most of these structures also show a circular dot in the DNA-PAINT overlay rather than three distinct points indicating the labeled corners of the DNA base plate. A possible explanation for Type 2 defects is structures that are bound with only one biotin anchor, which could rotate along a single biotinylated staple strand. Movement would then still be restricted to the X-Y plane combined with a round, spot-like appearance of the base plate in the DNA-PAINT reconstruction.

Origami staple list for base plate

[0101]

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
32[167] 34[168]	AGACAAAAACACCACGG AATAAGTGTCAGAGG	basics	yes	yes	yes	yes	yes	yes	yes
38[103] 40[104]	ATAAAGTAGGCGTTAAA TAAGAATTTAACCTC	basics	yes	yes	yes	yes	yes	yes	yes
18[135] 20[136]	GGGACATTATGAAAAAT CTAAAGCATATCTTT	basics	yes	yes	yes	yes	yes	yes	yes
34[103] 36[104]	CAAGAAACAAATAAGAA ACGATTTACCTCCCG	basics	yes	yes	yes	yes	yes	yes	yes
36[63] 35[63]	GCTATTTTGCACCCAGT AATTTGCCAGTTACA	basics	yes	yes	yes	yes	yes	yes	yes
21[120] 19[119]	TTCATCATAACAACTAAT AGATGAGAGCCA	basics	yes	yes	yes	yes	yes	yes	yes
4[103]6 [104]	TAGAGCTTTGTTTAGCT ATATTTTCCTGTAAT	basics	yes	yes	yes	yes	yes	yes	yes
30[39] 32[40]	TCACAAAGAAACGTCAC CAATGAAAATCAC	basics	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
19[56] 17[63]	GATAAAACTTTTTGAATG GCTATTTTGATTAGTAAT AACA	basics	yes	yes	yes	yes	yes	yes	yes
13[120] 11[119]	GTTTGCCTAACTCACAT TAATTCGGGATCC	basics	yes	yes	yes	yes	yes	yes	yes
28[39] 30[40]	AGTACCGAGAATGGAAA GCGCACTTGATAT	basics	yes	yes	yes	yes	yes	yes	yes
40[135] 42[136]	CATAGGTTATGTGAGTG AATAACAGATGAA	basics	yes	yes	yes	yes	yes	yes	yes
40[167] 42[168]	CTGAGAAGCGTCGCTAT TAATTAAAAAGAAAT	basics	yes	yes	yes	yes	yes	yes	yes
8[135] 10[136]	AGAAAAGCTTGACCGTA ATGGGATCCAGCTTT	basics	yes	yes	yes	yes	yes	yes	no
33[120] 31[119]	ACATACATGTAAATATTG ACGGAATGTAGCGC	basics	yes	yes	yes	yes	yes	yes	yes
34[135] 36[136]	ACAAGAAAATGAAAATA GCAGCGGTATTCT	basics	yes	yes	yes	yes	yes	yes	yes
36[95] 35[87]	GAGGTTTTGAAGCCTTA TTTAT	basics	yes	yes	yes	yes	yes	yes	yes
40[39] 42[40]	AACGCGAGATGATGAAA CAAACAGGCGAAT	basics	yes	yes	yes	yes	yes	yes	yes
16[71] 18[72]	TCCTGAGATCACTTGCC TGAGTAGTGGCAC	dock down 3'	yes	yes	yes	yes	yes	yes	*no*
19[120] 17[127]	GCAGCAACTGGCCAACA GAGATATCCAGAACAAT ATT	basics	yes	yes	yes	yes	yes	yes	yes
2[103]4 [104]	AAAAGAAGTATAGTCAG AAGCAAAGGATGGCT	basics	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
22[135] 24[136]	CCAAATCCGGTCAATCA TAAGGTTTCATGA	basics	yes	yes	yes	yes	yes	yes	yes
32[39] 34[40]	CAGTAGCAGGAAACGCA ATAATAAGCAGAT	basics	yes	yes	yes	yes	yes	yes	yes
18[39] 20[40]	ATGCGCGAATACCGAAC GAACCACCAACTCGT	basics	yes	yes	yes	yes	yes	yes	yes
12[167] 14[168]	AAGCATAACCGAAATCG GCAAAAGGGTTGA	dock right 5'	yes	yes	yes	yes	no	yes	yes
34[71] 36[72]	ACCGAAGCAAATAAACA GCCATATTAAATCAA	basics	yes	yes	yes	yes	yes	yes	yes
4[71]6 [72]	CTCAACATATTAGATACA TTTCGTCAACGC	dock up 5'	yes	yes	yes	yes	yes	yes	no
32[71] 34[72]	AGCCATTTGAACTGGCA TGATTAAGCTATCTT	basics	yes	yes	yes	yes	yes	yes	yes
31[120] 29[119]	GTTTTCATCCCTCAGAG CCGCCACGTAATAAG	basics	yes	yes	yes	yes	yes	yes	yes
22[71] 24[72]	GAACGAGTCCTGATAAA TTGTGTCTAAAACGA	basics	yes	yes	yes	yes	yes	yes	yes
18[71] 20[72]	AGACAATAAGAGGTGAG GCGGTCTTAGAAG	dock down 5'	yes	yes	yes	yes	yes	yes	yes
21[88]	TCATCATATAATACATTT GAGGATAGTATTAA	basics	yes	yes	yes	yes	yes	yes	yes
16[135] 18[136]	CAGAGCGGACCGCCAG CCATTGCATAATAAAA	basics	yes	yes	yes	yes	yes	yes	no
40[103] 42[104]	CGGCTTAGCTTTTTTAAT GGAAACATCGGGAG	basics	yes	yes	yes	yes	yes	yes	yes
20[71] 21[87]	TATTAGACAACCACCAG AAGGAGCGGAATTA	basics	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
36[127] 35[119]	CGAGGCGTTTTAGCGAT TTGTTTA	basics	yes	yes	yes	yes	yes	yes	yes
1[32]2 [40]	TTTAAGAACTGGCTCAA ATACTGC	basics	yes	yes	yes	yes	yes	yes	yes
2[135]4 [136]	GATAAAAAAAGATTAAG AGGAAGCATTGCTCC	basics	yes	yes	yes	yes	yes	yes	yes
6[167]8 [168]	AGCAATAAGCCTGAGAG TCTGGAAAACTAG	basics	yes	yes	yes	yes	yes	yes	yes
7[88]5 [95]	GTTCTAGCGGGAGAAG CCTTTATTCAAATGGTCA ATAACC	basics	yes	yes	yes	yes	yes	yes	yes
2[71]4 [72]	AAATGTTTAAATCAAAAA TCAGGGCTGTAG	dock up 3'	yes	yes	yes	yes	yes	yes	yes
36[159] 35[159]	TATAGAAGGCTTATCCC TTTACAGAGAGAATA	basics	yes	yes	yes	yes	yes	yes	yes
26[167] 28[168]	TTTCTGTACAGCCCTCA TAGTTAGTTAAGAGG	basics	yes	yes	yes	yes	yes	yes	yes
30[167] 32[168]	GAGCCGCCGTTTGCCAT CTTTTCAAGCGCCAA	basics	yes	yes	yes	yes	yes	yes	yes
23[120] 22[104]	GGCGCAGAAACGTAACA AAGCTGCTCATTCAG	basics	yes	yes	yes	yes	yes	yes	yes
28[71] 30[72]	GGAATAGGTTCCAGTAA GCGTCATGACAGGAG	basics	yes	yes	yes	yes	yes	yes	yes
32[135] 34[136]	AGGGAAGAAAGGTGGC AACATAGATAACCC	basics	yes	yes	yes	yes	yes	yes	yes
21[152] 19[151]	TACTTCTGAGGAAGGTT ATCTAAAATCACCTT	basics	yes	yes	yes	yes	yes	yes	yes
26[71] 28[72]	**[Biotin]** TTTT CACGTTGAATTTTCAGG GATAGCATATAGCCC	biotin	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
1[120]2 [136]	GGTAGAAAGATTCATCA GTTGAGCAGACGAC	basics	yes	yes	yes	yes	yes	yes	yes
24[39] 26[40]	TTTGACCGCTTGCTTTC GAGGTGGCTCCAA	basics	yes	yes	yes	yes	yes	yes	yes
32[103] 34[104]	TTAAAGGTAGTATGTTA GCAAACGAATAAGAG	basics	yes	yes	yes	yes	yes	yes	yes
12[103] 14[104]	CTCACTGCAGTTGCAGC AAGCGGTCAAAGGGC	basics	yes	yes	yes	yes	yes	yes	yes
38[135] 40[136]	**[Biotin]** TTTT AGAGGCAATTACTAGAA AAAGCATCAAAAT	biotin	yes	yes	yes	yes	yes	yes	yes
34[167] 36[168]	GTAATTGAACATAAAAA CAGGGAATAGCAAGC	basics	yes	yes	yes	yes	yes	yes	yes
38[71] 40[72]	**[Biotin]** TTTT GTCCAGACTGGTTTGAA ATACCGATATATGTA	biotin	yes	yes	yes	yes	yes	yes	yes
28[167] 30[168]	CTGAGACTAAACAGTTA ATGCCCCCTCCCTCA	basics	yes	yes	yes	yes	yes	yes	yes
6[103]8 [104]	ACTTTTGCTGATAAATTA ATGCCGATTGTATA	basics	yes	yes	yes	yes	yes	yes	yes
36[71] 38[72]	GATTAGTTCCCATCCTA ATTTACGGTAATTCT	basics	yes	yes	yes	yes	yes	yes	yes
7[120]5 [127]	AGCTATTCAAAAACATTA TGACCATTTGGGGCGC GAG	basics	yes	yes	yes	yes	yes	yes	yes
38[39] 40[40]	CTAATGCTAGTTAATTTC ATCTAGACAAAG	basics	yes	yes	yes	yes	yes	yes	yes
8[71]10 [72]	TTGTTAAACATCAACATT AAATGGCGCAAC	basics	yes	yes	yes	yes	yes	yes	no

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
6[135]8 [136]	GGTTGTACTTTGAGAGA TCTACAATGATAATC	basics	yes	yes	yes	yes	yes	yes	no
28[63] 27[63]	TGTATCACCGTACTCAC AGAGCCACCACCCTC	basics	yes	yes	yes	yes	yes	yes	yes
30[71] 32[72]	GTTGAGGCCACCGTAAT CAGTAGCCCGACTTG	basics	yes	yes	yes	yes	yes	yes	yes
18[103] 20[104]	TCTGACCTGCAACAGTG CCACGCTTAGAGCCG	basics	yes	yes	yes	yes	yes	yes	yes
41[88] 39[95]	TGAATTACGTTGGGTTA TATAACCCGTGTGATAA ATAA	basics	yes	yes	yes	yes	yes	yes	yes
12[135] 14[136]	GAGTGAGCCCAGCAGG CGAAAATCGTCCACTA	basics	yes	yes	yes	yes	yes	yes	no
4[39]6 [40]	GGTGTCTGCAATTCTGC GAACGAGCATATATT	basics	yes	yes	yes	yes	yes	yes	yes
42[135] 41[119]	TATACAGTAACAGTACC TTTTACAGTACATA	basics	yes	yes	yes	yes	yes	yes	yes
19[152] 17[159]	GCTGAACCCCAGTCACA CGACCAGACAGGAAAAA CGCTCA	basics	yes	yes	yes	yes	yes	yes	yes
21[56] 19[55]	AACAAAGATTTACAAAC AATTCGACAGCAGAA	basics	yes	yes	yes	yes	yes	yes	yes
14[135] 16[136]	TTAAAGAACAAGTGTAG CGGTCACGTTAGAAT	basics	yes	yes	yes	yes	yes	yes	no
42[71] 41[55]	ATACCAAGTTACAAAAT CGCGCAGATCAAGAA	basics	yes	yes	yes	yes	yes	yes	yes
22[175] 24[168]	TCATCAAGAGTAATCTC TTTGAAAGAGGACAGAC GGCTAC	basics	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
14[159] 13[159]	CCAGTTTGGAACAAGAC TGTTTGATGGTGGTT	basics	yes	yes	yes	yes	yes	yes	no
24[71] 26[72]	AAGAGGCATTGATACCG ATAGTTGAATTTTTT	basics	yes	yes	yes	yes	yes	yes	yes
10[39] 12[40]	GCTATTACGGCGATTAA GTTGGGTGGCCAACG	dock left 3'	yes	no	yes	no	no	no	yes
24[135] 26[136]	GGAAGTTGTCGCTGAG GCTTGCAACTTTCA	basics	yes	yes	yes	yes	yes	yes	yes
16[167] 18[168]	GAGCACGTTGGAAATAC CTACATACATTGG	basics	yes	yes	yes	yes	yes	yes	yes
10[71] 12[72]	TGTTGGGACAGTCACGA CGTTGTAAACCTG	basics	yes	yes	yes	yes	yes	yes	no
2[95]1 [87]	TTTTGCCAGAGGGGGTC TACGTTA	basics	yes	yes	yes	yes	yes	yes	yes
36[103] 38[104]	ACTTGCGGATCAATAAT CGGCTGTAAGAGAAT	basics	yes	yes	yes	yes	yes	yes	yes
9[88]7 [87]	TAACAACCTTTAAATTGT AAACGTATTCAACC	basics	yes	yes	yes	yes	yes	yes	no
2[127]1 [119]	CCAAAATAGCGAGAGTT ATTACA	basics	yes	yes	yes	yes	yes	yes	yes
18[167] 20[168]	CAGATTCATCAAATATCA AACCCAGTTGAA	basics	yes	yes	yes	yes	yes	yes	yes
29[88] 27[95]	TTTTGATGGAGGGTTGA TATAAGAGCCCAATAGG AACC	basics	yes	yes	yes	yes	yes	yes	yes
14[127] 13[119]	CGTGGACTCCAACGTCC ACGCTG	basics	yes	yes	yes	yes	yes	yes	no
30[103] 32[104]	**[Biotin]** TTTT CCACCAGAGCCTTTAGC GTCAGACATTATTCA	biotin	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
32[63] 31[63]	GGGAATTAGAGCCAGCA AACCATCGATAGCAG	basics	yes	yes	yes	yes	yes	yes	yes
2[63]1 [55]	AGACTGGATAGCGTCCT TATACCA	basics	yes	yes	yes	yes	yes	yes	yes
35[120] 33[119]	ACGTCAAATTGAGTTAA GCCCAATTAGAAAAT	basics	yes	yes	yes	yes	yes	yes	yes
14[71] 16[72]	ACGTGAACGCCGGCGA ACGTGGCGCCAGAA	basics	yes	yes	yes	yes	yes	yes	no
22[103] 24[104]	TGAATAAGCTCCATGTT ACTTAGCAATACGTA	basics	yes	yes	yes	yes	yes	yes	yes
14[103] 16[104]	GAAAAACCAAAGCGAAA GGAGCGGCCGATTAA	basics	yes	yes	yes	yes	yes	yes	yes
24[167] 26[168]	AGAGGCTTCTTTTGCGG GATCGTCAAATGAAT	basics	yes	yes	yes	yes	yes	yes	yes
23[56] 22[40]	TATCATCGAGTAAATTG GGCTTGAGATGGTTT	basics	yes	yes	yes	yes	yes	yes	yes
11[88]9 [87]	GGCCAGTGATTCGCCAT TCAGGCTTGAGCGAG	basics	yes	yes	yes	yes	yes	yes	yes
8[103] 10[104]	AGCAAATACGTCGGATT CTCCGTGAACCAGGC	basics	yes	yes	yes	yes	yes	yes	yes
31[88] 29[87]	TCAAGTTTGCCGCCGCC AGCATTACATGGC	basics	yes	yes	yes	yes	yes	yes	yes
16[39] 18[40]	ACCGAGTATTGTAGCAA TACTTCTAGTCTTTA	basics	yes	yes	yes	yes	yes	yes	yes
41[152] 39[159]	CTGTAAATAGTCAATAG TGAATTTCTGTTTAGTAT CATAT	basics	yes	yes	yes	yes	yes	yes	yes
10[103] 12[104]	AAAGCGCCCCAAGCTTT CTTTAGGGCGTTGCG	basics	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
1[56]2 [72]	GTCAGGACGTTGGGAA GAAAAATAATAGTA	basics	yes	yes	yes	yes	yes	yes	yes
6[63]5 [63]	AAATTTTTAGAACCCTTA GATTTAGTTTGACC	basics	yes	yes	yes	yes	yes	yes	yes
33[88] 31[87]	TATTACGCGAATTATCA CCGTCAGACAGAA	basics	yes	yes	yes	yes	yes	yes	yes
2[167]4 [168]	AACACTATATCGCGTTTT AATTCTCCAACA	basics	yes	yes	yes	yes	yes	yes	yes
6[39]8 [40]	TTAAATGCAAAAGGGTG AGAAAGGTGTTAAAT	basics	yes	yes	yes	yes	yes	yes	yes
4[135]6 [136]	TTTTGATACTGAAAAGG TGGCATCGCTAAATC	basics	yes	yes	yes	yes	yes	yes	no
4[167]6 [168]	GGTCAGGAGTAGCATTA ACATCCAAAATTA	basics	yes	yes	yes	yes	yes	yes	yes
30[135] 32[136]	GCCACCACGGCATTTTC GGTCAATTGAGGG	basics	yes	yes	yes	yes	yes	yes	yes
38[167] 40[168]	CATATTTAGCGTTATACA AATTCTTTAAGACG	basics	yes	yes	yes	yes	yes	yes	yes
8[39]10[40]	CAGCTCATAATTCGCGT CTGGCCTGCCTCTTC	basics	yes	yes	yes	yes	no	yes	yes
10[167] 12[168]	GGCCTCAGGTTTCCTGT GTGAAAGAGCCGG	dock right 3'	no	no	yes	no	no	no	yes
1[152]2 [168]	ATACCACATTCAACTAAT GCAGATAAGAGC	basics	yes	yes	yes	yes	yes	yes	yes
2[159]1 [151]	CATAACCCTCGTTTACA TTTAGGA	basics	yes	yes	yes	yes	yes	yes	yes
40[71] 42[72]	AATGCTGATAATTACATT TAACAATGCTTTGA	basics	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
28[159] 27[159]	CCTCAAGAGAAGGATTT GTAGCATTCCACAGA	basics	yes	yes	yes	yes	yes	yes	yes
9[120]7 [119]	CGGCGGACCCAAAAAC AGGAAGGAGAGGGT	basics	yes	yes	yes	yes	yes	yes	no
20[39] 21[55]	ATTAAATCTTGAGTAACA TTATCATTTTGCGG	basics	yes	yes	yes	yes	yes	yes	yes
29[120] 27[127]	TTTTAACGTTGCTCAGTA CCAGGCGAGTTTCGTCA CCAGT	basics	yes	yes	yes	yes	yes	yes	yes
13[88] 11[87]	CCTGAGAGCCGCTTTCC AGTCGGGAAAACGAC	basics	yes	yes	yes	yes	yes	yes	yes
23[88] 22[72]	GCGACCTGGCTTGCCCT GACGAGAAACACCA	basics	yes	yes	yes	yes	yes	yes	yes
42[103] 41[87]	AAACAATAACGGATTCG CCTGATTTTCATT	basics	yes	yes	yes	yes	yes	yes	yes
10[159] 9[159]	GAAGATCGCACTCCAGA GGTCACGTTGGTGTA	basics	yes	yes	yes	yes	yes	yes	no
19[88] 17[95]	CACCGCCTGAAAGCGTA AGAATACGAAGAACTCA AACTAT	basics	yes	yes	yes	yes	yes	yes	yes
24[63] 23[55]	AAAGAATACACTAAAAG AGATTTG	basics	yes	yes	yes	yes	yes	yes	yes
12[71] 14[72]	TCGTGCCACTGATTGCC CTTCACGCCCACT	basics	yes	yes	yes	yes	yes	yes	no
20[103] 21[119]	TCAATAGATTCCTGATTA TCAGATGATGGCAA	basics	yes	yes	yes	yes	yes	yes	yes
14[63]1 3[63]	CATCACCCAAATCAAGG TGAGACGGGCAACAG	basics	yes	yes	yes	yes	yes	yes	no

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
32[159] 31[159]	GGGCGACATTCAACCGT AGCCCCCTTATTAGC	basics	yes	yes	yes	yes	yes	yes	yes
26[135] 28[136]	**[Biotin]** TTTT ACAGTTTACAAACTACA ACGCCAGGATTAG	biotin	yes	yes	yes	yes	yes	yes	yes
6[159]5 [159]	AGCCTCAGAGCATAAAA ATTCTACTAATAGTA	basics	yes	yes	yes	yes	yes	yes	yes
36[39] 38[40]	TTATCCTATAGATAAGTC CTGAATGTTCAG	basics	yes	yes	yes	yes	yes	yes	yes
11[120] 9[119]	CCGGGTAGCTTCTGGTG CCGGAGGAACAAA	basics	yes	yes	yes	yes	yes	yes	yes
28[103] 30[104]	GCCGTCGAATACAGGA GTGTACTGCAGAACCA	basics	yes	yes	yes	yes	yes	yes	yes
24[127] 23[119]	TCCATTAAACGGGTAAC GGAACGA	basics	yes	yes	yes	yes	yes	yes	yes
26[103] 28[104]	CAACTAAACATGTACCG TAACACTGGATAAGT	basics	yes	yes	yes	yes	yes	yes	yes
6[71]8 [72]	AAGGATAACACCATCAA TATGATTAATATT	basics	yes	yes	yes	yes	yes	yes	no
26[39] 28[40]	AAGGAGCCAGAACCGC CACCCTGGAGGTTT	basics	yes	yes	yes	yes	yes	yes	yes
10[63]9 [63]	AGGGCGATCGGTGCGG TCCTGTAGCCAGCTTT	basics	yes	yes	yes	yes	yes	yes	no
23[152] 22[136]	CTGACCAATGACAAGAA CCGGATATTCATTAC	basics	yes	yes	yes	yes	yes	yes	yes
14[95] 13[87]	GTCTATCAGGGCGATGC GCCTGGC	basics	yes	yes	yes	yes	yes	yes	no
42[167] 41[151]	TGCGTAGATTTTCAGGT TTAACGTCCTTGCTT	basics	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
24[159] 23[151]	TGAGGACTAAAGACTTG AACCGAA	basics	yes	yes	yes	yes	yes	yes	yes
24[95] 23[87]	ACGAAGGCACCAACCG AAATCC	basics	yes	yes	yes	yes	yes	yes	yes
36[135] 38[136]	AAGAACGAAGAACGGGT ATTAAATTTAGGC	basics	yes	yes	yes	yes	yes	yes	yes
14[167] 16[168]	GTGTTGTTACACCCGCC GCGCTTCTTTGAC	basics	yes	yes	yes	yes	yes	yes	yes
41[120] 39[127]	AATCAATACTGAGAGAC TACCTTTAAACACCGGA ATCATA	basics	yes	yes	yes	yes	yes	yes	yes
28[135] 30[136]	CGGGGTTGGGTCAGTG CCTTGACCCTCAGA	basics	yes	yes	yes	yes	yes	yes	yes
36[167] 38[168]	AAATCAGAATCGAGAAC AAGCAAGAGAATCGC	basics	yes	yes	yes	yes	yes	yes	yes
16[103] 18[104]	AGGGATTTCGGCCTTGC TGGTAATAGAACCCT	basics	yes	yes	yes	yes	yes	yes	yes
41[56] 39[63]	AACAAAATTGCAAATCC AATCGCATCTGACCTAA ATTTAA	basics	yes	yes	yes	yes	yes	yes	yes
20[135] 21[151]	AGGAGCACATATAATCC TGATTGTTTGGATTA	basics	yes	yes	yes	yes	yes	yes	yes
2[39]4 [40]	GGAATCGTCTTTAAACA GTTCAGATAAAGTAC	basics	yes	yes	yes	yes	yes	yes	yes
8[167] 10[168]	CATGTCAAGATGGGCGC ATCGTACAGTATC	basics	yes	yes	yes	yes	yes	yes	yes
24[103] 26[104]	ATGCCACTCAACCATCG CCCACGCGAAAGGAA	basics	yes	yes	yes	yes	yes	yes	yes
1[88]2 [104]	ATAAAACGAACTAACGG AACAACAGCTTTTGC	basics	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
14[39] 16[40]	GGTCGAGGGGGAGCCC CCGATTTAGTGAGGCC	basics	yes	yes	yes	yes	yes	yes	yes
22[39] 24[40]	AATTTCAAAACAAAGTAC AACGCACTCATC	basics	yes	yes	yes	yes	yes	yes	yes
10[135] 12[136]	CCGGCACCCCGAGCTC GAATTCGTTGCCTAAT	basics	yes	yes	yes	yes	yes	yes	no
35[88] 33[87]	CCCAATCCAATGAAATA GCAATAGACTCCT	basics	yes	yes	yes	yes	yes	yes	yes
12[39] 14[40]	CGCGGGGAGTTTTTCTT TTCACCATTTTTTGG	dock left 5'	yes	yes	yes	yes	no	yes	yes
34[39] 36[40]	AGCCGAACGTCTTTCCA GAGCCCTACAATT	basics	yes	yes	yes	yes	yes	yes	yes
3T38 [95]7 [159]	CCTTTTTAATTTTTGCGC GGATTGCATCAAA	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T26 [127]11 [63]	GAGCTAAATCAGAGATA AAAGAAACGCAAAG	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T34	CCGACAAAACCCCGGTA	crossover	yes	yes	yes	yes	yes	yes	yes
[63]3 [127]	GGCTATCAGGTCATT	top / bottom layer							
3T8 [159] 37[95]	ATTCGCATGAATAATCG CCGACAATGACAA	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T4 [159]37 [63]	TGGGATTTTATAATCAG AGCTTGACGGGGAAA	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T16 [95]29 [159]	GTTTTAAAAAAAAAAAGA ATTTCTTAAACAGC	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T30 [159]15 [95]	TAGACAGGAACCGCCA GTAACAGTGCCCGTAT	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
3T26 [95]7 [63]	AGGTCAGAAATATAATT CTTTACCCTGACTAT	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T16 [159]37 [159]	AGTGTAAACCAGTAATC TTTCCTTATCATTCC	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T38 [63]3 [159]	AGAGGTCAGAAAAGTAA CGGAATACCCAAAA	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T34 [159]15 [127]	GCTGCATTTGAGAATAA TAACCGATATATTCG	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T30 [63]3 [95]	GGAATTGCTAAATTTTC CGGAGACAGTCAAAT	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T38 [159]15 [159]	AATTGCTGCGATTGGCG TCTCTGAATTTACCG	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T16 [63]25 [159]	ACAACGCCCTTTCCTCG CTGCGCGTAACCACC	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T16 [127]33 [159]	TCATATGTAGGTAAAAG CATGTAGAAACCA	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T12 [63]25 [127]	CAGCGGAGAATGAATCA ACGCCAGGGTTTTCC	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T8[63] 25[95]	TTAGAGAGTAAACAACA CAAGAAAAATAATAT	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T4[63] 25[63]	TTTTCGAGGCCTGGGGA ATCATGGTCATAGCT	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T12 [159]37 [127]	GACGACAATACCTTTAC CGAAAGACTTCAAAT	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
		crossover							

Oligo	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
3T4[95]29[63]	AGTGTTTTTGCTAAACA GGGAGTTAAAGGCCG	top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T4[127]33[63]	GCGCTAATACAGGAGG GCGCTAGGGCGCTGG	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T38[127]11[159]	AAATCTCCTATGCAACA AACGAGAATGACCAT	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T26[159]15[63]	ACCCTCAGAACGGTACG AGAAAGGAAGGGAAG	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes
3T26[63]3[63]	ATAACGTGAACATGTAA CCAAGTACCGCACTC	crossover top / bottom layer	yes	yes	yes	yes	yes	yes	yes

6HB Arm StSw

[0102]

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
1[63]3[76]	GGAAGCAGTTCCCAGT CACGATTCATGC	basics	yes	yes	no	no	no	no	no
1[13]2[20]	TTTAGGGCTTAAGCTAC GTGGTTCTGACGTTGGT TTT	basics	yes	yes	no	no	no	no	no
4[62]3[48]	AACCCCGCTTCTAATCT ATTTGGTGGAT	basics	yes	yes	no	no	no	no	no
2[55]3[62]	AGCCAGGGTTCTTCTAA GTGG	basics	yes	yes	no	no	no	no	no
3[20]4[16]	TTTCGGCCCTAGGAGA AGCCAGACGCTCGCCC TGGAGTGACTCTATTT	basics	yes	yes	no	no	no	no	no
2[90]0[70]	CGGTCTTGCCCAGACT GAGACTCGGCTGACGC	basics	yes	yes	no	no	no	no	no

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
	ATT								
2[48]0[28]	TGACATTGAGTGCGGC TTGTTCCTCCTGGTTGG TG	basics	yes	yes	no	no	no	no	no
5[70]3[69]	GAATATATGTCCCGCCA AAATTTGTGAA	basics	yes	yes	no	no	no	no	no
5[49]0[63]	AAGCAACTCGTCGGTG GGCACTCACATA	basics	yes	yes	no	no	no	no	no
0[85]1[105]	AACGACCATGGGGAAC TCAACTTT	basics	yes	yes	no	no	no	no	no
5[16]0[13]	TTTTGATACCGATAATG AGTAAACTTT	basics	yes	yes	no	no	no	no	no
3[77]5[88]	GCACGACATGACAAGG GGCCTTGTTT	basics	yes	yes	no	no	no	no	no
5[28]1[55]	CAGTGCGGCCCTGCCA TCTGTACTCTGAACCTC GATAAAGAC	basics	yes	yes	no	no	no	no	no
2[69]0[49]	CACCTGACAAACCCGG AAGTTAATCATTTCTCC GA	basics	yes	yes	no	no	no	no	no
4[102]3[90]	TTTCTGAATTGTCAACC TTTTAAGTG	FRET Donor	yes	no	no	no	no	no	no

6HB Arm linear extension

[0103]

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
1[50]3[62]	AAAGACAGCCAGGG TTCTTCTAAGTGG	basics	no	no	yes	no	no	no	no
1[30]3[41]		basics	no	no	yes	no	no	no	no

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
	GTGGTTCTGACGTTG GTTTTTTTCGGCCCT AGGAGAAGCCAG								
4[62]3[48]	AACCCCGCTTCTAAT CTATTTGGTGGAT	basics	no	no	yes	no	no	no	no
2[48]0[34]	TGACATTGAGTGCGG CTTGTTCCTCCTGG	basics	no	no	yes	no	no	no	no
0[53]1[71]	TCCGAAAGCAACTCG TCGGTGGGCACTCA CATAGGAAGCAGT I	basics	no	no	yes	no	no	no	no
0[21]1[29]	GTAAACTTTTTTAGG GCTTAAGCTAC	basics	no	no	yes	no	no	no	no
4[41]0[22]	ACGCTCGCCCTGGA GTGACTCTATTTTTTT GATACCGATAATGA	basics	no	no	yes	no	no	no	no
0[33]1[49]	TTGGTGCAGTGCGG CCCTGCCATCTGTAC TCTGAACCTCGAT	basics	no	no	yes	no	no	no	no
2[69]0[54]	CACCTGACAAACCCG	basics	no	no	yes	no	no	no	no
	GAAGTTAATCATTTC								
4[111]3[90]	GTAAGCGTCATACTG AATTGTCAACCTTTTA AGTG	Crossover Arm to 6hb Ext	no	no	yes	no	no	no	no
2[114]6[77]	TTAAAGGCCGCTAAC AGCAGTTGCTCCTTA GTGTTATAGTTGTAT AA	Crossover Arm to 6hb Ext, Arm Extension to Dock	no	no	yes	no	no	no	no
1[71]5[97]	TTCCCAGTCACGATT CATGCGCACGACATG ACAAGGGGCCTTGA GAGTCTGGAGC	Crossover Arm to 6hb Ext	no	no	yes	no	no	no	no
0[97]3[69]	GGTCATTGCCTGAAT CGGCTGACGCATTGA ATATATGTCCCGCCA AAATTTGTGAA	Crossover Arm to 6hb Ext	no	no	yes	no	no	no	no

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
2[90]1[114]	CGGTCTTGCCCAGAC TGAGACCGACCATG GGGAACTCAACTTTG CGGGATCG	Crossover Arm to 6hb Ext	no	no	yes	no	no	no	no

6HB Arm High Torque Extension

[0104]

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
5[209]3 [223]	AGCAACTCATCATTTC GTGGTGCTTGTTAAAC TCAATGGTTGT	AuNRExt	no	no	no	yes	yes	no	no
3[203]2 [189]	GATGTTCCTAATCTATT TACGCTCGCCCGAGAA GCCCCAGAG	Basics	no	no	no	yes	yes	yes	yes
1[176]3 [202]	CGGAATACGTAATGAG TAAACAGGGCTGGTCT TGCAGGGTG	Crossover to Extension, AuNRExt	no	no	no	yes	yes	yes	no
6[224]4 [231]	TTCTGAATTGTCAACC TTATGACAATGT	Crossover to Extension, 5PrDockExtensi on	no	no	no	yes	no	yes	yes
0[247]1 [256]	TTTTCTGAATCGGCTG AAAAGACGGAAGTTGG AAGCCGGATAA	Crossover to Extension, AuNRExt	no	no	no	yes	yes	yes	no
3[224]5 [250]	GAATTCACCCGCCAGG CACGAATATAGGGGCC TGGTCATAG	Crossover to Extension	no	no	no	yes	yes	yes	yes
2[253]6 [255]	CAGGAGTTCCCACTGA GACTTAAGTGTCCTTA GTGTT	Crossover to Extension, 3PrDockExtensi on	no	no	no	no	no	no	yes
5[175]0 [175]	CAATGATACCGACAGT GCGGCCTCCTGGTTG GTCCAAAAGAA	Crossover to Extension	no	no	no	yes	yes	yes	yes
2[188]4 [171]	TCACGACACCTGACCG TTGGTCGGCCAGTGG	Crossover to Extension, AuNRExt	no	no	no	yes	yes	yes	no

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
	AGTGACTCTCAAGAA								
3[154]2 [152]	CCTTTCATTGAGTGCG TCTGAAAACCCAGCCA GGTGATTAAGAA	Crossover to Extension, AuNRExt	no	no	no	yes	yes	yes	no
7[217]3 [216]	CAATAGACACATAAGT CGGTGAAATAACCCCG CTTTTCTAAG	Crossover to Extension, AuNRExt	no	no	no	yes	yes	yes	no
3[231]7 [230]	TGCGCACGACCGACC ATGGGGCCTCGATCG CATTTAAATTCA	Crossover to Extension	no	no	no	yes	yes	yes	yes
2[216]7 [209]	CAACAGCAGTTGCCTA AGCTACTCCGAATATT TTG	Crossover to Extension, AuNRExt	no	no	no	yes	yes	yes	no
7[196]5 [208]	ATAAGTTCTCTGACCC TGCCATCTGTA	Crossover to Extension	no	no	no	yes	yes	yes	yes

6HB Arm High Torque Extension AuNR

[0105]

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
1[176]Short Au8ADist	CGGAATACGTAATGAGTA AAAAAAAAA	8A 3Prime	no	no	no	no	no	no	yes
3[154]Short Au8ADist	CCTTTCATTGAGTGCGTC TGAAAACCCAAAAAAAA	8A 3Prime	no	no	no	no	no	no	yes
5[209]Short Au8ADist	AGCAACTCATCATTTCGT GGTGAAAAAAAA	8A 3Prime	no	no	no	no	no	no	yes
0[247]Short Au8ADist	TTTTCTGAATCGGCTGAA AAGACGAAAAAAAA	8A 3Prime	no	no	no	no	no	no	yes
7[217]Short Au8ADist	CAATAGACACATAAGTCG GTGAAATAACCCCGCTTT TCTAAGCAACAGCAAAAA AAA	8A 3Prime	no	no	no	no	no	no	yes

Oligo Position	Sequence	Staple Type	Figure						
			1	7	8	9A,B	9C,D	10A,B	10C,D
2[188]Short Au8AProx	AAAAAAAATCACGACACC TGACCGTTGGTCGGCCAG TGGAGTGACTCTCAAGAA	8A 5Prime	no	no	no	no	no	no	yes
1[195]Short Au8AProx	AAAAAAAAACAGGGCTGG TCTTGCAGGGTG	8A 5Prime	no	no	no	no	no	no	yes
1[217]Short Au8AProx	AAAAAAAACTTGTTAAACT CAATGGTTGT	8A 5Prime	no	no	no	no	no	no	yes
2[209]Short Au8AProx	AAAAAAAAAGTTGCCTAA GCTACTCCGAATATTTTG	8A 5Prime	no	no	no	no	no	no	yes
1[238]Short Au8AProx	AAAAAAAAGAAGTTGGAA GCCGGATAA	8A 5Prime	no	no	no	no	no	no	yes
2[168]Short Au8AProx	AAAAAAAAAGCCAGGTGA TTAAGAA	8A 5Prime	no	no	no	no	no	no	yes

Linear Extension

[0106]

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
0[391]3 [384]	TAGCAAAACGGCGGTTTCGG TCATAGCCCCTCAGA	basics	no	no	yes	no	no	no	no
0[517]3 [510]	TTCGCAACCGGCACTAGCAC CATTACCATGAATAA	basics	no	no	yes	no	no	no	no
0[223]3 [216]	AAGATTCAACGTTACAGCATT GACAGGATATTATT	basics	no	no	yes	no	no	no	no
0[643]3 [636]	TATAATGCTGCAAGCAAAAGG GCGACATCTGAGAG	basics	no	no	yes	no	no	no	no
1[868]3 [881]	CTCGTTTAGAAGGATATGCGT TATACAA	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
1 [343]3 [356]	TATCATCGTTTCAGTGTATCA CCGTACT	basics	no	no	yes	no	no	no	no
1[994]3 [1007]	AGAGTCTATTTGAGGAATATA AAGTACC	basics	no	no	yes	no	no	no	no
0[412]3 [405]	CATACAGGATAGGTGTAGCG CGTTTTCAAACCGCC	basics	no	no	yes	no	no	no	no
0[265]3 [258]	CCTCATAATCAGCTCACCCTC AGAGCCGCAAGAGA	basics	no	no	yes	no	no	no	no
1 [889]3 [902]	AAAACCATTGCGGACCAGTAT AAAGCCA	basics	no	no	yes	no	no	no	no
0[580]3 [573]	TCCATATGTTGGGAAAGGTGA ATTATCAATAGCGA	basics	no	no	yes	no	no	no	no
1[1057] 3[1070]	CTTGCCTGTTATCTTCAGCTA ATGCAGA	basics	no	no	yes	no	no	no	no
1[931]3 [944]	AGAGGGGCCGAACGTCGCCA TATTTAAC	basics	no	no	yes	no	no	no	no
1 [826]3 [839]	AAAGGAATGGCAATACACCG GAATCATA	basics	no	no	yes	no	no	no	no
1[1036] 3[1049]	CTTTGATAGCACTACGACGAC AATAAAC	basics	no	no	yes	no	no	no	no
0[475]3 [468]	GGGCGCGCGACAGTAACCAT CGATAGCATACCGTA	basics	no	no	yes	no	no	no	no
1[1078] 3[1091]	AAACTATAGTTGAATGTTTATC AACAAT	basics	no	no	yes	no	no	no	no
0[496]4 [483]	GTTTAGCGATCGCAGGCCGG AAACGTCA	basics	no	no	yes	no	no	no	no
0[979]3 [972]	TACGCCAGGTTTGCCTAATAT CAGAGAGCAGAGGC	basics	no	no	yes	no	no	no	no
1[910]3 [923]	TTTTGCAAGTTTGAACAGTAG	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
	GGCTTAA								
1[700]3 [713]	AGGACGTTTTAACGCCAATCG CAAGACA	basics	no	no	yes	no	no	no	no
0[601]3 [594]	TACGGTGGGGCCTCATTGAC GGAAATTAACGCTGA	basics	no	no	yes	no	no	no	no
0[202]3 [195]	GGCCGGATAAGCAAGCAGGT CAGACGATCCCCCTG	basics	no	no	yes	no	no	no	no
0[328]3 [321]	GACCCTGGCCAGCTAGCCAC CACCGGAAGGTTGAT	basics	no	no	yes	no	no	no	no
1[280]3 [293]	AAACACTTTGAAAATTGCTCA GTACCAG	basics	no	no	yes	no	no	no	no
1[322]3 [335]	ACAAAGTAAAGGAAATAAGTA TAGCCCG	basics	no	no	yes	no	no	no	no
0[181]3 [174]	CATCAATCCCAAAAGATATTC ACAAACATGCCCGT	basics	no	no	yes	no	no	no	no
1[1162] 3[1175]	TTTTGACAGCAAATGGCTGTC TTTCCTT	basics	no	no	yes	no	no	no	no
1[1120] 3[1133]	CCAGCCATATCAAATCCCATC CTAATTT	basics	no	no	yes	no	no	no	no
1[1183] 3[1196]	AATGGATAGTGCCACAAGAAC GGGTATT	basics	no	no	yes	no	no	no	no
0[1000] 3[993]	AGGGATTGGTGGTTAAGTCA GAGGGTAAAATAAGA	basics	no	no	yes	no	no	no	no
1 [427]3 [440]	GGGAACCGCGTAACATTTTCA GGGATAG	basics	no	no	yes	no	no	no	no
0[1021] 3[1014]	GCTAAACTGAGACGATTAACT GAACACCGACAAAA	basics	no	no	yes	no	no	no	no
0[1168] 3[1161]	GCGGGCGCCCGAGAAGCCTA ATTTGCCAAATAATC	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
1 [385]3 [398]	CATGTTAAATGAATACCGCCA CCCTCAG	basics	no	no	yes	no	no	no	no
0[1042] 3[1035]	CTCGTTAGCCCTTCGGAAGC GCATTAGAGTCCAGA	basics	no	no	yes	no	no	no	no
1[196]3 [209]	AGGAAGTCAGCTTGCCTATTT CGGAACC	basics	no	no	yes	no	no	no	no
1 [847]3 [860]	AAGAGCAATATTCCGAAAAAG CCTGTTT	basics	no	no	yes	no	no	no	no
1[406]3 [419]	GGCGCAGTCGTCTTACCCTC AGAGCCAC	basics	no	no	yes	no	no	no	no
1[805]3 [818]	TAATGCACTGATTGTAAGGCG TTAAATA	basics	no	no	yes	no	no	no	no
0[1063] 3[1056]	GAGCACGAGAGAGTGAGAGA ATAACATAAACATGT	basics	no	no	yes	no	no	no	no
1[259]3 [272]	AAGAGGCGCTCCAAAGGATT AGGATTAG	basics	no	no	yes	no	no	no	no
0[664]3 [657]	GCTTAGATAACGCCATGGTTT ACCAGCGCTCCGGC	basics	no	no	yes	no	no	no	no
1[763]3 [776]	AGAAAGAACCTACCTGACCTA AATTTAA	basics	no	no	yes	no	no	no	no
0[790]3 [783]	AAGACTTCCTGTGTAAGACTC CTTATTATGGTTTG	basics	no	no	yes	no	no	no	no
0[748]3 [741]	CCAGACCCGGGTACCATACA TAAAGGTGCAAATAT	basics	no	no	yes	no	no	no	no
1 [469]3 [503]	TGTACAGACTACAAACACTGA GTTTCGTCAATAAATCAATATA TGTGAG	basics	no	no	yes	no	no	no	no
0[685]3 [678]	AAGAGGTCACGACGCACAAT CAATAGAAATAACTA	basics	no	no	yes	no	no	no	no
0[160]3		basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
[153]	TTCTAGCCCGGTTGCCTCATT AAAGCCAGGTCAGT								
0[706]3 [699]	CCTTTAACCAGTGCCACGGAA TAAGTTTTGCAAAT	basics	no	no	yes	no	no	no	no
0[769]3 [762]	TAATTCGTAATCATTGTTAGCA AACGTACATCTTC	basics	no	no	yes	no	no	no	no
0[349]3 [342]	CGGTTGTATGTGAGAATCAAA ATCACCGGAATAGG	basics	no	no	yes	no	no	no	no
1[364]3 [377]	GTCGAAATTTGCTATTTAGTA CCGCCAC	basics	no	no	yes	no	no	no	no
0[727]3 [720]	ACAGGTCAGGTCGAATAAAAG AAACGCAAAGAACG	basics	no	no	yes	no	no	no	no
0[433]3 [426]	TAGCATTTGGGCGCGTTTGCC TTTAGCGCACCCTC	basics	no	no	yes	no	no	no	no
0[1126] 3[1119]	GTAACCAGGTTCCGTCCCAAT CCAAATAAATAATA	basics	no	no	yes	no	no	no	no
1[784]3 [797]	TTTAGGACTGAATAAAATACC GACCGTG	basics	no	no	yes	no	no	no	no
1[511]3 [524]	TAATCTTCATTTGACCTTGCTT CTGTAA	basics	no	no	yes	no	no	no	no
0[286]3 [279]	AAGGATATAGGAACAACCGC CACCCTCACGGGGTT	basics	no	no	yes	no	no	no	no
0[832]3 [825]	AAGCAAACGAGCCGAAACGC AATAATAAAGAATAA	basics	no	no	yes	no	no	no	no
0[1084] 3[1077]	GCGTACTCACGCTGATGAAAA TAGCAGCACGCGCC	basics	no	no	yes	no	no	no	no
1[175]3 [188]	AGGACTAGCCGACAATAAACA GTTAATG	basics	no	no	yes	no	no	no	no
0[1147] 3[1140]	AGTGTAGCCTTATAAATAAAC AGCCATAACGAGCA	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
5[98]0[98]	AAACAAGAGAATCGTACAAAG GCTATCA	basics	no	no	yes	no	no	no	no
1[532]3[545]	ATTCATTATTAATTCTATTAAT TAATTT	basics	no	no	yes	no	no	no	no
0[811]3[804]	AAAGATTCTCACAACCCAAAA GAACTGGTGATAAA	basics	no	no	yes	no	no	no	no
1[238]3[251]	GAAGGCATGTATCGAGGCTG AGACTCCT	basics	no	no	yes	no	no	no	no
0[118]4[112]	AGAGATCATGAACGCGTTCCA	basics	no	no	yes	no	no	no	no
1[448]3[461]	TGAAAGACACAGACAATAGGA ACCCATG	basics	no	no	yes	no	no	no	no
0[139]3[132]	CGGAGAGAGCATGTAAGCGC AGTCTCTGACTGGTA	basics	no	no	yes	no	no	no	no
0[853]3[846]	TACCCTGAAAGCCTGTTACCA GAAGGAAATTACTA	basics	no	no	yes	no	no	no	no
1[574]3[587]	AATAAGGCTGAGCATAGCTTA GATTAAG	basics	no	no	yes	no	no	no	no
0[895]3[888]	GTTCAGAGCGTTGCCCGAAG CCCTTTTTATTCTTA	basics	no	no	yes	no	no	no	no
0[1189]3[1182]	GAAGGGAGTTCCAGCGCTAA CGAGCGTCATCATTC	basics	no	no	yes	no	no	no	no
1[301]3[314]	AGCGATTGCGAATAAGTGCC GTCGAGAG	basics	no	no	yes	no	no	no	no
0[244]3[237]	TGCCTGATTCGCATAACCACC ACCAGAGTATTAAG	basics	no	no	yes	no	no	no	no
0[1210]3[1203]	CCGGCGACCACTATTTTTATC CTGAATCAAACCAA	basics	no	no	yes	no	no	no	no
1[217]3[230]	TAAAATATTTCGAGCTGAAAC ATGAAAG	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
	ATGAAAG								
1[553]3[566]	AACAAAGAACAAACGAATCCTTGAAAAC	basics	no	no	yes	no	no	no	no
1[658]3[671]	ATTACCTGGGAGAATTAGGTTGGGTTAT	basics	no	no	yes	no	no	no	no
1[595]3[608]	AAACACCCGAATTAGAAGAGTCAATAGT	basics	no	no	yes	no	no	no	no
1[1015]3[1028]	TTAACCGAGAGCCGGGTAAAGTAATTCT	basics	no	no	yes	no	no	no	no
1 [679]3[692]	AACTGGCAGTAACATATGTAAATGCTGA	basics	no	no	yes	no	no	no	no
1[616]3[629]	ATTGGGCAGTTACATCAAAATCATAGGT	basics	no	no	yes	no	no	no	no
1 [637]3[650]	TTTCAACGCCTGATACTACCTTTTTAAC	basics	no	no	yes	no	no	no	no
1[1141]3[1154]	ACGCTCAATCACCTTGTAGAAACCAATC	basics	no	no	yes	no	no	no	no
0[874]3[867]	ATAAATCGTGAGCTGTAAGCAGATAGCCAGTATCA	basics	no	no	yes	no	no	no	no
0[1105]3[1098]	CTTAATGGCGAAAAATTTTTTGTTTAACAGATAAG	basics	no	no	yes	no	no	no	no
0[916]3[909]	CCCCCTCTTCCAGTGAAATAGCAATAGCACGCTCA	basics	no	no	yes	no	no	no	no
0[538]3[531]	TAGTTTGGAAACCATAGAGCCAGCAAAAATCGTCG	basics	no	no	yes	no	no	no	no
0[937]3[930]	CGTCATATGCCAGCATAATAAGAGCAAGTTGAGAA	basics	no	no	yes	no	no	no	no
1[133]3[146]	GACAGCATTCGGTCATAAGTTTTAACGG	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
0[454]3 [447]	CATCAATTCTGCCAAATCAGT AGCGACACAAGCCC	basics	no	no	yes	no	no	no	no
0[958]3 [951]	TAGCGTCGGCCAACACAAGA ATTGAGTTAACGCCA	basics	no	no	yes	no	no	no	no
0[622]3 [615]	GTTTTAAAGCTGGCATTGAGG GAGGGAAGAATTTA	basics	no	no	yes	no	no	no	no
0[307]3 [300]	GAGAAGCTTCGCGTCCTCAG AGCCGCCAGCGGATA	basics	no	no	yes	no	no	no	no
1[721]3 [734]	TACGTTAGAAATTGCGAGAAA ACTTTTT	basics	no	no	yes	no	no	no	no
1[154]3 [167]	GCAACGGCGCCCACGCCTTG AGTAACAG	basics	no	no	yes	no	no	no	no
1[742]3 [755]	CGGAACATGCACGTATTTTAG TTAATTT	basics	no	no	yes	no	no	no	no
1 [1099] 3[1112]	ATATCCACTGGTCATCCTGAA CAAGAAA	basics	no	no	yes	no	no	no	no
0[370]3 [363]	CCTCAGATCGGATTTAGCGTT TGCCATCCAGGAGG	basics	no	no	yes	no	no	no	no
0[559]3 [552]	AATTCTGCGCCATTCGACTTG AGCCATTTCCCTTA	basics	no	no	yes	no	no	no	no
1[973]3 [986]	TCAGTGAAGACTTTATTTTCG AGCCAGT	basics	no	no	yes	no	no	no	no
3[100]3 [125]	CATGGCTTTTGATGATACAGG AGTGT	basics	no	no	yes	no	no	no	no
4[419]1 [426]	TCAGACTCACGTTGGTGTAGA AACATCCATCATAA	basics	no	no	yes	no	no	no	no
4[461]1 [468]	GCACCGTGTTTGAGGGGACG AAGCTGAATGAACGG	basics	no	no	yes	no	no	no	no
2[1140] 0[1127]	TGCTGAACCTCAAATTGCAAC	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
	GCTGCGC								
2[405]0 [392]	TCCAGACGTTAGTACTTAGCC AAAGAAT	basics	no	no	yes	no	no	no	no
4[692]1 [699]	ATTTTGTTTGTAAAACGACGG TTGCTCCACCAGTC	basics	no	no	yes	no	no	no	no
4[1070] 1[1077]	CTTTACATGCAGCAAGCGGTC ATGGTTGAGAACTC	basics	no	no	yes	no	no	no	no
4[1259] 1[1266]	TTTTGAAATCAGGGCGATGGC AAGCACTACCCTTC	basics	no	no	yes	no	no	no	no
2[552]0 [539]	ATCAAGAAAACAAAACCCAAA GTAGATT	basics	no	no	yes	no	no	no	no
4[167]1 [174]	AATAAATATAATCAGAAAAGC ATGATATGGCTTTG	basics	no	no	yes	no	no	no	no
5[959]0 [959]	GCGCGGGGAGAGGCGAATCC TGAGAAGA	basics	no	no	yes	no	no	no	no
2[1245] 0[1232]	CCACCAGCAGAAGAAAGGGA CCCCCCGA	basics	no	no	yes	no	no	no	no
2[1077] 0[1064]	AGGAATTGAGGAAGGAGTAG ACTTTGAC	basics	no	no	yes	no	no	no	no
2[783]0 [770]	ATGGAAGGGTTAGATTCATCA CGCGTTT	basics	no	no	yes	no	no	no	no
2[195]0 [182]	ATACCGATAGTTGCAAGACTT AAATCAC	basics	no	no	yes	no	no	no	no
4[314]1 [321]	CCGCCTCCTGGCCTTCCTGTA TAATACTGCGCGAA	basics	no	no	yes	no	no	no	no
4[1238] 1[1245]	TTAGTTGTCAAAGGGCGAAAA AAGGGAGATTCTGG	basics	no	no	yes	no	no	no	no
4[1028] 1[1035]	CGGGAGAGGCAACAGCTGAT TGAATCAGAATACTT	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
4[734]1[741]	GCAACATCTCTAGAGGATCCC GGAAGCAGAACTAA	basics	no	no	yes	no	no	no	no
2[846]0[833]	TGATTATCAGATGATTACGAG TAGTCAG	basics	no	no	yes	no	no	no	no
4[881]1[888]	AAGAAAAAACTCACATTAATTA AACGAGGACGATA	basics	no	no	yes	no	no	no	no
4[377]1[384]	CCCTTATCTCCGTGGGAACAA ATTAAGCCCTGCTC	basics	no	no	yes	no	no	no	no
4[482]1[489]	CCAATGAATCGGCCTCAGGA ATATATTTGCATAGG	basics	no	no	yes	no	no	no	no
2[1224]0[1211]	GAGGTGAGGCGGTCCAGTCA CGGGAAAG	basics	no	no	yes	no	no	no	no
2[741]0[728]	AAAACAGAAATAAAATAAAAC AACTCCA	basics	no	no	yes	no	no	no	no
2[951]0[938]	ATTAAATCCTTTGCGTAATAG GCGGAAT	basics	no	no	yes	no	no	no	no
4[230]1[237]	CCGCCGCATATTTTGTTAAAA GTAATGTCCACTAC	basics	no	no	yes	no	no	no	no
4[440]1[447]	GAATCAAATCGTAACCGTGCA TCTACTACCAACTT	basics	no	no	yes	no	no	no	no
4[1175]1[1182]	TTTCCAGTAGGGTTGAGTGTT AGAAAGCCGTCTGA	basics	no	no	yes	no	no	no	no
4[587]1[594]	TTCATTAAGGGCGATCGGTGC TCTGGAATGACGAG	basics	no	no	yes	no	no	no	no
4[209]1[216]	GGTTGAGATATTTAAATTGTA AAAAGGGAAACGGG	basics	no	no	yes	no	no	no	no
2[342]0[329]	CGGAGTGAGAATAGACAACG GACATTAT	basics	no	no	yes	no	no	no	no
4[1007]1[1014]	CTGAACATTTCTTTTCACCAG	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
	AGGAGGCACGCAAA								
4[272]1 [279]	GAGCCACCATTTTTTAACCAA AAAATTTTACACTA	basics	no	no	yes	no	no	no	no
2[1287] 0[1274]	ACTGATAGCCCTAAAAAGCGT GTCGAGG	basics	no	no	yes	no	no	no	no
4[1217] 1[1224]	GCTACAATAAAGAACGTGGAC CTTGACGACGACCA	basics	no	no	yes	no	no	no	no
2[510]0 [497]	ATTACCTTTTTTAAACCTTCAA TAACCT	basics	no	no	yes	no	no	no	no
2[132]2 [115]	GCTGAGGCTTGCAGGGAG	basics	no	no	yes	no	no	no	no
2[1014] 0[1001]	TCAATAGATAATACGTCCATC CGATTAA	basics	no	no	yes	no	no	no	no
4[503]1 [510]	TTAGCAACTCCAGCCAGCTTT ATGGTCATCAAGAG	basics	no	no	yes	no	no	no	no
2[384]0 [371]	TTTCTGTATGGGATTCCGCGA AATAAAG	basics	no	no	yes	no	no	no	no
4[986]1 [993]	TTGAGCGGTATTGGGCGCCA GTTAGACAGAGTAAA	basics	no	no	yes	no	no	no	no
4[125]1 [132]	AATTTACGTAATCGTAAAACT GGTAGCTAGCGAAA	basics	no	no	yes	no	no	no	no
4[671]1 [678]	AATTCATAGGGTTTTCCCAGT CATTTTTTTTTAAG	basics	no	no	yes	no	no	no	no
2[888]0 [875]	ACAAAGAAACCACCACCAGAC AATGACC	basics	no	no	yes	no	no	no	no
4[566]1 [573]	CCGTCACCAGGCTGCGCAAC TAACAGTTTTCAGTG	basics	no	no	yes	no	no	no	no
1[952]1 [972]	TTTAGACTGGTGTTTTTATAA	basics	no	no	yes	no	no	no	no
2[300]0 [287]	ATAATTTTTTCACGCATCTTTT CAACGC	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
2[1182]0[1169]	CGCTGAGAGCCAGCGCTCAATGAAAGGA	basics	no	no	yes	no	no	no	no
2[174]0[161]	ATGACAACAACCATCTACAGATCAACCG	basics	no	no	yes	no	no	no	no
4[1154]1[1161]	GTTACAAAATCAAAAGAATAGCTAGGGCACCTACA	basics	no	no	yes	no	no	no	no
2[1056]0[1043]	AAAATATCTTTAGGTAGTAATTGCTTTC	basics	no	no	yes	no	no	no	no
2[930]0[917]	TTATTAATTTTAAAAAAGAAGATTGAAT	basics	no	no	yes	no	no	no	no
4[335]1[342]	GAACCAGTTCATCAACATTAAACCAAAAAAGATTTG	basics	no	no	yes	no	no	no	no
4[524]1[531]	TCACCAGCGCTTCTGGTGCCGACCATTAACCGGAT	basics	no	no	yes	no	no	no	no
1[490]0[476]	CTGGCTGTGGAAACAGTACCCAGTACAAACCAGGCTCATTTG	basics	no	no	yes	no	no	no	no
4[1091]1[1098]	GTCAAAAGTTTGCCCCAGCAGCGCCGCTGCTGGTA	basics	no	no	yes	no	no	no	no
2[594]0[581]	TTCATTTCAATTACCTTGCCCGTTTCAT	basics	no	no	yes	no	no	no	no
2[762]0[749]	ATATCAAAATTATTACATTATAAGCGAA	basics	no	no	yes	no	no	no	no
4[629]1[636]	TCAACCGGAAAGGGGGATGTGCTGTAGCGGTTTAA	basics	no	no	yes	no	no	no	no
2[699]0[686]	TCAGATGAATATACTCATTATTTTTGAT	basics	no	no	yes	no	no	no	no
4[1133]1[1140]	TTATTTAAAATCGGCAAAATCCGGTCACAGGAAAA	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
2[426]0 [413]	GATCTAAAGTTTTGACGGTCA AATAAAT	basics	no	no	yes	no	no	no	no
2[363]0 [350]	AACAACTTTCAACAGCCTGAT GCTAAAT	basics	no	no	yes	no	no	no	no
2[1035] 0[1022]	ACAACTAATAGATTTTGTAGC AGCGGGA	basics	no	no	yes	no	no	no	no
1[115]0 [119]	TCACCCTCAGCATTTTTG	basics	no	no	yes	no	no	no	no
2[279]0 [266]	TCTCCAAAAAAAAGAAAAGAA TTAGAAC	basics	no	no	yes	no	no	no	no
4[818]1 [825]	CGGAATATTCCACACAACATA GCGGATTAACGCCA	basics	no	no	yes	no	no	no	no
4[776]1 [783]	CGCAGTAGGTCATAGCTGTTT CAAATATGTTGAGA	basics	no	no	yes	no	no	no	no
2[468]0 [455]	CGCCTGTAGCATTCGGACAG AAAGGTGG	basics	no	no	yes	no	no	no	no
4[944]1 [951]	AAGCCCATGCATTAATGAATC CAATACTTAAAATG	basics	no	no	yes	no	no	no	no
4[839]1 [846]	ACCGAGGGAAGCATAAAGTG TACTATTAGCATAGT	basics	no	no	yes	no	no	no	no
4[146]1 [153]	GAATGGACAATCATATGTACC TGATAAAGAGGGTA	basics	no	no	yes	no	no	no	no
4[860]1 [867]	GAACAAAGGGGTGCCTAATG AAAAAATCCATAACC	basics	no	no	yes	no	no	no	no
4[755]1 [762]	GAAAATACGAGCTCGAATTCG AGCTTCATACAGGT	basics	no	no	yes	no	no	no	no
2[636]0 [623]	TGCTTTGAATACCATTGAGAT TCAACAT	basics	no	no	yes	no	no	no	no
2[153]0 [140]	GCATAACCGATATATCGGAAC TTAATGC	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
2[657]0 [644]	ACAATAACGGATTCTTTAATCT GCTGAA	basics	no	no	yes	no	no	no	no
4[293]1 [300]	CCCTCAGGCCATCAAAAATAA CTTTATTGACCCCC	basics	no	no	yes	no	no	no	no
4[650]1 [657]	CCAAAGAGCGATTAAGTTGG GGCTTAATATTGTGA	basics	no	no	yes	no	no	no	no
2[321]0 [308]	CAACTAAAGGAATTATACCAA TTTGCGG	basics	no	no	yes	no	no	no	no
2[1203] 0[1190]	ACACCGCCTGCAACTATTTAC GAGAAAG	basics	no	no	yes	no	no	no	no
2[972]4 [959]	ACAAACAATTCGACAACTCGT ACATGTAATTTAGGATAACCC	basics	no	no	yes	no	no	no	no
2[993]0 [980]	GATTTAGAAGTATTGGCCACC GGAACGG	basics	no	no	yes	no	no	no	no
2[825]0 [812]	TCATCAATATAATCGATACAT GCATCAA	basics	no	no	yes	no	no	no	no
4[1112] 1[1119]	AGAAACGTCCTGTTTGATGGT CCACACCATTACCG	basics	no	no	yes	no	no	no	no
2[573]0 [560]	AAAGAAGATGATGACTGCTCA GATTCCC	basics	no	no	yes	no	no	no	no
4[713]1 [720]	AAGACACCAAGCTTTGCCTGC AGGATTAAAAAATC	basics	no	no	yes	no	no	no	no
2[258]0 [245]	AAGGAGCCTTTAATCCAACCT AATGCAA	basics	no	no	yes	no	no	no	no
2[531]0 [518]	ACATTTAACAATTTGACAAGA GATACAT	basics	no	no	yes	no	no	no	no
4[398]1 [405]	TCGGCATATTGACCGTAATGG GCAAGGCGGAACGA	basics	no	no	yes	no	no	no	no
4[1196]		basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
1[1203]	TTACCAATTTGGAACAAGAGT ACGTGGCATTGGCA								
2[678]0 [665]	GTACCTTTTACATCTATGCGA GCGGATG	basics	no	no	yes	no	no	no	no
4[902]1 [909]	TATCTTAGCTCACTGCCCGCT AAATGCTGAGAGGC	basics	no	no	yes	no	no	no	no
2[804]0 [791]	TTTGGATTATACTTATACCACA GCCCGA	basics	no	no	yes	no	no	no	no
2[216]0 [203]	GTGAATTTCTTAAATTCCATTT GAGAAA	basics	no	no	yes	no	no	no	no
2[909]0 [896]	GTAACATTATCATTAAATAGCT TAAACA	basics	no	no	yes	no	no	no	no
4[797]1 [804]	CATGATTGAAATTGTTATCCG AAGAGGAATTCAAC	basics	no	no	yes	no	no	no	no
2[720]0 [707]	CGTAGATTTTCAGGTGGGAAG GAGAGTA	basics	no	no	yes	no	no	no	no
2[867]0 [854]	GCGGAATTATCATCACACTAT AGGTCTT	basics	no	no	yes	no	no	no	no
2[447]0 [434]	AGCCCTCATAGTTAGAACTGA ATAGTAG	basics	no	no	yes	no	no	no	no
4[251]1 [258]	CCACCAGTAAATTTTTGTTAAT ATTTTAAAAACGA	basics	no	no	yes	no	no	no	no
4[1049] 1[1056]	AAAACAGACCGCCTGGCCCT GTATAACGAACATCA	basics	no	no	yes	no	no	no	no
4[923]1 [930]	AAACAATCGGGAAACCTGTCG AATATTCTTTTGCC	basics	no	no	yes	no	no	no	no
4[356]1 [363]	TTTTCATCGAGTAACAACCCG GCATAAAAAATTGT	basics	no	no	yes	no	no	no	no
2[1098] 0[1085]	GTTGGCAAATCAACCGGCCTT ACAGGGC	basics	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
2[237]0 [224]	GTTTATCAGCTTGCCGTAATG GTAGGTA	basics	no	no	yes	no	no	no	no
4[188]1 [195]	TGGCCTTACAGGAAGATTGTA GACAGTCTTTCATG	basics	no	no	yes	no	no	no	no
2[1119] 0[1106]	CCCTCAATCAATATGAACAAT CGCCGCG	basics	no	no	yes	no	no	no	no
2[1266] 0[1253]	CCATTAAAAATACCAGATAGA AAATCGG	basics	no	no	yes	no	no	no	no
2[615]0 [602]	AAATCGCGCAGAGGAGAACG AACTAAAG	basics	no	no	yes	no	no	no	no
4[545]1 [552]	TGGGAATGGCAAAGCGCCAT TCGAACGATCAACGT	basics	no	no	yes	no	no	no	no
4[608]1 [615]	GGTAAATTTCGCTATTACGCC ATATGCAGTAGTAA	basics	no	no	yes	no	no	no	no
2[1161] 0[1148]	GAAAAATCTAAAGCTGGAAAT GCTGGCA	basics	no	no	yes	no	no	no	no
2[1315] 1[1315]	taagtgagacccgtacatatTTTGGCT ATTAGTCTTTAACAGACAATAT TTTTGAATTtaagtgagacccgtacat at	A655 Marker Extensio ns	no	no	yes	no	no	no	no
4[1280] 5[1296]	taagtgagacccgtacatatAACCTCC GTGAACCATCACCCAAATCTTt aagtgagacccgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no
0[1296] 1[1287]	taagtgagacccgtacatatTTAAGTTT TTTGGGAAGAATAtaagtgagacc cgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no
4[1310] 3[1287]	taagtgagacccgtacatatTTTTCTAA GAACGCGAGGCGTTTTAGCG ATCAGATtaagtgagacccgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no
1[1288] 3[1310]	taagtgagacccgtacatatCGTGGCA TGCGCGAATAGAAGGCTTATC CGGTATTtaagtgagacccgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no

Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
1[1246] 3[1259]	taagtgagacccgtacatatCCAACAG GAACGAATCGTAGGAATCATT Ttaagtgagacccgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no
1[1204] 3[1217]	taagtgagacccgtacatatGATTCAC AGTATTAGTACCGCACTCATC Ttaagtgagacccgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no
1[1267] 3[1280]	taagtgagacccgtacatatTGACCTG AACATCGCCAATAGCAAGCAA Ttaagtgagacccgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no
0[1231] 3[1224]	taagtgagacccgtacatatTTTAGAG TCCAACGCTATTTTGCACCCA GAGAACATtaagtgagacccgtacat at	A655 Marker Extensio ns	no	no	yes	no	no	no	no
1[1225] 3[1238]	taagtgagacccgtacatatGTAATAA TAAAACAAGCAAGCCGTTTTT Ttaagtgagacccgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no
0[1273] 3[1266]	taagtgagacccgtacatatTGCCGTA CCACTACCGACTTGCGGGAG GACCGCGCTtaagtgagacccgtac atat	A655 Marker Extensio ns	no	no	yes	no	no	no	no
0[1252] 3[1245]	taagtgagacccgtacatatAACCCTA ACCGTCTGCCTTAAATCAAGA ATTTTCATtaagtgagacccgtacatat	A655 Marker Extensio ns	no	no	yes	no	no	no	no

High Torque Extension

[0107]

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
12[447]9 [440]	TTTACGAACGCCTGCTTCA AAGCGAACCTCAAATC	basics	no	no	no	yes	yes	yes	yes
11[315]9 [328]	GACCAGTCGTTAGAGGGAG AAGCCTTTA	basics	no	no	no	yes	yes	yes	yes
11[336]9 [349]	TCTGGCCGCACGTAGCAAG GATAAAAAT	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
11[672]9[685]	TAGGAGCAGTTTGGCGTTAATATTTTGT	basics	no	no	no	yes	yes	yes	yes
12[1077]9[1070]	GAGTGAACGAAATCTATTCATTACCCAAACGCCAG	basics	no	no	no	yes	yes	yes	yes
12[615]9[608]	AGGCAGAAATAATTTATTCATTGAATCCGTACCCC	basics	no	no	no	yes	yes	yes	yes
12[636]9[629]	AACAACGATCTCCAATACTGCGGAATCGAAAGCCC	basics	no	no	no	yes	yes	yes	yes
11[609]9[622]	ATATCTGCTATCAGGGTTGATAATCAGA	basics	no	no	no	yes	yes	yes	yes
12[657]9[650]	TAATTGAAAAGGAGGTTTAGACTGGATATTGTATA	basics	no	no	no	yes	yes	yes	yes
12[1035]9[1028]	TTTTCCCAAAGTACGAATAAGGCTTGCCCAACTGT	basics	no	no	no	yes	yes	yes	yes
11[399]9[412]	TTTTTGAAACCACCTAAAGATTCAAAAG	basics	no	no	no	yes	yes	yes	yes
1[315]3[328]	GAGGTTTAGTACCGTCTGAAAGGTAATA	basics	no	no	no	yes	yes	yes	yes
12[195]9[188]	TATTTTGCCACGGAGGTCAATAACCTGTTAATAGT	basics	no	no	no	yes	yes	yes	yes
12[804]9[797]	TAATGGTAAAGGCCCTAATGCAGATACAATTAAAT	basics	no	no	no	yes	yes	yes	yes
11[840]9[853]	CACCAGACGGGCAAGGCGGATTGACCGT	basics	no	no	no	yes	yes	yes	yes
11[630]9[643]	CAACAGTCGTCAAACAAAAACAGGAAGA	basics	no	no	no	yes	yes	yes	yes
11[966]9[979]	TATTTGCGCGCTCAGGCACCGCTTCTGG	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
5[154]1[175]	GCTAATATCAGAGAGATAA CCCTGGCATAATAATAA	basics	no	no	no	yes	yes	yes	yes
12[1014]9[1007]	AACATAGCGATTATGAAACA CCAGAACGCCATTCG	basics	no	no	no	yes	yes	yes	yes
11[882]9[895]	ATGATGGGCGTATTGGCGC ATCGTAACC	basics	no	no	no	yes	yes	yes	yes
12[699]9[692]	CAAATTCGGTGAATCTTTTG CAAAAGAATAAAATT	basics	no	no	no	yes	yes	yes	yes
12[384]9[377]	ATTAAACATAGCAAGCTCCT TTTGATAATAAATGC	basics	no	no	no	yes	yes	yes	yes
12[909]9[902]	TATATAAGAAGTTTCAGGAC GTTGGGAAGTGCATC	basics	no	no	no	yes	yes	yes	yes
12[720]9[713]	TTTAGTAGATACCGAAAAAC CAAAATAGGTTAAAT	basics	no	no	no	yes	yes	yes	yes
3[329]0[336]	AGTTTTACAGGAGGAGCCG CCACCCTCACGTCACC	basics	no	no	no	yes	yes	yes	yes
12[678]9[671]	CCAACGCGGTTTATCAGAG GGGGTAATATTGTAAA	basics	no	no	no	yes	yes	yes	yes
11[735]9[748]	TATTAGACGAAATCGGAAC GCCATCAAA	basics	no	no	no	yes	yes	yes	yes
11[819]9[832]	CATTTTGTCACCGCGGATT CTCCGTGGG	basics	no	no	no	yes	yes	yes	yes
5[251]0[248]	CCCCCTTATTTCATCGGCA	basics	no	no	no	yes	yes	yes	yes
8[349]3[342]	TTAGAGCGAGCCATCCGGA AAGAACCGCGCCGCCAGC ATTGAACGGGGT	basics	no	no	no	yes	yes	yes	yes
7[125]12[132]	TTTATGAAAAAACGTAGAAA ATAGCGTCTTTCCATTT	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
12[888]9[881]	TGATGCAGACTAAACTACGTTAATAAAAGTAGATG	basics	no	no	no	yes	yes	yes	yes
1[336]3[349]	CAGAACCGCCACCCGCCTATTCAGTGCC	basics	no	no	no	yes	yes	yes	yes
12[741]9[734]	ATAATTAAATGACACCTCGTTTACCAGAACCAATA	basics	no	no	no	yes	yes	yes	yes
11[252]9[265]	CTACATTCGCCAGAAGCCTCAGAGCATA	basics	no	no	no	yes	yes	yes	yes
12[237]9[230]	GACTTGCTATGGTTAACGAGTAGATTTAGCAAAGA	basics	no	no	no	yes	yes	yes	yes
11[273]9[286]	TCTGAAAGGATTTTATCGGTTGTACCAA	basics	no	no	no	yes	yes	yes	yes
11[987]9[1000]	TAAAGAACTAACTCAACCAGGCAAAGCG	basics	no	no	no	yes	yes	yes	yes
8[142]9[139]	TGTTTAACGTCAAAATTTTTTCATATTATT	basics	no	no	no	yes	yes	yes	yes
0[132]1[146]	GCAGCCTTTACATTTTTTGAGAGAATAACATAAACAAAGTTACC	basics	no	no	no	yes	yes	yes	yes
3[350]0[357]	TTGAGTACAGAGCCCACCCTCAGAGCCATACCATT	basics	no	no	no	yes	yes	yes	yes
11[546]9[559]	CAGCAGCCCGTAAAGGAGCAAACAAGAG	basics	no	no	no	yes	yes	yes	yes
12[216]9[209]	CCTTAAATCACAATCATTAGATACATTTCCAATAA	basics	no	no	no	yes	yes	yes	yes
11[420]9[433]	TTAATGCTGTAGCGAAGGCCGGAGACAG	basics	no	no	no	yes	yes	yes	yes
11[924]9[937]	ACTTCTGGCTGCATACAGTATCGGCCTC	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
12[258]9[251]	AGGCGTTACAAAAGCAGTTGATTCCCAAGCAATAA	basics	no	no	no	yes	yes	yes	yes
11[462]9[475]	TACCGAAAGGGAAGCGTTCTAGCTGATA	basics	no	no	no	yes	yes	yes	yes
12[174]8[168]	TTTATCCTATAAAATATTTTC	basics	no	no	no	yes	yes	yes	yes
11[1050]9[1063]	CATCGGGAATTCCAGCCTCTTCGCTATT	basics	no	no	no	yes	yes	yes	yes
0[385]5[378]	TTTTTTTCAGCAGTAGCACCATCCACCCTCAGAGTTT	basics	no	no	no	yes	yes	yes	yes
11[861]9[874]	CATCATATTTTTCTTAGGTCACGTTGGT	basics	no	no	no	yes	yes	yes	yes
12[1056]9[1049]	TAAATCGTCATCGCTAACAAAGCTGCTCGGTGCGG	basics	no	no	no	yes	yes	yes	yes
11[441]9[454]	CTAAAACGGGCGCTACCATCAATATGAT	basics	no	no	no	yes	yes	yes	yes
11[945]9[958]	TAGAACCGTCGGGATCGCACTCCAGCCA	basics	no	no	no	yes	yes	yes	yes
11[378]9[391]	GAATACGTAATGCGAATGCCTGAGTAAT	basics	no	no	no	yes	yes	yes	yes
12[573]9[566]	ACCGACAGCGGAGTACGAGAATGACCATAATCGAT	basics	no	no	no	yes	yes	yes	yes
11[483]9[496]	AAGATAAGGCGAACGCCGGAGAGGGTAG	basics	no	no	no	yes	yes	yes	yes
12[594]9[587]	AGTAATAACAACTAATGCTTTAAACAGTAAACTAG	basics	no	no	no	yes	yes	yes	yes
8[307]3[300]	TTTAAATGGAAATTTCAGTAGGAGCCACGCCTTGATATTCACATGGCTT	basics	no	no	no	yes	yes	yes	yes
1[257]2[		basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
254]	GTGCCGTCGTTTGCTCAGT AC								
11[504]9 [517]	GGTCAGTTAGAGCTTGAGA GATCTACAA	basics	no	no	no	yes	yes	yes	yes
12[762]9 [755]	ATAAGAACGCATAATAAGA GCAACACTAAATAATT	basics	no	no	no	yes	yes	yes	yes
12[930]9 [923]	AACCTCCAAATACGGAACT GGCTCATTAGACGACG	basics	no	no	no	yes	yes	yes	yes
0[146]5[146]	AGTATGTTAGCATAAAAGTC AGAGGGTA	basics	no	no	no	yes	yes	yes	yes
12[783]9 [776]	GTGTGATCGCTGAGAAAAG GAATTACGACTGTAGC	basics	no	no	no	yes	yes	yes	yes
7[147]0[154]	ACATACATAAAGGTACTCCT T	basics	no	no	no	yes	yes	yes	yes
12[825]9 [818]	TTTCATCGTCACCCATTTAG GAATACCAACCCGTC	basics	no	no	no	yes	yes	yes	yes
12[846]9 [839]	TTTCAAACAGCATCTAGAAA GATTCATCAACAAAC	basics	no	no	no	yes	yes	yes	yes
1[294]3[307]	TAGGTGTATCACCGGAGGC TGTTGATGA	basics	no	no	no	yes	yes	yes	yes
12[279]9 [272]	ATCCGGTGATTGAGTGGAA GTTTCATTCAAGCTAA	basics	no	no	no	yes	yes	yes	yes
11[525]9 [538]	CAACAGTCCCTAAACAGGT CATTGCCTG	basics	no	no	no	yes	yes	yes	yes
2[371]0[350]	TTTTAAACAGTTAATGCCCC CTTCAGAACAGCAAGG	basics	no	no	no	yes	yes	yes	yes
3[287]0[294]	GTCATACAAACAAAAATCAC CGGAACCACGACAGA	basics	no	no	no	yes	yes	yes	yes
11[588]9		basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
[601]	CAAATATACGTGAACATGTC AATCATAT								
11[903]9 [916]	AATCCTGACGCGCGTGCCA GTTTGAGGG	basics	no	no	no	yes	yes	yes	yes
12[230]1 1[237]	GGGAGGTGCAACAGGAAAA AC	basics	no	no	no	yes	yes	yes	yes
4[146]5[132]	CAAGAAACAATGAAATACT GAACTTTTTTACCCTGAAC	basics	no	no	no	yes	yes	yes	yes
12[321]9 [314]	ATTACCGAAAGGTGGTAGC TCAACATGTCTTTTGC	basics	no	no	no	yes	yes	yes	yes
11[168]9 [181]	AACTCAACAATACTGGCAT CAATTCTAC	basics	no	no	no	yes	yes	yes	yes
8[167]8[143]	ATTTGGGGCGCGAGAAACG ATTTTT	basics	no	no	no	yes	yes	yes	yes
1[273]3[286]	TGATATAAGTATAGAAGGAT TAGTAAGC	basics	no	no	no	yes	yes	yes	yes
11[1008] 9[1021]	CAGGTTTCTGGGGTCCATT CAGGCTGCG	basics	no	no	no	yes	yes	yes	yes
11[1029] 9[1042]	ATACAGTCGGAAGCTGGGA AGGGCGATC	basics	no	no	no	yes	yes	yes	yes
5[147]1[160]	ATTGAGCATTACGCAGAAG GAAACCGAG	basics	no	no	no	yes	yes	yes	yes
12[300]9 [293]	CAAATCATATTGACATGCAA CTAAAGTAAAACATT	basics	no	no	no	yes	yes	yes	yes
11[357]9 [370]	CCTTCTGGTACTATACCCTC ATATATTT	basics	no	no	no	yes	yes	yes	yes
12[468]9 [461]	AAAAATACAGCCCTAATATC GCGTTTTAATTCAAC	basics	no	no	no	yes	yes	yes	yes
11[132]1		basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
2[147]	TTTGAGCCTAATTTGCCTCA CTTGCCTGATACCAACGCT AACG								
11[693]9 [706]	GATTAGAGATAGGGCGCAT TAAATTTTT	basics	no	no	no	yes	yes	yes	yes
10[237]7 [244]	TTTTATAATTAGCAAAATTA ATTCTGCGTACCAGC	basics	no	no	no	yes	yes	yes	yes
9[140]9[167]	TATCCCAATCCAAATAAGCT GAAAAGGT	basics	no	no	no	yes	yes	yes	yes
8[286]3[279]	CGGTGTCGGAGGGATTGC CTTTAATCAATAAATCCTCA TTAACCGTTCC	basics	no	no	no	yes	yes	yes	yes
3[114]3[146]	TTTAGACGGGAGAATTAAG CAATAGCTATCTTA	basics	no	no	no	yes	yes	yes	yes
12[209]8 [217]	TCAAGATACAATATTACCGC CCGAGTAAATCATACAGGC AAGGTTTGAC	basics	no	no	no	yes	yes	yes	yes
12[510]9 [503]	AGAACGCTTCCAGAGGATT GCATCAAAACTATTTT	basics	no	no	no	yes	yes	yes	yes
11[189]8 [196]	TGGTAATCACGCAAAGTAG CATTAACATCGCAAAT	basics	no	no	no	yes	yes	yes	yes
11[651]9 [664]	GAAGGTTATTAAAGAGCAA ATATTTAAA	basics	no	no	no	yes	yes	yes	yes
11[714]9 [727]	ATACATTTAAATCACAGCTC ATTTTTTA	basics	no	no	no	yes	yes	yes	yes
12[531]9 [524]	AACAACATTTTCTGTATTAT AGTCAGAAAGGCTAT	basics	no	no	no	yes	yes	yes	yes
12[489]9 [482]	AATAGATCGATCTAGAGGA AGCCCGAAAAATTAAT	basics	no	no	no	yes	yes	yes	yes
12[552]9 [545]	TCTGTCCAAACAACAAATCA GGTCTTTAAGAGTCT	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
11[567]9[580]	AAGCATCAAGTTTTGAACGGTAATCGTA	basics	no	no	no	yes	yes	yes	yes
12[342]9[335]	TTTATTTCCGACTTTTAATTGCTGAATATTTCAAC	basics	no	no	no	yes	yes	yes	yes
11[294]9[307]	TGGCAGATAAACAGATGACCCTGTAATA	basics	no	no	no	yes	yes	yes	yes
12[363]9[356]	ATCGAGATTAGAGCTTTTTGCGGATGGCTTTTAGA	basics	no	no	no	yes	yes	yes	yes
4[378]3[371]	TTTCCGCCACCAGAACCACCACACAGTGCCCGTATTT	basics	no	no	no	yes	yes	yes	yes
11[777]9[790]	TTGCCCGTGGTTTGCAGCTTTCATCAAC	basics	no	no	no	yes	yes	yes	yes
12[972]9[965]	AGTGAATGAGGCAAATTTCAACTTTAATGCTTTCC	basics	no	no	no	yes	yes	yes	yes
1[357]1[385]	CGCCACCCTCAGAGCCACCACCCTCATTT	basics	no	no	no	yes	yes	yes	yes
11[798]9[811]	TAAAAGTGTTGCAGGTGAGCGAGTAACA	basics	no	no	no	yes	yes	yes	yes
8[328]3[321]	TAATGCTAATTATCCCATCGACCCTCAGTTGAGGCAGGTCAGGTGTACT	basics	no	no	no	yes	yes	yes	yes
12[993]9[986]	AAGACGCACACTCAAATTGGGCTTGAGATGCCGGA	basics	no	no	no	yes	yes	yes	yes
11[756]9[769]	CGACAACAATCCTGCGCGTCTGGCCTTC	basics	no	no	no	yes	yes	yes	yes
12[951]9[944]	GGTCTGAAGGCACCAATTACCTTATGCGAGGAAGA	basics	no	no	no	yes	yes	yes	yes
12[405]9[398]	CTTATCACATGTACGATTAGAGAGTACCGTGTAGG	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
12[867]9[860]	ACAAAGAAACGGCTACGGAACAACATTAAATGGGA	basics	no	no	no	yes	yes	yes	yes
4[170]3[153]	TTGAGTTAAGCCCAATAATAAGAGCCGAAGC	basics	no	no	no	yes	yes	yes	yes
12[426]9[419]	ATCAATATCGTCACAAGCAAACTCCAACGGTGAGA	basics	no	no	no	yes	yes	yes	yes
8[265]0[273]	CATATAAGGCGACAAGCGCGTTTAGCGTTTGCCATCTTTTCATAGCGTC	basics	no	no	no	yes	yes	yes	yes
10[167]10[128]	TCTTTGATTAGTAATAACAAGTTACAAAATAAACAGCTTT	basics	no	no	no	yes	yes	yes	yes
2[151]2[114]	AAGTAAGCAGATAGCCGAAAACAGGGAAGCGCATTTTT	basics	no	no	no	yes	yes	yes	yes
3[308]0[315]	TACAGGAACGATTGCACCGGAACCGCCTTAGCAGC	basics	no	no	no	yes	yes	yes	yes
10[293]12[280]	GAGGCCGATTAAAGTGGATTAAAGGCTT	basics	no	no	no	yes	yes	yes	yes
8[916]11[923]	TACCAGTCCATTAAACGGGTAGGCTTAGGGATTAT	basics	no	no	no	yes	yes	yes	yes
10[965]12[952]	CTGCCCGCTTTCCATACCATAAATCATA	basics	no	no	no	yes	yes	yes	yes
8[685]11[692]	GTTTTGCCAGCTTGCTTTCGATTACCAGACTAATA	basics	no	no	no	yes	yes	yes	yes
10[1028]12[1015]	ATAAAGTGTAAAGCAACGTCACCTTGAA	basics	no	no	no	yes	yes	yes	yes
2[321]11[314]	CATGAAAGTATTAATACTCAGACCGTAAATTCATTCGCCCAAGTCACAC	basics	no	no	no	yes	yes	yes	yes
8[391]11		basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
[398]	TTTAATTGCCCAATAGGAAC CTTCCAAGGACAATA								
10[608]12[595]	GGCGATGGCCCACTCAAAC CCTCGAGCC	basics	no	no	no	yes	yes	yes	yes
8[622]11[629]	TCATAAATTTTCACGTTGAA ACCAACATGGCAAAT	basics	no	no	no	yes	yes	yes	yes
10[671]12[658]	AACAAGAGTCCACTATCTAA ATAGGGCT	basics	no	no	no	yes	yes	yes	yes
8[979]11[986]	TGGTTTAAAGAATACACTAA ATGAGAAGACAGAAA	basics	no	no	no	yes	yes	yes	yes
8[475]11[482]	GACTTCACATAGTTAGCGT AAAAGTCCTCCAGCAG	basics	no	no	no	yes	yes	yes	yes
2[300]11[293]	AGACTCCTCAAGAGCCCGG AAATCAAGTAGGTAAAGATA TAGTTTACAT	basics	no	no	no	yes	yes	yes	yes
10[503]12[490]	TGACGGGGAAAGCCAACAG AGTATCAAC	basics	no	no	no	yes	yes	yes	yes
7[350]11[356]	TTGGGAAACAAGCAATAGA AC	basics	no	no	no	yes	yes	yes	yes
10[335]12[322]	TAACGTGCTTTCCTAATAAA AAGGAATC	basics	no	no	no	yes	yes	yes	yes
10[1091]12[1078]	TAGCTGTTTCCTGTTGATTG CTATATGT	basics	no	no	no	yes	yes	yes	yes
10[692]12[679]	TTGAGTGTTGTTCCACTAAC ATATAAAG	basics	no	no	no	yes	yes	yes	yes
10[755]12[742]	TTTGATGGTGGTTCCTTTAC ACGGAATC	basics	no	no	no	yes	yes	yes	yes
10[419]12[406]	GTCACGCTGCGCGTATGGC TAGTCTTTC	basics	no	no	no	yes	yes	yes	yes
10[398]1		basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
2[385]	ACACCCGCCGCGCTTGGCA CAAACGGGT								
10[797]12[784]	CAAGCGGTCCACGCAACGT TAACCGACC	basics	no	no	no	yes	yes	yes	yes
10[482]12[469]	GTGGCGAGAAAGGACGAA CCAGAACAAG	basics	no	no	no	yes	yes	yes	yes
7[245]11[251]	GCCAAAGTTAGCGAGAAAT AC	basics	no	no	no	yes	yes	yes	yes
10[734]12[721]	GGCAAAATCCCTTATGAGG ATAAGCCTG	basics	no	no	no	yes	yes	yes	yes
8[496]11[503]	AGATTAAAAGTTTTGTCGTC TGCCTGTTGTGAGGC	basics	no	no	no	yes	yes	yes	yes
8[1042]11[1049]	ATTCAGTAACGGAGATTTGT ATCGCTATCCTTTTA	basics	no	no	no	yes	yes	yes	yes
10[566]12[553]	TTGGGGTCGAGGTGAAATG AAAAGTAAT	basics	no	no	no	yes	yes	yes	yes
8[412]11[419]	AGGTCAGCGTAACACTGAG TTATCGGCTTTAGTCT	basics	no	no	no	yes	yes	yes	yes
8[664]11[671]	GTAAAATCCTTTAATTGTAT CTCAACAGATATCTT	basics	no	no	no	yes	yes	yes	yes
10[839]12[826]	CAGCTGATTGCCCTCGGAA CATAGTTAA	basics	no	no	no	yes	yes	yes	yes
8[181]11[188]	TTAGCTAGAAACGCAAAGA CACACCCAGGCCTTGC	basics	no	no	no	yes	yes	yes	yes
10[188]12[175]	ATTAACCGTTGTAGACTATC GCTACAAT	basics	no	no	no	yes	yes	yes	yes
10[440]12[427]	AGGGCGCTGGCAAGGCGA ACTGAAACCA	basics	no	no	no	yes	yes	yes	yes
10[860]1		basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
2[847]	TTTCACCAGTGAGAAGGAG CGAAAACTT								
2[279]11 [272]	AGGATTAGCGGGGTAGAG GGTAGACTGTTTCAACCATT CTAATCAATCG	basics	no	no	no	yes	yes	yes	yes
8[706]11 [713]	CGAGAGGTTCTTAAACAGC TTTCATATGATAGATA	basics	no	no	no	yes	yes	yes	yes
8[454]11 [461]	ATTCGAGTAGCATTCCACA GAATATCCCTTAAAAA	basics	no	no	no	yes	yes	yes	yes
10[314]1 2[301]	ATCAGAGCGGGAGCTTCAC CATAGCAAG	basics	no	no	no	yes	yes	yes	yes
8[1000]1 1[1007]	AGTAGTATCTTTGACCCCC AGCGATAGCAGATTTT	basics	no	no	no	yes	yes	yes	yes
8[790]11 [797]	TAACGCCGCTTGCAGGGAG TTTTGAAATTTAATTT	basics	no	no	no	yes	yes	yes	yes
10[629]1 2[616]	GGGCGAAAAACCGTGTCAG TTGTAATTT	basics	no	no	no	yes	yes	yes	yes
10[251]1 2[238]	ATCCTGAGAAGTGTGCTCA TGACCTCCC	basics	no	no	no	yes	yes	yes	yes
10[923]1 2[910]	TAATGAATCGGCCAATTGTT TGTTGGGT	basics	no	no	no	yes	yes	yes	yes
8[811]11 [818]	CATTCAAGCTTTTGCGGGA TCTTCTGACACATTAT	basics	no	no	no	yes	yes	yes	yes
8[559]11 [566]	AAATCAATTTCAACAGTTTC AAAAGGTAAAATCTA	basics	no	no	no	yes	yes	yes	yes
8[580]11 [587]	TCAGAAAGAGAATAGAAAG GAAGAGAATTGAACCT	basics	no	no	no	yes	yes	yes	yes
2[342]11 [335]	TCGGAACCTATTATCCACC CTAATGAAAACCGTCATCAT CGTGGGACAT	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
10[461]12[448]	AAAGCGAAAGGAGCATCGCCAATCCTAA	basics	no	no	no	yes	yes	yes	yes
10[1070]12[1057]	TGTTATCCGCTCACAGAAACAGCTTCTG	basics	no	no	no	yes	yes	yes	yes
10[524]12[511]	GGGAGCCCCCGATTATTAACACTAATGC	basics	no	no	no	yes	yes	yes	yes
10[818]12[805]	CTGGCCCTGAGAGATTGAGTACTAAATT	basics	no	no	no	yes	yes	yes	yes
10[986]12[973]	ACATTAATTGCGTTACGTAAAAGTCAAT	basics	no	no	no	yes	yes	yes	yes
1[161]11[167]	GAAACGCGATTAAGGGCAACATGAATCTGTAGAAG	basics	no	no	no	yes	yes	yes	yes
8[1063]11[1077]	ATCAACGCTGATAAATTGTGTTAACCTTATAACGGATTCGCC	basics	no	no	no	yes	yes	yes	yes
8[601]11[608]	CCCTCAAAAGGAATTGCGAATGGCATTTTCAATCA	basics	no	no	no	yes	yes	yes	yes
8[517]11[524]	GCAAAGCCGTTAGTAAATGAATGTTCAGCCGCCTG	basics	no	no	no	yes	yes	yes	yes
8[538]11[545]	CCCTGACTATGGGATTTTGCTAGACGACTGAGAGC	basics	no	no	no	yes	yes	yes	yes
10[356]12[343]	GGTTGCTTTGACGAAACAGAGAGCCGTT	basics	no	no	no	yes	yes	yes	yes
8[370]11[377]	GAGGTCACAGCAAAATCACGGCAAGTACAGCGTAA	basics	no	no	no	yes	yes	yes	yes
10[902]12[889]	GGGAGAGGCGGTTTCAATTCATAAATGC	basics	no	no	no	yes	yes	yes	yes
8[895]11[902]	GAAAAATGACTTTTTCATGAGCTATATGTCAATAT	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
8[832]11[839]	AGTTGAGTCAGCAGCGAAAGATATATTTAAGAAAC	basics	no	no	no	yes	yes	yes	yes
8[769]11[776]	GGCATAGCCGATATATTCGGTAAATAAGAAATCCT	basics	no	no	no	yes	yes	yes	yes
10[209]12[196]	AAGAGTCTGTCCATATCCAGATAGTTGC	basics	no	no	no	yes	yes	yes	yes
10[881]12[868]	GGGCGCCAGGGTGGTTCCTGATCGCAAG	basics	no	no	no	yes	yes	yes	yes
8[748]11[755]	TCATAACACAACCATCGCCCATAAACACAACAATT	basics	no	no	no	yes	yes	yes	yes
8[727]11[734]	CGACGATATAGTTGCGCCGACCTAGAAATTAGAAG	basics	no	no	no	yes	yes	yes	yes
8[643]11[650]	GCGTCCAAAAAAAAGGCTCCAGAATCGCAATTGAG	basics	no	no	no	yes	yes	yes	yes
8[1021]11[1028]	CTGACGAACCAAGCGCGAAACTTAGAATGATGAAT	basics	no	no	no	yes	yes	yes	yes
10[1049]12[1036]	CACAACATACGAGCAACAGTATAATTAA	basics	no	no	no	yes	yes	yes	yes
8[433]11[440]	AGACCGGCAGTACAAACTACAGCATGTAGATAGCC	basics	no	no	no	yes	yes	yes	yes
10[650]12[637]	AACGTGGACTCCAATGAAAGGCATATTT	basics	no	no	no	yes	yes	yes	yes
10[587]12[574]	CCATCACCCAAATCACCTTGCATAAAGT	basics	no	no	no	yes	yes	yes	yes
10[1007]12[994]	GCCTAATGAGTGAGATTGCGTTTAGATT	basics	no	no	no	yes	yes	yes	yes
8[958]11[965]	CATTGTGAACCTAAAACGAAATTATCAATCAAAAT	basics	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
10[944]12[931]	AACCTGTCGTGCCAAATAATGCCTTTTT	basics	no	no	no	yes	yes	yes	yes
8[937]11[944]	ATTTTAATAATGCCACTACGAGAGACTAGAAGGGT	basics	no	no	no	yes	yes	yes	yes
8[874]11[881]	CGAACTAACAGAGGCTTTGAGAATCCAATTATCAG	basics	no	no	no	yes	yes	yes	yes
10[377]12[364]	CCGCTACAGGGCGCACCTGAACGCACTC	basics	no	no	no	yes	yes	yes	yes
10[776]12[763]	CCCCAGCAGGCGAATCGTATTGCGTTAA	basics	no	no	no	yes	yes	yes	yes
10[713]12[700]	AAAGAATAGCCCGAGCCGTCACGTTATA	basics	no	no	no	yes	yes	yes	yes
10[272]12[259]	AGACAGGAACGGTATTGACGCGAACGCG	basics	no	no	no	yes	yes	yes	yes
10[545]12[532]	GCACTAAATCGGAAGCCACGCGACAATA	basics	no	no	no	yes	yes	yes	yes
8[853]11[860]	TTACAGGGGAACGAGGGTAGCACGCGAGGAATTAT	basics	no	no	no	yes	yes	yes	yes
10[230]12[217]	ATCAGTGAGGCCACAGCCATTTTTGAAG	basics	no	no	no	yes	yes	yes	yes
7[1099]11[1171]	TAGCCGGAACGAGGTTTTTAATCGCGCATTtaagtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
7[1078]11[1174]	CGCGACCTGCTCCAAAATCAATTTGAATTTtaagtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
10[1133]12[1169]	GAGGATCCCCGGGTATTATTCCATTTGATTtaagtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
12[1098]9[1175]	AGTACATTGTTACTGTAATCTTGACAAGATGTGCTTTtaag	A655 Marker Extensions	no	no	no	yes	yes	yes	yes

Oligo	Sequence	Staple	Figure						
Position		Type	1	7	8	9A,B	9C,D	10A,B	10C,D
	TTGACAAGATGTGCTTTtaag tgagacccgtacatat								
11[1113] 8[1160]	GAGGCGAACCGAGCACGC CAGGGTTTTCCGCATAGTTt aagtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
8[1159]7 [1158]	TTTAGAGGACAGATGAACG ACTGACCAACTTTGAATTtaa gtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
12[1166] 11[1165]	TTTACATCAAGAAAACAAAG AAGATGATGAAACAATTtaag tgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
10[1112] 12[1172]	TCGAATTCGTAATCTACAAA ATGGAAACTTtaagtgagacccgt acatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
10[1162] 12[1167]	TTTCAAGCTTTGCCTGCAG GTCAGCAAAAATTAATTTTta agtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
7[1120]11 1[1168]	GGTCAATCATAAGGACAAT TTATTTCAATTtaagtgagacccg tacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
10[1077] 8[1166]	GTGAAATCTGGCGAAAGGG GGAACCGGATTtaagtgagacc cgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
12[1140] 9[1169]	ACATTTAGAACCGAGTGTA CAGACCAGGCCAGTCATTta agtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
12[1119] 9[1172]	ATTACCTCGCAGACGCTGG CTGACCTTCTTGGGTATTtaa gtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
11[1092] 8[1163]	ACCAAGTATGGTCAGCAAG GCGATTAAGATCAAGATTta agtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes
11[1134] 9[1161]	TTACCTGGACTCTACGACG TTGTAAAACGACGGCCAGT GCTTtaagtgagacccgtacatat	A655 Marker Extensions	no	no	no	yes	yes	yes	yes

Additional Staple Strands

[0108]

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
Base Plate	10[39]12 [40]	Dock Left 3' A565	GCTATTACGGCGATT AAGTTGGGTGGCCAA CG TT TT ATACAACTAT T [ATTO565]	no	yes	no	no	no	yes	no
Base Plate	10[167] 12[168]	Dock Right 3' A647N	GGCCTCAGGTTTCCT GTGTGAAAGAGCCGG TT TT ATACAACTAT T [ATTO647N]	no	yes	no	no	no	yes	no
6hb Arm Lin	4[102]3 [90]	A488 Donor	[Alexa488] TT TTTCTGAATTGTCAAC CTTTTAAGTG	no	yes	no	no	no	no	no
6hb Arm Lin	2[105]3 [121]	Dock arm 8nt	TTTAACAGCAGTTGC TCCTTAGTG TT ATAGTTGT	no	yes	no	no	no	no	no
6hb Arm Lin	2[105]3 [121]	Dock arm 9nt	TTTAACAGCAGTTGC TCCTTAGTG TT ATAGTTGTA	no	yes	no	no	no	no	no
6hb Arm Lin	2[105]3 [121]	Dock arm 10nt	TTTAACAGCAGTTGC TCCTTAGTG TT ATAGTTGTAT	yes	yes	no	no	no	no	no
Base Plate	10[39]12 [40]	Dock Left 3'	GCTATTACGGCGATT AAGTTGGGTGGCCAA CG TT TT ATACAACTAT	no	no	no	yes	no	no	no
Base Plate	10[167] 12[168]	Dock Right 3'	GGCCTCAGGTTTCCT GTGTGAAAGAGCCGG TT TT ATACAACTAT	no	no	no	yes	no	no	no
Base Plate	2[71]4 [72]	Dock Up 3'	AAATGTTTAAATCAAA AATCAGGGCTGTAG TT TT ATACAACTAT	no	no	no	no	no	no	no
Base Plate	16[71]18 [72]	Dock Down 3'	TCCTGAGATCACTTG CCTGAGTAGTGGCAC TT TT ATACAACTAT	no	no	no	no	no	no	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
Base Plate	12[39]14[40]	Unzip Dock Left 20nt 5'	GGAAGTTGAGATGGTAGAGG TT GCAAGGTGGCTT CGCGGGGAGTTTTTC TTTTCACCATTTTTTG G	no	no	no	no	yes	no	no
Base Plate	10[39]12[40]	Unzip Dock Left helper	GCTATTACGGCGATTAAGTTGGGTGGCCAACG TT GCCACCTTGC	no	no	no	no	yes	no	no
Base Plate	12[167]14[168]	Unzip Dock Right 20nt 5'	GGAAGTTGAGATGGTAGAGG TT GCAAGGTGGCTT AAGCATAACCGAAAT CGGCAAAAGGGTTGA	no	no	no	no	yes	no	no
Base Plate	10[167]12[168]	Unzip Dock Right helper	GGCCTCAGGTTTCCTGTGTGAAAGAGCCGG TT GCCACCTTGC	no	no	no	no	yes	no	no
6hb Arm HT	4[231]	A488 Donor HT	[Alexa488] TT CTGAATTGTCAACCTTATGACAATGT	no	no	no	no	no	yes	no
6hb Arm HT	2[253]	Dock arm 9nt HT	CAGGAGTTCCCACTGAGACTTAAGTGTCCTTAGTG TT ATAGTTGTA	no	no	no	yes	no	yes	no
6hb Arm HT	2[253]	Unzip Dock Arm 20nt HT	TTAAAGGCCGCTAACAGCAGTTGCTCCTTAGTG TTGCTAGCACGC TT	no	no	no	no	yes	no	no
			CCTCTACCATCTCAACTTCC							
6hb Arm HT	4[231]	Unzip Dock Arm 20nt helper	GCGTGCTAGCTTCATGGCTTTTGATGATACAGGAGTGT	no	no	no	no	yes	no	no
CQO_Parking1 6A	10[39]	Park12 ntLeft	AGATGGTAGAGG TT GCTATTACGGCGATTAAGTTGGGTGGCCAACG	no	no	no	no	no	no	no
CQO_Par	10[167]	Park12 ntRight	AGATGGTAGAGG	no	no	no	no	no	no	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
king1 2nt			TT GGCCTCAGGTTT CCTGTGTGAAAGAGC CGG							
CQO _Par king1 6A	10[39]	Park16 A 10[39]	AAAAAAAAAAAAAAAA CC GCTATTACGGCG ATTAAGTTGGGTGGC CAACG	no	no	no	no	no	no	no
CQO _Par king1 6A	10[167]	Park16 A10[16 7]	AAAAAAAAAAAAAAAA CC GGCCTCAGGTTT CCTGTGTGAAAGAGC CGG	no	no	no	no	no	no	no
CQO _Par king1 6A	12[39]	Park16 A 12[39]	AAAAAAAAAAAAAAAA CC CGCGGGGAGTTT TTCTTTTCACCATTTT TTGG	no	no	no	no	no	no	no
CQO _Par king1 6A	12[167]	Park16 A12[16 7]	AAAAAAAAAAAAAAAA CC AAGCATAACCGA AATCGGCAAAAGGGT TGA	no	no	no	no	no	no	no
CQO _Par king1 6A	20[103]	Park16 A20[10 3]	AAAAAAAAAAAAAAAA CC TCAATAGATTCCT GATTATCAGATGATG GCAA	no	no	no	no	no	no	no
CQO _Par king1 6A	18[71]	Park16 A 18[71]	AAAAAAAAAAAAAAAA CC AGACAATAAGAG GTGAGGCGGTCTTAG AAG	no	no	no	no	no	no	no
CQO _Par king1 6A	16[167]	Park16 A16[16 7]	AAAAAAAAAAAAAAAA CC GAGCACGTTGGA AATACCTACATACATT GG	no	no	no	no	no	no	no
CQO _Par king1 6A	2[71]	Park16 A2[71]	AAAAAAAAAAAAAAAA CC AAATGTTTAAATC AAAAATCAGGGCTGT AG	no	no	no	no	no	no	no
CQO _Par king1 6A	6[39]	Park16 A6[39]	AAAAAAAAAAAAAAAA CC TTAAATGCAAAAG GGTGAGAAAGGTGTT AAAT	no	no	no	no	no	no	no
CQO _Par	14[39]	Park16 A 14[39]	AAAAAAAAAAAAAAAA	no	no	no	no	no	no	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
king1 6A			CC GGTCGAGGGGG AGCCCCCGATTTAGT GAGGCC							
CQO _Par king1 6A	16[39]	Park16 A16[39]	AAAAAAAAAAAAAAAA CC ACCGAGTATTGT AGCAATACTTCTAGT CTTTA	no	no	no	no	no	no	no
CQO _Par king1 6A	14[167]	Park16 A14[16 7]	AAAAAAAAAAAAAAAA CC GTGTTGTTACAC CCGCCGCGCTTCTTT GAC	no	no	no	no	no	no	no
CQO _Par king1 6A	19[56]	Park16 A19[56]	AAAAAAAAAAAAAAAA CC GATAAAACTTTTT GAATGGCTATTTTGAT TAGTAATAACA	no	no	no	no	no	no	no
CQO _Par king1 6A	18[103]	Park16 A18[10 3]	AAAAAAAAAAAAAAAA CC TCTGACCTGCAA CAGTGCCACGCTTAG AGCCG	no	no	no	no	no	no	no
CQO _Par king1 6A	19[120]	Park16 A19[12 0]	AAAAAAAAAAAAAAAA CC GCAGCAACTGGC CAACAGAGATATCCA GAACAATATT	no	no	no	no	no	no	no
CQO _Par king1 6A	19[152]	Park16 A19[15 2]	AAAAAAAAAAAAAAAA CC GCTGAACCCCAG TCACACGACCAGACA GGAAAAACGCTCA	no	no	no	no	no	no	no
CQO _Par king1 6A	18[135]	Park16 A18[13 5]	AAAAAAAAAAAAAAAA CC GGGACATTATGA AAAATCTAAAGCATAT CTTT	no	no	no	no	no	no	no
CQO _Par king1 6A	8[39]	Park16 A8[39]	AAAAAAAAAAAAAAAA CC CAGCTCATAATTC GCGTCTGGCCTGCCT CTTC	no	no	no	no	no	no	no
CQO _Par king1 6A	6[159]	Park16 A6[159]	AAAAAAAAAAAAAAAA CC AGCCTCAGAGCA TAAAAATTCTACTAAT AGTA	no	no	no	no	no	no	no
CQO _Par	19[88]	Park16 A 19[88]	AAAAAAAAAAAAAAAA	no	no	no	no	no	no	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
king1 6A			CC CACCGCCTGAAA GCGTAAGAATACGAA GAACTCAAACTAT							
CQO _Par king1 6A	4[39]	Park16 A4[39]	AAAAAAAAAAAAAAAA CC GGTGTCTGCAAT TCTGCGAACGAGCAT ATATT	no	no	no	no	no	no	no
CQO _Par king1 6A	4[103]	Park16 A4[103]	AAAAAAAAAAAAAAAA CC TAGAGCTTTGTTT AGCTATATTTTCCTGT AAT	no	no	no	no	no	no	no
CQO _Par king1 6A	4[167]	Park16 A4[167]	AAAAAAAAAAAAAAAA CC GGTCAGGAGTAG CATTAACATCCAAAAT TA	no	no	no	no	no	no	no
CQO _Par king1	4[135]	Park16 A4[135]	AAAAAAAAAAAAAAAA CC TTTTGATACTGAA AAGGTGGCATCGCTA	no	no	no	no	no	no	no
6A			AATC							
CQO _Par king1 6A	4[71]	Park16 A4[71]	AAAAAAAAAAAAAAAA CC CTCAACATATTAG ATACATTTCGTCAAC GC	no	no	no	no	no	no	no
CQO _Par king1 6A	2[103]	Park16 A2[103]	AAAAAAAAAAAAAAAA CC AAAAGAAGTATA GTCAGAAGCAAAGGA TGGCT	no	no	no	no	no	no	no
CQO _Par king1 6A	18[39]	Park16 A 18[39]	AAAAAAAAAAAAAAAA CC ATGCGCGAATAC CGAACGAACCACCAA CTCGT	no	no	no	no	no	no	no
CQO _Par king1 6A	2[135]	Park16 A2[135]	AAAAAAAAAAAAAAAA CC GATAAAAAAAGAT TAAGAGGAAGCATTG CTCC	no	no	no	no	no	no	no
CQO _Par king1 6A	8[167]	Park16 A8[167]	AAAAAAAAAAAAAAAA CC CATGTCAAGATG GGCGCATCGTACAGT ATC	no	no	no	no	no	no	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
6hb Arm HT	6[224]4 [231]	HTD2_ 0T_5Pr	GCGTGCTAGCTT TTCTGAATTGTCAACC TTATGACAATGT	no	no	no	no	no	no	no
6hb Arm HT	2[253]6 [255]	HTD2_ 16T_3P r	CAGGAGTTCCCACTG AGACTTAAGTGTCCT TAGTGTT TTGCTAGCACGC CC TTTTTTTTTTTTTTT	no	no	no	no	no	no	no
Base Plate	9[120]7 [119]	Plate A655 1	CGGCGGACCCAAAAA CAGGAAGGAGAGGG TTT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base Plate	10[135] 12[136]	Plate A655 2	CCGGCACCCCGAGC TCGAATTCGTTGCCT AATTT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base Plate	8[135]10 [136]	Plate A655 3	AGAAAAGCTTGACCG TAATGGGATCCAGCT TTTT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base Plate	14[159] 13[159]	Plate A655 4	CCAGTTTGGAACAAG ACTGTTTGATGGTGG TTTT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base Plate	10[159] 9[159]	Plate A655 5	GAAGATCGCACTCCA GAGGTCACGTTGGTG TATT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base	14[127]	Plate	CGTGGACTCCAACGT	no	no	no	no	no	no	yes
Plate	13[119]	A655 6	CCACGCTGTT TAAGTGAGACCCGTA CATAT							
Base Plate	6[135]8 [136]	Plate A655 7	GGTTGTACTTTGAGA GATCTACAATGATAAT CTT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
Base Plate	12[135] 14[136]	Plate A655 8	GAGTGAGCCCAGCA GGCGAAAATCGTCCA CTATT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base Plate	16[135] 18[136]	Plate A655 9	CAGAGCGGACCGCC AGCCATTGCATAATA AAATT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base Plate	4[135]6 [136]	Plate A655 10	TTTTGATACTGAAAAG GTGGCATCGCTAAAT CTT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base Plate	14[135] 16[136]	Plate A655 11	TTAAAGAACAAGTGT AGCGGTCACGTTAGA ATTT TAAGTGAGACCCGTA CATAT	no	no	no	no	no	no	yes
Base Plate	12[71]14 [72]	Plate A565 1	TCGTGCCACTGATTG CCCTTCACGCCCACT TT CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
Base Plate	4[71]6 [72]	Plate A565 2	CTCAACATATTAGATA CATTTCGTCAACGCT T CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
Base Plate	10[63]9 [63]	Plate A565 3	AGGGCGATCGGTGC GGTCCTGTAGCCAGC TTTTT CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
Base Plate	14[95]13 [87]	Plate A565 4	GTCTATCAGGGCGAT GCGCCTGGCTT CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
Base Plate	9[88]7 [87]	Plate A565 5	TAACAACCTTTAAATT GTAAACGTATTCAAC CTT CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
Base Plate	14[63]13 [63]	Plate A565 6	CATCACCCAAATCAA GGTGAGACGGGCAA CAGTT CAACCTACTTAACCT	no	no	no	no	no	no	yes
			CCG							
Base Plate	6[71]8 [72]	Plate A565 7	AAGGATAACACCATC AATATGATTAATATTT T CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
Base Plate	10[71]12 [72]	Plate A565 8	TGTTGGGACAGTCAC GACGTTGTAAACCTG TT CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
Base Plate	16[71]18 [72]	Plate A565 9	TCCTGAGATCACTTG CCTGAGTAGTGGCAC TT CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
Base Plate	8[71]10 [72]	Plate A565 10	TTGTTAAACATCAACA TTAAATGGCGCAACT T CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
Base Plate	14[71]16 [72]	Plate A565 11	ACGTGAACGCCGGC GAACGTGGCGCCAG AATT CAACCTACTTAACCT CCG	no	no	no	no	no	no	yes
6hb Arm HT	11[252]	AuNRE xt 1	AAAAAAAACTACATTC GCCAGAAGCCTCAGA GCATA	no	no	no	no	no	no	yes
6hb Arm HT	12[258]	AuNRE xt 2	AAAAAAAAAGGCGTT ACAAAAGCAGTTGAT TCCCAAGCAATAA	no	no	no	no	no	no	yes
6hb Arm HT	11[273]	AuNRE xt 3	AAAAAAAATCTGAAA GGATTTTATCGGTTG TACCAA	no	no	no	no	no	no	yes
6hb Arm	11[168]	AuNRE xt 4		no	no	no	no	no	no	yes

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
HT			AAAAAAAAAACTCAAC AATACTGGCATCAATT CTAC							
6hb Arm HT	12[174]	AuNRE xt 5	AAAAAAAATTTATCCT ATAAAATATTTTC	no	no	no	no	no	no	yes
6hb Arm HT	12[195]	AuNRE xt 6	AAAAAAAATATTTTGC CACGGAGGTCAATAA CCTGTTAATAGT	no	no	no	no	no	no	yes
6hb Arm HT	11[189]	AuNRE xt 7	AAAAAAAATGGTAATC ACGCAAAGTAGCATT AACATCGCAAAT	no	no	no	no	no	no	yes
6hb Arm HT	12[216]	AuNRE xt 8	AAAAAAAACCTTAAAT CACAATCATTAGATAC ATTTCCAATAA	no	no	no	no	no	no	yes
6hb Arm HT	2[279]	AuNRE xt 9	AGGATTAGCGGGGTA GAGGGTAGACTGTTT CAACCATTCTAATCAA TCGAAAAAAAA	no	no	no	no	no	no	yes
6hb	1[161]	AuNRE	GAAACGCGATTAAGG	no	no	no	no	no	no	yes
Arm HT		xt 10	GCAACATGAATCTGT AGAAGAAAAAAAA							
6hb Arm HT	8[181]	AuNRE xt 11	TTAGCTAGAAACGCA AAGACACACCCAGGC CTTGCAAAAAAAA	no	no	no	no	no	no	yes
6hb Arm HT	10[230]	AuNRE xt 12	ATCAGTGAGGCCACA GCCATTTTTGAAGAA AAAAAA	no	no	no	no	no	no	yes
6hb Arm HT	7[245]	AuNRE xt 13	GCCAAAGTTAGCGAG AAATACAAAAAAAA	no	no	no	no	no	no	yes
6hb Arm HT	10[188]	AuNRE xt 14	ATTAACCGTTGTAGA CTATCGCTACAATAAA AAAAA	no	no	no	no	no	no	yes
6hb Arm HT	10[209]	AuNRE xt 15	AAGAGTCTGTCCATA TCCAGATAGTTGCAA AAAAAA	no	no	no	no	no	no	yes

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
6hb Arm HT	10[251]	AuNRE xt 16	ATCCTGAGAAGTGTG CTCATGACCTCCCAA AAAAAA	no	no	no	no	no	no	yes
6hb Arm HT	10[272]	AuNRE xt 17	AGACAGGAACGGTAT TGACGCGAACGCGAA AAAAAA	no	no	no	no	no	no	yes
Base Plate	15[12]14 [12]	Edge Passiva tion 4C	CCCCAATCGGAACCC TAAATGCCGTAAAGC ACTACCCC	no	no	no	no	no	no	yes
Base Plate	6[195]5[195]	Edge Passiva tion 4C	CCCCAAGGCAAAGAA TTAGCAATAAATCATA CAGGCCCCC	no	no	no	no	no	no	yes
Base Plate	23[17]22 [14]	Edge Passiva tion 4C	CCCCACCAAGCGCGA CTTTAATCATCCCC	no	no	no	no	no	no	yes
Base Plate	39[17]38 [17]	Edge Passiva tion 4C	CCCCCAAATATATTTA GAACGCGCCTCCCC	no	no	no	no	no	no	yes
Base Plate	8[195]7 [195]	Edge Passiva tion 4C	CCCCATGAACGGTAA TCGTAGCAAACAAGA GAATCGCCCC	no	no	no	no	no	no	yes
Base Plate	29[17]28 [17]	Edge Passiva tion 4C	CCCCTCATTAAAGCC CCACCCTCAGACCCC	no	no	no	no	no	no	yes
Base Plate	16[195] 15[195]	Edge Passiva tion 4C	CCCCGCGCGTACTAT GGTTGAATGCGCCGC TACAGGCCCC	no	no	no	no	no	no	yes
Base Plate	40[200] 39[200]	Edge Passiva tion 4C	CCCCAAACATAGCGA TAGCTTAGATACCAG TATAAAGCCAACGCC CCC	no	no	no	no	no	no	yes
Base Plate	24[200] 23[200]	Edge Passiva tion 4C	CCCCGCATCGGAACG AGGGTAGCAATGAAC GGTGTACAGACCAGC CCC	no	no	no	no	no	no	yes
Base Plate	28[200] 27[200]	Edge Passiva tion 4C	CCCCTATTCTGAAAC ATGAAAGTACGTAAC GATCTAAAGTTTTGC	no	no	no	no	no	no	yes

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
			CCC							
Base Plate	40[39]42 [17]	Edge Passivation 4C	AACGCGAGATGATGAAACAAACAGGCGAATTATTCATTTCAATTACCTCCCC	no	no	no	no	no	no	yes
Base Plate	33[17]32 [17]	Edge Passivation 4C	CCCCGAAGGAAACCGACCATTACCATCCCC	no	no	no	no	no	no	yes
Base Plate	7[12]6 [12]	Edge Passivation 4C	CCCCTGTAGGTAAAGATTCAATGCCTGAGTAATGCCCC	no	no	no	no	no	no	yes
Base Plate	5[12]4 [12]	Edge Passivation 4C	CCCCATAACAGTTGATTCCGAAGTTTCATTCCATCCCC	no	no	no	no	no	no	yes
Base Plate	42[203] 41[200]	Edge Passivation 4C	CCCCTTTGCACGTAAAACAGAAATTTTTCCCTTAGAATCCTTGACCCC	no	no	no	no	no	no	yes
Base Plate	20[167] 21[198]	Edge Passivation 4C	AGGAATTGAATAATGGAAGGGTTAGAACCTACCATATCACCCC	no	no	no	no	no	no	yes
Base Plate	35[17]34 [17]	Edge Passivation 4C	CCCCACGCTAACGAGCAAAGTTACCACCCC	no	no	no	no	no	no	yes
Base Plate	20[195] 19[195]	Edge Passivation 4C	CCCCCAGTTGGCAAATCAACTCAATCAATATCTGGTCCCC	no	no	no	no	no	no	yes
Base Plate	36[200] 35[200]	Edge Passivation 4C	CCCCGGAATCATTACCGCGCCCAAGCGCATTAGACGGGAGAATTCCCC	no	no	no	no	no	no	yes
Base Plate	34[200] 33[200]	Edge Passivation 4C	CCCCAACTGAACACCCTGAACAAATTATTTTGTCACAATCAATACCCC	no	no	no	no	no	no	yes
Base Plate	1 [8]2[40]	Edge Passivation 4C	CCCCATTACCTTATGCGATTTTAAGAACTG	no	no	no	no	no	no	yes

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
			GCTCAAATACTGC							
Base Plate	41[17]40 [17]	Edge Passivation 4C	CCCCGAGCAAAAGAA GAAAACTTTTTCCCC	no	no	no	no	no	no	yes
Base Plate	4[195]3 [195]	Edge Passivation 4C	CCCCCAGACCGGAA GCAAACGAGCTTCAA AGCGAACCCCC	no	no	no	no	no	no	yes
Base Plate	11[12]10 [12]	Edge Passivation 4C	CCCCGGGGATGTGCT GCAAGCCAGCTGGC GAAAGCCCC	no	no	no	no	no	no	yes
Base Plate	31[17]30 [17]	Edge Passivation 4C	CCCCTAGCAAGGCCG CAAATAAATCCCCCC	no	no	no	no	no	no	yes
Base Plate	3[12]2 [12]	Edge Passivation 4C	CCCCAATCCCCCTCA AATGCATAAATATTCA TTGCCCC	no	no	no	no	no	no	yes
Base Plate	13[12]12 [12]	Edge Passivation 4C	CCCCTTGGGCGCCA GGGTGGAGGCGGTT	no	no	no	no	no	no	yes
			TGCGTACCCC							
Base Plate	14[195] 13[195]	Edge Passivation 4C	CCCCAGAATAGCCCG AGATATCCCTTATAAA TCAAACCCC	no	no	no	no	no	no	yes
Base Plate	27[17]26 [17]	Edge Passivation 4C	CCCCACCGCCACCCT CTTTAATTGTACCCC	no	no	no	no	no	no	yes
Base Plate	22[200] 22[168]	Edge Passivation 4C	CCCCGCGCATAGGCT GGCTGACCTTCATCA AG	no	no	no	no	no	no	yes
Base Plate	32[200] 31[200]	Edge Passivation 4C	CCCCGAAAATTCATA TGGTTTACCTAATCAA AATCACCGGAACCCC CC	no	no	no	no	no	no	yes
Base Plate	9[12]8 [12]	Edge Passivation 4C	CCCCAACGCCATCAA AAATTTTTTAACCAAT AGGCCCC	no	no	no	no	no	no	yes
Base	37[17]36	Edge Passiva		no	no	no	no	no	no	yes

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
Plate	[17]	tion 4C	CCCCGTTTATCAACA GAATCTTACCACCCC							
Base Plate	12[195] 11[195]	Edge Passiva tion 4C	CCCCATTCCACACAA CATACTTGTTATCCG CTCACACCCC	no	no	no	no	no	no	yes
Base Plate	26[200] 25[200]	Edge Passiva tion 4C	CCCCTCGTCTTTCCA GACGTTAGTACCCTC AGCAGCGAAAGACAC CCC	no	no	no	no	no	no	yes
Base Plate	2[195]1 [195]	Edge Passiva tion 4C	CCCCGAATTACGAGG CATAGTACATAACGC CAAAAGCCCC	no	no	no	no	no	no	yes
Base Plate	30[200] 29[200]	Edge Passiva tion 4C	CCCCAGAGCCACCAC CGGAACCGCCTGCCT ATTTCGGAACCTATC CCC	no	no	no	no	no	no	yes
Base Plate	38[200] 37[200]	Edge Passiva tion 4C	CCCCTCAACAGTAGG GCTTAATTGCCGTTTT TATTTTCATCGTACCC C	no	no	no	no	no	no	yes
Base Plate	21[12]20 [12]	Edge Passiva tion 4C	CCCCATTAATTTTAAA AGTCTTTGCCCGAAC GTTCCCC	no	no	no	no	no	no	yes
Base Plate	18[195] 17[195]	Edge Passiva tion 4C	CCCCCTGAAATGGAT TATTTTTTGACGCTCA ATCGTCCCC	no	no	no	no	no	no	yes
Base Plate	19[12]18 [12]	Edge Passiva tion 4C	CCCCACATCGCCATT AAAAACTGATAGCCC TAAACCCC	no	no	no	no	no	no	yes
Base Plate	10[195]9 [195]	Edge Passiva tion 4C	CCCCTTTGAGGGGAC GACGAACCGTGCATC TGCCAGCCCC	no	no	no	no	no	no	yes
Base Plate	25[17]24 [17]	Edge Passiva tion 4C	CCCCTCGGTTTATCA CCCAGCGATTACCCC	no	no	no	no	no	no	yes
Base Plate	17[12]16 [12]	Edge Passivation 4C	CCCCCACGCAAATTA ACCGAAAGAGTCTGT	no	no	no	no	no	no	yes

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
			CCATCCCC							
Base Plate	15[12]14[12]	Edge Passivation 4T	TTTTAATCGGAACCCTAAATGCCGTAAAGCACTATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	6[195]5[195]	Edge Passivation 4T	TTTTAAGGCAAAGAATTAGCAATAAATCATACAGGCTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	23[17]22[14]	Edge Passivation 4T	TTTTACCAAGCGCGACTTTAATCATTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	39[17]38[17]	Edge Passivation 4T	TTTTCAAATATATTTAGAACGCGCCTTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	8[195]7[195]	Edge Passivation 4T	TTTTATGAACGGTAATCGTAGCAAACAAGAGAATCGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	29[17]28[17]	Edge Passivation 4T	TTTTTCATTAAAGCCCCACCCTCAGATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	16[195]15[195]	Edge Passivation 4T	TTTTGCGCGTACTATGGTTGAATGCGCCGCTACAGGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	40[200]39[200]	Edge Passivation 4T	TTTTAAACATAGCGATAGCTTAGATACCAGTATAAAGCCAACGCTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	24[200]23[200]	Edge Passivation 4T	TTTTGCATCGGAACGAGGGTAGCAATGAACGGTGTACAGACCAGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	28[200]27[200]	Edge Passivation 4T	TTTTTATTCTGAAACATGAAAGTACGTAACGATCTAAAGTTTTGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	40[39]42[17]	Edge Passivation 4T	AACGCGAGATGATGAAACAAACAGGCGAATTATTCATTTCAATTACCTTTTT	yes	yes	yes	yes	yes	yes	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
Base Plate	33[17]32[17]	Edge Passivation 4T	TTTTGAAGGAAACCGACCATTACCATTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	7[12]6[12]	Edge Passivation 4T	TTTTTGTAGGTAAAGATTCAATGCCTGAGTAATGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	5[12]4[12]	Edge Passivation 4T	TTTTATAACAGTTGATTCCGAAGTTTCATTCCATTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	42[203]41[200]	Edge Passivation 4T	TTTTTTTGCACGTAAAACAGAAATTTTTCCCTTAGAATCCTTGATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	20[167]21[198]	Edge Passivation 4T	AGGAATTGAATAATGGAAGGGTTAGAACCTACCATATCATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	35[17]34[17]	Edge Passivation 4T	TTTTACGCTAACGAGCAAAGTTACCATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	20[195]19[195]	Edge Passivation 4T	TTTTCAGTTGGCAAATCAACTCAATCAATATCTGGTTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	36[200]35[200]	Edge Passivation 4T	TTTTGGAATCATTACCGCGCCCAAGCGCATTAGACGGGAGAATTTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	34[200]33[200]	Edge Passivation 4T	TTTTAACTGAACACCCTGAACAAATTATTTTGTCACAATCAATATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	1[8]2[40]	Edge Passivation 4T	TTTTATTACCTTATGCGATTTTAAGAACTGGCTCAAATACTGC	yes	yes	yes	yes	yes	yes	no
Base Plate	41[17]40[17]	Edge Passivation 4T	TTTTGAGCAAAAGAAGAAAACTTTTTTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	4[195]3[195]	Edge Passivation 4T	TTTTCAGACCGGAAGCAAACGAGCTTCAAAGCGAACTTTT	yes	yes	yes	yes	yes	yes	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
Base Plate	11[12]10 [12]	Edge Passivation 4T	TTTTGGGGATGTGCTGCAAGCCAGCTGGCGAAAGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	31[17]30 [17]	Edge Passivation 4T	TTTTTAGCAAGGCCGCAAATAAATCCTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	3[12]2 [12]	Edge Passivation 4T	TTTTAATCCCCCTCAAATGCATAAATATTCATTGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	13[12]12 [12]	Edge Passivation 4T	TTTTTTGGGCGCCAGGGTGGAGGCGGTTTGCGTATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	14[195] 13[195]	Edge Passivation 4T	TTTTAGAATAGCCCGAGATATCCCTTATAAATCAAATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	27[17]26 [17]	Edge Passivation 4T	TTTTACCGCCACCCTCTTTAATTGTATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	22[200] 22[168]	Edge Passivation 4T	TTTTGCGCATAGGCTGGCTGACCTTCATCAAG	yes	yes	yes	yes	yes	yes	no
Base Plate	32[200] 31[200]	Edge Passivation 4T	TTTTGAAAATTCATATGGTTTACCTAATCAAAATCACCGGAACCTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	9[12]8 [12]	Edge Passivation 4T	TTTTAACGCCATCAAAAATTTTTTAACCAATAGGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	37[17]36 [17]	Edge Passivation 4T	TTTTGTTTATCAACAGAATCTTACCATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	12[195] 11[195]	Edge Passivation 4T	TTTTATTCCACACAACATACTTGTTATCCGCTCACATTTT	yes	yes	yes	yes	yes	yes	no
Base	26[200]	Edge	TTTTTCGTCTTTCCAG	yes	yes	yes	yes	yes	yes	no
Plate	25[200]	Passivation 4T	ACGTTAGTACCCTCAGCAGCGAAAGACATT							

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
			TT							
Base Plate	2[195]1[195]	Edge Passivation 4T	TTTTGAATTACGAGGCATAGTACATAACGCCAAAAGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	30[200]29[200]	Edge Passivation 4T	TTTTAGAGCCACCACCGGAACCGCCTGCCTATTTCGGAACCTATTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	38[200]37[200]	Edge Passivation 4T	TTTTTCAACAGTAGGGCTTAATTGCCGTTTTTATTTTCATCGTATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	21[12]20[12]	Edge Passivation 4T	TTTTATTAATTTTAAAAGTCTTTGCCCGAACGTTTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	18[195]17[195]	Edge Passivation 4T	TTTTCTGAAATGGATTATTTTTTGACGCTCAATCGTTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	19[12]18[12]	Edge Passivation 4T	TTTTACATCGCCATTAAAAACTGATAGCCCTAAATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	10[195]9[195]	Edge Passivation 4T	TTTTTTTGAGGGGACGACGAACCGTGCATCTGCCAGTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	25[17]24[17]	Edge Passivation 4T	TTTTTCGGTTTATCACCCAGCGATTATTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	17[12]16[12]	Edge Passivation 4T	TTTTCACGCAAATTAACCGAAAGAGTCTGTCCATTTTT	yes	yes	yes	yes	yes	yes	no
Base Plate	37[28]36[190]	Bottom Layer Polymerization	AACAGAATCTTACCAGGAATCA	no	no	no	no	no	no	no
Base Plate	33[28]32[190]	Bottom Layer Polymerization	ACCGACCATTACCATGAAAATT	no	no	no	no	no	no	no
Base Plate	31[28]30[190]	Bottom Layer Polyme	GCCGCAAATAAATCC	no	no	no	no	no	no	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
		rization	AGAGCCA							
Base Plate	42[39]42 [21]	Bottom Layer Polyme rization	TATTCATTTCAATTAC CT	no	no	no	no	no	no	no
Base Plate	41[28]40 [190]	Bottom Layer Polyme rization	AGAAGAAAACTTTTTA AACATA	no	no	no	no	no	no	no
Base Plate	27[28]26 [190]	Bottom Layer Polymerization	CCCTCTTTAATTGTAT CGTCTT	no	no	no	no	no	no	no
Base Plate	29[28]28 [190]	Bottom Layer Polyme rization	AGCCCCACCCTCAGA TATTCTG	no	no	no	no	no	no	no
Base Plate	22[31]22 [176]	Bottom Layer Polyme rization	ACTTTAATCATGCGC ATAGGCTGGCTGACC T	no	no	no	no	no	no	no
Base Plate	25[28]24 [190]	Bottom Layer Polyme rization	ATCACCCAGCGATTA GCATCGG	no	no	no	no	no	no	no
Base Plate	35[28]34 [190]	Bottom Layer Polyme rization	CGAGCAAAGTTACCA AACTGAA	no	no	no	no	no	no	no
Base Plate	39[28]38 [190]	Bottom Layer Polyme rization	ATTTAGAACGCGCCT TCAACAG	no	no	no	no	no	no	no
Base Plate	28[189] 27[27]	Bottom Layer Polyme rization	AAACATGAAAGTACG TAACGATCTAAAGTTT TGACCGCCA	no	no	no	no	no	no	no
Base Plate	24[189] 23[31]	Bottom Layer Polyme rization	AACGAGGGTAGCAAT GAACGGTGTACAGAC CAGTACCAAGCGCG	no	no	no	no	no	no	no
Base Plate	30[189] 29[27]	Bottom Layer Polyme rization	CCACCGGAACCGCCT GCCTATTTCGGAACC TATTCATTAA	no	no	no	no	no	no	no
Base Plate	36[189] 35[27]	Bottom Layer Polyme rization	TTACCGCGCCCAAGC GCATTAGACGGGAGA ATTACGCTAA	no	no	no	no	no	no	no
Base Plate	26[189] 25[27]	Bottom Layer Polyme rization	TCCAGACGTTAGTAC CCTCAGCAGCGAAAG ACATCGGTTT	no	no	no	no	no	no	no

Structure	Pos. in Structure	Oligo Name	Sequence	Figure						
				1	7	8	9A,B	9C,D	10A,B	10C,D
			~~AGATCGGTTT~~							
Base Plate	40[189] 39[27]	Bottom Layer Polymerization	GCGATAGCTTAGATACCAGTATAAAGCCAACGCCAAATAT	no	no	no	no	no	no	no
Base Plate	38[189] 37[27]	Bottom Layer Polymerization	TAGGGCTTAATTGCCGTTTTTATTTTCATCGTAGTTTATC	no	no	no	no	no	no	no
Base Plate	42[196] 41[27]	Bottom Layer Polymerization	TTTGCACGTAAAACAGAAATTTTTCCCTTAGAATCCTTGAGAGCAAA	no	no	no	no	no	no	no
Base Plate	34[189] 33[27]	Bottom Layer	CACCCTGAACAAATTATTTTGTCACAATCAA	no	no	no	no	no	no	no
		Polymerization	TAGAAGGAA							
Base Plate	32[189] 31[27]	Bottom Layer Polymerization	CATATGGTTTACCTAATCAAAATCACCGGAACCTAGCAAG	no	no	no	no	no	no	no

Additional Strands

[0109]

Oligo Name	Sequence	Figure						
		1	7	8	9A,B	9C,D	10A,B	10C,D
HybrA655	**[Atto655]** TT ATATGTACGGGTCTCACTTA	no	no	no	no	no	no	yes
HybrA565	**[Atto565]** TT CGGAGGTTAAGTAGGTTG	no	no	no	no	no	no	yes
Thiol_10T	[thiol] TTTTTTTTTT	no	no	no	no	no	no	yes

Fixation of platform

[0110] Optional orientation control of the platform 4 during sample preparation is shown in figure 11. Figure 11-A shows a sketch of the designed structures. A long handle 18 is attached to the platform 4, which has the shape of a square plate in this embodiment. The protruding end of the handle 18 is functionalized with a single biotin molecule 22, which can flexibly anchor the construct to an avidin modified surface and hence functions

as a primary anchor 19. The edges of the platform 4 can be fixed via secondary anchors 20. Therefore, the platform 4 is extended with secondary anchoring sequences 21. These secondary anchoring sequences 21 allow subsequent fixation upon addition of biotin modified complimentary strands 23. For superresolution optical microscopy various points on the construct are labelled with DNA-PAINT docking sites 24. The workflow of fixation of the platform 4 including orientation control is illustrated in figure 11-B. First, the construct comprising platform 4 and handle 18 is flexibly anchored with the primary anchor 19. Second, the handle 18 and the platform 4 are aligned in the direction 25 of an externally applied electric field. This is performed in the same way as aligning the positioning arm 5 after fixation of the platform 4. Third, while aligned, the biotin modified complimentary strands 23 (biotin modified oligonucleotides) are added to facilitate fixation of the secondary anchoring sequences 21 in order to generate the secondary anchors 20. As a result, the platform 4 and the handle 18 stay fixed in the alignment direction after the external field is switched off.

[0111] Figure 11-C shows a DNA-PAINT localization image of aligned structures including platform 4 and handle 18 after the external field has been switched off. The DNA-PAINT localization image shows the positions of the DNA-PAINT docking sites 24. The inset shows a histogram of the angular distribution of structures that were measured in a larger field of view that exhibits a strong preference between 150° and 210°. In the histogram, the circumferential dimension denotes the alignment angle and the radial dimension denotes the number of structures comprising platform 4 and handle 18.

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[0112]

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List of reference signs

[0113]

1
molecular machine
2
movement part
3
control part
4
platform (first molecular element)
5
positioning arm(second molecular element)
6
linking element
7
first electrical device
8
second electrical device
9

first fluidic channel

10

second fluidic channel

11

electrode

12

intersection area

13

isolating element

14

additional lever/pointer structure

15

donor dye

16

first acceptor dye

17

second acceptor dye

18

handle

19

primary anchor

20

secondary anchor

21

secondary anchoring sequences

22

biotin molecule

23

biotin modified complimentary strand

24

DNA-PAINT docking sites

25

direction of electrical field

SEQUENCE LISTING

[0114]

<110> Technische Universität München

<120> Molecular machine

<130> TUM180801PEP

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<151> 2017-04-06

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ttagttgtta gtgctcctaa agatatttta gataaccttc ctcaattcct ttcaactgtt 5760

gatttgccaa ctgaccagat attgattgag ggtttgatat ttgaggttca gcaaggtgat 5820

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ccttttatta ctggtcgtgt gactggtgaa tctgccaatg taaataatcc atttcagacg 6120

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attcgagctc ggtacccggg gatcctctag agtcgacctg caggcatgc                 7249
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REFERENCES CITED IN THE DESCRIPTION

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Patentkrav

1. Molekylær maskine (1) omfattende

- en bevægelsesdel (2), som inkluderer
  - et første molekylært element (4),
  - et andet molekylært element (5), og
  - et forbindelseselement (6) til at begrænse en relativ bevægelse af det første molekylære element (4) og det andet molekylære element (5), og **kendetegnet ved, at** den yderligere omfatter
- en kontroldel (3) konfigureret til at generere et elektrisk felt omkring bevægelsesdelen (2),
- hvor det første molekylære element (4) er fikseret i forhold til kontroldelen (3),
- hvor det andet molekylære element (5) er bevægeligt i forhold til det første molekylære element (4) i mindst én frihedsgrad, og
- hvor det andet molekylære element (5) er elektrisk ladet således at det andet molekylære element (5) bringes på linje med nævnte elektriske felt.

2. Molekylær maskine (1) ifølge krav 1, **kendetegnet ved, at** kontroldelen (3) omfatter en fluidkanal (9, 10), i hvilken bevægelsesdelen (2) er tilvejebragt, hvor kontroldelen (3) har en elektrisk indretning (7, 8) som inkluderer elektroder (11), der er forbundet til fluidkanalen (9, 10), for at skabe det elektriske felt.

3. Molekylær maskine (1) ifølge krav 2, **kendetegnet ved, at** kontroldelen (3) omfatter mindst to elektriske indretninger (7, 8) og fluidkanaler (9, 10) med forskellige orienteringer for at skabe mindst to uafhængigt overliggende elektriske felter, hvor fluidkanalerne (9, 10) er indrettet til at krydse ved et skæringsområde (12) og bevægelsesdelen (2) er placeret ved skæringsområdet (12).

4. Molekylær maskine (1) ifølge krav 2 eller 3, **kendetegnet ved, at** det første molekylære element (4) er fikseret til fluidkanalen (9, 10).

5. Molekylær maskine (1) ifølge et hvilket som helst af kravene 2 til 4, **kendetegnet ved, at** den elektriske indretning (7, 8) inkluderer et isoleringselement (13) til at isolere elektroderne (11) fra bevægelsesdelen (2).

6. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** forbindelseselementet (6) er en del af det første molekylære element (4) eller det andet molekylære element (5).

7. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** det første molekylære element (4) og/eller det andet molekylære element (5) og/eller forbindelseselementet (6) er biomolekyler, fortrinsvis lavet af DNA, fortrinsvis DNA-origami, og/eller RNA og/eller protein og/eller kunstigtladede supramolekylære strukturer.

8. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** det første molekylære element (4) er en platform og det andet molekylære element (5) er en positioneringsarm, hvor forbindelseselementet (6) begrænser al relativ bevægelse af det første molekylære element (4) og det andet molekylære element (5) bortset fra en rotation af det andet molekylære element (5) inden for et plan parallelt med det første molekylære element (4).

9. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** svingninger af det første molekylære element (4) og/eller det andet molekylære element (5) på grund af diffusion er inden for en tolerance på højst 10 nm, fortrinsvis højst 1 nm, i særdeleshed foretrukket højst 0,5 nm.

10. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** enhver dimension af det første molekylære element (4) og det andet molekylære element (5) er mindre end 1.000 nm.

11. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** det første molekylære element (4) er lavet af en krydset

tolagsskabelonføring, i hvilken et øverste lag er fortrinsvis roteret i forhold til et nederste lag med en vinkel mellem 80° og 100°, i særdeleshed 90°.

12. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** det andet molekylære element (5) er lavet af et DNA seks-helix-bundt.

13. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** forbindelseselementet (6) er skabt af to tilstødende skabelonkrydsninger med tre og fire uparrede baser.

14. Molekylær maskine (1) ifølge et hvilket som helst af de foregående krav, **kendetegnet ved, at** det andet molekylære element (5) er indrettet til at transportere uorganiske nanopartikler.

DRAWINGS

Fig. 1

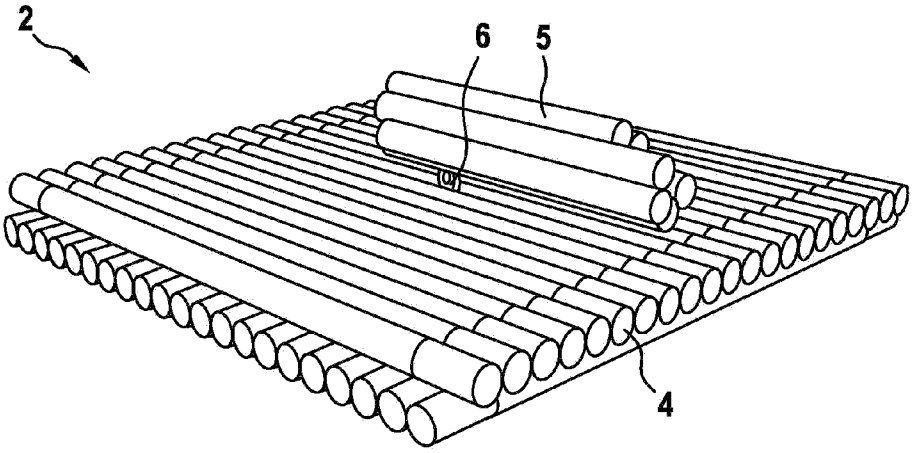


Fig. 2

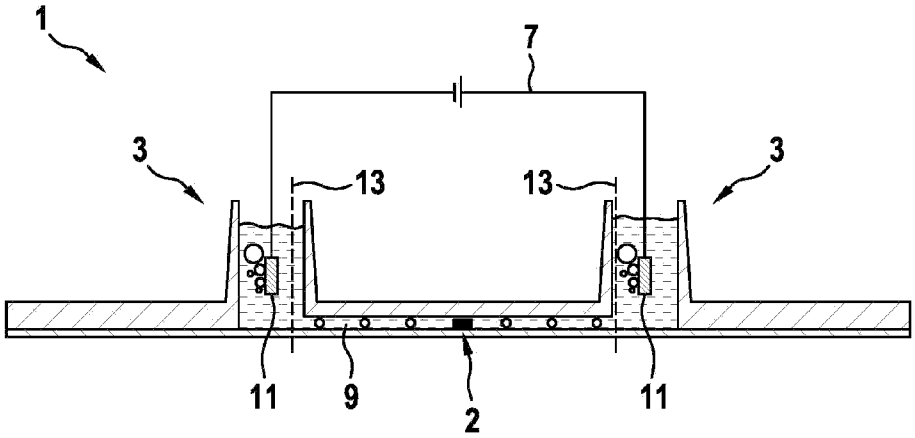


Fig. 3

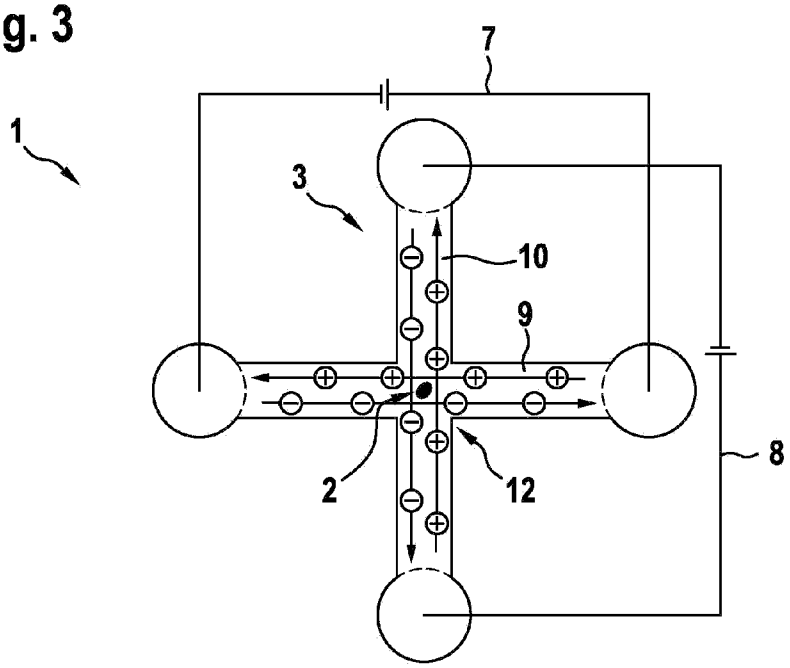


Fig. 4

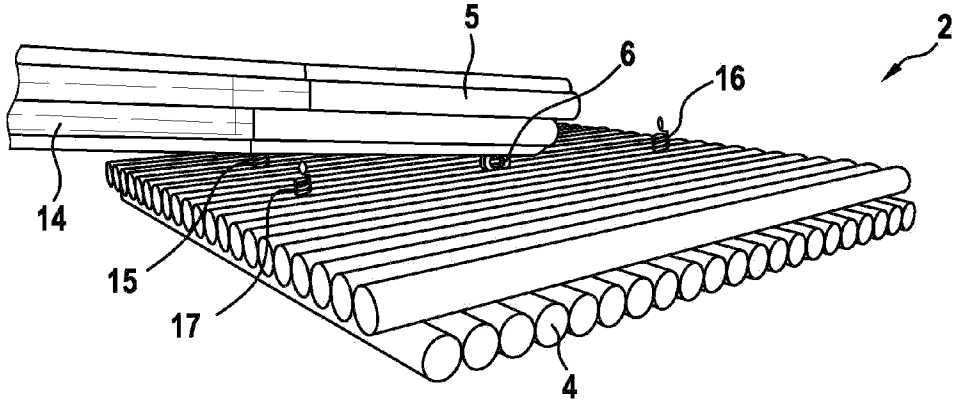


Fig. 5

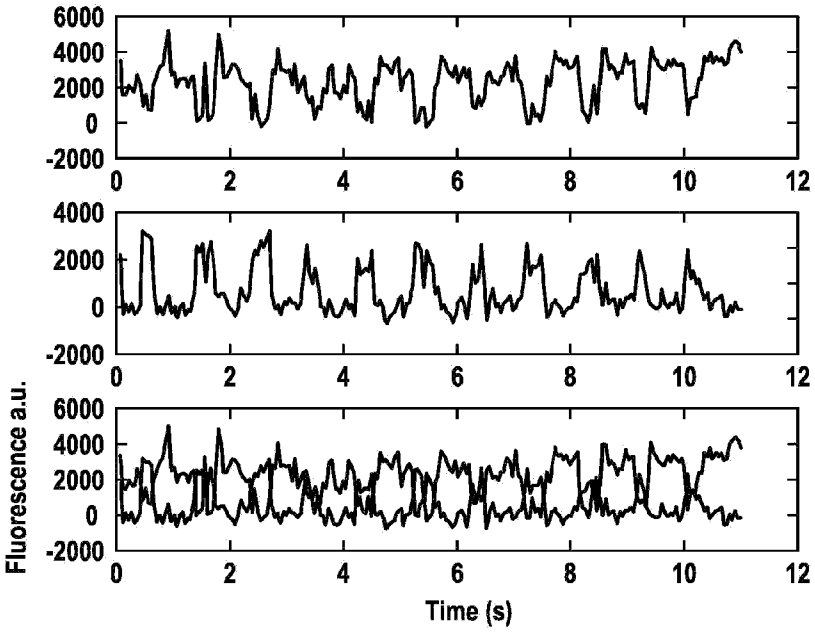


Fig. 6

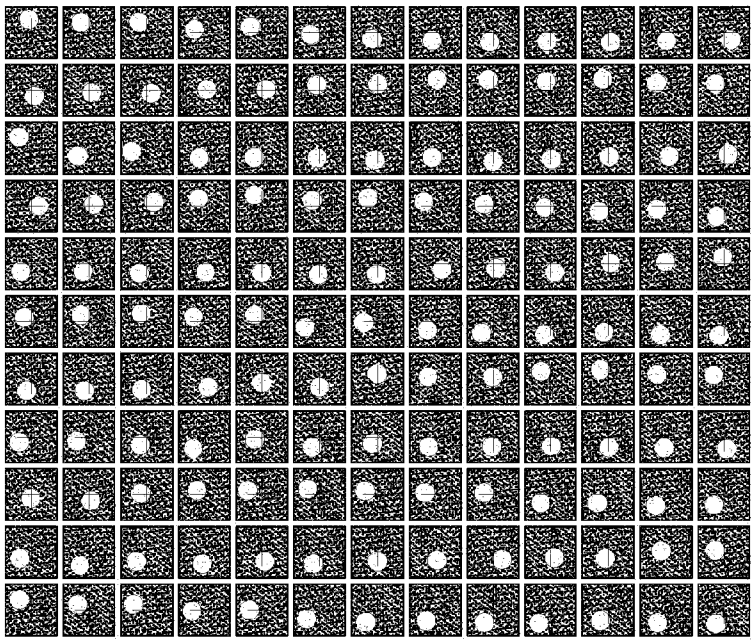


Fig. 7A

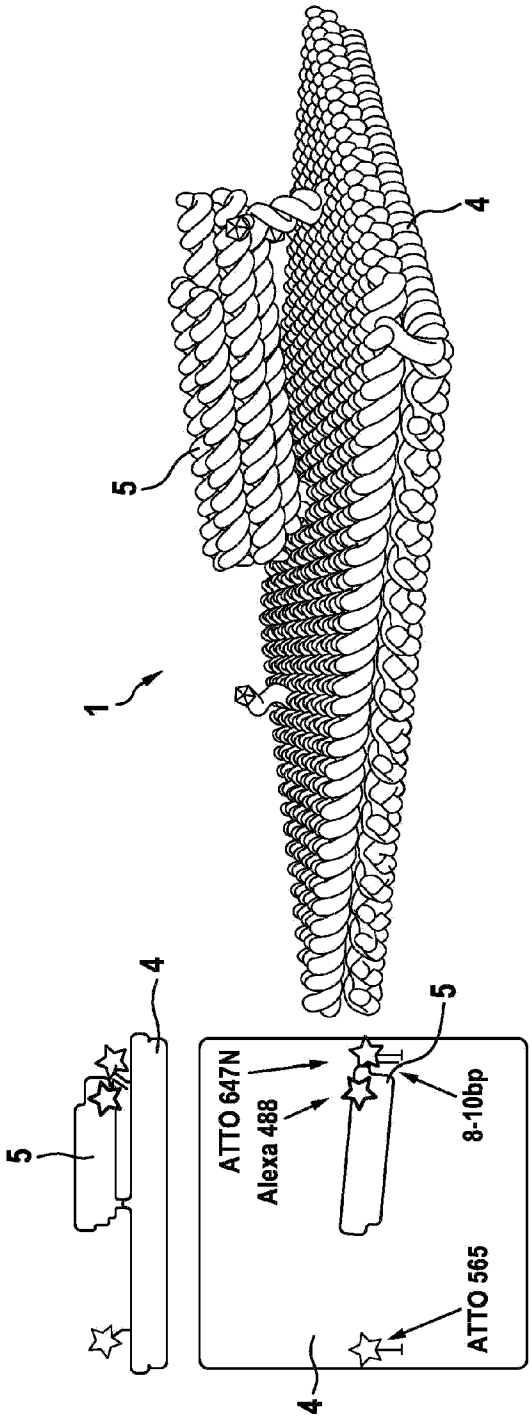


Fig. 7B

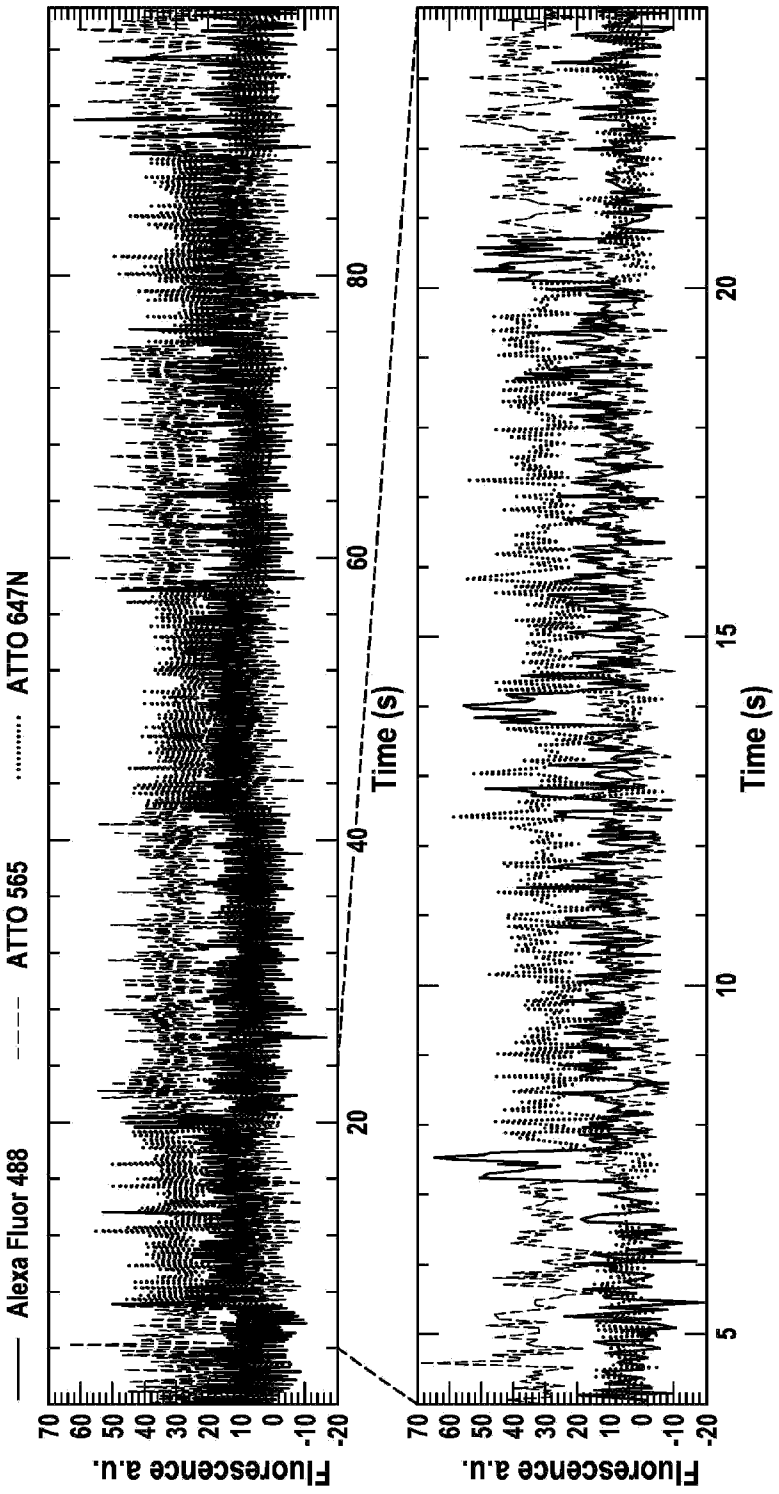

Alexa Fluor 488
ATTO 565
ATTO 647N
Fluorescence a.u.
Time (s)
70
60
50
40
30
20
10
0
-10
-20
20
40
60
80
5
10
15
20

Fig. 7C

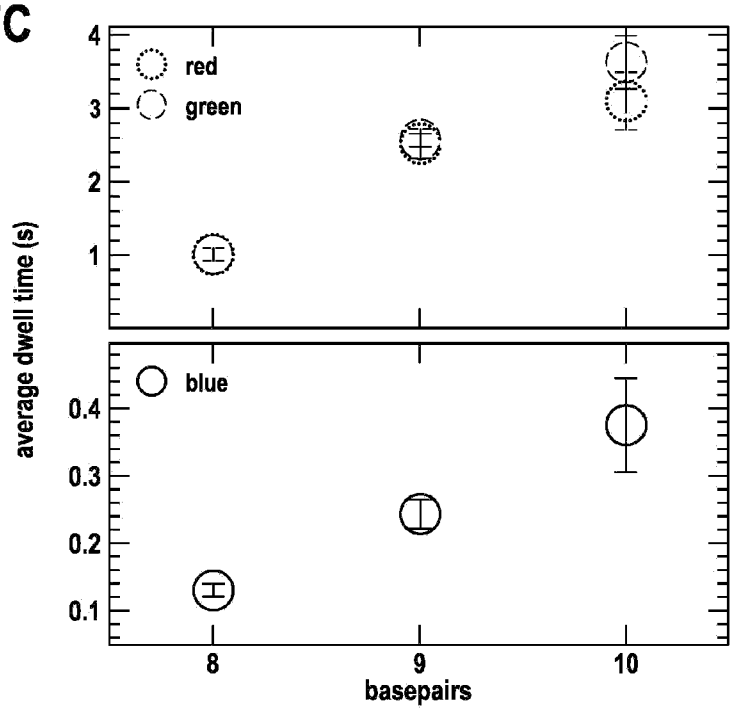

red
green
blue
average dwell time (s)
basepairs
4
3
2
1
0.4
0.3
0.2
0.1
8
9
10

Fig. 7D

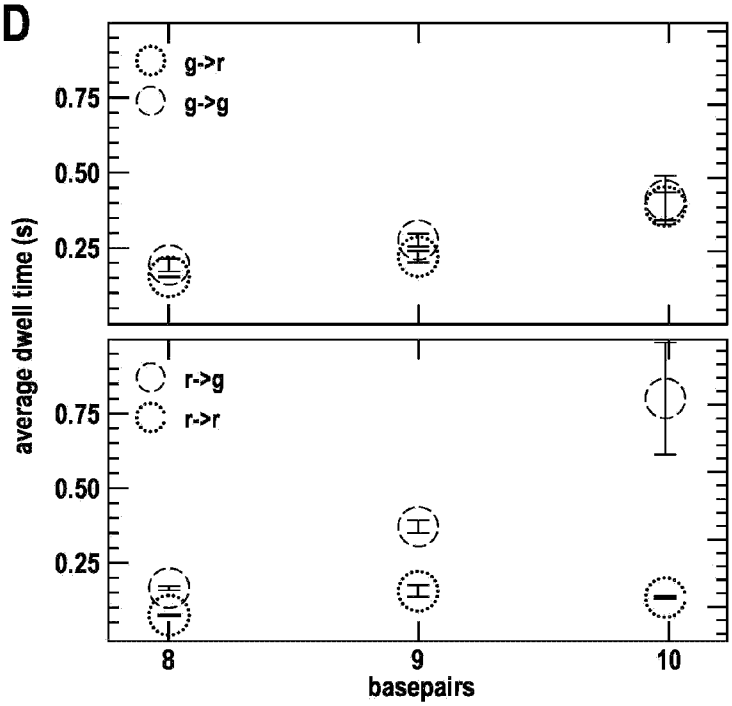

g->r
g->g
r->g
r->r
average dwell time (s)
basepairs
0.75
0.50
0.25
8
9
10

Fig. 8A

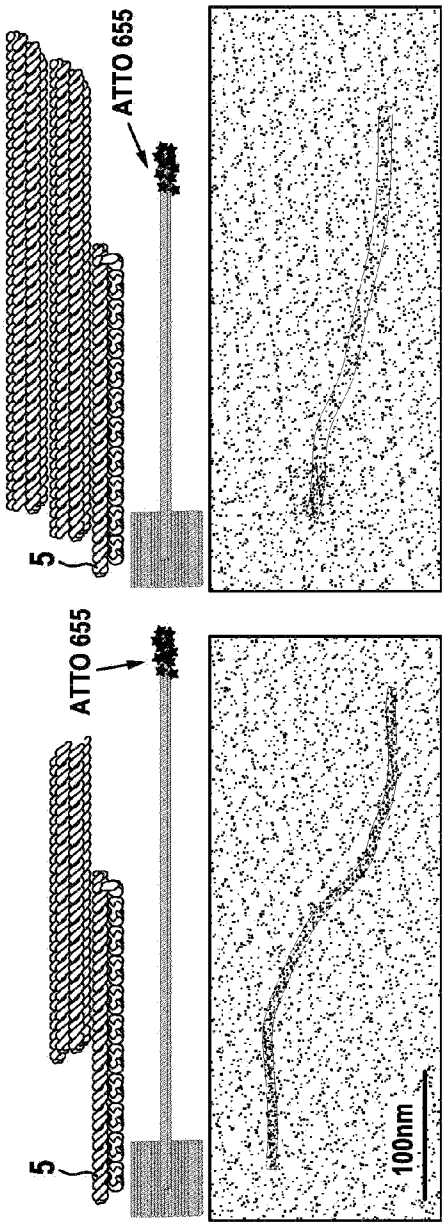

ATTO 655
5
ATTO 655
5
100nm

Fig. 8B

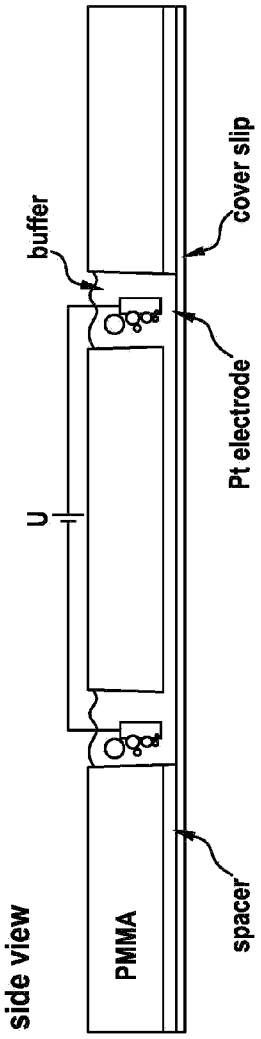
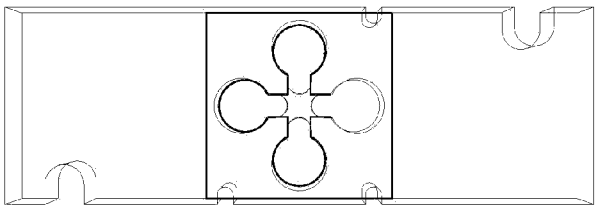

buffer
cover slip
U
Pt electrode
side view
PMMA
spacer

Fig. 8C

top view



isometric view

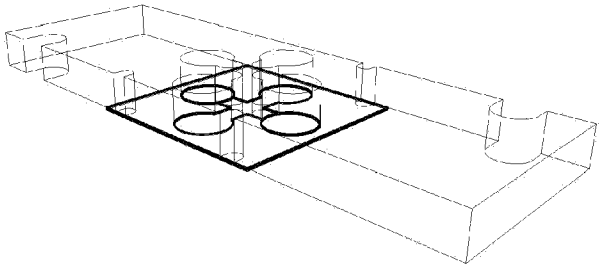


Fig. 8D

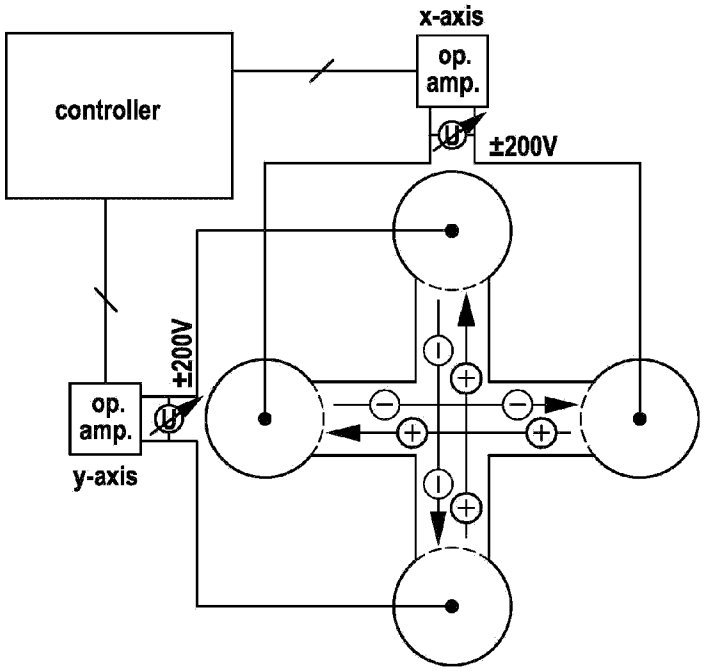


Fig. 8E

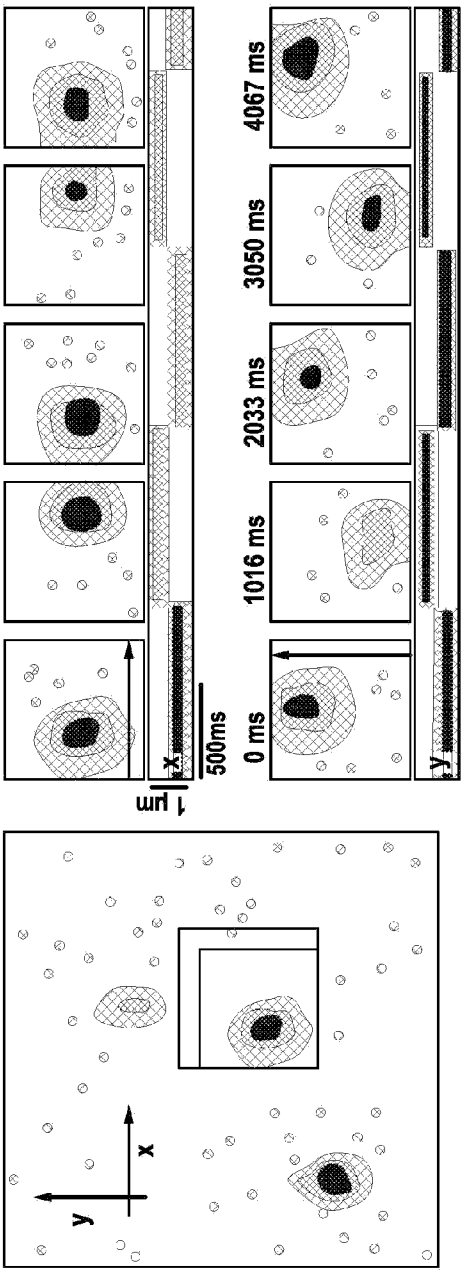

0 ms
1016 ms
2033 ms
3050 ms
4067 ms
x
y
1 µm
500ms

Fig. 8F

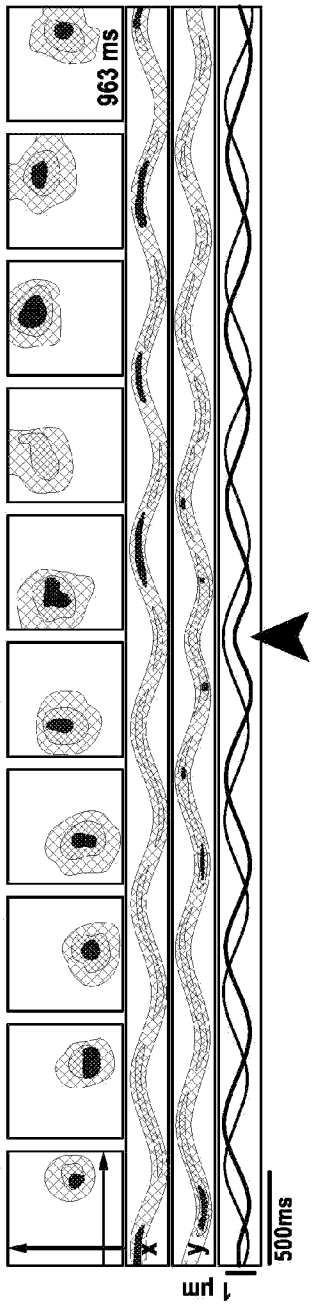

0 ms
107 ms
214 ms
321 ms
428 ms
535 ms
642 ms
749 ms
856 ms
963 ms
x
y
1 µm
500ms

Fig. 8G


1 µm
500ms

Fig. 8H

25 Hz rotation
0 ms
2.1 ms
4.1 ms
6.1 ms
8.2 ms
10.2 ms
12.3 ms
14.3 ms
16.3 ms
18.4 ms
20.4 ms
22.5 ms
24.5 ms
26.5 ms
28.6 ms
30.6 ms
32.7 ms
34.7 ms
36.7 ms
38.8 ms
x
y
1 µm
40ms

Fig. 9A

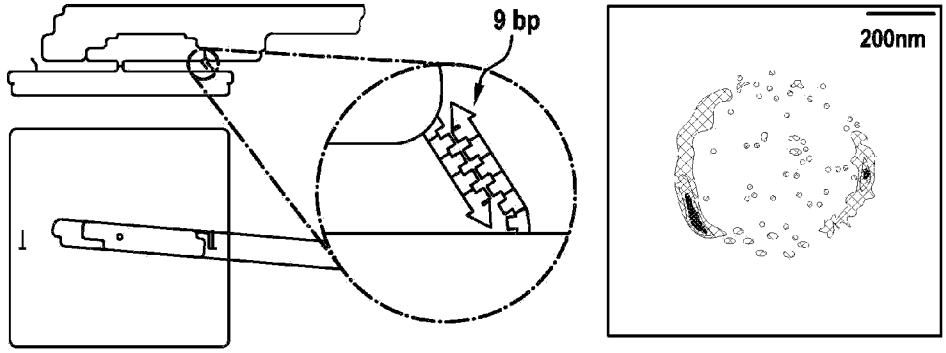


Fig. 9B

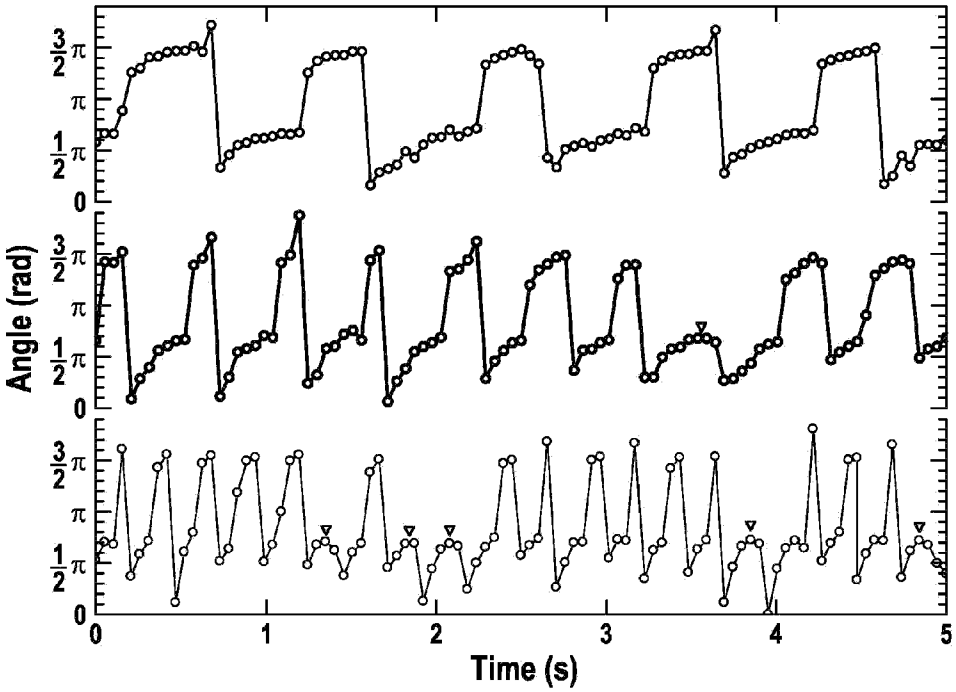


Fig. 9C

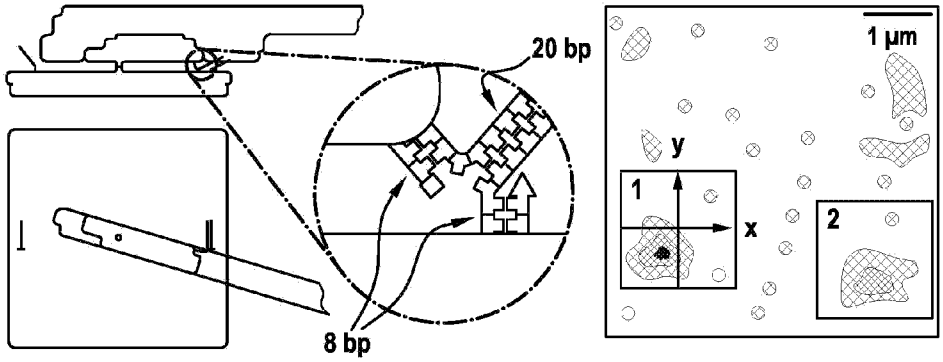
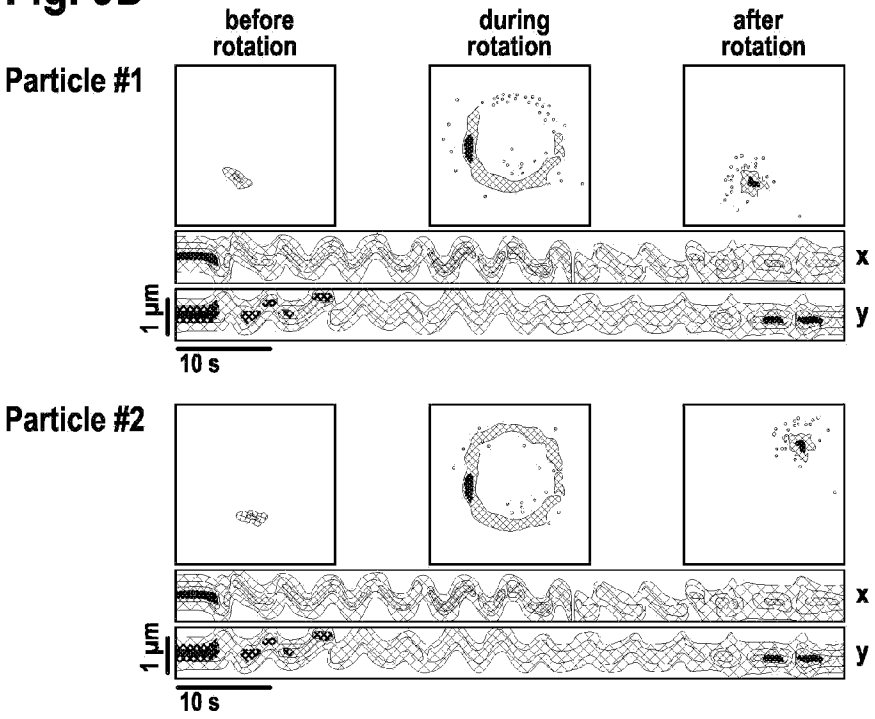

20 bp
8 bp
1 µm
y
1
x
2

Fig. 9D


before rotation
during rotation
after rotation
Particle #1
x
y
1 µm
10 s
Particle #2
x
y
1 µm
10 s

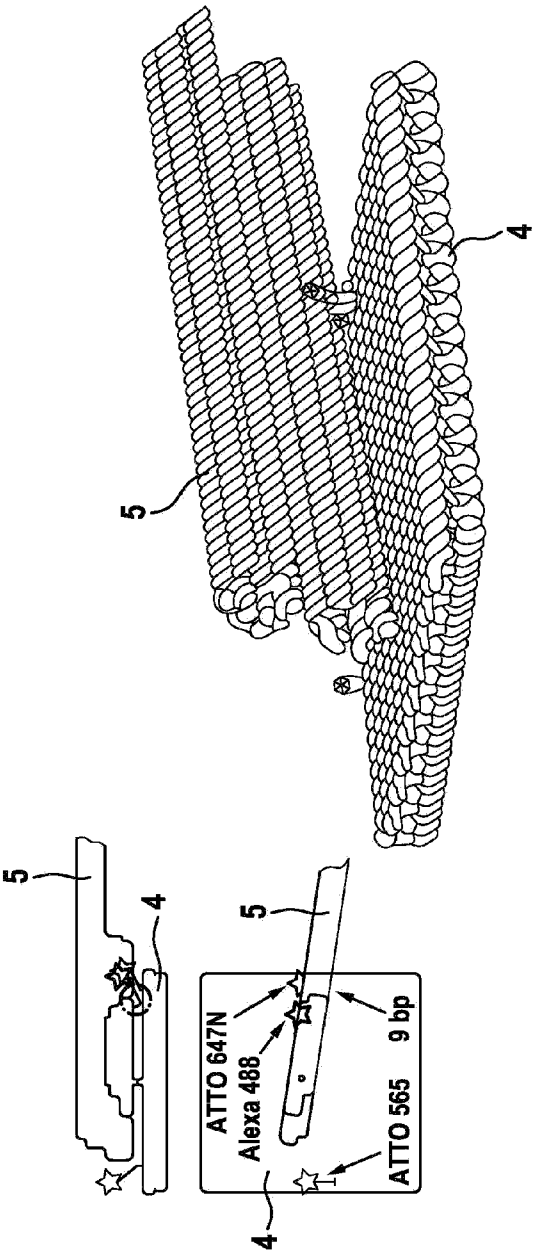
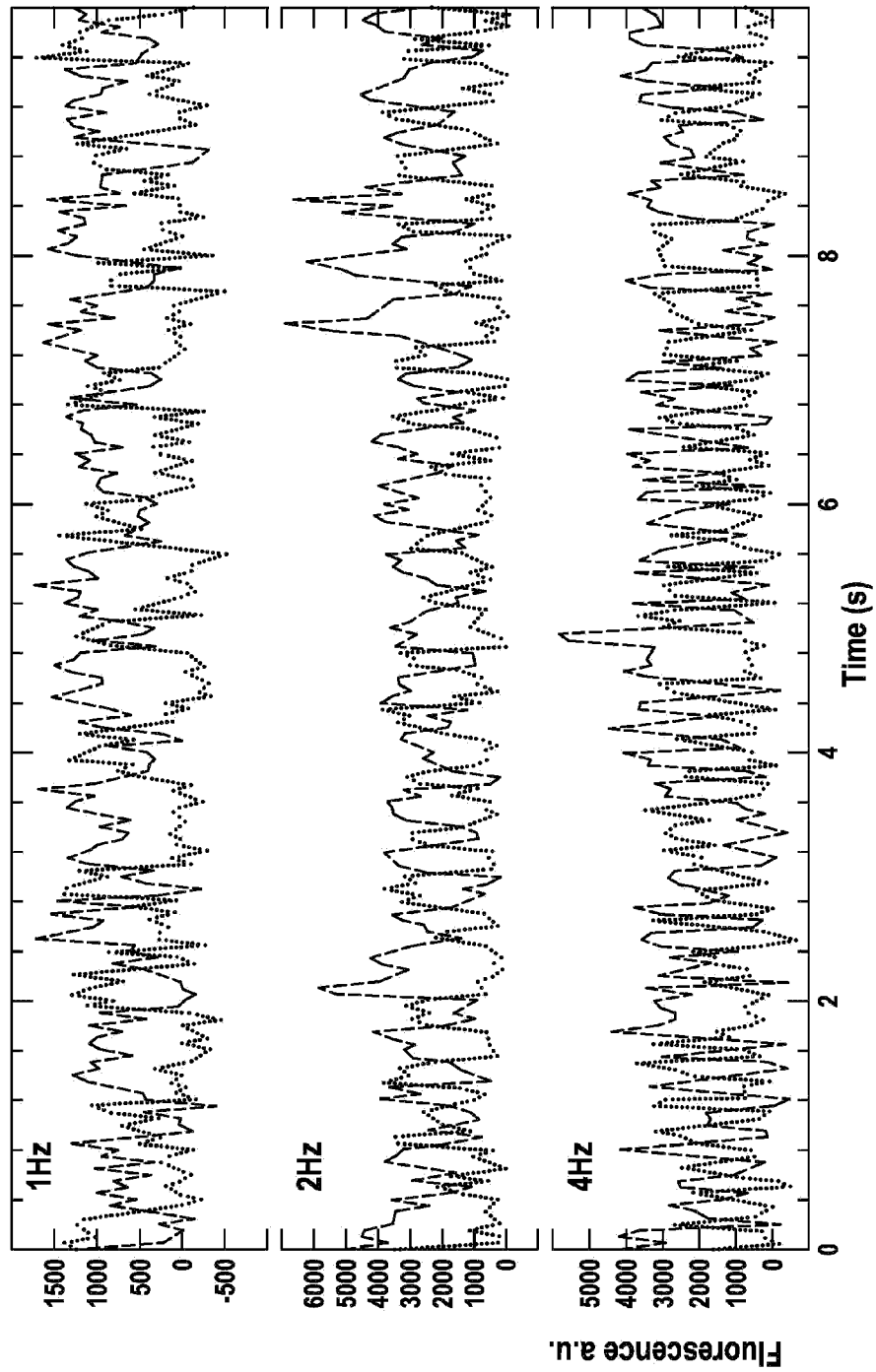


Fig. 10A

Fig. 10B


ATTO 565
ATTO 647N
1Hz
2Hz
4Hz
Fluorescence a.u.
Time (s)
1500
1000
500
0
-500
6000
5000
4000
3000
2000
1000
0
5000
4000
3000
2000
1000
0
0
2
4
6
8

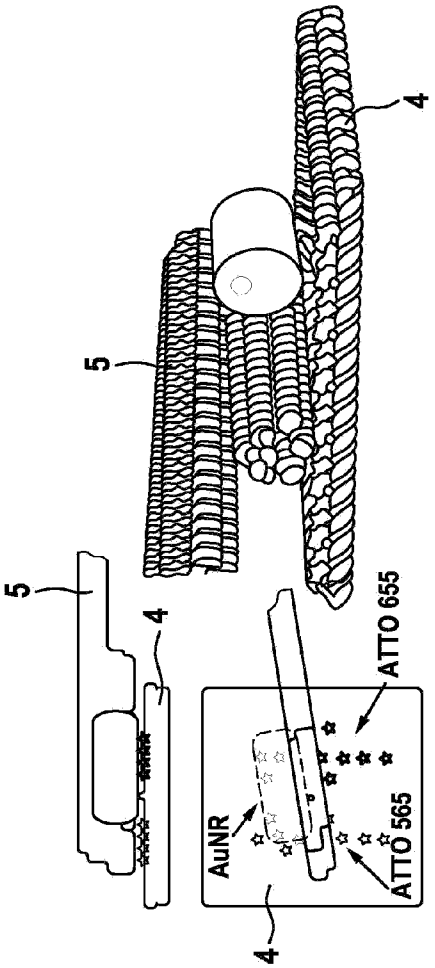
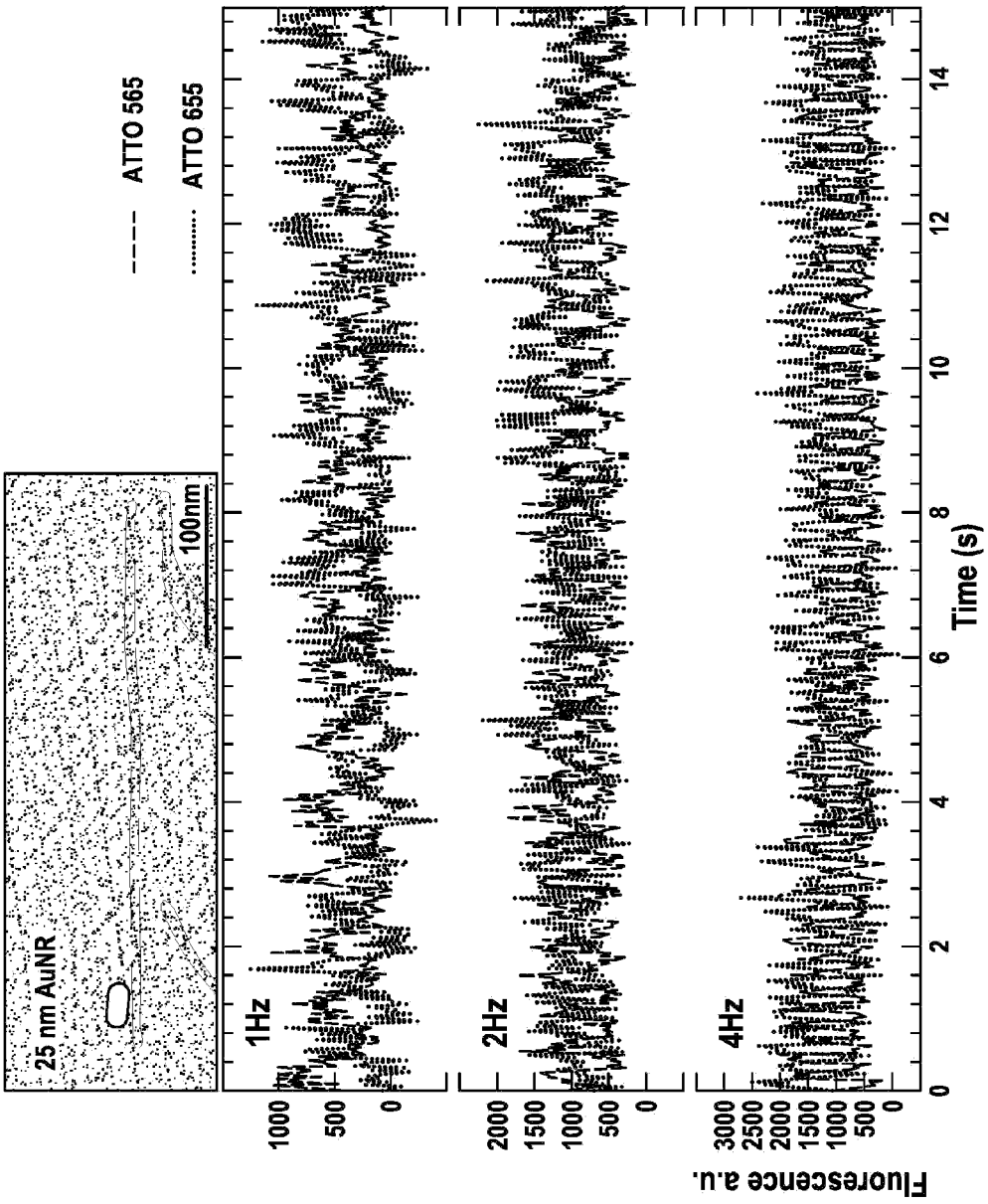


Fig. 10C

Fig. 10D


25 nm AuNR
100nm
ATTO 565
ATTO 655
1Hz
2Hz
4Hz
Fluorescence a.u.
Time (s)

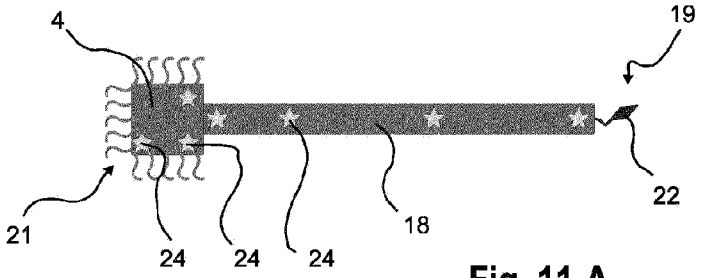


Fig. 11-A

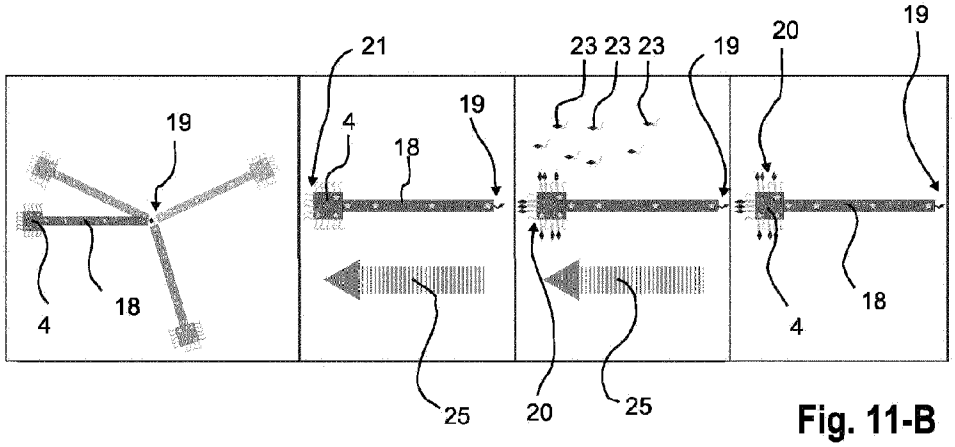


Fig. 11-B

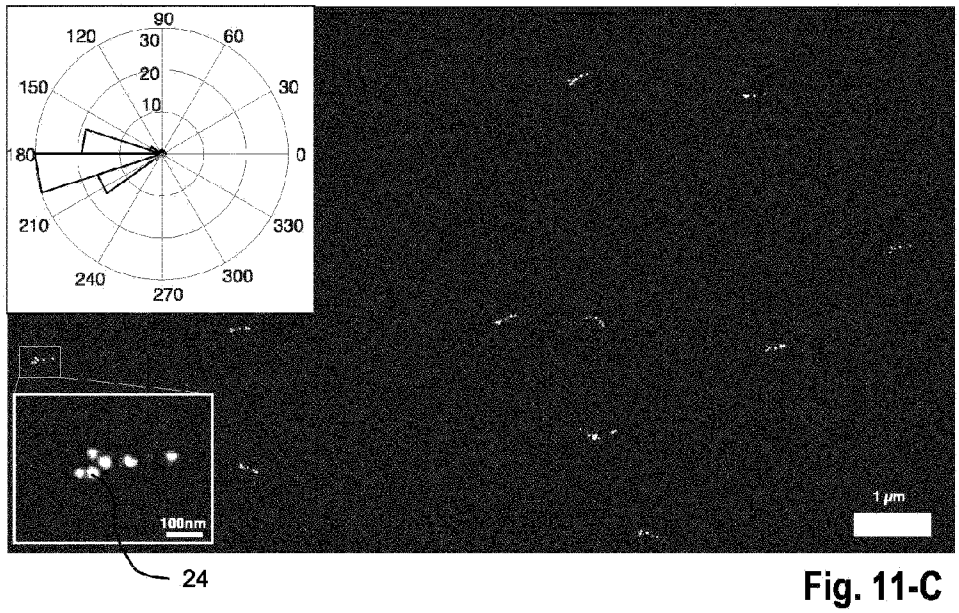


Fig. 11-C