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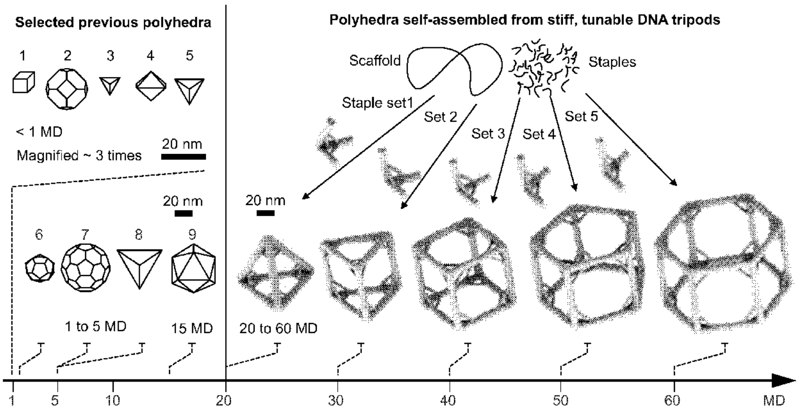

FIG. 1A

(57) Abstract: Provided herein are compositions comprising nucleic acid structures comprising three or more arms arranged at fixed angles from each other, composites thereof such as DNA cages, and methods for their synthesis and use.

NUCLEIC ACID POLYHEDRA FROM SELF-ASSEMBLED VERTEX-CONTAINING FIXED-ANGLE NUCLEIC ACID STRUCTURES

RELATED APPLICATION

This application claims the benefit under 35 U.S.C. § 119(e) of U.S. provisional application number 61/950,098, filed March 8, 2014, which is incorporated by reference herein in its entirety.

FEDERALLY SPONSORED RESEARCH

This invention was made with U.S. Government support under grant number N000141110914, N000141010827 and N00014130593, awarded by the Office of Naval Research; grant number W911NF1210238, awarded by the Army Research Office; grant numbers 1DP2OD007292, 1R01EB018659 and 5R21HD072481, awarded by the National Institutes of Health; and grant numbers CCF1054898, CCF1317291, CCF1162459 and CMM11333215, awarded by the National Science Foundation. The U.S. Government has certain rights in the invention.

FIELD OF INVENTION

Provided herein are a novel compositions and methods for generating nucleic acid structures such as DNA cages.

BACKGROUND OF INVENTION

DNA nanotechnology has produced a wide range of shape-controlled nanostructures (1-10). Hollow polyhedra (1, 5, 11-26) are particularly interesting, as they resemble natural structures such as viral capsids and promise applications for scaffolding and encapsulating functional materials. Previous work has constructed diverse polyhedra, such as tetrahedra (13, 16, 20, 24), cubes (1, 19, 23), bipyramids (15), truncated octahedra (11), octahedra (12), dodecahedra (16, 18), icosahedra (17, 21), nano-prisms (14, 22, 25, 26), and buckyballs (16), with sub-80 nm sizes and sub-5 megadalton (MD) molecular weights (*e.g.* structures 1–8 in FIG. 1A). Assembly strategies include step-wise synthesis (1, 11, 21, 22), folding of a long scaffold (12, 19, 20, 24, 25), cooperative assembly of individual strands (13-15, 18, 26), and hierarchical assembly of branched DNA tiles (16, 17, 23).

Another route to scaling up polyhedra is the hierarchical assembly of larger monomers. Previous work using small three-arm-junction (16, 21) (80 kD) and five-arm junction tiles (17) (130 kD) has produced several sub-5 MD polyhedra (*e.g.* structures 5-7 in FIG. 1A). Additionally, a 15 MD icosahedron (5) (FIG. 1A, structure 9) was assembled from three double-triangle shaped origami monomers. However, this icosahedron was generated in low yield (5) and this method has not been generalized to construct more complex polyhedra.

SUMMARY OF INVENTION

The invention provides a novel, general strategy for, optionally, one-step self-assembly of wireframe DNA polyhedra that are larger than previous structures and that are produced at higher yield than previous structures. A stiff three-arm-junction tile motif, which can be made using for example DNA origami, with precisely controlled angles and arm lengths is used for hierarchical assembly of polyhedra. Using these methods, it was possible to construct a tetrahedron (20 megadaltons or MD), a triangular prism (30 MD), a cube (40 MD), a pentagonal prism (50 MD), and a hexagonal prism (60 MD) with edge widths of 100 nanometers. The structures were visualized by transmission electron microscopy and by three-dimensional DNA-PAINT super-resolution fluorescent microscopy of single molecules in solution.

Thus, in one aspect, provided herein is a nucleic acid structure comprising a first (x), a second (y), and a third (z) nucleic acid arm, each connected at one end to the other arms to form a vertex, and a first, a second, and a third nucleic strut, wherein the first nucleic acid strut connects the first (x) nucleic arm to the second (y) nucleic arm, the second nucleic acid strut connects the second (y) nucleic arm to the third (z) nucleic arm, and the third nucleic acid strut connects the third (z) arm to the first (x) nucleic acid strut.

In another aspect, provided herein is a nucleic acid structure comprising three nucleic acid arms radiating from a vertex at fixed angles.

In another aspect, provided herein is a nucleic acid structure comprising N nucleic acid arms radiating from a vertex, wherein N is the number of nucleic acid arms and is 3 or more, and M nucleic acid struts, each strut connecting two nucleic acid arms to each other, wherein M is the number of nucleic acid struts and is 3 or more. In some embodiments, N is equal to M. In some embodiments, N is less than M.

Embodiments relating to one or more of the foregoing aspects are now provided.

In some embodiments, the nucleic acid structure comprises 4 nucleic acids and at least 4 nucleic acid struts, or 5 nucleic acid arms and at 5 nucleic acid struts.

In some embodiments, the nucleic acid arms are equally spaced apart from each other (or the arms are separated from each other by the same angle). In some embodiments, the nucleic acid arms are not equally separated from each other (or the arms are separated from each other by different angles).

In some embodiments, the nucleic acid structure comprises three nucleic acid arms separated from each other by 60° - 60° - 60°. When four such structures are connected to each other at their free ends, they form a tetrahedron.

In some embodiments, the nucleic acid structure comprises three nucleic acid arms separated from each other by 60° - 90° - 90°. When six such structures are connected to each other at their free ends, they form a triangular prism.

In some embodiments, the nucleic acid structure comprises three nucleic acid arms separated from each other by 90° - 90° - 90°. When eight such structures are connected to each other at their free ends, they form a cube.

In some embodiments, the nucleic acid structure comprises three nucleic acid arms separated from each other by 108° - 90° - 90°. When ten such structures are connected to each other at their free ends, they form a pentagonal prism. In some instances, pentagonal prisms may be formed by connecting nucleic acid structures defined as 120° - 90° - 90°.

In some embodiments, the nucleic acid structure comprises three nucleic acid arms separated from each other by 120° - 90° - 90°. When twelve such structures are connected to each other at their free ends, they form a hexagonal prism. In some instances, pentagonal prisms may be formed by connecting nucleic acid structures defined as 140° - 90° - 90°.

In some embodiments, the nucleic acid structure further comprises a vertex nucleic acid.

In some embodiments, the nucleic acid structure further comprises a connector nucleic acid.

In some embodiments, the nucleic acid arms, nucleic acid struts, and/or vertex nucleic acid are comprised of parallel double helices.

In some embodiments, nucleic acid arms are of identical length.

In some embodiments, the nucleic acid struts are of identical length. In some embodiments, the nucleic acid struts are of different lengths.

In some embodiments, at least one nucleic acid arm comprises a blunt end.

In some embodiments, at least one nucleic acid arm comprises a connector nucleic acid at its free (non-vertex) end that is up to 16 nucleotides in length. In some embodiments, at least one nucleic acid arm comprises a connector nucleic acid at its free (non-vertex) end, thereby comprising a 1 or 2 nucleotide overhang.

In some embodiments, the nucleic acid structure is up to 5 megadaltons (MD) in size.

In some embodiments, the nucleic acid arms are 50 nm in length.

In another aspect, provided herein is a composite nucleic acid structure comprising L nucleic acid structures selected from any of the foregoing nucleic acid structures, wherein L is an even number of nucleic acid structures, and wherein the L nucleic acid structures are connected to each other at free (non-vertex) ends of the nucleic acid arms.

In some embodiments, the two more nucleic acid structures are two, four, six, eight, ten, twelve or more nucleic acid structures.

In some embodiments, the composite nucleic acid structure is a tetrahedron, a triangular prism, a cube, a pentagonal prism, or a hexagonal prism.

In some embodiments, the composite nucleic acid structure is 20 megadaltons (MD), 30 MD, 40 MD, 50 MD, or 60 MD in size.

In some embodiments, the composite nucleic acid structure has edge widths, comprised of two nucleic acid arms from adjacent nucleic acid structures, of 100 nm.

In another aspect, provided herein are methods of synthesis of any of the foregoing nucleic acid structures and the composite nucleic acid structures. In some embodiments, the methods comprise combining a nucleic acid scaffold strand with nucleic acid staple strands in a reaction vessel, wherein the nucleic acid staple strands are selected to form any of the foregoing nucleic acid structures when hybridized to the nucleic acid scaffold strand. In some embodiments, the methods further comprise combining the nucleic acid scaffold strand, the nucleic acid staple strands, and nucleic acid connector strands, wherein when the nucleic acid scaffold strand, the nucleic acid staple strands, and nucleic acid connector strands are hybridized to each other, they form a composite nucleic acid structure, such as any of the foregoing composite nucleic acid structures.

These and other aspects and embodiments provided herein are described in greater detail herein.

BRIEF DESCRIPTION OF DRAWINGS

FIGs. 1A-1B. DNA-origami polyhedra. (FIG. 1A) Polyhedra self-assembled from DNA tripods with tunable inter-arm angles, and comparison of their sizes and molecular weights with selected previous polyhedra (structures 1-9; see FIG. 5 for details). (FIG. 1B) Design diagram of a tripod. Cylinders represent DNA double helices. See FIG. 6 for details of the arm connection at the vertex. (FIG. 1C) Cylinder model illustrating the connection between two tripod monomers. (FIG. 1D and FIG. 1E) Connection schemes for assembling

(FIG. 1E) the tetrahedron and (FIG. 1D) other polyhedra (represented here by the cube design).

FIGs. 2A-2F. Self-assembly of DNA tripods and polyhedra. (FIG. 2A) Gel electrophoresis and (FIG. 2B) TEM images of the 60°-60°-60° (lane 1 in the gel) and 90°-90°-90° (lane 2) tripods. Gel lane 3: 1kb ladder. Gel electrophoresis: 1.5 % native agarose gel, ice water bath. (FIGS. 2C and 2D) Two schemes of connector designs and corresponding gel electrophoresis results. For each scheme, the strand model depicts the connection between two pairs of DNA duplexes. The number above a gel lane denotes the number of connected helices between two adjacent arms. Lane L: 1 kb ladder. Lane S: scaffold. Arrowheads indicate the bands corresponding to assembled cubes. (FIG. 2C) Scheme i: long (30 nt) connector (colored red) including a 2 nt sticky end. The complete 30 nt connector is only shown on the left, with a 28 nt segment anchored on the left helices and a 2 nt exposed sticky end available for hybridization with the 90°-90°-90° right neighbor (dashed circle depicts hybridization site). (FIG. 2D) Scheme ii: short (11 nt) connector including a 2 nt sticky end. (FIG. 2E) Assembly yields of the cubes, calculated as intensity ratio between a cube band and the corresponding scaffold band. (FIG. 2F) Agarose gel electrophoresis of the polyhedra. Lane 1: 90°-90°-90° monomer. Lanes 2-6: polyhedra. Lane 7: assembly reaction containing tripods without struts. Lane 8: assembly reaction containing 90°-90°-90° tripods without vertex helices. Lane 9: 1 kb ladder. Gel bands corresponding to desired products are marked with arrowheads. Gel electrophoresis: 0.8% native agarose gel, ice water bath.

FIGs. 3A-3E. TEM images of polyhedra. The zoomed-in (columns 1 and 2) and zoomed-out (column 3) images are shown for the tetrahedron (FIG. 3A), the triangular prism (FIG. 3B), the cube (FIG. 3C), the pentagonal prism (FIG. 3D), and the hexagonal prism (FIG. 3E). Images of the tetrahedron, the triangular prism, and the cube were acquired from purified samples. Images of the pentagonal prism and hexagonal prism were collected from crude samples (denoted with “*”). Scale bars are 100 nm in the zoomed-in TEM images and 500 nm in the zoomed-out images. Note that aggregates are clearly visible for unpurified samples (*e.g.* in the rightmost panel of D).

FIGs. 4A1-4G. 3D DNA-PAINT super-resolution fluorescence imaging of polyhedra. (FIG. 4A1) Staple strands at the vertices of each polyhedron were extended with single-stranded docking sequences for 3D DNA-PAINT super-resolution imaging. (FIGs. 4A1–4E1) Schematics of polyhedra with DNA-PAINT sites highlighted. (FIGs. 4A2–4E2) 3D DNA-PAINT super-resolution reconstruction of typical polyhedra shown in the same perspective as depicted in A1–E1. (FIGs. 4A3–4E3) 2D x-y-projection. (FIGs. 4A4–4E4) 2D x-z-projection. (FIG2. 4A5–4E5) Height measurements of the polyhedra obtained from the cross-sectional histograms in the x-z-projections. (FIG. 4F) A larger 2D super-resolution x-y-projection view of tetrahedra and drift markers (bright individual dots). The diffraction-limited image is super imposed on the super-resolution image in the upper half. (FIG. 4G) Tilted 3D view of a larger field of view image of the tetrahedron. Drift markers appear as bright individual dots. Scale bars: 200 nm. Color indicates height in the z direction.

FIG. 5. 20-60 megadalton DNA polyhedra. 20-60 megadalton DNA wireframe polyhedra assembled from tunable DNA-origami tripods. Top, schematics showing the assembly process of tripod monomers and the polyhedra; middle, TEM images of polyhedra; bottom, super-resolution fluorescence images of polyhedra. These polyhedra are significantly larger than previous DNA polyhedra in FIG. 1A, including (1) a cube (1), a truncated octahedron (11), a tetrahedron (13), an octahedron (12), (2) a tetrahedron, a dodecahedron, and a buckyball assembled from three-arm DNA tiles (16), (3) a DNA-origami tetrahedron (24), and (4) an icosahedron assembled from three DNA-origami monomers (5).

FIG. 6. Connections at the vertex the three-arm monomer. Three layers of connections at the vertex: (1) the first-layer (innermost) connections are formed by the scaffold strand only. There are no extra bases between the duplexes. (2) the second-layer (middle) connections and (3) the third-layer (outmost) connections are DNA duplexes (*i.e.*, the vertex helices) formed by staple strands and their complementary strands. Each polyhedron used different number of vertex helices with different lengths (see Table 2), which were estimated on the distances between the ends of the 16-helix arms at the vertexes. For detailed design and sequence information, refer to FIG. 8 to FIG. 13. The "*"s denote the helices where DNA handles were placed for DNA-PAINT.

FIGs. 7A-7C. Connection pattern. (FIG. 7A) A three-arm tripod monomer. (FIG. 7B) The cross-section of an arm of the three-arm monomer. The arrows in A and B indicate the same direction. The dotted line indicates the line of reflection symmetry. (FIG. 7C) The connection patterns that were implemented in FIG. 2B to FIG. 2E. See FIG. 8 to FIG. 13 for design and sequence details.

FIG. 8. Strand diagrams of the tetrahedron. The sequences used are provided in Table 4. The horizontal axis provides the position or length of the helix from the first base thereof. The vertical axis provides the helix number. As illustrated, there are three groupings of helices, each representing an arm. The 3 protrusions on the right side correspond to the 3

struts. The right end of the helices represents the free ends, while the left ends represent the ends at the vertex. Similarly renderings are provided in FIGs. 9-13.

FIG. 9. Strand diagrams of the triangular prism. The sequences used are provided in Table 5.

FIG. 10. Strand diagrams of the cube (short connectors). The sequences used are provided in Table 6.

FIG. 11. Strand diagrams of the cube (long connectors). The sequences used are provided in Table 7.

FIG. 12. Strand diagrams of the pentagonal prism. The sequences used are provided in Table 8.

FIG. 13. Strand diagrams of the hexagonal prism. The sequences used are provided in Table 9.

FIGs. 14A-14B. Schematics of nucleic acid structures having N arms, and N or more nucleic acid struts.

DETAILED DESCRIPTION OF INVENTION

The invention is based, in part, on the discovery and development of a general strategy for hierarchical self-assembly of polyhedra from megadalton monomers using a DNA "tripod", a 5 MD three-arm-junction origami tile that is 60 times more massive than previous three-arm tiles (16). The tripod motif features inter-arm angles controlled by supporting struts and strengthened by vertex helices. The invention further provides self-assembly of tripods into wireframe polyhedra using a dynamic connector design. Using this robust methodology, we constructed a tetrahedron (~20 MD), a triangular prism (~30 MD), a cube (~40 MD), a pentagonal prism (~50 MD), and a hexagonal prism (~60 MD) (FIG. 1A and FIG. 5).

These structures have a variety of applications including but not limited to biological applications. For example, when generated having edges widths on the order of about 100 nm, these polyhedra have a size comparable to bacterial microcompartments such as carboxysomes. Additional applications include without limitation use in or as photonic devices, nanoelectronics and drug delivery systems.

To characterize the 3D single-molecule morphology of these polyhedra, we used a DNA-based super-resolution fluorescence imaging method (resolution below the diffraction limit) called DNA-PAINT (28, 29) (a variation of point accumulation for imaging in nanoscale topography (30)). Unlike traditional transmission electron microscopy (TEM) which images the samples in a vacuum under dried and stained conditions and thus may not render the structure in its native form, 3D DNA-PAINT introduces minimal distortion to the structures by rendering them in a more "native" hydrated imaging environment.

General Tripod Design and Methodology

Disclosed herein are nucleic acid structures (alternatively referred to herein as structures) comprising at a minimum three nucleic acid arms (or arms). Such three arm structures are referred to herein as tripods. As will be understood, given the structure of a tripod, the three arms meet each other at a vertex and radiate outwards towards a free end on each arm. This disclosure contemplates and provides nucleic acid structures comprising more than three nucleic acid arms, including structures comprising four, five, six, seven, or more arms. Examples of such structures are provided in FIG. 14. In FIG. 14A, the longer thicker lines correspond to nucleic acid arms and the shorter thinner lines correspond to nucleic acid struts. In FIG. 14B and C, only nucleic acid arms are illustrated but it is to be understood that such nucleic acid structures comprise nucleic acid struts also.

The nucleic acid arms within a structure (or within a composite structure) are typically of identical length. They are not however so limited and may differ in length depending on the embodiment.

Of particular significance and as provided herein, the nucleic acid arms exist at fixed angles with each other. This is achieved through the use of nucleic acids that are positioned between arms of a structure; these nucleic acids are referred to as nucleic acid struts (or struts). Each nucleic acid strut is connected to two nucleic acid arms in a single structure, thereby maintaining the angular distance between the two arms. The nucleic acid struts may be positioned anywhere along the length of the arms. The position of the strut along the length of the arm (from the vertex) and the length of the strut together can influence the angular distance between the arms. The angular distance between the arms can also be controlled in part by the vertex nucleic acids and other connections existing at the vertex including the nucleic acid connectors interactions. Examples of strut lengths and strut positions along an arm from the vertex are provided in Table 1 for a number of nucleic acid structures. As will be clear from the Table and from the remaining disclosure, struts in a structure (or within a composite structure) may be of identical length or of differing length.

It is to be understood nucleic acid structures may be produced having any particular defined angular distance between their arms, and any number of arms, based on the methodology provided herein. In this respect, the structures are considered to be "tunable" because an end user is able to modify the synthesis method in order to obtain structures of choice.

The arms of the structure may be referred to herein for clarity as the x, y and z arms, for example in the context of a tripod structure. In this structure, typically one (but optionally more than one) strut connects arms x and y, typically one (but optionally more than one) strut connects arms y and z, and typically one (but optionally more than one) strut connects arms z and x. These struts may be referred to, again for clarity, as the xy strut, the yz strut, and the zx strut. In the case of a tripod, each arm is connected to every other arm in the structure. In the case of a structure having more than three arms, all adjacent arms will typically be connected to each other by struts, and optionally non-adjacent arms may also be connected to each other by struts as well. It may be desirable to include struts between non-adjacent arms in order to provide greater structural integrity. As an example, in FIG. 14A, the second structure shown comprises four arms, and four struts between adjacent arms. This structure may also comprise additional struts between non-adjacent arms such as between the "north" and "south" arms and/or the "west" and "east" arms, imagining that the arms are directions on a compass for the sake of explanation.

Thus, the minimum number of arms is 3, and the minimum number of struts is 3. The disclosure contemplates structures having 3 or more arms and 3 or more struts. The number of struts is typically equal to or greater than the number of arms.

Accordingly, provided herein is a nucleic acid structure comprising a first (x), a second (y), and a third (z) nucleic acid arm, each connected at one end to the other arms to form a vertex, and a first, a second, and a third nucleic strut, wherein the first nucleic acid strut connects the first (x) nucleic arm to the second (y) nucleic arm, the second nucleic acid strut connects the second (y) nucleic arm to the third (z) nucleic arm, and the third nucleic acid strut connects the third (z) arm to the first (x) nucleic acid strut.

Provided herein is a nucleic acid structure comprising three nucleic acid arms radiating from a vertex at fixed angles. Such structures may have more than three arms, including 4, 5, 6, 7 or more arms.

Further provided herein is a nucleic acid structure comprising N nucleic acid arms radiating from a vertex, wherein N is the number of nucleic acid arms and is 3 or more, and M nucleic acid struts, each strut connecting two nucleic acid arms to each other, wherein M is the number of nucleic acid struts and is 3 or more. N may be equal to M or it may be less than M. Examples include a nucleic acid structure that comprises 4 nucleic acids and at least

4 nucleic acid struts, or a nucleic acid structure that comprises 5 nucleic acid arms and at 5 nucleic acid struts.

In some embodiments, nucleic acid arms (including adjacent arms) within a structure are equally spaced apart from each other. In other words, the arms are separated from each other by the same angle, or the angular distance between the arms is the same. An example of this is a three arm structure in which adjacent arms are separated from each other by a 60°C angle. This tripod is referred to as 60°C - 60°C - 60°C. Tripods of this type, when connected to each other, will form a tetrahedron. Thus, it will be understood that the angular distance between the arms also dictates how to such structures will connect with each other and the ultimate 3D shape (or composite nucleic acid structure) to be formed. Another example is a three arm structure in which adjacent arms are separated from each other by a 90°C angle. This tripod is referred to as 90°C - 90°C - 90°C. Tripods of this type, when connected to each other, will form a cube.

In some embodiments, nucleic acid arms (including adjacent arms) within a structure are not equally spaced apart from each other. In other words, the arms are separated from each other by a different angle, or the angular distance between the arms is different. An example of this is a three arm structure in which some adjacent arms are separated from each other by a 60°C angle and other adjacent arms are separated from each other by a 90°C angle. Such a tripod may be referred to as 90°C - 90°C - 60°C. Tripods of this type, when connected to each other, will form a triangular prism. Another example is a three arm structure in which some adjacent arms are separated from each other by a 108°C angle and other adjacent arms are separated from each other by a 90°C angle. This tripod is referred to as 90°C - 90°C - 108°C. Tripods of this type, when connected to each other, will form a pentagonal prism. Another example is a three arm structure in which some adjacent arms are separated from each other by a 120°C angle and other adjacent arms are separated from each other by a 90°C angle. This tripod is referred to as 90°C - 90°C - 120°C. Tripods of this type, when connected to each other, will form a hexagonal prism.

As will be understood based on this disclosure, the nucleic acid structures arrange their arms (three or more of their arms) so as to form a vertex. The arm ends that exist at the vertex may be connected to each other through nucleic acid helices or through nucleic acid connectors (or connector strands), or through a combination of helices and connector strands. Examples of this are illustrated in FIG. 6. The lengths of vertex helices in the first and second layers are provided in Table 2. Typically 0-6 vertex helices are present in a structure. Thus, the structures may further comprise vertex nucleic acids such as vertex helices. Some composite structures may not comprise vertex helices. An example is the tetrahedron which can be formed from the attachment of two tripod structures without vertex helices.

The structures may further comprise connector nucleic acids. These connector nucleic acids may be located at the vertex and/or at the free ends of arms. In the latter instance, such connector nucleic acids facilitate the attachment of two nucleic acid structures to each other, thereby forming a composite nucleic acid structure.

Each nucleic acid arm in a structure therefore typically has one end located at the vertex and one free end (*i.e.*, an end not located at the vertex). The free end may be a blunt end, meaning that it lack any single stranded nucleic acid sequence. Alternatively it may be a sticky end, meaning that it comprises a single-stranded nucleic acid sequence. That sequence, referred to as an overhang, may be 1 or 2 nucleotides in length. It may be longer, although 1-2 nucleotides are suitable and in some instances may result in more efficient synthesis of composite nucleic acids (and thus greater yields of such composites). The overhang may be provided by connector nucleic acids. Such connector nucleic acids may be present in the initial hybridization reaction or they may be added post-synthesis of the nucleic acid structures, with or without purification of the synthesized structures. The connector nucleic acids (also referred to herein as connector strands) may be of any length although it has been found that shorter lengths result in higher composite nucleic acid structure yields. FIG. 2 C provides a schematic of a longer connector strand (on the order of 30 nucleotides with a 2 nucleotide overhang). FIG. 2D provides a schematic of a shorter connector strand (on the order of 11 nucleotides with a 2 nucleotide overhang). The structures of FIG. 2C and 2D were used to form composite nucleic acid structures that are cubes. The yields of such cubes are shown in FIG. 2E. The top line corresponds to the shorter connector and the bottom line corresponds to the longer connector. Thus, the shorter connector led to higher yield of its composite cube. Although not intending to be bound by any theory, the lower yields using the longer connector strands may be because mismatched composites (or mismatched composite intermediates) comprising longer connector strands may be more stable while mismatched composites (or mismatched composite intermediates) comprising shorter connectors may be less stable and therefore more likely to dissociate and re-associate to form properly matched composite and composite intermediates. As used herein, a composite intermediate comprises a subset of the nucleic acid structures needed to form a composite structure. For example, if the desired composite is a cube (which requires 4 structures), then an intermediate may consist of 2 or 3 structures.

The disclosure contemplates that the connector may be of any length, including lengths of 50 or fewer nucleotides, 40 or fewer nucleotides, 30 or fewer nucleotides, 25 or fewer nucleotides, 20 or fewer nucleotides, 15 or fewer nucleotides, 10 or fewer nucleotides, or 5 or fewer nucleotides. The connector may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more nucleotides.

The nucleic acid structures may be of any size although typically they are in the range of up to about 5 megadaltons (MD). Thus, they may be 3, 4, 5, or 6 MD in some embodiments. The length of the nucleic acid arms is dictated by the desired rigidity and by their method of synthesis. For example, the structures described herein have arms made of 16 parallel double helices. Since they were made using DNA origami techniques starting with the M13 scaffold strand, the length of the arms is typically about 50 nm. It is to be understood that if a scaffolds of a different length was used, or if the arms were designed to have a different number of double helices (for example if more or less rigidity and strength was desired), then the length of the arm could vary from that described herein. Assuming the nucleic acid structures have arms of 50 nm, and assuming all arms are of equal length, then it will be understood that composite nucleic acid structures will have edges widths on the order of 100 nm. Thus the composites that may be generated according to this disclosure may be defined as having edge widths that are at least 100 nm, including 120, 140, 160, 180, 200, or more nm. In some instances, the composites may have edge widths of 80 nm or more.

The nucleic acid arms, nucleic acid struts and vertex nucleic acids may be comprised of double helices such as parallel double helices. Illustrated herein are arms comprised of 16 parallel double helices each, struts comprised of 2 parallel double helices each, and vertex nucleic acids comprised of a single double helix each. When more than one double helix is present, there typically be cross-over strands that hybridize to parallel helices and thereby promote the proximity of the helices and ultimately rigidity thereof.

It is to further understood that the nucleic acid structures disclosed herein may be synthesized using any number of nucleic acid nanostructure synthesis methods including without limitation DNA origami and DNA single stranded tiles (SST). These techniques are known in the art, and are described in greater detail in U.S. Patent Nos. 7,745,594 and 7,842,793; U.S. Patent Publication No. 2010/00696621; and Goodman et al. Nature Nanotechnology.

The nucleic acid structures may be used to generate larger structures referred to herein as composite nucleic acid structures (or composites or composite structures). Composite structures are formed through the connection of nucleic acid structures to each other.

Typically the nucleic acid structures are identical in terms of length and angle definition. Thus a plurality of identical nucleic acid structures are combined in a single reaction vessel, and allowed to attached to each other to form larger 3D structures via connections of their free arm ends. Such connections may be facilitated by the presence (or inclusion) of connector strands, although the synthesis method is not so limited.

Therefore, disclosed and provided herein is a composite nucleic acid structure comprising L nucleic acid structures, wherein L is the number of nucleic acid structures, and wherein the L nucleic acid structures are connected to each other at free (non-vertex) ends of the nucleic acid arms. The number of structures needed to make a composite will depend on the composite structure desired and the structures used as components. In some instances, the composite structure may comprise two, four, six, eight, ten, twelve or more nucleic acid structures each of which has three arms. As illustrated throughout, this methodology may be used to generate composite nucleic acid structures that are tetrahedrons, triangular prisms, cubes, pentagonal prisms, or hexagonal prisms. It is to be understood that any arbitrary composite structure may be made using the methodology provided herein. These composites may be of virtually any size, including but not limited to . Illustrated herein are composite nucleic acid structures that are 20 megadaltons (MD), 30 MD, 40 MD, 50 MD, and 60 MD in size.

The composites may be generated immediately following the generation of the nucleic acid structures and thus in the same vessel as the structures. Connector strands, if used, may be present at the beginning of the hybridization reaction or may be added once the structures are formed and prior to formation of the composites. Such single reaction vessel synthesis is referred to as “one-pot” annealing.

Below are more detailed and exemplary descriptions of the particular nucleic acid structures, and particular composite nucleic acid structures, and their methods of synthesis. These descriptions are meant to be exemplary and not limiting as to the breadth of this disclosure. For example, it is to be understood that although much of the following description and exemplification involves 3-arm “tripod” nucleic acid structures, the teachings may be generalized to structures of any number of arms as described herein.

Exemplary Tripod Design and Methodology

Assembly strategy of polyhedra and design features of tripods.

In one-pot annealing, the scaffold and staple strands first assemble into a tripod origami monomer, and then the tripods (without intermediate purification) assemble into the polyhedron (FIG. 1A). It is also contemplated that the tripod monomers may be purified prior to the final assembly into composite nucleic acid structures. Diverse polyhedra can be constructed by using tripods with different designed inter-arm angles. The tripod has three typically equal-length (*e.g.*, ~50 nm) stiff arms connected at the vertex (see FIG. 6 for connection details) with controlled inter-arm angles (FIG. 1B). To ensure stiffness, each arm contains a sufficient number (*e.g.*, 16) of parallel double-helices packed on a honeycomb lattice (*5*) with twofold rotational symmetry. A supporting "strut" consisting of two double-helices controls the angle between the two arms. The tripod is named according to its three inter-arm angles (*e.g.* the tetrahedron and the cube are respectively assembled from 60°-60°-60° and 90°-90°-90° tripods). To avoid potential unwanted aggregation resulting from blunt-end stacking of DNA helices (*5*), up to six short DNA double-helices (denoted "vertex helices") are included at the vertex to partially conceal its blunt duplex ends (FIG. 1B; the number of helices and their lengths vary for different polyhedra, see FIG. 6 and Table 2 for details). Additionally, the vertex helices are expected to help maintain inter-arm angles by increasing rigidity of the vertices. Two connection strategies are used to assemble tripods into polyhedra. To facilitate exposition, the three arms are denoted as X-arm, Y-arm, and Z-arm (FIG. 1C). Connecting X-arm to X-arm and Y-arm to Z-arm produces polyhedra (such as a cube; FIG. 1D) other than the tetrahedron, which is assembled by connecting X to X, Y to Y, and Z to Z (FIG. 1E).

Tripod conformation control with struts.

First, we verified that the inter-arm angle was controlled by the length of the supporting strut. Gel electrophoresis of 60°-60°-60° and 90°-90°-90° tripods revealed a dominant band for each tripod (FIG. 2A), confirming their correct formation. Consistent with its more compact designed conformation, the 60°-60°-60° tripod migrated slightly faster than the 90°-90°-90° one. The two tripod bands were each purified, imaged by TEM, and showed designed tripod-like morphologies (FIG. 2B). The measured inter-arm angles were slightly smaller than designed (53±5° [SD, $n = 60$] for 60°-60°-60° tripods; 87±4° [SD, $n = 60$] for 90°-90°-90° tripods), possibly reflecting a small degree of strut bending.

Connector designs.

The strands connecting the tripods are called "connectors." Connector designs affected the polyhedra assembly yields. Two designs were tested for the cube. In scheme i, each 30-base connector spanned two adjacent tripods, with a 28-base segment anchored on one tripod and another 2-base (sticky end) on the other (FIG. 6; see FIG. 7 for details). Gel electrophoresis (quantified in FIG. 2E) revealed that the assembly yield was affected by the number of connected helices (n): a product band was only observed for $4 \leq n \leq 12$; for $n < 4$, the dominant band were monomers, likely reflecting overly weak inter-monomer connections; for $n > 12$, aggregations dominated.

In scheme i, the connectors were stably anchored (forming 28 base pairs) on tripods before inter-monomer connection occurred. In scheme ii, the connector was shortened from 30 to 11 bases so that it should only be anchored to two adjacent tripods by 9-base and 2-base segments in the assembled cube (FIG. 2D), and only dynamically binds to a monomeric tripod. Compared with the stably attached connector design, the dynamic connector design is expected to reduce inter-monomer mismatches that may occur during the assembly, as such mismatches would be less likely frozen in a kinetic trap. Indeed, scheme ii showed substantially increased assembly yield (FIG. 2E). It was thus used for subsequent polyhedra designs, except for the tetrahedron, where scheme i produced sufficient yield for this relatively simple structure. The assembly yields were estimated from the gel (FIG. 2F). The 90°-90°-90° monomer sample (FIG. 2F, lane 1) showed a strong monomer band and a putative dimer band (not studied by TEM, ~27% intensity compared to the monomer). We define the assembly yield of a polyhedron as the ratio between its product band intensity and the combined intensity of the 90°-90°-90° monomer and dimer bands (lane 1), and obtained yields of 45%, 24%, 20%, 4.2%, and 0.11% for the tetrahedron, the triangular prism, the cube, the pentagonal prism, and the hexagonal prism, respectively (FIG. 2F).

Polyhedra assembly.

The lengths and the attachment points of the struts varied for each polyhedron (Table 1). The tetrahedron, the triangular prism, the cube, the pentagonal prism, and the hexagonal prism should be assembled from monomers with designed 60°-60°-60°, 90°-90°-60°, 90°-90°-90°, 90°-90°-108°, and 90°-90°-120° angles, respectively (FIG. 1B). The first three monomers indeed produced tetrahedra, triangular prisms, and cubes [verified by gel electrophoresis (FIG. 2F) and TEM imaging (FIG. 3, A to C)], suggesting accurate control for angles within 90°. However, the pentagonal prism was assembled from monomers with designed angles of 90°-90°-120° (instead of 90°-90°-108°), and the hexagonal prism from 90°-90°-140° (instead of 90°-90°-120°). Thus the assembly of these two polyhedra requires monomers with designed Y-Z angles greater than the design criteria. This requirement likely reflects slight bending of the relevant struts, which could be compensated by using longer struts.

Effects of struts and vertex helices on polyhedra assembly.

We next verified that both the struts and the vertex helices were required for the tripods to assemble into the designed polyhedron. Three samples were prepared for cube assembly using tripods that contain (i) both the struts and the vertex helices (FIG. 2F, lane 4), (ii) the vertex helices but not the struts (lane 7), and (iii) the struts but not the vertex helices (lane 8; the samples were subjected to gel electrophoresis after annealing). The first sample showed a sharp strong band corresponding to the cube (verified by TEM, FIG. 3B). The second failed to produce any clear product band. The third produced substantial aggregates, and a clear but weak band with mobility comparable to the triangular prism. This band may correspond to a hexamer, but its molecular morphology was not investigated. Based on the above experiments, we included both the struts and the vertex helices in the tripods for subsequent polyhedra assembly.

TEM characterization.

Product bands were purified and imaged under TEM. For the tetrahedron, the triangular prism, and the cube, most structures appeared as intact polyhedra; a small fraction of broken structures (< 20%) were likely ruptured during the purification and imaging (FIG. 3, A to C). In contrast, few intact structures were observed for the purified pentagonal and hexagonal prisms (data not shown). Thus, unpurified samples for these two were directly imaged and the expected molecular morphologies were observed (FIG. 3, D and E, for exemplary images, further images available but not shown). The struts are clearly visible in many images.

3D DNA-PAINT super-resolution microscopy.

Localization-based 3D super-resolution fluorescence microscopy (*31-33*) offers a minimally invasive way to obtain true single molecule 3D images of DNA nanostructures in their “native” hydrated environment. In stochastic reconstruction microscopy (*34*), most molecules are switched to a fluorescent dark (OFF) state, and only a few emit fluorescence (ON state). Each molecule is localized with nanometer precision by fitting its emission to a 2D Gaussian function. In DNA-PAINT, the “switching” between ON- and OFF-states is facilitated by repetitive, transient binding of fluorescently labeled oligonucleotides ("imager" strands) to complementary "docking" strands (*24, 28, 29, 35*).

We extended DNA-PAINT to 3D imaging (*29*) by using optical astigmatism (*31, 36*), in which a cylindrical lens used in the imaging path "converts" the spherical point spread function (PSF) of a molecule to an elliptical PSF when imaged out of focus. The degree and orientation of the elliptical PSF depends on the displacement and direction of the point source from the current focal imaging plane, and is used to determine its *z* position (*31, 36*). We applied 3D DNA-PAINT to obtain sub-diffraction-resolution single-molecule images of the polyhedra. To ensure all the vertices of a polyhedron will be imaged, each vertex is modified with multiple (about eighteen) 9-nt docking strands (Staple–TTATCTACATA–3'; SEQ ID NO: 1) (FIG. 4A1) in a symmetric arrangement (FIG. 6). For surface immobilization, a subset of strands along the polyhedron edges were modified with 21-nt extensions (Staple–TTCGGTTGTACTGTGACCGATTC–3'; SEQ ID NO: 2), which were hybridized to biotinylated complementary strands attached to a streptavidin covered glass slide (Biotin–GAATCGGTCACAGTACAACCG–3'; SEQ ID NO: 3).

Using 3D DNA-PAINT microscopy, all five polyhedra showed designed 3D patterns of vertices (FIG. 4, columns 1-4) with expected heights (FIG. 4, A5-E5), suggesting that the solution shape of the structures is maintained during surface immobilization and imaging. We quantified the tetrahedra formation and imaging yields (FIG. 4, F and G). 253 out of 285 structures (89%) contained 4 spots in the expected tetrahedral geometry. Height measurement yielded 82±15 nm, consistent with the designed value (82 nm). Single DNA-PAINT binding events were localized with an accuracy of 5.4 nm in *x-y* and 9.8 nm in *z* [see below for how localization accuracy was determined]. This *z* localization accuracy almost completely accounts for the 15 nm spread in the height measurement distribution. The calculated localization precisions translate to an obtainable resolution of ~13 nm in *x* and *y*, and ~24 nm in *z*.

Previous work demonstrated diverse DNA polyhedra self-assembled from small 3-arm-junction tiles (~80 kD) (*16*), which consist of three double-helix arms connected by flexible single-stranded hinges. However, straightforward implementation of megadalton 3-arm origami tiles using similar flexible inter-arm hinges (*i.e.* tripods with no struts or vertex helices) failed to produce well-formed polyhedra (Fig. 2B, lane 7). An origami tripod contains 50 times more distinct strands than previous 3-arm-junction tiles (formed from 3 distinct strands) and is 60 times more massive in molecular weight. Apart from the challenges associated with the more error-prone construction of the more complex monomers from individual strands, successful hierarchical assembly of such large monomers into polyhedra also needs to overcome much slower reaction kinetics, caused by the larger size and lower concentration of the tripod monomers. The stiff DNA tripods, with rationally designed inter-arm angles controlled by supporting struts and vertex helices, lead to successful construction of diverse polyhedra, suggesting that conformation control of branched megadalton monomers can facilitate their successful assembly into higher order structures.

The design principles of DNA tripods may be extended to stiff megadalton *n*-arm ($n \geq 4$) branched motifs with controlled inter-arm angles. Self-assembly with such *n*-arm motifs could be used to construct more sophisticated polyhedra, and potentially extended 2D and 3D lattices with sub-100 nm tunable cavities.

Such structures could potentially be used to template guest molecules for diverse applications, *e.g.* spatially arranging multiple enzymes into efficient reaction cascades (*37*) or nanoparticles to achieve useful photonic properties (*38, 39*). Furthermore, the DNA polyhedra constructed here, with a size comparable to bacterial microcompartments, may potentially be used as skeletons for making compartments with precisely controlled dimensions and shapes by wrapping lipid membranes around their outer surfaces (*40*). Such membrane-enclosed microcompartments could potentially serve as bioreactors for synthesis of useful products or as delivery vehicles for therapeutic cargo (*25*).

For 3D characterization of DNA nanostructures, super-resolution fluorescence microscopy (*e.g.* 3D DNA-PAINT) provides complementary capabilities to present electron microscopy (*e.g.* cryo-EM (*12, 16, 17, 23*)). While cryo-EM offers higher spatial resolution imaging of unlabeled structures, DNA-PAINT is less technically involved to implement, obtains true single molecule images of individual structures (rather than relying on class averaging), and preserves the multi-color capability of fluorescence microscopy (*29*). Additionally, DNA-PAINT in principle allows for observation of dynamic structural changes of nanostructures in their "native" hydrated environment, currently suitable for slow changes on the minutes timescale (*e.g.* locomotion of synthetic DNA walkers) and potentially for faster motions with further development.

Table 1. Strut designs of the polyhedra. All units are nanometers. Designed length of the strut connecting (i) Y-arm and Z-arm, (ii) X-arm and Z-arm, or (iii) X-arm and Y-arm. Designed distance from the vertex to the strut attachment point on (iv) X-, (v) Y-, or (vi) Z-arm.

	i	ii	iii	iv	v	vi
Tetrahedron	28	28	28	29	29	29
Triangular prism	18	26	26	18	18	18
Cube	30	30	30	21	21	21
Pentagonal prism	32	26	26	19	18	18
Hexagonal prism	37	28	28	20	20	20

Table 2.

	Number of 1st-layer helices	length of 1st-layer helices	Number of 2nd-layer helices	Length of 2nd-layer helices
Tetrahedron	0	n/a	0	n/a
Triangular prism	3	15bp, 15bp, 18bp	0	n/a
Cube	3	15bp, 15bp, 15bp	3	15bp, 15bp, 15bp
Pentagonal prism	3	15bp, 15bp, 12bp	0	n/a
Hexagonal prism	3	24bp, 24bp, 12bp	3	19bp, 19bp, 15bp

Nucleic Acid Nanostructure Methodology Generally

The nucleic acid structures provided herein may be formed using any nucleic acid folding or hybridization approach. One such approach is DNA origami (Rothemund, 2006, Nature, 440:297-302, incorporated herein by reference in its entirety). In a DNA origami approach, a structure is produced by the folding of a longer "scaffold" nucleic acid strand through its hybridization to a plurality of shorter "staple" oligonucleotides, each of which hybridize to two or more non-contiguous regions within the scaffold strand. In some embodiments, a scaffold strand is at least 100 nucleotides in length. In some embodiments, a scaffold strand is at least 500, at least 1000, at least 2000, at least 3000, at least 4000, at least 5000, at least 6000, at least 7000, or at least 8000 nucleotides in length. The scaffold strand may be naturally or non-naturally occurring. The scaffold typically used in the M13mp18 viral genomic DNA, which is approximately 7 kb. Other single stranded scaffolds may be used including for example lambda genomic DNA. Staple strands are typically less than 100 nucleotides in length; however, they may be longer or shorter depending on the application and depending upon the length of the scaffold strand. In some embodiments, a staple strand may be about 15 to about 100 nucleotides in length. In some embodiments the staple strand is about 25 to about 50 nucleotides in length.

In some embodiments, a nucleic acid structure may be assembled in the absence of a scaffold strand (*e.g.*, a scaffold-free structure). For example, a number of oligonucleotides (*e.g.*,< 200 nucleotides or less than 100 nucleotides in length) may be assembled to form a nucleic acid nanostructure. This approach is described in WO 2013/022694 and WO 2014/018675, each of which is incorporated herein by reference in its entirety.

Other methods for assembling nucleic acid structures are known in the art, any one of which may be used herein. (See for example Kuzuya and Komiyama, 2010, Nanoscale, 2:310-322. It is also to be understood that a combination or hybrid of these methods may also be used to generate the nucleic acid structures disclosed herein. These methods may be modified based on the teaching provided herein in order to obtain the fixed-angle nucleic acid structures of this disclosure.

Nucleic acids

The nucleic acid structures may comprise naturally occurring and/or non-naturally occurring nucleic acids. If naturally occurring, the nucleic acids may be isolated from natural sources or they may be synthesized apart from their naturally occurring sources. Non-naturally occurring nucleic acids are synthetic.

The terms “nucleic acid”, “oligonucleotide”, and “strand” are used interchangeably to mean multiple nucleotides attached to each other in a contiguous manner. A nucleotide is a molecule comprising a sugar (*e.g.* a deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a pyrimidine (*e.g.*, cytosine (C), thymidine (T) or uracil (U)) or a purine (*e.g.*, adenine (A) or guanine (G)). In some embodiments, the nucleic acid may be L-DNA. In some embodiments, the nucleic acid is not RNA or an oligoribonucleotide. In these embodiments, the nucleic acid structure may be referred to as a DNA structure. A DNA structure however may still comprise base, sugar and backbone modifications.

Modifications

A nucleic acid structure may be made of DNA, modified DNA, and combinations thereof. The oligodeoxyribonucleotides (also referred to herein as oligonucleotides, and which may be staple strands, connector strands, and the like) that are used to generate the nucleic acid structure or that are present in the nucleic acid structure may have a homogeneous or heterogeneous (*i.e.*, chimeric) backbone. The backbone may be a naturally occurring backbone such as a phosphodiester backbone or it may comprise backbone modification(s). In some instances, backbone modification results in a longer half-life for the oligonucleotides due to reduced nuclease-mediated degradation. This is turn results in a longer half-life. Examples of suitable backbone modifications include but are not limited to phosphorothioate modifications, phosphorodithioate modifications, p-ethoxy modifications, methylphosphonate modifications, methylphosphorothioate modifications, alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), alkylphosphotriesters (in which the charged oxygen moiety is alkylated), peptide nucleic acid (PNA) backbone modifications, locked nucleic acid (LNA) backbone modifications, and the like. These modifications may be used in combination with each other and/or in combination with phosphodiester backbone linkages.

Alternatively or additionally, the oligonucleotides may comprise other modifications, including modifications at the base or the sugar moieties. Examples include nucleic acids having sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position (*e.g.*, a 2'-O-alkylated ribose), nucleic acids having sugars such as arabinose instead of ribose. Nucleic acids also embrace substituted purines and pyrimidines such as C-5 propyne modified bases (Wagner *et al.*, *Nature Biotechnology* 14:840-844, 1996). Other purines and pyrimidines include but are not limited to 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine. Other such modifications are well known to those of skill in the art.

Modified backbones such as phosphorothioates may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl-and alkyl-phosphonates can be made, *e.g.*, as described in U.S. Pat. No. 4,469,863, and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092574) can be prepared by automated solid phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described (Uhlmann, E. and Peyman, A., Chem. Rev. 90:544, 1990; Goodchild, J., *Bioconjugate Chem.* 1:165, 1990).

Nucleic acids can be synthesized *de novo* using any of a number of procedures known in the art including, for example, the b-cyanoethyl phosphoramidite method (Beaucage and Caruthers *Tet. Let.* 22:1859, 1981), and the nucleoside H-phosphonate method (Garegg *et al.*, *Tet. Let.* 27:4051-4054, 1986; Froehler *et al.*, *Nucl. Acid. Res.* 14:5399-5407, 1986; Garegg *et al.*, *Tet. Let.* 27:4055-4058, 1986, Gaffney *et al.*, *Tet. Let.* 29:2619-2622, 1988). These chemistries can be performed by a variety of automated nucleic acid synthesizers available in the market. These nucleic acids are referred to as synthetic nucleic acids. Modified and unmodified nucleic acids may also be purchased from commercial sources such as IDT and Bioneer.

An isolated nucleic acid generally refers to a nucleic acid that is separated from components with which it normally associates in nature. As an example, an isolated nucleic acid may be one that is separated from a cell, from a nucleus, from mitochondria, or from chromatin.

The nucleic acid structures and the composite nucleic acid structures may be isolated and/or purified. Isolation, as used herein, refers to the physical separation of the desired entity (*e.g.*, nucleic acid structures, etc.) from the environment in which it normally or naturally exists or the environment in which it was generated. The isolation may be partial or complete.

Isolation of the nucleic acid structure may be carried out by running a hybridization reaction mixture on a gel and isolating nucleic acid structures that migrate at a particular molecular weight and are thereby distinguished from the nucleic acid substrates and the spurious products of the hybridization reaction. As another example, isolation of nucleic acid structures may be carried out using a buoyant density gradient, sedimentation gradient centrifugation, or through filtration means.

Agents

The composite nucleic acid structures may contain an agent that is intended for use *in vivo* and/or *in vitro*, in a biological or non-biological application. For example, an agent may be any atom, molecule, or compound that can be used to provide benefit to a subject (including without limitation prophylactic or therapeutic benefit) or that can be used for diagnosis and/or detection (for example, imaging) *in vivo*, or that may be used for effect in an *in vitro* setting (for example, a tissue or organ culture, a clean-up process, and the like). The agents may be without limitation therapeutic agents and diagnostic agents. Examples of agents for use with any one of the embodiments described herein are described below.

In some aspects, the composite nucleic acid structures are used to deliver agent either systemically or to localized regions, such as for example tissues or cells. Any agent may be delivered using the methods of the invention provided that it can be loaded into the composite strucure.

The agent may be without limitation a chemical compound including a small molecule, a protein, a polypeptide, a peptide, a nucleic acid, a virus-like particle, a steroid, a proteoglycan, a lipid, a carbohydrate, and analogs, derivatives, mixtures, fusions, combinations or conjugates thereof. The agent may be a prodrug that is metabolized and thus converted *in vivo* to its active (and/or stable) form. The invention further contemplates the loading of more than one type of agent in a composite structure and/or the combined use of composite structures comprising different agents.

One class of agent is peptide-based agents such as (single or multi-chain) proteins and peptides. Examples of peptide-based agents include without limitation antibodies, single chain antibodies, antibody fragments, enzymes, co-factors, receptors, ligands, transcription factors and other regulatory factors, some antigens (as discussed below), cytokines, chemokines, hormones, and the like.

Another class of agents includes chemical compounds that are non-naturally occurring.

A variety of agents that are currently used for therapeutic or diagnostic purposes include without limitation imaging agents, immunomodulatory agents such as immunostimulatory agents and immunoinhibitory agents (*e.g.*, cyclosporine), antigens, adjuvants, cytokines, chemokines, anti-cancer agents, anti-infective agents, nucleic acids, antibodies or fragments thereof, fusion proteins such as cytokine-antibody fusion proteins, Fc-fusion proteins, analgesics, opioids, enzyme inhibitors, neurotoxins, hypnotics, anti-histamines, lubricants, tranquilizers, anti-convulsants, muscle relaxants, anti-Parkinson agents, anti-spasmodics, muscle contractants including channel blockers, miotics and anti-cholinergics, anti-glaucoma compounds, modulators of cell-extracellular matrix interactions including cell growth inhibitors and anti-adhesion molecules, vasodilating agents, inhibitors of DNA, RNA or protein synthesis, anti-hypertensives, anti-pyretics, steroidal and non-steroidal anti-inflammatory agents, anti-angiogenic factors, anti-secretory factors, anticoagulants and/or antithrombotic agents, local anesthetics, ophthalmics, prostaglandins, targeting agents, neurotransmitters, proteins, cell response modifiers, and vaccines.

In some embodiments, an agent is a diagnostic agent such as an imaging agent. As used herein, an imaging agent is an agent that emits signal directly or indirectly thereby allowing its detection *in vivo*. Imaging agents such as contrast agents and radioactive agents can be detected using medical imaging techniques such as nuclear medicine scans and magnetic resonance imaging (MRI). Imaging agents for magnetic resonance imaging (MRI) include Gd(DOTA), iron oxide or gold nanoparticles; imaging agents for nuclear medicine include ^{201}Tl, gamma-emitting radionuclide 99 mTc; imaging agents for positron-emission tomography (PET) include positron-emitting isotopes, (18)F-fluorodeoxyglucose ((18)FDG), (18)F-fluoride, copper-64, gadoamide, and radioisotopes of Pb(II) such as 203Pb, and 11In; imaging agents for *in vivo* fluorescence imaging such as fluorescent dyes or dye-conjugated nanoparticles.

The present disclosure further provides the following numbered embodiments:

1. A nucleic acid structure comprising

a first (x), a second (y), and a third (z) nucleic acid arm, each connected at one end to the other arms to form a vertex, and

a first, a second, and a third nucleic strut, wherein the first nucleic acid strut connects the first (x) nucleic arm to the second (y) nucleic arm, the second nucleic acid strut connects the second (y) nucleic arm to the third (z) nucleic arm, and the third nucleic acid strut connects the third (z) arm to the first (x) nucleic acid strut.

2. A nucleic acid structure comprising

three nucleic acid arms radiating from a vertex at fixed angles.

3. A nucleic acid structure comprising

N nucleic acid arms radiating from a vertex, wherein N is the number of nucleic acid arms and is 3 or more, and

M nucleic acid struts, each strut connecting two nucleic acid arms to each other, wherein M is the number of nucleic acid struts and is 3 or more.

4. The nucleic acid structure of embodiment 3, wherein N is equal to M.

5. The nucleic acid structure of embodiment 3, wherein N is less than M.

6. The nucleic acid structure of any one of embodiments 1-5, wherein the nucleic acid structure comprises 4 nucleic acids and at least 4 nucleic acid struts, or 5 nucleic acid arms and at 5 nucleic acid struts.

7. The nucleic acid structure of any one of embodiments 1-6, wherein the nucleic acid arms are equally spaced apart from each other (or the arms are separated from each other by the same angle).

8. The nucleic acid structure of any one of embodiments 1-7, wherein the nucleic acid arms are not equally separated from each other (or the arms are separated from each other by different angles).

9. The nucleic acid structure of any one of embodiments 1-8, further comprising a vertex nucleic acid.

10. The nucleic acid structure of any one of embodiments 1-9, further comprising a connector nucleic acid.

11. The nucleic acid structure of any one of embodiments 1-10, wherein the nucleic acid arms, nucleic acid struts, and/or vertex nucleic acid are comprised of parallel double helices.

12. The nucleic acid structure of any one of embodiments 1-11, wherein nucleic acid arms are of identical length.

13. The nucleic acid structure of any one of embodiments 1-12, wherein the nucleic acid struts are of identical length.

14. The nucleic acid structure of any one of embodiments 1-13, wherein the nucleic acid struts are of different lengths.

15. The nucleic acid structure of any one of embodiments 1-14, wherein at least one nucleic acid arm comprises a blunt end.

16. The nucleic acid structure of any one of embodiments 1-15, wherein at least one nucleic acid arm comprises a connector nucleic acid at its free (non-vertex) end that is up to 16 nucleotides in length.

17. The nucleic acid structure of any one of embodiments 1-16, wherein at least one nucleic acid arm comprises a connector nucleic acid at its free (non-vertex) end, thereby comprising a 1 or 2 nucleotide overhang.

18. The nucleic acid structure of any one of embodiments 1-17, wherein the nucleic acid structure is up to 5 megadaltons (MD) in size.

19. The nucleic acid structure of any one of embodiments 1-18, wherein the nucleic acid arms are 50 nm in length.

20. The nucleic acid structure of any one of embodiments 1-19, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 60° - 60° - 60° (tetrahedron).

21. The nucleic acid structure of any one of embodiments 1-20, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 60° - 90° - 90° (triangular prism).

22. The nucleic acid structure of any one of embodiments 1-21, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 90° - 90° - 90° (cube).

23. The nucleic acid structure of any one of embodiments 1-22, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 108° - 90° - 90° (pentagonal prism).

24. The nucleic acid structure of any one of embodiments 1-23, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 120° - 90° - 90° (hexagonal prism).

25. A composite nucleic acid structure comprising L nucleic acid structures selected from the nucleic acid structures of any one of embodiments 1-24, wherein L is an even number of nucleic acid structures, and wherein the L nucleic acid structures are connected to each other at free (non-vertex) ends of the nucleic acid arms.

26. The composite nucleic acid structure of embodiment 25, wherein the two more nucleic acid structures are two, four, six, eight, ten, twelve or more nucleic acid structures.

27. The composite nucleic acid structure of embodiment 25 or 26, wherein the composite nucleic acid structure is a tetrahedron, a triangular prism, a cube, a pentagonal prism, or a hexagonal prism.

28. The composite nucleic acid structure of any one of embodiments 25-27, wherein the composite nucleic acid structure is 20 megadaltons (MD), 30 MD, 40 MD, 50 MD, or 60 MD in size.

29. The composite nucleic acid structure of any one of embodiments 25-28, wherein the composite nucleic acid structure has edge widths, comprised of two nucleic acid arms from adjacent nucleic acid structures, of 100 nm.

EXAMPLES

Materials and sample preparation.

DNA strands were synthesized by Integrated DNA Technology, Inc. or Bioneer Corporation. To assemble the structures, unpurified 100 μM DNA strands were mixed with p8064 scaffold in a molar stoichiometric ratio of 10:1 in 0.5 x TE buffer (5 mM Tris, pH 7.9, 1 mM EDTA) supplemented with 12 mM $MgCl_2$. The final concentration of p8064 scaffold was adjusted to 10 nM. Cy3b-modified DNA oligonucleotides were purchased from Biosynthesis (Lewisville, TX) (5'-TATGTAGATC-Cy3b; SEQ ID NO: 4). Streptavidin was purchased from Invitrogen (S-888, Carlsbad, CA). Bovine serum albumin (BSA), and BSA-Biotin was obtained from Sigma Aldrich (A8549, St. Louis, MO). Glass slides and coverslips were purchased from VWR (Radnor, PA). Two buffers were used for sample preparation and imaging for super-resolution DNA-PAINT imaging: Buffer A (10 mM Tris-HCl, 100 mM NaCl, 0.05% Tween-20, pH 7.5), buffer B (5 mM Tris-HCl, 10 mM $MgCl_2$, 1 mM EDTA, 0.05% Tween-20, pH 8).

Annealing ramps.

The strand mixture was then annealed in a PCR thermo cycler using a fast linear cooling step from 80 °C to 65 °C over 1 hour, then a 42 hour linear cooling ramp from 64°C to 24°C.

Agarose gel electrophoresis.

Annealed samples were subjected to gel electrophoresis in 0.5% TBE buffer that includes 10 mM of $MgCl_2$, at 90V for 3 hours in an ice-water bath. Gels were stained with Syber® Safe before imaging.

TEM imaging.

For imaging, 2.5 μL of annealed sample were adsorbed for 2 minutes onto glow-discharged, carbon-coated TEM grids. The grids were then stained for 10 seconds using a 2% aqueous uranyl formate solution containing 25 mM NaOH. Imaging was performed using a JEOL JEM-1400 TEM operated at 80 kV.

Super-resolution imaging.

Fluorescence imaging was carried out on an inverted Nikon Eclipse Ti microscope (Nikon Instruments, Melville, NY) with the Perfect Focus System, applying an objective-type TIRF configuration using a Nikon TIRF illuminator with an oil-immersion objective (CFI Apo TIRF 100, NA 1.49, Oil). For Cy3b excitation a 561 nm laser (200 mW nominal, Coherent Sapphire) was used. The laser beam was passed through cleanup filters (ZET561/10, Chroma Technology, Bellows Falls, VT) and coupled into the microscope objective using a multi-band beam splitter (ZT488rdc/ZT561rdc/ZT640rdc, Chroma

Technology). Fluorescence light was spectrally filtered with an emission filter (ET600/50m, Chroma Technology) and imaged on an EMCCD camera (iXon X3 DU-897, Andor Technologies, North Ireland). Imaging was performed without additional magnification in the detection path, yielding 160 nm pixel size.

Sample preparation and imaging.

For sample preparation, a piece of coverslip (No. 1.5, 18x18 mm^2, 0.17 mm thick) and a glass slide (3x1 inch^2, 1 mm thick) were sandwiched together by two strips of double-sided tape to form a flow chamber with inner volume of 20 μL. First, 20 μL of biotin-labeled bovine albumin (1 mg/mL, dissolved in buffer A) was flown into the chamber and incubated for 2 min. The chamber was then washed using 40 μL of buffer A. 20 μL of streptavidin (0.5 mg/mL, dissolved in buffer A) was then flown through the chamber and allowed to bind for 2 min. After washing with 40 μL of buffer A and subsequently with 40 μL of buffer B, 20 μL of biotin-labeled microtubule-like DNA structures (≈ 300 pM monomer concentration) and DNA origami drift markers (≈ 100 pM) in buffer B were finally flown into the chamber and incubated for 5 min. The chamber was washed using 40 μL of buffer B. The final imaging buffer solution contained 3 nM Cy3b-labeled imager strands in buffer B. The chamber was sealed with epoxy before subsequent imaging. The CCD readout bandwidth was set to 3 MHz at 14 bit and 5.1 pre-amp gain. No EM gain was used. Imaging was performed using inclined illumination with an excitation intensity of ~200 W/cm^2 at 561 nm. 3D images were acquired with a cylindrical lens in the detection path (Nikon). All images were reconstructed from 5000 frame long time-lapsed movies acquired with 200 ms integration time, resulting in ≈17 min imaging time.

Image processing and drift correction.

Super-resolution DNA-PAINT images were reconstructed using spot-finding and 2DGaussian fitting algorithms programmed in LabVIEW (Jungmann, R., et al. Nature Methods, advance online publication, 2014). A simplified version of this software is available for download at the “dna-paint” website. The N-STORM analysis package for NIS Elements (Nikon) was used for data processing. 3D calibration was carried out according to the manufacturer’s instructions. DNA origami drift markers (Lin, C., et al. Nature Chemistry 4, 832-839, 2012) were used as fiducial markers. The high binding site density increases the probability to observe one bound imager strand per structure in each image frame. Furthermore, the fluorescence intensity of the origami drift markers is similar to single imager strand binding events and the markers never “bleach”. These properties render DNA origami structures as ideal drift markers. Drift correction was performed by tracking the position of each origami drift marker structure throughout the duration of each movie. The trajectories of all detected drift markers were then averaged and used to correct the drift in the final super-resolution reconstruction.

Determination of localization accuracy.

Fitting a 1D-Gaussian function to the distribution of z localizations from DNA origami drift markers and calculating the standard deviation was used to determine the localization accuracy in z. As origami drift markers are 2D structures, all binding events occur in a 2D plane on the surface, and thus at the same z location. Localization accuracy in x and y was determined by calculating the average separation of single-molecule localizations in neighboring frames, which can be attributed to an imager strand binding to a single docking strand. As multiple docking strands are used in each vertex of the polyhedral (~18 strands per vertex), one cannot fit the distribution of binding events per vertex, as this would result in an overestimation of the localization accuracy. The measured value per vertex would represent a convolution of the actual localization accuracy with the spatial extent of the binding sites in this vertex.

Spatial vs. temporal imaging resolution.

In stochastic super-resolution microscopy such as DNA-PAINT, one can generally make the statement that there is a tradeoff between spatial and temporal resolution. Higher spatial resolution can be obtained by collecting a larger amount of photons per binding or photoswitching event. This can be achieved by increasing fluorescence ON times and matching the camera integration time to these ON times. In DNA-PAINT imaging, this can be accomplished by increasing the binding stability of the imager/docking complex (*i.e.* going from a 9 to a 10-nt interaction region) and increasing the camera integration time to match the longer binding time, which in turn results in a longer image acquisition time. Higher temporal resolution can be obtained by reducing the binding stability of the imager/docking complex (*i.e.* going from a 9 to a 8-nt interaction region) and decreasing the camera integration time to match the shorter binding time.

Table 3. Sequences for super-resolution DNA-PAINT imaging.

Description	Sequence
Cy3b imager strand	5'–TATGTAGATC–Cy3b (SEQ ID NO: 1)
9nt docking site for P2 imager	Staple–TTATCTACATA–3' (SEQ ID NO: 2)
Biotinylated surface strand for structure immobilization	Biotin–GAATCGGTCACAGTACAACCG–3'
Handle strand on the DNA structure for surface immobilization; 7 staples (5' ends are 48[69], 43[130], 27[129], 11[88], 9[130], 26[65]) are modified. See Table 4 for sequence details.	Staple–TTCGGTTGTACTGTGACCGATTC–3'(SEQ ID NO: 4)

Table 4. Sequences of the tetrahedron.

5' — end	Sequence	Note	SEQ ID NO:
1[84]	TGAGGCCAACGCTCATGGACGTACTATGGTTTTTACAGCCTCCGGA	Core staple	5
0[54]	ACGTATTACGCCACCAAACATCCCTTAGCCAGCGAAAG	Core staple	6
3[102]	TCGATTGCAACAGGAAAACCGAGTGTTTTTTTGGT	Core staple	7
3[144]	CACTCGGCCTTGCTGGTAGCAATATAATTACATTTATGTATT	Core staple	8
2[44]	AACATAAATCAAAAGAAGCAGCAAGTTTTTCTCCA	Core staple	9
2[51]	ATTGTGCCGGCACTGCGGCACGCGGTCATAGCTGTTTCCATA	Core staple	10
2[72]	AGTGACGGATTCGCCTGTCGCTGGTAATCAG	Core staple	11
2[93]	ATGTGAATACACCTTTTTGATCAATATAATCTTTC	Core staple	12
2[107]	GACCATCGCCATTAAAAATGAAAATGGTCAGTACA	Core staple	13
2[114]	TGGGCGCAGAAGATGAATTTGGATTCCTGATTATCAGAATTA	Core staple	14
2[135]	ACCTTCAATTTAGATTTATGGAAGGGAGCGGAATTATCTTAT	Core staple	15
5[39]	CTTGTGGACTCGTAACCTTTCCTCGTTAGAAAGGG	Core staple	16
5[60]	CCGAAGAGTCGCTTAATTGACGAGC	Core staple	17
5[123]	CGAGTAAGAATTTACATAGAACAATATTACCATCACGCCCGT	Core staple	18
4[83]	CCCTTCAGTTAATGGTCTTTGCGAATACCTACATTTTGACGCTTGA	Core staple	19
7[32]	TATGCCAGCTATACGAGCCGGAAGCTGTGTGGGGGGTTTAAT	Core staple	20
7[74]	GCACGTTGCGTGAGTGAGCTAACTGGGTACCAGCCTCCCAAA	Core staple	21
7[81]	CTGGAGAAACAATAACGGTCCGTGGAGCTCGAATTCGTTGCC	Core staple	22
7[91]	ATCAAACATTAGACTTTACCATTAATTGACAG	Core staple	23
7[109]	ATCATCTAAAGCATCACCCTAAAAAATATTTTCAA	Core staple	24
6[51]	GTCTGTAAAGCCTGGGGAATCATGTGCC	Core staple	25
6[114]	TTTCCTTTGCCCGAACGATCATATTATACTTAAAT	Core staple	26
8[44]	TGTCAGGGTGGCGGTCCACGCTGGATCC	Core staple	27
8[65]	AGCCAGTGAGGCCCTGAGAGAGTTTAGC	Core staple	28
9[60]	TGTCCAACGCATAACGGAACGTGCCGGC	Core staple	29
9[130]	ATATCAGGTTATCAACAAGAGCCAGCAGCAAATAC	Core staple	30
11[88]	CTTGCTATTACGCGAACTGATAGCCTTGCTGAACCTTG	Core staple	31
11[130]	CATTGAAAGCACGAACCACCAGCACACGCTGGTTG	Core staple	32
10[37]	GGTTTAGACAGGAACGGAACGTGCACCACACCCGCCGCCACT	Core staple	33
10[58]	CATGAATCCTGAGAAGTGTTGCTTGCGCCGCTACAGGGTTCC	Core staple	34
10[65]	CAGTGCATCATTGGAACAGATAGGGTTGAGTCCGCCTGACGG	Core staple	35
10[100]	TCCAAAAGAGTCTGTCCGCCAGCCTCTGAAATGGATTATACG	Core staple	36
10[114]	TCCGGGTAAACGCTATTAATTAATCTGATTGTATACAGCAAT	Core staple	37
10[121]	TTGAAATTAACCGTTGTAATATCCTGGCAGATTCACCATCTG	Core staple	38
13[74]	CTTTTACCAGTATAAAGTCTTCGCATCC	Core staple	39
13[95]	GCTTCATATGCGTTATATCACAGTACATCGGATCAAAT	Core staple	40
12[37]	TGAAGGTTTCTTTGCTCGTCATTCTCAACAGTAGGGCTTCTGCCACGCC	Core staple	41
12[79]	TTCGTAGAACGTCAGCGCGTCTCGATTG	Core staple	42
12[100]	CCTGCTTTAGTGATGAAGGCAAACCAAAATCCACA	Core staple	43
12[121]	CGTGTTAAACGAACAATTTCATTTAACCTTGCTTCTGTCTGA	Core staple	44
15[46]	AAGGGGAAACCTGTCGTTGGGCGCGCACTCTACCTGCACACT	Core staple	45
15[67]	TAACTCACTGCCCGCTTTTTTCACGCAGTGTTGCCCCCAGCA	Core staple	46
15[88]	ACAATTCGACAACTCGTTGATGGCAATTCAGGATCCCCCAAA	Core staple	47
15[109]	AATGAGGATTTAGAAGTCCTCAATTAACAGTCAAGTTAGCGG	Core staple	48
15[130]	TAACCGTCAATAGATAATTGGCAATAACGTCGGCGAATCTGA	Core staple	49
17[147]	GTCTGGTCAGCAGCAACCGCAAAAAAAAGCCGCACAGGCGGC	Core staple	50
16[188]	ATCGACATAAAAAAATCCCGTAGAATGCCAACGGCAGCACCG	Core staple	51

5' — end	Sequence	Note	SEQ ID NO:
16[209]	AGCAGTTGGGCGGTTGTGTACTCGGTGGTGCCATCCCACGCA	Core staple	52
16[229]	ATTTCTGCTCATTTGCCGCCACCAGCTTACGGCTGGAGGT	Core staple	53
19[53]	GAACTGACCAACTTTGAATCAAGATAAT	Core staple	54
19[84]	CATTTCGAGCTAAATCGGTGAGCTTAATTTGACCAAGAG	Core staple	55
19[116]	ATAAGCAGCGCCGCTTTAGAAACAGCGGATCGGAAGATTATT	Core staple	56
18[44]	CATCTCCTTTTGATAAGCGCGTTTGTAA	Core staple	57
18[65]	GAATTTTGCGGATGGCTAGCC	Core staple	58
21[39]	TTGGTTTTAAATATGCATATAACACAGATGAACGG	Core staple	59
21[102]	GTAGCCTCAGAGCATAACAAATGGAACG	Core staple	60
21[144]	AAATCATACAGGCAAGGGCGAGCTCGGCGAAACGTAGTCAGT	Core staple	61
20[44]	TCGTCAGAAGCAAAGCGCCCCCTCGTAATAGGCAA	Core staple	62
20[65]	CTTTCAAAAAGATTAAGCGTCATATGGATAGGAAT	Core staple	63
20[72]	CGATAATTAAGTTGGGTCGGCTACTTAGATA	Core staple	64
20[93]	ATCGGGTTTTGCGAAAGTTGTATCGGCCTCAAAAC	Core staple	65
20[107]	CCGTAATGCCGGAGAGGGCATGTCGTATAAGAAAA	Core staple	66
20[114]	AGATGTAAAATCTTCGCCGCACTCTCTGCCAGTTTGAGTGAG	Core staple	67
20[135]	AGGAAGCTTTGAAGGGCGCACCGCTGGGCGCATCGTAAGATT	Core staple	68
23[60]	GCACAAATATAGGTCATTATAATGCTGTAGCCTGC	Core staple	69
23[123]	CTATCAAAAGGAAGCCTTTAGCAAAATTAAGAGCT	Core staple	70
22[97]	CGGTTGATAATCCTGCGGAATAGATATTCAACCGTTCTAGCT	Core staple	71
25[32]	AAGTTTACCAAGAAAGATTCATCATTAATAAATTGGGCGTTG	Core staple	72
25[60]	ATGCAAATCATGACAAGCTAAAGACGAGTAGATTTAGTTGCT	Core staple	73
24[51]	CACTTTAGGAATACCACCGTTGGGTTTCAACGCA	Core staple	74
24[72]	TACTAATGCAGATACATGGCTCATATTACCTGGGG	Core staple	75
24[90]	GCCAGCGCCAAAAGCGTCCAATGCTGCAAGGCGTTATTG	Core staple	76
24[114]	TAAGTAACAACCCGTCGCCGTGCACAGCCAGGAGA	Core staple	77
26[44]	CTGAGAGGGGAAATGCTTTAAACAATTATAGAGCTTCATTAA	Core staple	78
26[65]	ACCTTTAGACAATATTCATTGAATGATT	Core staple	79
26[86]	ATGTAAGAAAAGCCCCATCCTGTA	Core staple	80
26[107]	ACGGAAGATTAATCATATGTACCCGATAAATGAGACAGCCCT	Core staple	81
27[74]	TGATATACCAGTCAGGAATTCAACGAGGCATAGTAAGATAAA	Core staple	82
27[129]	TCCGGATCGGTTTAAATTTAATCGTAAAACTAGTAG	Core staple	83
29[39]	TTCAAGAGGAGTTGATTCCCAATTTCAA	Core staple	84
29[53]	TCTACGTAACGGTTTAAAAGAAAAATCTACGGTTG	Core staple	85
29[88]	CCAACCATCAATATGGATATGTACCAAAAACATTATGATCAA	Core staple	86
29[102]	GTCGCATCGGTCAATAACCTGTTTCAATAAAATACTTTTGCGGGAGGTG	Core staple	87
29[130]	GCCTAAAGATTTTTTGAGAGATCTTGAACGGGTAA	Core staple	88
28[72]	GCTTCCATTATTGCAGGCGCTTTCTTTAATCCATT	Core staple	89
28[93]	AGGGTAATGCAGTCCAGCATCAGCTATGCGAGGGG	Core staple	90
28[121]	CTCTTTTCATTTGGGGCCAAAGAATTATTTCAACGCAAGTGT	Core staple	91
30[37]	CGGATCATAAGGGAACCGAACTTTATCCGCCGGGCGCGTTGAGATAAAG	Core staple	92
30[59]	CTCATTCATGAGGAAGTTTTGAGGAAACCGGAAAGA	Core staple	93
30[79]	TCAAACGGGTAAAATACGTAGCAAAACG	Core staple	94
30[100]	TTACAGGGAGTTAAAGGAAAGACAACGACGTAAGG	Core staple	95
30[121]	CGCTGCGGGATCCAGCGCCATGTTCTCTCACGGAAAAACTT	Core staple	96
33[46]	AGATATCATAACCCTCGTTTTGCCCTCATTCGACC	Core staple	97
33[91]	ATCAACATTAAATGGGGACGACGACATTAAGAACTAACTTTC	Core staple	98
33[109]	CGATTCGCGTCTGGCCTAAAACAGCCAGCTGCCCA	Core staple	99
33[130]	CTCTAGGAACGCCATCACAAATATGCGGGCCCGACGGCCACC	Core staple	100
35[147]	ACTACGAAGGCACCAACCTAATATTCGGTCGCTGAGGCTTGC	Core staple	101
34[188]	ATCGCCCACGCATAACCGATAAACGAAAGAGGCAAAAGAATA	Core staple	102
34[209]	GCGCCGACAATGACAACAACCCACTAAAACACTCATCTTTGA	Core staple	103
34[229]	ACAGCTTGATACCGATAGTTCCCCCAGCGATTATACCAAG	Core staple	104
37[53]	TATAATAAGAGAATATAATGTTCAAGCA	Core staple	105
37[84]	GGTTTACCAAGGCCGGAAACTG	Core staple	106
37[116]	TTCTAACTATAACCTCCGCTTTCGAGGTGAACGCCACCAACT	Core staple	107
36[44]	TTACCGAGGAAACGCAAATGAAATGCTAATGTCCT	Core staple	108
36[65]	GACGGAATACCCAAAAGCAAT	Core staple	109
36[75]	GCATGATAGAAAAAGAACGCTTCATCTAGATTTG	Core staple	110
39[39]	AAAGCAAACGTAGAAAAACGCAAAGACAAAAAGGC	Core staple	111
39[102]	GCAACCATTACCATTAGCAGCGCCGCAAATCAATGGTTACGCGAA	Core staple	112
39[144]	GCGTTGAGCCATTTGGGGGGAAGGACAACTAAAGGATGTCTG	Core staple	113
38[44]	ATATAATATCAGAGAGAAATAACACCCAATCAATT	Core staple	114
38[65]	GCACAAGAATTGAGTTAAATAGCATTTTTTGTGCT	Core staple	115
38[72]	AATTTTTAGCGTAACGAAAGACAATTCATAT	Core staple	116
38[83]	GGAACCCAACGTCACCAATGAAACCATCCCAG	Core staple	117
38[93]	AGCTTTTGTCTAGCATTACGAGGTTTAGTACTTTC	Core staple	118
38[107]	ATCGAACCGCCACCCTCTATTCACACCGTTCCAGT	Core staple	119
38[114]	AATTAGTAAACAGTACACTCAGAACGGAATAGGTGTATATTA	Core staple	120
38[135]	TAGGGGATTTCGTAACAACCGCCAAGGGTTGATATAAGAAGA	Core staple	121

5' — end	Sequence	Note	SEQ ID NO:
41[60]	CCAAGAAACATAATAACTCCTTATTACGCAGAGTT	Core staple	122
41[123]	CCACATCTTTAGCGACAGCCAGCAAAATCACGACA	Core staple	123
40[97]	TCATTAAAGCCAAAAAATGAAAGCGCCTCCCTCAGAGCCGCC	Core staple	124
43[32]	ACAAACGCTAGAACGCGAGGCGTTAAGCAAAGTCTTTCTCCG	Core staple	125
43[60]	TAAAGATAAGCAGAACGCTTTTTCTTTGTCACAATCAATTAA	Core staple	126
43[130]	ATAACGATTGGCCTTGAAGAG	Core staple	127
42[51]	TTAACCTCCCGACTTGCATCATTAAACGGGTGCCT	Core staple	128
42[72]	ATTTTTGAAGCCTTAAAGTTTTTACGCACTCACAA	Core staple	129
42[90]	CCTATAAGATTAGTTTTAACGCAGCCCTCATAGATCAAG	Core staple	130
42[114]	TAAGGCTGAGACTCCTCTATAGCCCCGCCACTCAGCTTGGCTTAG	Core staple	131
44[51]	GAATTCCAAGCCGCGCCCAATAGCTTAG	Core staple	132
44[107]	ACATGAATTTAAACAAATAAATCCACCCTCAACCGGAAGATA	Core staple	133
45[46]	TCACAAGAAATATTTATTAAAAACAGGGAAGTGAGCGCGCTATCTAAGG	Core staple	134
45[74]	TACTTTTCATCGTAGGAGGGAGGTTTGCACCCAGCTACCAAA	Core staple	135
47[39]	AACAAGTACCGACACCACGGAATATATG	Core staple	136
47[102]	TTCTGCTGATAAAGACAAAAGGGCCAGTAGCGCACCGTAATCAGTTCAT	Core staple	137
47[130]	TATCGTTTGCCCACCCTCAGAGCCAGGTCAGCATGGCTGAGT	Core staple	138
46[121]	ATAAACCGATTGAGGGAAATTAGAGAATCAAGTTTGCCTTAT	Core staple	139
49[126]	GTATTGCGAATAATATTGTATCGGTTTACCTCAGACTGAGTTCGTC	Core staple	140
48[37]	CGAGGCATTTTCGAGCCAGTAAATAAATTGTGTCGAAACTTA	Core staple	141
48[58]	GATATATTTTAGTTAATGAGAAAACGCCTGTAAGA	Core staple	142
48[69]	TATCATCATTAAACCAACAATGAAACGAGCCTTTACAGAGAGTAAC	Core staple	143
48[79]	CGGTCTGACCTAAATTTCAATCGCTCTAAAGCACCACC	Core staple	144
48[90]	ACAAAGTATCGAGACCACAGATCGAATGGAAAGCGTTCGGAA	Core staple	145
48[100]	TTATAGACTACCTTTTTATGTAAACAGACGTCAAA	Core staple	146
50[104]	CACCGTACTCAGAAGCAAGCCTCTATTCTGAAACATGAAAGT	Core staple	147
51[46]	CGATCCTGAATCTTACCGCCATATAATAATAAAAC	Core staple	148
51[109]	AGATGCCCCCTGCCTATCAGTCTCACGCCTGGTCT	Core staple	149
51[130]	GAAAGTGCCCGTATAAACAGTAAGTCGTCACTGAATTTGGTT	Core staple	150
53[147]	GAAATACCGACCGTGTGATAATATCAAAATCATAGGTCTGAG	Core staple	151
52[188]	GAGAAGAGTCAATAGTGAATTATAAGGCGTTAAATAAGAATA	Core staple	152
52[209]	GATAGCTTAGATTAAGACGCTAACACCGGAATCATAATTACT	Core staple	153
52[229]	AGAATCCTTGAAAACATAGCAGAAAAAGCCTGTTTAGTAT	Core staple	154
7[137]	AAAATTAGAGTTTTAAAAGTTTGAACCAGAAGGTTAGAAGTG	Core staple	155
7[151]	AGGGCCTGCAACAGTGCGAAGATAGAACCCTGTCA	Core staple	156
6[146]	CTAATAGGGAATTGAATTGCGACCTGAGACAA	Core staple	157
12[142]	AATGAATTACCTTTTTTCAAGAAACAAA	Core staple	158
25[137]	ACGTAACCAACGTGGGAACAAACGGTGTAGATTCTGGTGGGA	Core staple	159
25[151]	TTAAACAAGAGAATCGAACAAAGGGAGTAATGGAT	Core staple	160
24[146]	CATTTTTTTAATATCTGTTGGCAGAGGTAAAC	Core staple	161
30[142]	TAGTACCAGTCCCGGAATCACCGGGGAG	Core staple	162
43[151]	AGGCAGGAGGTTGAGGCGCCACCAAGCCCCCTTTA	Core staple	163
42[135]	AACGGATTAGGATTAGCCGTCGAGCCCTCAGGCCT	Core staple	164
42[146]	GTGCCTTTTTGATGCATGTACTGCTAAAGAAA	Core staple	165
48[142]	TTAAATTTTTTCACGTTGAGAATACAAC	Core staple	166
0[166]	GAGTAGAAGAACTAATAACATCACTTGCGC	Connector staple	167
2[163]	TCTGGCCAACAGATGATGAGC	Connector staple	168
4[163]	TATTAACACCTTATCTAAAATAAT	Connector staple	169
6[163]	TTTAGGAGCATATCATTTTCT	Connector staple	170
8[166]	ACGTAAAACAGAAATATCAAAATTATTTAA	Connector staple	171
11[151]	AGAAGAGATAAAACAGAGGTGAGGCGGTCAG	Connector staple	172
10[142]	AATCTTCTTTGATTAGTCAAACTAGACCAGTAATAAAAGGGACTC	Connector staple	173
10[160]	CAAACATAATGGAAACAGTAC	Connector staple	174
12[163]	ATAAATCAATATATGTGACCTACCATAAAGAAGGA	Connector staple	175
14[160]	GGAACAAAGAAACCGTAACATCTAACAA	Connector staple	176
18[166]	TAGCATTAACATCAATTCTACTAATAGTGG	Connector staple	177
20[163]	TTTTAAATGCCCACGGGAAAT	Connector staple	178
22[163]	GTCTGGAGCAAAATTCGCATTATA	Connector staple	179
24[163]	TTTTTGTTAAGACCGTAATAG	Connector staple	180
26[166]	TCGCCATTCAGGCACCAGGCAAAGCGCCCG	Connector staple	181
29[151]	CCGAATGCCTCTATCAGGTCATTGCCTGAGA	Connector staple	182
28[142]	AATGAAAAGGTGGCATCCAATAAAAATTTTTAGAACCCTCATAAA	Connector staple	183
28[160]	GATAACCTTTGTGAGAGATAG	Connector staple	184
30[163]	ACTTTCTCCGTGGTGAAGCCGGAATGCGCAATTTG	Connector staple	185
32[160]	GATAGGTCACGTTGGCGGATTATCAGCT	Connector staple	186
36[166]	GAATTATCACCGTAATTATTCATTAAAGCC	Connector staple	187
38[163]	TCGGCATTTTCAACAGTTTGA	Connector staple	188
40[163]	CCAGCATTGAAGTGTACTGGTACA	Connector staple	189
42[163]	AAGTTTTAACTGCTCAGTAGT	Connector staple	190
44[166]	TAGCAAGCCCAATACCCTCATTTTCAGGCA	Connector staple	191

5' — end	Sequence	Note	SEQ ID NO:
47[151]	TTTCGGTCATGAACCACCACCAGAGCCGCCG	Connector staple	192
46[142]	GGATAAATATTGACGGACACCGACTCAGACTGTAGCGCGTTTTAT	Connector staple	193
46[160]	GCGGAGTGAAAATCTCCAAAA	Connector staple	194
48[163]	AAAAGGCTCCAAAAGGAAGCCACCAGGAACCATAC	Connector staple	195
50[160]	AGGCGGATAAGTGCGGGGTTTGGGGTCA	Connector staple	196
1[12]	ACAGGAGGCCGATTAATCAGAGCGCGGTCACGCTGCGCCAA	Vertex staple	197
1[32]	ATTGTGTTCATGGGTAAGAATCGCCATATTTAACAACG	Vertex staple	198
3[9]	TATCAAAGTGTAGGGAGCTAA	Vertex staple	199
2[30]	CGTCCGGGTTGTGGTGCTCATACCAAATTGTTATCCGCTCACA	Vertex staple	200
5[9]	TTGATGGTGGTTCGAAAAACCGTC	Vertex staple	201
7[9]	CGCGCGGGGAGAAGAATGCGG	Vertex staple	202
9[12]	CGGGCCGTTTTCACGGTGCGGCCGGCGGTTCAGCAGGCGAAAATCCTGT	Vertex staple	203
11[16]	CGGCATCAGATGCAAAGGGCCGAAATCGGCAAATTTGCCCTGCG	Vertex staple	204
13[14]	CCTGCGGCTGGTAAGCAAATCGTTAA	Vertex staple	205
15[16]	ATTCCACACAACGCATTAATGAATCGGCCAA	Vertex staple	206
19[12]	TGGAAGTTTCATTCCAACTAAAGATTAGAGAGTACCTAAG	Vertex staple	207
21[9]	CAACAGGTCAGGTACGGTGTC	Vertex staple	208
20[31]	CGAAGCTGGCTAGTGAATGTAGTAAAACGAACTAACGGAACAAC	Vertex staple	209
23[9]	TCAAAAATCAGGGGAAGCAAACTC	Vertex staple	210
25[9]	ATAGCGAGAGGCGCCCTGACG	Vertex staple	211
27[12]	AGAAACACCAGAACGAAAGGCTTTTTTGCAAAACGAGAATGACCATAAA	Vertex staple	212
29[16]	CCAGGCGCATAGCCAGACCTCTTTACCCTGACTGTTCAGAAAAG	Vertex staple	213
31[14]	GGAACGAGGCGCAGACGGTGTACAGA	Vertex staple	214
31[32]	TCATATGAGCCGGGTCACTGTTGC	Vertex staple	215
33[16]	ATTATTACAGGTGACGACGATAAAAACCAAA	Vertex staple	216
37[12]	GCAACATATAAAAGAATACATACAACAAAGTTACCAGTACC	Vertex staple	217
39[9]	AGCAGATAGCCGATAAAGGTG	Vertex staple	218
38[30]	GAACGACAATTCCCATCATCGGCTTCAGATATAGAAGGCTTAT	Vertex staple	219
41[9]	CACCCTGAACAATTAAGAAAAGTA	Vertex staple	220
43[9]	CTAATTTGCCAGACGAGCATG	Vertex staple	221
45[12]	TAGAAACCAATCAATACTAATTTTTACAAAGACGGGAGAATTAACTGAA	Vertex staple	222
47[16]	CTGTCCAGACGAGCCCTTTAGTCAGAGGGTAATCGCATTAATAA	Vertex staple	223
49[14]	CCAACATGTAATTTGGTAAAGTAATT	Vertex staple	224
49[32]	AGACCTGCTCCATGTTACTTAGCC	Vertex staple	225
51[16]	CCGGTATTCTAAACGAGCGTCTTTCCAGAGC	Vertex staple	226

Table 5. Sequences of the triangular prism.

5' — end	Sequence	Note	SEQ ID NO:
1[53]	CGCCAACCGCAAGAAAAGTTACCTGTCC	Core staple	227
1[84]	AGTGAGGAAAACGCTCATGCGCGTACTAGTGTTTTTGGT	Core staple	228
0[44]	CGTCCACCACACCCGCCAACAAGAGCAG	Core staple	229
3[102]	AATCCATTGCAACAGGACCACCGACGGACTTGCGGTCCCTTAGAA	Core staple	230
3[144]	CACTATCGGCCTTGCTGGTAGCAAATTAATTACATTGCATTA	Core staple	231
2[44]	ACTAAAATCCCTTATAATGAGAGACGCCAGGCTGC	Core staple	232
2[65]	TCCGAATAGCCCGAGATTTGCCCTCACC	Core staple	233
2[72]	GTGCCAACGGATTCGCCGTCAGCGTATAATC	Core staple	234
2[93]	GAATTTGAATGTACCTTTCTCATCAATATAAATTT	Core staple	235
2[107]	CAGAACATCGCCATTAAAAATGAATCTGGTCAATA	Core staple	236
2[114]	CGTTCGCGCATCAGATGTGTTTGGATTCCTGATTATCAGTAT	Core staple	237
2[135]	TGAATTTCAACGTAGATTAATGGAAAGGAGCGGAATTACGTT	Core staple	238
5[60]	AAAAGTTTGGGCGCTTATTTGACGAGCACGTGGTA	Core staple	239
5[123]	ACCGCGTAAGTATTTACCCAGAACAATATTACCATCACCATC	Core staple	240
4[41]	CAAGCGGAATCGGCATTAAAGCGCGTAAGCTTTCC	Core staple	241
4[97]	ACCTTGCTGAACAACAGCTGAAGTTTAATGCGCGAACTGATA	Core staple	242
4[135]	CGCCAGTTGAAGATTAGAATTTTAAAAGTTTCCAC	Core staple	243
7[32]	GCGAACCTGTTCCACACAACATACTAGCTGTCGGTCATTGAG	Core staple	244
7[60]	TTTACGATCCGCGGTGCTCAG	Core staple	245
7[74]	AGTACATTAAGGGTGCCTAATGAGGAGGATCCGCGTCCAAAC	Core staple	246
7[109]	ATAAAATCTAAAGCATCGCCCTAAACAATATGCTC	Core staple	247

5’ — end	Sequence	Note	SEQ ID NO:
6[51]	CCGAAGCATAAAGTGTATCGAATTCCAG	Core staple	248
6[90]	ACTTTAGCTAACTCGAGACGGGGGAGAAACAATCTTGTTCTTCCCGGGT	Core staple	249
6[114]	CATATCCTTTGCCCGAATCATCATATTATACGTAA	Core staple	250
8[65]	CAGTTCTTTTTCACCGCCTGGCCCATCA	Core staple	251
9[60]	CACCGCTCAACACCGTCGGTGATGGGTCTGGCGGTGCCTTGT	Core staple	252
9[130]	GAATTTCAGGAAATCAATGAGAGCCAGCAGCAAAT	Core staple	253
11[39]	CGGACATCCCTTTTAGACAGGAACATAA	Core staple	254
11[53]	CCAAGCGCAGGTTTCTGCGTAATCATGGTCAGAGC	Core staple	255
11[88]	TGCTGGCTATTAGTCGGGGGAAATACCTACATTTTGACTTTT	Core staple	256
11[130]	TTCCCTGAAAGAACGAACCACCAGGCCA	Core staple	257
10[58]	CAGCAGAATCCTGAGAATGGTTGCATGCGCCGCTACAGTTGA	Core staple	258
10[72]	GCTCTGATTGCCGTTCCGGCAAACGTAGAACTGAT	Core staple	259
10[100]	TGCGTAAAAGAGTCTGTCCGCCAGCGTCTGAAATGGATAATA	Core staple	260
10[114]	CTCTCGCTGGGTCGCTATTAATTATCCTGATAATATACATCA	Core staple	261
10[121]	GCAGCAAATTAACCGTTGTAATATATTGGCAGATTCACCTTC	Core staple	262
12[37]	AATGCTCGTCATTGCCAACGGCAGCAGTAGG	Core staple	263
12[48]	GCTTAATACCGGGGTGTCACTTATTGGGGTTGCAG	Core staple	264
12[79]	ATAGCGATAGCTTACAAGCGTGCCGCAT	Core staple	265
12[90]	TCCTTGAGTGAGCCTTACATCGCCTCAAATATCAAGTATTAG	Core staple	266
12[100]	TCCGTTTTTTCGTCTCGATAACGGTACAAAAGGCA	Core staple	267
12[121]	ATCCAGCCTCCGTAACAATTTCATATAACCTTGCTTCTTTCT	Core staple	268
14[69]	ACCGAGCAAGCCTGTTGCGTTGCGCTCAGTGG	Core staple	269
15[46]	CGGCTTTCCAGTCGGGAGTTTGCGGCGCGCCATGC	Core staple	270
15[98]	ACAACTCGATGATGGCAATCTCACAGTTTGACAAACAATTCG	Core staple	271
15[109]	TAATTGAGGATTTAGAAACCCTCAAGTAACAACCAAGTAACG	Core staple	272
15[130]	ATTAGCCGTCAATAGATAGTTGGCTTTAACGGAGGCGACAGA	Core staple	273
17[130]	GTGCCATCCCACGCAACAAGGGTAAAGTTAAACG	Core staple	274
16[167]	CACAGGCGGCCTTTAGTGATGCAGCTTACGGCTGGAGGTGTC	Core staple	275
16[188]	AAAATCCCGTAAAAAAAGCCGCAGCATCAGCGGGGTCATTGC	Core staple	276
16[205]	GTGTACATCGACATAAAAGGCGCTTTCGCACTCA	Core staple	277
19[53]	GAGCACCAACCTAAAGAAGAGTAATCGA	Core staple	278
19[84]	TCGCAAAAAATCGGTTGTATTAATTGCTCCATTAGTACG	Core staple	279
18[44]	TTTTTTTGATAAGAGGTTTTTAATTCTT	Core staple	280
21[102]	TACCAGAGCATAAAGCTTGGTCAAGTTTCCAACAGCATTCTGCTC	Core staple	281
21[144]	ATTACAGGCAAGGCAAAGCTGAAAGAAACGTACAGCTTGCCA	Core staple	282
20[44]	GCTAAGCAAAGCGGATTCTCAAATTAGTAAACACT	Core staple	283
20[65]	AAAAAAGATTAAGAGGAATAAATATAGC	Core staple	284
20[72]	AGACAAGTTGGGTAACGGGTAAAAATACATT	Core staple	285
20[93]	CCATTTCCCAAAGGGGGAACGGCCTCAGGAATTAA	Core staple	286
20[107]	AGAGCCGGAGAGGGTAGGTCAATCAAGCAAATAAT	Core staple	287
20[114]	AGGAAACGACCGCTATTCTCCAGCCCAGTTTGAGGGGACGAG	Core staple	288
20[135]	AAATTTCAGAGGCGATCCGCTTCTCGCATCGTAACCGTCTCC	Core staple	289
23[60]	CAATATCGCGCATTTTTATGCTGTAGCTCAAGAAC	Core staple	290
23[123]	TTTAAGGGTGCCTTTATCAAAATTAAGCAATATATTTTTAAA	Core staple	291
22[41]	ACAGTTCTAGTCAGTCAAAGCTTGCTCCTAAATAT	Core staple	292
22[97]	TGATAATCAGAAGGAATCGTCAGTCAACCGTTCTAGCTGATA	Core staple	293
22[135]	AATACGTTAACAATAGGGGAACAAACGGCGGAGAT	Core staple	294
25[32]	TTTCCAGACGAGATTCATCAGTTGTAAAACGGGCTTGAGAGC	Core staple	295
25[60]	TTATCAACGTAAGAACCACGA	Core staple	296
25[74]	GTCTACGAGGGCAGATACATAACGCATTATACCTTATGGCCA	Core staple	297

5' — end	Sequence	Note	SEQ ID NO:
24[51]	ATCGGAATACCACATTCGGGAAGAAACT	Core staple	298
24[90]	GCTTTAAAAGGAATCAATACTGCAAGGCGATTATTTGAATTACCAGTCA	Core staple	299
24[114]	TCGCAACCCGTCGGATTGCATCTGCAGCTTTCGCA	Core staple	300
26[65]	AAAGACTGGATTCATTGAATCCCCGCAT	Core staple	301
26[107]	CAGATTGTATATATGTACCCCGGTAATTAATCAGTCAAGTAA	Core staple	302
27[60]	TTACGCCGGGAAAGAATACACGATTGCCACTGGATATTCTTC	Core staple	303
27[129]	GCACGGTGCGGATTGTAACGTAAAACTAGCATCTAT	Core staple	304
29[39]	TCAGGACAGAATTCCCAATTCTGCCATG	Core staple	305
29[53]	GACAACAAAGTAATTTCAAAATCTACGTTAAAGAT	Core staple	306
29[88]	GGTTCAATATGATATCCGCCCAAAAACATTATGACCCTATCA	Core staple	307
29[130]	AGCGATTCAATGAGAGATCTACAACGGT	Core staple	308
28[58]	AGGTAGATTTAGTTTGAGAATATAGCGGATGGCTTAGACGAA	Core staple	309
28[72]	TAACGTCACCCTCAGCAGCGAAAGTTAAACGCCAG	Core staple	310
28[100]	GAATAACCTGTTTAGCTAAAGCCTTTTTGCGGGAGAAGAGAA	Core staple	311
28[114]	GACCAACGGCACAGCGGATCAAACGATCGCAACGC	Core staple	312
28[121]	GACCATTTGGGGCGCGAGAATTAGTTCAACGCAAGGATAGGT	Core staple	313
30[37]	CGGACTTTGAAAACGAAAGAGGCACGCGGTT	Core staple	314
30[48]	GCGGTATGATGGTTCTGCTCAGGGGTAAGCTTTAA	Core staple	315
30[79]	GCAGTTGGGCGGTTATCATCATTGACCC	Core staple	316
30[90]	ATTTGCCCGATTTTATGTGCTGCAAGCCCCAAAAAGTAGCCA	Core staple	317
30[100]	ATTCGGAACGAGGGTAGTTTTTCACGTTGTACCGG	Core staple	318
30[121]	GAATACAGAGGCGCCATGTTTACCCACGGAAAAAGAGACCG	Core staple	319
32[69]	GGACGTTAACTAATCATAGTAAGAGCAAATGT	Core staple	320
33[46]	TTAATAACCCTCGTTTAGCCAGAGTTCAGTGTTCA	Core staple	321
33[98]	ATGTGAGCGACGACAGTATGAACTGGCTCCCATCAACATTAA	Core staple	322
33[109]	TAACGTCTGGCCTTCCTCAGGAAGCTGGCGAGTCACGATGAG	Core staple	323
33[130]	GTGAACGCCATCAAAAATATTTAAGCCTCTTGGCCAGTTGAG	Core staple	324
35[132]	TAAAACACTCATCTTAGGCCGCTTTTGCGG	Core staple	325
34[224]	TAGTTGCGCCGACAATAAATTGTGTCGAAA	Core staple	326
37[53]	CACCGACCGTGTGATCAGACGACACAAG	Core staple	327
37[84]	AATAGAAGCACCATTACCAGGAATACCCATTTTGTAAAT	Core staple	328
36[44]	CTTAGTTACCAGAAGGAATAAGAGATAA	Core staple	329
36[65]	GAAGAAACGCAATAATAAGAA	Core staple	330
39[102]	AATCAAAATCACCAGTAAATTCATGTTAATTTGTAAATCGAGGTG	Core staple	331
39[144]	ATCTATCACCGTCACCGTCAACCGGTGAGAATAGAAACGTTA	Core staple	332
38[44]	AAAGAGGGTAATTGAGCCAGCCTTCAGCCATTTTT	Core staple	333
38[65]	AAGTCAGAGAGATAACCTAACGTCTCCA	Core staple	334
38[72]	TTGTGCAGACAGCCCTCCTGACCTCACAATC	Core staple	335
38[93]	AAAGCGTAACCAAACTAACGTATCACCGTACTTGC	Core staple	336
38[107]	TCTAGAGCCGCCACCCTAGACGATCGCAGTCACAG	Core staple	337
38[114]	TTTTCGTCTTCACTGAGGTTTAGTTGATATAAGTATAGTCTG	Core staple	338
38[135]	GTCAATGAATATAGGAAAACCGCCGATAAGTGCCGTCGGAGG	Core staple	339
41[60]	ATACCCAATAAACCGAGCTGGCATGATTAAGAAGA	Core staple	340
41[123]	ACCCCTTATTCAGCACCCCATTTGGGAATTACCAAAGAAACT	Core staple	341
40[41]	AGAATAAAAAGTCACAATGAACGAACAAATTACGC	Core staple	342
40[97]	ACAAACAAATAATTTTTTGTTCAGAGCCACCACCGGAACCGC	Core staple	343
40[135]	GGATCCAGTAACGGGGTAGACTCCTCAAGAGCCAG	Core staple	344
43[32]	GCCTATCCTGTTATCCGGTATTCTTACCGCGCAATCAAAGCC	Core staple	345
43[60]	TTTCCTGTTTACATGTTGAAA	Core staple	346
43[74]	AATTTAAATCCCGACTTGCGGGAGCGAGAACGTATTAATAAA	Core staple	347

5' — end	Sequence	Note	SEQ ID NO:
42[51]	GCACGAGGCGTTTTAGCTATTTTCTCCT	Core staple	348
42[90]	CCTGCTTTGAAGCCAAGAAACTGTAGCATTCCACAAGAACGGAAGCAAG	Core staple	349
42[114]	TGCCATGAAAGTATTAAAGAGGGTACCGCCATAAT	Core staple	350
44[65]	GCGATCCCAAAAAAATGAAAATAGGCTA	Core staple	351
44[107]	GTCTGGAAAGTGGCCTTGATATTCCTCCCTCTTTCATACACC	Core staple	352
45[60]	TATGCGACCTAAATAAGAATACTTATGGTTTCAGCTAAAGTT	Core staple	353
45[129]	TCAGCCCATGTTTACCGTGGTTGAGGCAGGTCCAGA	Core staple	354
47[39]	GACGTAATAAATAAAAGAAACGCAACTC	Core staple	355
47[53]	ACAATCAACACTGTCTTATCGTAGGAATCATAAGA	Core staple	356
47[88]	TTATCACCGGAACCACAACTTAGCAAGGCCGGAAACGTATCA	Core staple	357
47[130]	GTAATAGCCCGCCACCCTCAGAGCGACA	Core staple	358
46[58]	TACCACGGAATAAGTTTAAAA	Core staple	359
46[72]	TTAAGGTTGGGTTATATAACTATATCATCTTATAG	Core staple	360
46[100]	TTAATGGTTTACCAGCGGAGCCAGGAAACCATCGATAGAGCG	Core staple	361
46[114]	TTTAATCGCAATCGGTTTATCAGCTCAGGAGTTTC	Core staple	362
46[121]	GAACAAAAGGGCGACATACTTGAGGTAATCAGTAGCGATTCG	Core staple	363
48[37]	GGATTTTCGAGCAAATAAGGCGTTGCTCCAT	Core staple	364
48[48]	GTTACTTTAATCGGATAGATAAAATAAATACAGAG	Core staple	365
48[79]	CAGCTTGATACCGATCCCATTCCAGAAC	Core staple	366
48[90]	AATTTCTACCAAGTCAACGCCGAATCCTCATTAAAAATGCCC	Core staple	367
48[100]	TTTGCTGATGCAAATCCTCAAATAAGTTTTGGCCA	Core staple	368
48[121]	TGTAGACAAAGAAGGAACAACTAACCAAAAGGAGCCTTCCC	Core staple	369
50[69]	CCGTTTTGAACCTCAAGATTAGTTGCTAATTA	Core staple	370
51[46]	ACGCCCAGCTACAATTTAGTTACAAGTCCTGTCCA	Core staple	371
51[98]	CTATTATCCCGGAATAGGTCGCACTCATGTCTATTTCGGAAC	Core staple	372
51[109]	AAACCGTATAAACAGTTGCCAGAAACCAGTAGATCTAATATT	Core staple	373
51[130]	CTGCAGTGCCTTGAGTATCTGAATACCGTAATCCAGACGCGA	Core staple	374
53[130]	AACACCGGAATCATAATACCTTTTTAACCTCCGG	Core staple	375
52[167]	AAATCATAGGTCTGAGAGACTTACTAGAAAAAGCCTGTTTAG	Core staple	376
52[188]	GAGTCAATAGTGAATTTATCATATCATATGCGTTATACAAAT	Core staple	377
52[205]	GATTAAGACGCTGAGAATCTTACCAGTATAAAGC	Core staple	378
34[209]	TGACAACAACCAGCAGGGAGTTAATGACCCCCAGCGATCATCGCCTGA	Core staple	379
5[25]	GTGGTTCCGATCCACGCAGAG	Core staple	380
23[25]	CTGACTATTAAGAAAACAAGT	Core staple	381
41[25]	CACCCTGAACCATAAAAATTT	Core staple	382
0[166]	CTGAGTAGAAGAACTCAAACACGACCAGTA	Core staple	383
2[163]	ATTCTGGCCAACAGAGATAAAACAGAG	Core staple	384
4[163]	AGTATTAACACCGCCTGCAACAGTCAGAAGATAGAACCCAGT	Core staple	385
6[163]	TCTTTAGGAGCACTAACAACTAATAAGGAATGAAA	Core staple	386
8[142]	TTGTTACCTGAAACAAATACTTCTTTGATTAGTAATA	Core staple	387
8[166]	GCACGTAAAACAGAAATAAATGAGGAAGGT	Core staple	388
10[160]	AACAAACATCAAGAAGCAAAA	Core staple	389
12[163]	ACATAAATCAATATATGGAACCTACCATAT	Core staple	390
14[142]	CAGAGGGTTATGAGTGATTGAATTACCTTTTTTA	Core staple	391
14[160]	GCGGAACAAAGAAAGAGTAAC	Core staple	392
18[166]	ATTAACATCCAATAAATCATTTTAGAACCC	Core staple	393
20[163]	AAATGCAATGCCTGAGTCAGGTCATTG	Core staple	394
22[163]	GGAGCAAACAAGAGAATCGATGAAAGGCTATAATGTGTAAAA	Core staple	395
24[163]	TGTTAAATCAGCTCATTTTTTAACTATTTTGTGGG	Core staple	396
26[142]	AAGGGTGGAGAATCGGCAGGTGGCATCAATTCTACTA	Core staple	397

5’ — end	Sequence	Note	SEQ ID NO:
26[166]	CATTCAGGCTGCGCAACTGTTTAAAATTCG	Core staple	398
28[160]	ACCTCACCGGAAACCCGCCAC	Core staple	399
30[163]	TCTCCGTGGTGAAGGGAGAAACCAGGCAAA	Core staple	400
32[142]	GGGGGTGCCGTAGCTCTAGTCCCGGAATTTGTGA	Core staple	401
32[160]	GGTCACGTTGGTGTATTGACC	Core staple	402
36[166]	ATTATTCATTAAAGGTGAATAAGTTTGCCT	Core staple	403
38[163]	CTGTAGCGCGTTTTCATCTCAGAGCCG	Core staple	404
40[163]	ACCACCAGAGCCGCCGCCAGCATTCACCACCCGGCATTCAGA	Core staple	405
42[163]	GGAGTGTACTGGTAATAAGTTTTAAGCGTCAAAGC	Core staple	406
44[142]	CCATTTCTGTCAGCGGAATTGAGGGAGGGAAGGTAAA	Core staple	407
44[166]	CCCTCATTTTCAGGGATAGCTACATGGCTT	Core staple	408
46[160]	ACTTTCAACAGTTTATGGGAT	Core staple	409
48[163]	TTGAAAATCTCCAAAAAGAACCGCCACCCT	Core staple	410
50[142]	GCGACCCTCAAAAGGCTAGGAATTGCGAATAATA	Core staple	411
50[160]	GGTTTTGCTCAGTAAAGGATT	Core staple	412
9[160]	CAAAATTATGA	Connector staple	413
27[160]	GCGCCATTCCA	Connector staple	414
45[160]	CAGAGCCACTA	Connector staple	415
11[154]	GAAGATGATTT	Connector staple	416
29[154]	GGGAACGGACA	Connector staple	417
47[154]	TTTGCTAAAGC	Connector staple	418
7[157]	TATCTAAAAAC	Connector staple	419
25[157]	CATTAAATTGA	Connector staple	420
43[157]	TTGATGATATT	Connector staple	421
1[160]	ACATCACTTTT	Connector staple	422
19[160]	ATAGTAGTAGG	Connector staple	423
37[160]	TATTGACGGTA	Connector staple	424
3[157]	ATAAAAGGGTA	Connector staple	425
5[157]	GTGAGGCGGTC	Connector staple	426
13[157]	ATGGAAACAGT	Connector staple	427
15[154]	ATTATCATTGC	Connector staple	428
21[157]	TCATATATTCA	Connector staple	429
23[157]	CCTGAGAGTCC	Connector staple	430
31[157]	GAGATAGACCG	Connector staple	431
33[154]	GTAATGGGAAA	Connector staple	432
39[157]	TTAGCGTCATT	Connector staple	433
41[157]	CCACCAGAACT	Connector staple	434
49[157]	ATTTTTTCATT	Connector staple	435
51[154]	AGGATTAGCGC	Connector staple	436
1[12]	TTTTTAAACAGGAGGCCGATTAATCAGATCACGGTCACGCTGAACG	Vertex staple	437
0[34]	TCGTTAGAAAGGGATTACACTTTTCTTTCGCCATATTTAACAACGCCAATTTTT	Vertex staple	438
3[9]	TTTTTAAAAACCGTCTAGCGGGAGCTTTTTT	Vertex staple	439
2[30]	TGGGCATCAGTGTGCACGTTTTCATTCCTGTGTGAAATTGTTATTTTT	Vertex staple	440
9[12]	TTTTTCAGAATGCGGCGGGCCTCTGTGGCGC	Vertex staple	441
13[14]	TTTTTGTAATGGGTAAAGGGGTGTGTTCAGCTTTTT	Vertex staple	442
15[16]	TTTTTTCCGCTCACAATCGTGCCAGCTGCATTAATGTTTTT	Vertex staple	443
19[12]	TTTTTAGTTTCATTCCATATAAAGTACGGAGAGTACCTTTAAGAA	Vertex staple	444
18[34]	GCAACTAACAGTTGTGAACGGCTGACCAGTCACTGTTGCCCTGCGGCTGTTTTT	Vertex staple	445
21[9]	TTTTTAGGTCAGGATTAGTGTCTGGATTTTT	Vertex staple	446
20[31]	CCAGGCTGACCAATAAGGTAAATTGAACTAACGGAACAACATTATTT	Vertex staple	447

5' — end	Sequence	Note	SEQ ID NO:
	TT		
27[12]	TTTTTACACCAGAACGAGTAGCTTGCCCGCA	Vertex staple	448
31[14]	TTTTTATAAGGGAACCGAATGTACAGACCAGTTTTT	Vertex staple	449
33[16]	TTTTTTTACAGGTAGAAACGATAAAAACCAAAATAGTTTTT	Vertex staple	450
37[12]	TTTTTTACATACATAAAGGTGTAGCAAAAGTAAGCAGATAGCATAG	Vertex staple	451
36[34]	AGTATGTGCAACATGAGAATAAGAGGCAACGAGGCGCAGACGGTCAATCTTTTT	Vertex staple	452
39[9]	TTTTTCTTTTTAAGAAACGTAGAAAATTTTT	Vertex staple	453
38[30]	CAAAATTCTGAACAAGATAGAAACCCCAATAGCAAGCAAATCATTTTT	Vertex staple	454
45[12]	TTTTTCTAATTTACGAGCATGAAAATAAGAG	Vertex staple	455
49[14]	TTTTTCATGTAATTTAGGCTAAAGTACCGACTTTTT	Vertex staple	456
51[16]	TTTTTGATATAGAAGGCAATCTTACCAACGCTAACGTTTTT	Vertex staple	457
5[9]	TTTTTAAAATCCTGTTTCGTCAAAGGGCGTTTTT	Vertex staple	458
7[24]	GGGGTGGTTTGCCCCAGCAGGCGTTTTT	Vertex staple	459
23[9]	TTTTTAAATCAGGTCTTGCAAACTCCAACTTTTT	Vertex staple	460
25[24]	AAAGGAGAATGACCATAAATCAATTTTT	Vertex staple	461
41[9]	TTTTTGGGAGAATTAACCTTACCGAAGCCTTTTT	Vertex staple	462
43[24]	CCTAACAGGGAAGCGCATTAGACTTTTT	Vertex staple	463
7[9]	TTTTTAATCGGCCAACGTGCTGCGGCTTCACTAATCTGATGAAAAGGTAAAGTTAGCTATTGAA	Vertex bundle strand	464
25[9]	TTTTTCGAGAGGCTTTTTGACGAGAAGCAAAATTCTCATTGAAATCGTTAACGACTCCAAGATG	Vertex bundle strand	465
	TTTTTAGCGTCTTTCCATATCCCATC TTCACTAATCTTATGTACT		466
43[9]	GCGCATAGGCTGACCGGAATACC	Vertex bundle strand	467
	CATCAGATTAGTGAA	Vertex bundle strand (complementary)	468
	CAATGAGAATTTTGC	Vertex bundle strand (complementary)	469
	AGTACATAAGATTAGTGAA	Vertex bundle strand (complement-ary)	470

Table 6. Sequences of the cube with long connector staples.

5' — end	Sequence	Note	SEQ ID NO:
1[84]	AACGGTATATCCAGAACAAACCACCACAGGATTTTAACGGAATGGT	Core staple	471
0[54]	GCGCCGTAAACAGAGTGCTCGTCATAAGTTACCTGTCC	Core staple	472
3[102]	GGAGGCCTTGCTGGTAACGCCAGACCGGCCAAGTT	Core staple	473
3[144]	GTCAGTAATAACATCACCGAGTAAGCAAAAGAAGATTCTGCT	Core staple	474
2[44]	ACTAAAATCCCTTATAATGAGAGACGCCAGGCTGC	Core staple	475
2[51]	AGAGCAGCCAAGCGCAGGTTTCTGCGTAATCATGGTCAGAGC	Core staple	476
2[72]	GTGCCTATACAGTAACATCCTCATAGACAGG	Core staple	477
2[93]	CTGTTACATCGATTTTCTCAATTATCATCATTGAA	Core staple	478
2[107]	AGATGGCTATTAGTCTTACACCGCACCTTGCGAGC	Core staple	479
2[114]	CAGCGGATTCCAGAAATATTATCAAACAAAGAAACCACTTTA	Core staple	480
2[135]	TAAAATACCACAAAATTATCAATAAGTAACATTATCATAAAC	Core staple	481
5[25]	GTGGTTCCGATCCACGCAGAG	Core staple	482
5[60]	AAAAGTTTGGGTGTAGCCGCTTAAT	Core staple	483
5[123]	GCGATTCTGGAATACCTAGTAGAAGAACTCATTTTATATCGT	Core staple	484
4[41]	CAAGCGGAATCGGCATTAAAGCGGGCGCGCGCGTA	Core staple	485
4[83]	CAGCTGAAGTACGTAAGAAGGTATATTACCGCCAGCCATTGCTGAC	Core staple	486
7[32]	GCGAACCTGTTCCACACAACATACTAGCTGTCGGTCATAGTA	Core staple	487
7[74]	AGTACATTAAGGGTGCCTAATGAGGAGGATCCGCGTCCATCG	Core staple	488

7[81]	CGGACGTCAGATGAACTTGTTCTTCCCGGGTACCGAGCAAGC	Core staple	489
7[91]	AAATGAATAGAGCCGTCAAAGCTAACTCGAGA	Core staple	490
7[109]	ATCCTGCAACAGTGCCATTTTGAAACCCTTCAACA	Core staple	491
6[51]	CCGAAGCATAAAGTGTATCGAATTCCAG	Core staple	492
6[114]	ACTGTATTAGACTTTACTTTGCGGGATGATGACAT	Core staple	493
8[65]	CAGTTCTTTTTCACCGCCTGGCCCATCA	Core staple	494
9[60]	CACTGCGTTACGTCAGCGTGGTGCCGTG	Core staple	495
9[130]	TTCATTTGCACAAATATGGCGGTCAGTATTATAAT	Core staple	496
11[88]	CTTAAAGCGTGGCACAGACAATATCGCTGAGAGCCAAA	Core staple	497
11[130]	TTGAAGGGACCGAACTGATAGCCCGAGGTGACAAA	Core staple	498
10[37]	CCCATCAGAGCGGGAGCCTACAGGTAGGGCGCTGGCAAAACA	Core staple	499
10[58]	TGTGAGGCCGATTAAAGCCCGCCGGGTCACGCTGCGCGTTGA	Core staple	500
10[65]	CCGCGGTGCCTTGTTCCGAATAGCCCGAGATTTGCCCTCACC	Core staple	501
10[100]	CCTATCCTGAGAAGTGTAACTATCAAAACGCTCATGGACCAA	Core staple	502
10[114]	CTCGTTCCGGTCAATATATGTGAGATTCCTGAAAGAAAAAGC	Core staple	503
10[121]	TTTATCAGTGAGGCCACTTGCCTGACATTTTGACGCTCGTAA	Core staple	504
13[74]	CTGGTGATGAAGGGTAAGAGCACAGTAC	Core staple	505
13[95]	AAACCTTGCTTCTGTAAGTGAGCCAGGTTTAGCGCAGC	Core staple	506
12[37]	TAATAATGGGTAAAGGTTTCTTAATACAAAT	Core staple	507
12[48]	TCTTACCACCGGGGTGTCACTTATTGGGGTTGCAG	Core staple	508
12[79]	TCGCTTTTAGTATCATAGCGTGCCGCAT	Core staple	509
12[100]	TAACGATGCTGATTGCCGTCGCTGACAATAAAGAT	Core staple	510
12[121]	AAACAAACGCGGGATGAAACAAACTTAATGGAAACAGTGCAA	Core staple	511
15[46]	CGGCTTTCCAGTCGGGAGTTTGCGGCGCGCCATGCCGGACAT	Core staple	512
15[67]	CTGTTGCGTTGCGCTCAGTGGTTTACGATCCGCGGTGCGACT	Core staple	513
15[88]	GATAATACATTTGAGGACAGAAGGAGCGGCTCACAGTTTGTA	Core staple	514
15[109]	GAAAACAACTAATAGATAAATCTATTGCGTAGGGAGAAGCAG	Core staple	515
15[130]	AATTAAAATATCTTTAGTGAACCTCGTAAAAGCCTGATCGTT	Core staple	516
17[134]	CAGCAGCAACCGCGGCGGCCTTTAGT	Core staple	517
16[167]	TCCCGTAAAAAAAGCCGCACAAAGAATGCCAACGGCAGCACC	Core staple	518
16[188]	GTGTACATCGACATAAAAAAAGTCGGTGGTGCCATCCCACGC	Core staple	519
16[209]	GCCGCCAGCAGTTGGGCGGTTAACCAGCTTACGGCTGGAGGT	Core staple	520
16[221]	TTCTGCTCATTTGTCCAGCATCAG	Core staple	521
19[53]	CAGTTAATCATAAGGGAGCATAGGAGAC	Core staple	522
19[84]	TTTAGTTAATAAAGCCTCATCATTTTTGTGCGAACAAGA	Core staple	523
19[116]	GGTTCGGAACTCACCCTTCTCACGGAAAAAGCGACGACATCG	Core staple	524
18[44]	AATTTAGAGAGTACCTTGCCCGAACTGG	Core staple	525
18[65]	TGGTCCTTTTGATAAGACATC	Core staple	526
21[102]	ACCTAGCAAAATTAAGCTGACCATCTAC	Core staple	527
21[144]	CTTTAGCATTAACATCCGCTATATATAACCTCACCGAACGAC	Core staple	528
20[44]	TTCCTTTACCCTGACTAGTCATAAAAGAAGTAATT	Core staple	529
20[65]	TTACAGAAGCAAAGCGGAGCGTCCTAATAGTCAGA	Core staple	530
20[72]	AAATAGGGGGATGTGCTAGGACTAGAGTAGA	Core staple	531
20[93]	GAAGATTAAGCTTCGCTTTAGTTTGAGGGGAAGAC	Core staple	532
20[107]	ATTAACCGTTCTAGCTGGAACGGTGCCCCAAAACC	Core staple	533
20[114]	GGTGGTTTTCAAGGGCGAGTATCGGGGCGCATCGTAACGCTT	Core staple	534
20[135]	GCAGTAAAACTCAGGCTGCACTCCATAGGTCACGTTGGGAGC	Core staple	535
23[25]	TAAATCAAAACCCCTCAAATA	Core staple	536
23[60]	AGTAGAGGAATAATTGCCTTAGAGCTTAATTATAA	Core staple	537
23[123]	ATTAGTAATGCCTGTAACATACAGGCAAGGCAAAT	Core staple	538
22[41]	TTGAATCATCAGGTAAATATCGTCAGGAATAATGC	Core staple	539
22[97]	CATGTCAATCATAGACTGGATATGTCAAATCACCATCAATAT	Core staple	540

25[32]	GCGCAACACTGGAACAACATTATTGTTGGGAAACACCAGCCG	Core staple	541
25[60]	CCAAGAACCGACCTTCAAGGAAGTTTGATTCCCAATTCCGGA	Core staple	542
24[51]	ACGGAAAGATTCATCAGGCTCATTTTGGGCTAGG	Core staple	543
24[72]	TACTTAGGAATACCACACTTATGCTTCAACTAACT	Core staple	544
24[90]	TCGCGCAACTAATGAAAATGTCAGCTGGCGAAAATGTTT	Core staple	545
24[114]	AATTCAACATTAAATGTTGTAGATGCCTCAGGGAT	Core staple	546
26[65]	ACAGAGGGGGAATACTGCGGAATCTTAT	Core staple	547
26[86]	CGCTTATGTACCCCGGTAAATAAT	Core staple	548
26[107]	GTGCAGAAAAAATCGTAAAACTAGGATATTCCAAAAGGTTGT	Core staple	549
27[74]	AATGATTTTAAGAACTGTTGAGATATAACGCCAAAAGGTTTG	Core staple	550
27[129]	GATCGCGCAACAAGATTGACAAGAGAATCGATATAA	Core staple	551
29[39]	GGCACCGAACAAGTTTCATTCCATGCTG	Core staple	552
29[53]	CTGGATATTCTAGTAAAATACCAGTCAGGACACAG	Core staple	553
29[88]	GGCAGGCCGGAGACATGGGGAGCATAAAGCTAAATCGGGTGA	Core staple	554
29[102]	GTAGCAACGGTAGATACATTTCGCAAAGAATAAAAACATTATGACTGTA	Core staple	555
29[130]	GTTATGCCTGAATGCCGGAGAGGGGGAGCAATATA	Core staple	556
28[72]	CTTATACGTAATTGCAGGGAGTTAGGCTTTGGCAA	Core staple	557
28[93]	AGAAAGGCCGGAAACAGCGGATCATTAATCAATTA	Core staple	558
28[121]	GCACAATAACCTGTTTAAATAAATTACTTTTGCGGGAGAAAT	Core staple	559
30[37]	GGCGAACGAGGCGCAGACGGTCCCTTCGCAC	Core staple	560
30[48]	TCAATCCGAACGAGATTACCCTTTGCAAATATTCA	Core staple	561
30[59]	CGCTATTAAACGGGTAAATTTCATGTCAAGAGAAGA	Core staple	562
30[79]	TAAATCGGGGTCATTGCTGAGATGCTTG	Core staple	563
30[100]	GCACTTTTGCGGGATCGGAGGGTAACGCCAGAAAG	Core staple	564
30[121]	AGCCAGCAGCGAGAAACAATCGGCTCTCCGTGGTGAAGGAA	Core staple	565
33[46]	GTAAGGCATAGTAAGAGAGAGGCTAAATCAAACCA	Core staple	566
33[91]	CCTTCCTGTAGCCACGTGCATCTGCCGTGAATTACTTTCTGG	Core staple	567
33[109]	TCAAGGAACGCCATCAATGATAATCGGGCCTTTGG	Core staple	568
33[130]	GAGTCAGCTCATTTTTTAAACAGGTGTTGGGCCAGTCAGACA	Core staple	569
35[134]	GCCACTACGAAGGGGTCGCTGAGGCT	Core staple	570
34[167]	CCACGCATAACCGATATATTCCACCAACCTAAAACGAAAGAG	Core staple	571
34[188]	GACAATGACAACAACCATCGCGCAAAAGAATACACTAAAACA	Core staple	572
34[209]	CTTGATACCGATAGTTGCGCCCTCATCTTTGACCCCCAGCGA	Core staple	573
34[221]	TTTCTTAAACAGTTATACCAAGCG	Core staple	574
37[53]	AAGTTATTTAGGCAGAGAATTCTGCCCA	Core staple	575
37[84]	ATTTTGTCAAAATCACCAGAAC	Core staple	576
37[116]	TTTATGTAAAGGCTTAGGAGCCTTTAATTGTGTGTATCACCG	Core staple	577
36[44]	CATAGATAGCCGAACAAAGTTAAGTCCAGACGAAC	Core staple	578
36[65]	CGGAGAAGGAAACCGAGAGAG	Core staple	579
36[75]	GCAATACACGGAAGAGAAAATCTGACCTATCATA	Core staple	580
39[102]	CCGGGAATTAGAGCCAGCACAATCCAATCGCGAGACTATATCAGC	Core staple	581
39[144]	TCACATTAAAGGTGAATCAAAAGGACAGTTTCAGCGTATCGT	Core staple	582
38[44]	ATACCTGAACAAAGTCAAAAAATGAGTTACAAAGA	Core staple	583
38[65]	ACAATTGAGCGCTAATAAACGATTATTATTTGAGG	Core staple	584
38[72]	ATAACCCTGTAGCATTCAGAACGCTAAGTTT	Core staple	585
38[83]	ATCAAAGGATAGCACCATTACCATTAGCGCCA	Core staple	586
38[93]	TCTAGCCCTCTTTCGTCGTAGCCCGGAATAGATCG	Core staple	587
38[107]	ATTGAACCGCCTCCCTCGGTTGAGGCCAGAACAGT	Core staple	588
38[114]	CCCGATCTAACCCATGTACCGTACGCCGTCGAGAGGGTTCGG	Core staple	589
38[135]	CATTCCAGACGGATAGCACCGCCACTCAGTACCAGGCGCATG	Core staple	590
41[25]	GAGAATTAACTACAGAGCTTT	Core staple	591
41[60]	GTAAGAATTGAGTTACCAATACCCAAAAGAAATAA	Core staple	592

41[123]	CCGTTCGGTCGAAACCAGTCACCGACTTGAGATGG	Core staple	593
40[41]	CAGCCTTTGAACACATAAGAGAGTAAGCGATTAAG	Core staple	594
40[97]	TGGCCTTGATATCAAATAAGATCAATCACCGGAACCAGAGCC	Core staple	595
43[32]	CCACCCAGCTCAGATATAGAAGGCATCGTAGGAGCATGCCTG	Core staple	596
43[60]	AAATAATGCAGACGACAAAATATAAAACGCAAAGACACATAA	Core staple	597
43[130]	GTCCAGCATTGACAGGAAGAG	Core staple	598
42[51]	TTAGTATTCTAAGAACGAAGCAAGTAATCGGCAAC	Core staple	599
42[72]	TTTTTTTAGCGAACCTCAGTACCGCATTCCACGAGGTGAACGAAA	Core staple	600
42[90]	AACAGGACTTGCGGATCCCAACAAACTACAACGATTCCT	Core staple	601
42[114]	GCCCTATTATTCTGAAAGATAAGTTCAGGAGCCAAAAGGTTGGGT	Core staple	602
44[51]	GCGCAATCAACCGTTTTTATTTTCTTAT	Core staple	603
44[107]	TAACATTAAAGCAGGTCAGACGATACCACCGAGCGTTTAAGG	Core staple	604
45[74]	TATCACTCATCGAGAACCGAGGCGTGAAGCCTTAAATCAAAT	Core staple	605
47[39]	AGTGCATTTTAAAGGTGGCAACATCTGG	Core staple	606
47[102]	TTAGCAAATCAATAGAAAATTCATCCATTTGGAAACGTCACCAATATAG	Core staple	607
47[130]	CTTCGGCATTCCACCCTCAGAACCCCGCCGCTCTGAATGGTA	Core staple	608
46[121]	TATACCAGCGCCAAAGATATCACCTCGATAGCAGCACCTTTT	Core staple	609
49[84]	GGTCTGAAAGACAACACAGACTTTCATA	Core staple	610
49[126]	TAGAGTGAGAATAGCCAAAAAAAAGGCTGTTTAGTAAGCCCACGCA	Core staple	611
48[37]	ATATTAACAACGCCAACATGTATTGATTTGT	Core staple	612
48[48]	ATCATCGTAGAAACCCTGTTTATTTGCCAAAATAG	Core staple	613
48[58]	GGAAGTTAATTTCATCTCTTTTTCATAAACAACCC	Core staple	614
48[69]	CAAAGTACTGTCTTGTTCAGCCAGCCATTTTTGTTTAACGTCGAGG	Core staple	615
48[90]	TTGCTTTAGAACGGACCAGTATCTCACAAACAAATCCGTATA	Core staple	616
48[100]	GTTCCTTTTTAACCTCCTGCTGATGCGTAACCCTT	Core staple	617
50[104]	TGATATAAGTATATTAAACCACCTTAATGCCCCCTGCCTATT	Core staple	618
51[46]	CCGGTTGCTATTTTGCAGAGCCTAATCAACAGTAA	Core staple	619
51[109]	AACTTGAGTAACAGTGCAAATCCTCACTGAGATAG	Core staple	620
51[130]	AAAAGTTTTAACGGGGTTGGAAAGATAGGAAAGTTTTGTAAC	Core staple	621
53[134]	AATTTAATGGTTTGAATTTATCAAAA	Core staple	622
52[167]	ACGCTGAGAAGAGTCAATAGTGAAATACCGACCGTGTGATAA	Core staple	623
52[188]	ATAGCGATAGCTTAGATTAAGATAAGGCGTTAAATAAGAATA	Core staple	624
52[209]	TCCCTTAGAATCCTTGAAAACAACACCGGAATCATAATTACT	Core staple	625
52[221]	ATTAATTAATTTAGAAAAAGCCTG	Core staple	626
7[137]	CCCGGTTATCTCGACAACTCGTATAAGTTTGTAATCCTACCT	Core staple	627
7[151]	CTGCAGAAGATAAAACATAAAACAACGACCAAATC	Core staple	628
6[146]	TGAGGAATCAATCAACCATATAGTTACATACCTGAAAGAGTC	Core staple	629
12[142]	TTTATCAAGAAAACAAATTTCAATAAATCGCCAGTCAC	Core staple	630
12[163]	ACAATTTCATTTGAATTGATTGTTAGAACCTATAT	Core staple	631
14[160]	GTTATTAATTTTAATAAATCCAAGGAAT	Core staple	632
25[137]	AGCTGTTAAATAACAACCCGTCGGTAATGGGAGCCAGCTAGA	Core staple	633
25[151]	TTGTTGCCTGAGAGTCTTAGCTATATATTTTAAGC	Core staple	634
24[146]	AAATTTTAAATATTTCGCCATGACGGCCGGAACGGTTTCATT	Core staple	635
30[142]	CTTGAAACGTACAGCGCCGCCACGAGTGCCACCCTCAT	Core staple	636
30[163]	CCGGAATTTGTGAGAGATTTCCGGGCGCCATTAAA	Core staple	637
32[160]	CGGCGGATTGACCGATTCTCCTCGCATT	Core staple	638
43[151]	GTAAACCACCACCAGAGGCCACCCTAGCGCGGTAA	Core staple	639
42[135]	ATAGTATTAAGAGGCTGGGTTTTGCCCTCAGAAAA	Core staple	640
42[146]	GTGTACTTTACCGTTTTTCAGGTTAGTAACTTTCAGCGACAT	Core staple	641
48[142]	TCTAAAGGAACAACTAACTAAACAAATGAATCAGACTG	Core staple	642
48[163]	ATAATTTTTTCACGTTGAACCGCCACCCTCATCCA	Core staple	643
50[160]	ATTAGGATTAGCGGAGACTCCTACAGGA	Core staple	644

10[160]	TTATTCAATTAATTACATTTA	Connector staple	645
28[160]	GTGGAGCCATGTTTACCAGTA	Connector staple	646
46[160]	GATTTTGAGGAATTGCGAATC	Connector staple	647
8[166]	TAATGGAAGGGTTTGGATTATACTTCTGAA	Connector staple	648
26[166]	GAAACCAGGCAAACACCGCTTCTGGTGCGG	Connector staple	649
44[166]	CCTCAGAGCCACCACCCTCAGAACCGCCAG	Connector staple	650
2[163]	GCAGATTCACGCAGAGGCGAA	Connector staple	651
20[163]	ATTTTTAGAAAGCTTTCAGAC	Connector staple	652
38[163]	CCTTTAGCGTTTTCTGTATCG	Connector staple	653
4[163]	GAACCACCAGGTCAGTTGGCAATG	Connector staple	654
22[163]	TATCAGGTCATAAACGTTAATATG	Connector staple	655
40[163]	CCGCCACCAGAGCGTCATACATAA	Connector staple	656
5[147]	TCGCCATTAAAAATACCGAAC	Connector staple	657
23[147]	TTTTGAGAGATCTACAAAGAG	Connector staple	658
41[147]	TCAGAGCCACCACCCTCAGGC	Connector staple	659
1[147]	TGTCCATTTTGATTTGAAATGGATTATTTACATAT	Connector staple	660
19[147]	TGGGGCGATAGTAGTATTTCAACGCAAGGATAAGG	Connector staple	661
37[147]	TCAACCGAATTATTGTAGCGACAGAATCAAGTTTT	Connector staple	662
6[163]	CAACAGTTGATTTGCCCGATT	Connector staple	663
24[163]	TTGTTAAAATGTGGGAACAGT	Connector staple	664
42[163]	CTTTTGATGATCAAGAGAAGC	Connector staple	665
0[166]	GTAGCAATACTTCCACGCAAATTAACCGAC	Connector staple	666
18[166]	ATCAATTCTACTACGAGCTGAAAAGGTGGG	Connector staple	667
36[166]	AAATATTGACGGAATTGAGGGAGGGAAGAA	Connector staple	668
9[12]	TTTTTCAGAATGCGGCGGGCCTCTGTGGCGC	Vertex staple	669
15[16]	TTTTTTCCGCTCACAATCGTGCCAGCTGCATTAATGTTTTT	Vertex staple	670
38[30]	AAAACAAAAGATAGATAAATTTACGAATCATTACCGCGCCCAATTTTT	Vertex staple	671
36[34]	ACTCCTTCATACATCGAGCCAGCCATATAATTGTGTCGAAATCCGCGACTTTTT	Vertex staple	672
49[14]	TTTTTCTTAATTGAGAATCGTAATAAGAGAATTTTT	Vertex staple	673
45[12]	TTTTTAATAATATCCCATCCTAGTCCTGCGA	Vertex staple	674
51[16]	TTTTTTAGCAAGCAAATACAATTTTATCCTGAATCTTTTTT	Vertex staple	675
37[12]	TTTTTGCAAACGTAGAAAATAATTACGCCCCTTTTTAAGAAACAAG	Vertex staple	676
39[9]	TTTTTATCTTACCGAAGAGTATGTTATTTTT	Vertex staple	677
20[31]	TTTTTGTACAGCGTAACAGACGAGAAGAAAAATCTACGTTAATATTTTT	Vertex staple	678
18[34]	TGTAGCTTGTCTGGTGACCAATTAGCCGGCGGTTGCGGTATGAGCCGGGTTTTT	Vertex staple	679
31[14]	TTTTTCTGCTCCATGTTACCTTTGAAAGAGGTTTTT	Vertex staple	680
27[12]	TTTTTGAATAAGGCTTGCCCTAAGCTGCAAA	Vertex staple	681
33[16]	TTTTTAAACGAACTAACATCATAACCCTCGTTTACCTTTTT	Vertex staple	682
19[12]	TTTTTTGCAACTAAAGTACGGCAACATGGCAAACTCCAACAGGCG	Vertex staple	683
1[12]	TTTTTTATAACGTGCTTTCCTTGCTTTGTCAAGCGAAAGGAGAACG	Vertex staple	684
21[9]	TTTTTACCAGACCGGAATTTTAAATATTTTT	Vertex staple	685
2[30]	TGGGCATCAGTGTGCACGTTTTCATTCCTGTGTGAAATTGTTATTTTT	Vertex staple	686
0[34]	CTATGGTCGTTAGATTACACTCGGCTGGAGCCAACGCTCAACAGTAGGGTTTTT	Vertex staple	687
13[14]	TTTTTTCACTGTTGCCCTGGGTGTGTTCAGCTTTTT	Vertex staple	688
3[9]	TTTTTAAAAACCGTCTAACGAGCACGTTTTT	Vertex staple	689
7[24]	GGGGTGGTTTGCCCCAGCAGGCGTTCACTAATCTGATGGAAGCGCATTAGATAGCAATAGCTTTTTT	Vertex bundle strand	690
25[24]	CCAAAATGCTTTAAACAGTTCAGGCAAAATTCTCATTGAAAATCCTGTTTCGTCAAAGGGCGTTTTT	Vertex bundle strand	691
43[24]	GCGTAGAATAACATAAAAACAGGAATGTCGATATCTAGAAAACGAGAATGGCTTCAAAGCGATTTTT	Vertex bundle strand	692
7[9]	TTTTTAATCGGCCAACGTGCTGCGGCTTCACTAATCTGATGTATAAAGTACCGCAATGAAACGG	Vertex bundle strand	693

25[9]	TTTTTAGACGACGATAATCATTCAGTGCAAAATTCTCATTGAAATCGTTAACGACTCCAAGATG	Vertex bundle strand	694
43[9]	TTTTTTACCAACGCTAAAACAAGAAAAATGTCGATATCTAGACAGATGAACGGAATTCGAACCA	Vertex bundle strand	695
	CATCAGATTAGTGAA	Vertex bundle strand (complement-ary)	696
	CAATGAGAATTTTGC	Vertex bundle strand (complement-ary)	697
	CTAGATATCGACATT	Vertex bundle strand (complement-ary)	698

Table 7. Sequences of the cube with short connector staples.

5' — end	Sequence	Note	SEQ ID NO:
1[84]	AACGGTATATCCAGAACAAACCACCACAGGATTTTAACGGAATGGT	Core staple	699
0[54]	GCGCCGTAAACAGAGTGCTCGTCATAAGTTACCTGTCC	Core staple	700
3[102]	GGAGGCCTTGCTGGTAACGCCAGACCGGCCAAGTT	Core staple	701
3[144]	GTCAGTAATAACATCACCGAGTAAGCAAAAGAAGATTCTGCT	Core staple	702
2[44]	ACTAAAATCCCTTATAATGAGAGACGCCAGGCTGC	Core staple	703
2[51]	AGAGCAGCCAAGCGCAGGTTTCTGCGTAATCATGGTCAGAGC	Core staple	704
2[72]	GTGCCTATACAGTAACATCCTCATAGACAGG	Core staple	705
2[93]	CTGTTACATCGATTTTCTCAATTATCATCATTGAA	Core staple	706
2[107]	AGATGGCTATTAGTCTTACACCGCACCTTGCGAGC	Core staple	707
2[114]	CAGCGGATTCCAGAAATATTATCAAACAAAGAAACCACTTTA	Core staple	708
2[135]	TAAAATACCACAAAATTATCAATAAGTAACATTATCATAAAC	Core staple	709
5[25]	GTGGTTCCGATCCACGCAGAG	Core staple	710
5[60]	AAAAGTTTGGGTGTAGCCGCTTAAT	Core staple	711
5[123]	GCGATTCTGGAATACCTAGTAGAAGAACTCATTTTATATCGT	Core staple	712
4[41]	CAAGCGGAATCGGCATTAAAGCGGGCGCGCGTA	Core staple	713
4[83]	CAGCTGAAGTACGTAAGAAGGTATATTACCGCCAGCCATTGCTGAC	Core staple	714
7[32]	GCGAACCTGTTCCACACAACATACTAGCTGTCGGTCATAGTA	Core staple	715
7[74]	AGTACATTAAGGGTGCCTAATGAGGAGGATCCGCGTCCATCG	Core staple	716
7[81]	CGGACGTCAGATGAACTTGTTCTTCCCGGGTACCGAGCAAGC	Core staple	717
7[91]	AAATGAATAGAGCCGTCAAAGCTAACTCGAGA	Core staple	718
7[109]	ATCCTGCAACAGTGCCATTTTGAAACCCTTCAACA	Core staple	719
6[51]	CCGAAGCATAAAGTGTATCGAATTCCAG	Core staple	720
6[114]	ACTGTATTAGACTTTACTTTGCGGGATGATGACAT	Core staple	721
8[65]	CAGTTCTTTTTCACCGCCTGGCCCATCA	Core staple	722
9[60]	CACTGCGTTACGTCAGCGTGGTGCCGTG	Core staple	723
9[130]	TTCATTTGCACAAATATGGCGGTCAGTATTATAAT	Core staple	724
11[88]	CTTAAAGCGTGGCACAGACAATATCGCTGAGAGCCAAA	Core staple	725
11[130]	TTGAAGGGACCGAACTGATAGCCCGAGGTGACAAA	Core staple	726
10[37]	CCCATCAGAGCGGGAGCCTACAGGTAGGGCGCTGGCAAAACA	Core staple	727
10[58]	TGTGAGGCCGATTAAAGCCCGCCGGGTCACGCTGCGCGTTGA	Core staple	728
10[65]	CCGCGGTGCCTTGTTCCGAATAGCCCGAGATTTGCCCTCACC	Core staple	729
10[100]	CCTATCCTGAGAAGTGTAACTATCAAAACGCTCATGGACCAA	Core staple	730
10[114]	CTCGTTCCGGTCAATATATGTGAGATTCCTGAAAGAAAAAGC	Core staple	731
10[121]	TTTATCAGTGAGGCCACTTGCCTGACATTTTGACGCTCGTAA	Core staple	732
13[74]	CTGGTGATGAAGGGTAAGAGCACAGTAC	Core staple	733
13[95]	AAACCTTGCTTCTGTAAGTGAGCCAGGTTTAGCGCAGC	Core staple	734
12[37]	TAATAATGGGTAAAGGTTTCTTAATACAAAT	Core staple	735
12[48]	TCTTACCACCGGGGTGTCACTTATTGGGGTTGCAG	Core staple	736
12[79]	TCGCTTTTAGTATCATAGCGTGCCGCAT	Core staple	737

5' — end	Sequence	Note	SEQ ID NO:
12[100]	TAACGATGCTGATTGCCGTCGCTGACAATAAAGAT	Core staple	738
12[121]	AAACAAACGCGGGATGAAACAAACTTAATGGAAACAGTGCAA	Core staple	739
15[46]	CGGCTTTCCAGTCGGGAGTTTGCGGCGCGCCATGCCGGACAT	Core staple	740
15[67]	CTGTTGCGTTGCGCTCAGTGGTTTACGATCCGCGGTGCGACT	Core staple	741
15[88]	GATAATACATTTGAGGACAGAAGGAGCGGCTCACAGTTTGTA	Core staple	742
15[109]	GAAAACAACTAATAGATAAATCTATTGCGTAGGGAGAAGCAG	Core staple	743
15[130]	AATTAAAATATCTTTAGTGAACCTCGTAAAAGCCTGATCGTT	Core staple	744
17[134]	CAGCAGCAACCGCGGCGGCCTTTAGT	Core staple	745
16[167]	TCCCGTAAAAAAAGCCGCACAAAGAATGCCAACGGCAGCACC	Core staple	746
16[188]	GTGTACATCGACATAAAAAAAGTCGGTGGTGCCATCCCACGC	Core staple	747
16[209]	GCCGCCAGCAGTTGGGCGGTTAACCAGCTTACGGCTGGAGGT	Core staple	748
16[221]	TTCTGCTCATTTGTCCAGCATCAG	Core staple	749
19[53]	CAGTTAATCATAAGGGAGCATAGGAGAC	Core staple	750
19[84]	TTTAGTTAATAAAGCCTCATCATTTTTGTGCGAACAAGA	Core staple	751
19[116]	GGTTCGGAACTCACCCTTCTCACGGAAAAAGCGACGACATCG	Core staple	752
18[44]	AATTTAGAGAGTACCTTGCCCGAACTGG	Core staple	753
18[65]	TGGTCCTTTTGATAAGACATC	Core staple	754
21[102]	ACCTAGCAAAATTAAGCTGACCATCTAC	Core staple	755
21[144]	CTTTAGCATTAACATCCGCTATATATAACCTCACCGAACGAC	Core staple	756
20[44]	TTCCTTTACCCTGACTAGTCATAAAAGAAGTAATT	Core staple	757
20[65]	TTACAGAAGCAAAGCGGAGCGTCCTAATAGTCAGA	Core staple	758
20[72]	AAATAGGGGGATGTGCTAGGACTAGAGTAGA	Core staple	759
20[93]	GAAGATTAAGCTTCGCTTTAGTTTGAGGGGAAGAC	Core staple	760
20[107]	ATTAACCGTTCTAGCTGGAACGGTGCCCCAAAACC	Core staple	761
20[114]	GGTGGTTTTCAAGGGCGAGTATCGGGGCGCATCGTAACGCTT	Core staple	762
20[135]	GCAGTAAAACTCAGGCTGCACTCCATAGGTCACGTTGGGAGC	Core staple	763
23[25]	TAAATCAAAACCCCTCAAATA	Core staple	764
23[60]	AGTAGAGGAATAATTGCCTTAGAGCTTAATTATAA	Core staple	765
23[123]	ATTAGTAATGCCTGTAACATACAGGCAAGGCAAAT	Core staple	766
22[41]	TTGAATCATCAGGTAAATATCGTCAGGAATAATGC	Core staple	767
22[97]	CATGTCAATCATAGACTGGATATGTCAAATCACCATCAATAT	Core staple	768
25[32]	GCGCAACACTGGAACAACATTATTGTTGGGAAACACCAGCCG	Core staple	769
25[60]	CCAAGAACCGACCTTCAAGGAAGTTTGATTCCCAATTCCGGA	Core staple	770
24[51]	ACGGAAAGATTCATCAGGCTCATTTTGGGCTAGG	Core staple	771
24[72]	TACTTAGGAATACCACACTTATGCTTCAACTAACT	Core staple	772
24[90]	TCGCGCAACTAATGAAAATGTCAGCTGGCGAAAATGTTT	Core staple	773
24[114]	AATTCAACATTAAATGTTGTAGATGCCTCAGGGAT	Core staple	774
26[65]	ACAGAGGGGGAATACTGCGGAATCTTAT	Core staple	775
26[86]	CGCTTATGTACCCCGGTAAATAAT	Core staple	776
26[107]	GTGCAGAAAAAATCGTAAAACTAGGATATTCCAAAAGGTTGT	Core staple	777
27[74]	AATGATTTTAAGAACTGTTGAGATATAACGCCAAAAGGTTTG	Core staple	778
27[129]	GATCGCGCAACAAGATTGACAAGAGAATCGATATAA	Core staple	779
29[39]	GGCACCGAACAAGTTTCATTCCATGCTG	Core staple	780
29[53]	CTGGATATTCTAGTAAAATACCAGTCAGGACACAG	Core staple	781
29[88]	GGCAGGCCGGAGACATGGGGAGCATAAAGCTAAATCGGGTGA	Core staple	782
29[102]	GTAGCAACGGTAGATACATTTCGCAAAGAATAAAAACATTATGACTGTA	Core staple	783
29[130]	GTTATGCCTGAATGCCGGAGAGGGGGAGCAATATA	Core staple	784
28[72]	CTTATACGTAATTGCAGGGAGTTAGGCTTTGGCAA	Core staple	785
28[93]	AGAAAGGCCGGAAACAGCGGATCATTAATCAATTA	Core staple	786
28[121]	GCACAATAACCTGTTTAAATAAATTACTTTTGCGGGAGAAAT	Core staple	787

5' — end	Sequence	Note	SEQ ID NO:
30[37]	GGCGAACGAGGCGCAGACGGTCCCTTCGCAC	Core staple	788
30[48]	TCAATCCGAACGAGATTACCCTTTGCAAATATTCA	Core staple	789
30[59]	CGCTATTAAACGGGTAAATTTCATGTCAAGAGAAGA	Core staple	790
30[79]	TAAATCGGGGTCATTGCTGAGATGCTTG	Core staple	791
30[100]	GCACTTTTGCGGGATCGGAGGGTAACGCCAGAAAG	Core staple	792
30[121]	AGCCAGCAGCGAGAAACAATCGGCTCTCCGTGGTGAAGGAA	Core staple	793
33[46]	GTAAGGCATAGTAAGAGAGAGGCTAAATCAAACCA	Core staple	794
33[91]	CCTTCCTGTAGCCACGTGCATCTGCCGTGAATTACTTTCTGG	Core staple	795
33[109]	TCAAGGAACGCCATCAATGATAATCGGGCCTTTGG	Core staple	796
33[130]	GAGTCAGCTCATTTTTTAAACAGGTGTTGGGCCAGTCAGACA	Core staple	797
35[134]	GCCACTACGAAGGGGTCGCTGAGGCT	Core staple	798
34[167]	CCACGCATAACCGATATATTCCACCAACCTAAAACGAAAGAG	Core staple	799
34[188]	GACAATGACAACAACCATCGCGCAAAAGAATACACTAAAACA	Core staple	800
34[209]	CTTGATACCGATAGTTGCGCCCTCATCTTTGACCCCCAGCGA	Core staple	801
34[221]	TTTCTTAAACAGTTATACCAAGCG	Core staple	802
37[53]	AAGTTATTTAGGCAGAGAATTCTGCCCA	Core staple	803
37[84]	ATTTTGTCAAAATCACCAGAAC	Core staple	804
37[116]	TTTATGTAAAGGCTTAGGAGCCTTTAATTGTGTGTATCACCG	Core staple	805
36[44]	CATAGATAGCCGAACAAAGTTAAGTCCAGACGAAC	Core staple	806
36[65]	CGGAGAAGGAAACCGAGAGAG	Core staple	807
36[75]	GCAATACACGGAAGAGAAAATCTGACCTATCATA	Core staple	808
39[102]	CCGGGAATTAGAGCCAGCACAATCCAATCGCGAGACTATATCAGC	Core staple	809
39[144]	TCACATTAAAGGTGAATCAAAAGGACAGTTTCAGCGTATCGT	Core staple	810
38[44]	ATACCTGAACAAAGTCAAAAAATGAGTTACAAAGA	Core staple	811
38[65]	ACAATTGAGCGCTAATAAACGATTATTATTTGAGG	Core staple	812
38[72]	ATAACCCTGTAGCATTCAGAACGCTAAGTTT	Core staple	813
38[83]	ATCAAAGGATAGCACCATTACCATTAGCGCCA	Core staple	814
38[93]	TCTAGCCCTCTTTCGTCGTAGCCCGGAATAGATCG	Core staple	815
38[107]	ATTGAACCGCCTCCCTCGGTTGAGGCCAGAACAGT	Core staple	816
38[114]	CCCGATCTAACCCATGTACCGTACGCCGTCGAGAGGGTTCGG	Core staple	817
38[135]	CATTCCAGACGGATAGCACCGCCACTCAGTACCAGGCGCATG	Core staple	818
41[25]	GAGAATTAACTACAGAGCTTT	Core staple	819
41[60]	GTAAGAATTGAGTTACCAATACCCAAAAGAAATAA	Core staple	820
41[123]	CCGTTCGGTCGAAACCAGTCACCGACTTGAGATGG	Core staple	821
40[41]	CAGCCTTTGAACACATAAGAGAGTAAGCGATTAAG	Core staple	822
40[97]	TGGCCTTGATATCAAATAAGATCAATCACCGGAACCAGAGCC	Core staple	823
43[32]	CCACCCAGCTCAGATATAGAAGGCATCGTAGGAGCATGCCTG	Core staple	824
43[60]	AAATAATGCAGACGACAAAATATAAAACGCAAAGACACATAA	Core staple	825
43[130]	GTCCAGCATTGACAGGAAGAG	Core staple	826
42[51]	TTAGTATTCTAAGAACGAAGCAAGTAATCGGCAAC	Core staple	827
42[72]	TTTTTTTAGCGAACCTCAGTACCGCATTCCACGAGGTGAACGAAA	Core staple	828
42[90]	AACAGGACTTGCGGATCCCAACAAACTACAACGATTCCT	Core staple	829
42[114]	GCCCTATTATTCTGAAAGATAAGTTCAGGAGCCAAAAGGTTGGGT	Core staple	830
44[51]	GCGCAATCAACCGTTTTTATTTTCTTAT	Core staple	831
44[107]	TAACATTAAAGCAGGTCAGACGATACCACCGAGCGTTTAAGG	Core staple	832
45[74]	TATCACTCATCGAGAACCGAGGCGTGAAGCCTTAAATCAAAT	Core staple	833
47[39]	AGTGCATTTTAAAGGTGGCAACATCTGG	Core staple	834
47[102]	TTAGCAAATCAATAGAAAATTCATCCATTTGGAAACGTCACCAATATAG	Core staple	835
47[130]	CTTCGGCATTCCACCCTCAGAACCCCGCCGCTCTGAATGGTA	Core staple	836
46[121]	TATACCAGCGCCAAAGATATCACCTCGATAGCAGCACCTTTT	Core staple	837
49[84]	GGTCTGAAAGACAACACAGACTTTCATA	Core staple	838
49[126]	TAGAGTGAGAATAGCCAAAAAAAAGGCTGTTTAGTAAGCCCACGCA	Core staple	839

5’ — end	Sequence	Note	SEQ ID NO:
48[37]	ATATTAACAACGCCAACATGTATTGATTTGT	Core staple	840
48[48]	ATCATCGTAGAAACCCTGTTTATTTGCCAAAATAG	Core staple	841
48[58]	GGAAGTTAATTTCATCTCTTTTTCATAAACAACCC	Core staple	842
48[69]	CAAAGTACTGTCTTGTTCAGCCAGCCATTTTTGTTTAACGTCGAGG	Core staple	843
48[90]	TTGCTTTAGAACGGACCAGTATCTCACAAACAAATCCGTATA	Core staple	844
48[100]	GTTCCTTTTTAACCTCCTGCTGATGCGTAACCCTT	Core staple	845
50[104]	TGATATAAGTATATTAAACCACCTTAATGCCCCCTGCCTATT	Core staple	846
51[46]	CCGGTTGCTATTTTGCAGAGCCTAATCAACAGTAA	Core staple	847
51[109]	AACTTGAGTAACAGTGCAAATCCTCACTGAGATAG	Core staple	848
51[130]	AAAAGTTTTAACGGGGTTGGAAAGATAGGAAAGTTTTGTAAC	Core staple	849
53[134]	AATTTAATGGTTTGAATTTATCAAAA	Core staple	850
52[167]	ACGCTGAGAAGAGTCAATAGTGAAATACCGACCGTGTGATAA	Core staple	851
52[188]	ATAGCGATAGCTTAGATTAAGATAAGGCGTTAAATAAGAATA	Core staple	852
52[209]	TCCCTTAGAATCCTTGAAAACAACACCGGAATCATAATTACT	Core staple	853
52[221]	ATTAATTAATTTAGAAAAAGCCTG	Core staple	854
0[166]	GTAGCAATACTTCTTTGATTTGAAATGGAT	Core staple	855
2[163]	GCAGATTCACCAGTCACTCGCCATTAA	Core staple	856
4[163]	GAACCACCAGCAGAAGATAAAACATAAAACAACGACCAAATC	Core staple	857
7[137]	CCCGGTTATCTCGACAACTCGTATAAGTTTGTAATCCTACCT	Core staple	858
6[163]	CAACAGTTGAAAGGAATTGAGGAATCAATCAACCATATAGTTACATACC	Core staple	859
8[166]	TAATGGAAGGGTTAGAACCTATATCTGGTC	Core staple	860
10[142]	TGAAAGAGTCTGTCCATCACGCA	Core staple	861
10[160]	TTATTCATTTCAATAAATCGC	Core staple	862
12[142]	TTTATCAAGAAAACAAAATT	Core staple	863
12[163]	ACAATTTCATTTGAATTGATTGTTTGGATT	Core staple	864
14[160]	GTTATTAATTTTAATAAATCC	Core staple	865
18[166]	ATCAATTCTACTAATAGTAGTATTTCAACG	Core staple	866
20[163]	ATTTTTAGAACCCTCATTTTTGAGAGA	Core staple	867
22[163]	TATCAGGTCATTGCCTGAGAGTCTTAGCTATATATTTTAAGC	Core staple	868
25[137]	AGCTGTTAAATAACAACCCGTCGGTAATGGGAGCCAGCTAGA	Core staple	869
24[163]	TTGTTAAAATTCGCATTAAATTTTAAATATTTCGCCATGACGGCCGGAA	Core staple	870
26[166]	GAAACCAGGCAAAGCGCCATTAAATTGTAA	Core staple	871
28[142]	CGGTTTCATTTGGGGCGCGAGCT	Core staple	872
28[160]	GTGGAGCCGCCACGAGTGCCA	Core staple	873
30[142]	CTTGAAACGTACAGCGCCAT	Core staple	874
30[163]	CCGGAATTTGTGAGAGATTTCCGGCACCGC	Core staple	875
32[160]	CGGCGGATTGACCGATTCTCC	Core staple	876
36[166]	AAATATTGACGGAAATTATTGTAGCGACAG	Core staple	877
38[163]	CCTTTAGCGTCAGACTGTCAGAGCCAC	Core staple	878
40[163]	CCGCCACCAGAACCACCACCAGAGGCCACCCTAGCGCGGTAA	Core staple	879
42[135]	ATAGTATTAAGAGGCTGGGTTTTGCCCTCAGAAAA	Core staple	880
42[163]	CTTTTGATGATACAGGAGTGTACTTTACCGTTTTTCAGGTTAGTAACTT	Core staple	881
44[166]	CCTCAGAGCCACCACCCTCATCCAGTAAGC	Core staple	882
46[142]	TCAGCGACATTCAACCGATTGAG	Core staple	883
46[160]	GATTTTGCTAAACAAATGAAT	Core staple	884
48[142]	TCTAAAGGAACAACTAAAGG	Core staple	885
48[163]	ATAATTTTTTCACGTTGAACCGCCACCCTC	Core staple	886
50[160]	ATTAGGATTAGCGGAGACTCC	Core staple	887
13[157]	AATTACATTTA	Connector staple	888
31[157]	GTTTACCAGTA	Connector staple	889
49[157]	AATTGCGAATC	Connector staple	890

5' — end	Sequence	Note	SEQ ID NO:
9[160]	ATACTTCTGAA	Connector staple	891
27[160]	TTCTGGTGCGG	Connector staple	892
45[160]	AGAACCGCCAG	Connector staple	893
11[154]	GCAGAGGCGAA	Connector staple	894
29[154]	AGCTTTCAGAC	Connector staple	895
47[154]	TTTCTGTATCG	Connector staple	896
7[157]	AGTTGGCAATG	Connector staple	897
25[157]	ACGTTAATATG	Connector staple	898
43[157]	GTCATACATAA	Connector staple	899
5[157]	AAATACCGAAC	Connector staple	900
23[157]	TCTACAAAGAG	Connector staple	901
41[157]	CACCCTCAGGC	Connector staple	902
3[157]	TATTTACATAT	Connector staple	903
21[157]	CAAGGATAAGG	Connector staple	904
39[157]	AATCAAGTTTT	Connector staple	905
15[154]	TTTGCCCGATT	Connector staple	906
33[154]	GTGGGAACAGT	Connector staple	907
51[154]	TCAAGAGAAGC	Connector staple	908
1[160]	AATTAACCGAC	Connector staple	909
19[160]	GAAAAGGTGGG	Connector staple	910
37[160]	GGAGGGAAGAA	Connector staple	911
9[12]	TTTTTCAGAATGCGGCGGGCCTCTGTGGCGC	Vertex staple	912
15[16]	TTTTTTCCGCTCACAATCGTGCCAGCTGCATTAATGTTTTT	Vertex staple	913
38[30]	AAAACAAAAGATAGATAAATTTACGAATCATTACCGCGCCCAATTTTT	Vertex staple	914
36[34]	ACTCCTTCATACATCGAGCCAGCCATATAATTGTGTCGAAATCCGCGACTTTTT	Vertex staple	915
49[14]	TTTTTCTTAATTGAGAATCGTAATAAGAGAATTTTT	Vertex staple	916
45[12]	TTTTTAATAATATCCCATCCTAGTCCTGCGA	Vertex staple	917
51[16]	TTTTTTAGCAAGCAAATACAATTTTATCCTGAATCTTTTTT	Vertex staple	918
37[12]	TTTTTGCAAACGTAGAAAATAATTACGCCCCTTTTTAAGAAACAAG	Vertex staple	919
39[9]	TTTTTATCTTACCGAAGAGTATGTTATTTTT	Vertex staple	920
20[31]	TTTTTGTACAGCGTAACAGACGAGAAGAAAAATCTACGTTAATATTTTT	Vertex staple	921
18[34]	TGTAGCTTGTCTGGTGACCAATTAGCCGGCGGTTGCGGTATGAGCCGGGTTTTT	Vertex staple	922
31[14]	TTTTTCTGCTCCATGTTACCTTTGAAAGAGGTTTTT	Vertex staple	923
27[12]	TTTTTGAATAAGGCTTGCCCTAAGCTGCAAA	Vertex staple	924
33[16]	TTTTTAAACGAACTAACATCATAACCCTCGTTTACCTTTTT	Vertex staple	925
19[12]	TTTTTTGCAACTAAAGTACGGCAACATGGCAAACTCCAACAGGCG	Vertex staple	926
1[12]	TTTTTTATAACGTGCTTTCCTTGCTTTGTCAAGCGAAAGGAGAACG	Vertex staple	927
21[9]	TTTTTACCAGACCGGAATTTTAAATATTTTT	Vertex staple	928
2[30]	TGGGCATCAGTGTGCACGTTTTCATTCCTGTGTGAAATTGTTATTTTT	Vertex staple	929
0[34]	CTATGGTCGTTAGATTACACTCGGCTGGAGCCAACGCTCAACAGTAGGGTTTTT	Vertex staple	930
13[14]	TTTTTTCACTGTTGCCCTGGGTGTGTTCAGCTTTTT	Vertex staple	931

5' — end	Sequence	Note	SEQ ID NO:
3[9]	TTTTTAAAAACCGTCTAACGAGCACGTTTTT	Vertex staple	932
7[24]	GGGGTGGTTTGCCCCAGCAGGCGTTCACTAATCTGATGGAAGCGCATTAGATAGCAATAGCTTTTTT	Vertex bundle strand	933
25[24]	CCAAAATGCTTTAAACAGTTCAGGCAAAATTCTCATTGAAAATCCTGTTTCGTCAAAGGGCGTTTTT	Vertex bundle strand	934
43[24]	GCGTAGAATAACATAAAAACAGGAATGTCGATATCTAGAAAACGAGAATGGCTTCAAAGCGATTTTT	Vertex bundle strand	935
7[9]	TTTTTAATCGGCCAACGTGCTGCGGCTTCACTAATCTGATGTATAAAGTACCGCAATGAAACGG	Vertex bundle strand	936
25[9]	TTTTTAGACGACGATAATCATTCAGTGCAAAATTCTCATTGAAATCGTTAACGACTCCAAGATG	Vertex bundle strand	937
43[9]	TTTTTTACCAACGCTAAAACAAGAAAAATGTCGATATCTAGACAGATGAACGGAATTCGAACCA	Vertex bundle strand	938
	CATCAGATTAGTGAA	Vertex bundle strand (complementary)	939
	CAATGAGAATTTTGC	Vertex bundle strand (complementary)	940
	CTAGATATCGACATT	Vertex bundle strand (complementary)	941

Table 8. Sequences of the pentagonal prism.

5' — end	Sequence	Note	SEQ ID NO:
1[53]	CGCCAACCGCAAGAAAAGTTACCTGTCC	Core staple	942
1[84]	AGTGAGGAAAACGCTCATGCGCGTACTAGTGTTTTTGGT	Core staple	943
0[44]	CGTCCACCACACCCGCCAACAAGAGCAG	Core staple	944
3[102]	AATCCATTGCAACAGGACCACCGACGGACTTGCGGTCCCTTAGAA	Core staple	945
3[144]	CACTATCGGCCTTGCTGGTAGCAAATTAATTACATTGCATTA	Core staple	946
2[44]	ACTAAAATCCCTTATAATGAGAGACGCCAGGCTGC	Core staple	947
2[65]	TCCGAATAGCCCGAGATTTGCCCTCACC	Core staple	948
2[72]	GTGCCAACGGATTCGCCGTCAGCGTATAATC	Core staple	949
2[93]	GAATTTGAATGTACCTTTCTCATCAATATAAATTT	Core staple	950
2[107]	CAGAACATCGCCATTAAAAATGAATCTGGTCAATA	Core staple	951
2[114]	CGTTCGCGCATCAGATGTGTTTGGATTCCTGATTATCAGTAT	Core staple	952
2[135]	TGAATTTCAACGTAGATTAATGGAAAGGAGCGGAATTACGTT	Core staple	953
5[25]	GTGGTTCCGATCCACGCAGAG	Core staple	954
5[60]	AAAAGTTTGGGCGCTTATTTGACGAGCACGTGGTA	Core staple	955
5[123]	ACCGCGTAAGTATTTACCCAGAACAATATTACCATCACCATC	Core staple	956
4[41]	CAAGCGGAATCGGCATTAAAGCGCGTAAGCTTTCC	Core staple	957
4[97]	ACCTTGCTGAACAACAGCTGAAGTTTAATGCGCGAACTGATA	Core staple	958
4[135]	CGCCAGTTGAAGATTAGAATTTTAAAAGTTTCCAC	Core staple	959
7[32]	GCGAACCTGTTCCACACAACATACTAGCTGTCGGTCATTGAG	Core staple	960
7[60]	TTTACGATCCGCGGTGCTCAG	Core staple	961
7[74]	AGTACATTAAGGGTGCCTAATGAGGAGGATCCGCGTCCAAAC	Core staple	962

5' — end	Sequence	Note	SEQ ID NO:
7[109]	ATAAAATCTAAAGCATCGCCCTAAACAATATGCTC	Core staple	963
6[51]	CCGAAGCATAAAGTGTATCGAATTCCAG	Core staple	964
6[90]	ACTTTAGCTAACTCGAGACGGGGGAGAAACAATCTTGTTCTTCCCGGGT	Core staple	965
6[114]	CATATCCTTTGCCCGAATCATCATATTATACGTAA	Core staple	966
8[65]	CAGTTCTTTTTCACCGCCTGGCCCATCA	Core staple	967
9[60]	CACCGCTCAACACCGTCGGTGATGGGTCTGGCGGTGCCTTGT	Core staple	968
9[130]	GAATTTCAGGAAATCAATGAGAGCCAGCAGCAAAT	Core staple	969
11[39]	CGGACATCCCTTTTAGACAGGAACATAA	Core staple	970
11[53]	CCAAGCGCAGGTTTCTGCGTAATCATGGTCAGAGC	Core staple	971
11[88]	TGCTGGCTATTAGTCGGGGGAAATACCTACATTTTGACTTTT	Core staple	972
11[130]	TTCCCTGAAAGAACGAACCACCAGGCCA	Core staple	973
10[58]	CAGCAGAATCCTGAGAATGGTTGCATGCGCCGCTACAGTTGA	Core staple	974
10[72]	GCTCTGATTGCCGTTCCGGCAAACGTAGAACTGAT	Core staple	975
10[100]	TGCGTAAAAGAGTCTGTCCGCCAGCGTCTGAAATGGATAATA	Core staple	976
10[114]	CTCTCGCTGGGTCGCTATTAATTATCCTGATAATATACATCA	Core staple	977
10[121]	GCAGCAAATTAACCGTTGTAATATATTGGCAGATTCACCTTC	Core staple	978
12[37]	AATGCTCGTCATTGCCAACGGCAGCAGTAGG	Core staple	979
12[48]	GCTTAATACCGGGGTGTCACTTATTGGGGTTGCAG	Core staple	980
12[79]	ATAGCGATAGCTTACAAGCGTGCCGCAT	Core staple	981
12[90]	TCCTTGAGTGAGCCTTACATCGCCTCAAATATCAAGTATTAG	Core staple	982
12[100]	TCCGTTTTTTCGTCTCGATAACGGTACAAAAGGCA	Core staple	983
12[121]	ATCCAGCCTCCGTAACAATTTCATATAACCTTGCTTCTTTCT	Core staple	984
14[69]	ACCGAGCAAGCCTGTTGCGTTGCGCTCAGTGG	Core staple	985
15[46]	CGGCTTTCCAGTCGGGAGTTTGCGGCGCGCCATGC	Core staple	986
15[98]	ACAACTCGATGATGGCAATCTCACAGTTTGACAAACAATTCG	Core staple	987
15[109]	TAATTGAGGATTTAGAAACCCTCAAGTAACAACCAAGTAACG	Core staple	988
15[130]	ATTAGCCGTCAATAGATAGTTGGCTTTAACGGAGGCGACAGA	Core staple	989
17[130]	GTGCCATCCCACGCAACAAGGGTAAAGTTAAACG	Core staple	990
16[167]	CACAGGCGGCCTTTAGTGATGCAGCTTACGGCTGGAGGTGTC	Core staple	991
16[188]	AAAATCCCGTAAAAAAAGCCGCAGCATCAGCGGGGTCATTGC	Core staple	992
16[205]	GTGTACATCGACATAAAAGGCGCTTTCGCACTCA	Core staple	993
19[53]	GAGCACCAACCTAAAGAAGAGTAATCGA	Core staple	994
19[84]	TCGCAAAAAATCGGTTGTATTAATTGCTCCATTAGTACG	Core staple	995
18[44]	TTTTTTTGATAAGAGGTTTTTAATTCTT	Core staple	996
21[102]	TACCAGAGCATAAAGCTTGGTCAAGTTTCCAACAGCATTCTGCTC	Core staple	997
21[144]	ATTACAGGCAAGGCAAAGCTGAAAGAAACGTACAGCTTGCCA	Core staple	998
20[44]	GCTAAGCAAAGCGGATTCTCAAATTAGTAAACACT	Core staple	999
20[65]	AAAAAAGATTAAGAGGAATAAATATAGC	Core staple	1000
20[72]	AGACAAGTTGGGTAACGGGTAAAAATACATT	Core staple	1001
20[93]	CCATTTCCCAAAGGGGGAACGGCCTCAGGAATTAA	Core staple	1002
20[107]	AGAGCCGGAGAGGGTAGGTCAATCAAGCAAATAAT	Core staple	1003
20[114]	AGGAAACGACCGCTATTCTCCAGCCCAGTTTGAGGGGACGAG	Core staple	1004
20[135]	AAATTTCAGAGGCGATCCGCTTCTCGCATCGTAACCGTCTCC	Core staple	1005
23[25]	CTGACTATTAAGAAAACAAGT	Core staple	1006
23[60]	CAATATCGCGCATTTTTATGCTGTAGCTCAAGAAC	Core staple	1007
23[123]	TTTAAGGGTGCCTTTATCAAAATTAAGCAATATATTTTTAAA	Core staple	1008
22[41]	ACAGTTCTAGTCAGTCAAAGCTTGCTCCTAAATAT	Core staple	1009
22[97]	TGATAATCAGAAGGAATCGTCAGTCAACCGTTCTAGCTGATA	Core staple	1010
22[135]	AATACGTTAACAATAGGGGAACAAACGGCGGAGAT	Core staple	1011
25[32]	TTTCCAGACGAGATTCATCAGTTGTAAAACGGGCTTGAGAGC	Core staple	1012

5' — end	Sequence	Note	SEQ ID NO:
25[60]	TTATCAACGTAAGAACCACGA	Core staple	1013
25[74]	GTCTACGAGGGCAGATACATAACGCATTATACCTTATGGCCA	Core staple	1014
24[51]	ATCGGAATACCACATTCGGGAAGAAACT	Core staple	1015
24[90]	GCTTTAAAAGGAATCAATACTGCAAGGCGATTATTTGAATTACCAGTCA	Core staple	1016
24[114]	TCGCAACCCGTCGGATTGCATCTGCAGCTTTCGCA	Core staple	1017
26[65]	AAAGACTGGATTCATTGAATCCCCGCAT	Core staple	1018
26[107]	CAGATTGTATATATGTACCCCGGTAATTAATCAGTCAAGTAA	Core staple	1019
27[60]	TTACGCCGGGAAAGAATACACGATTGCCACTGGATATTCTTC	Core staple	1020
27[129]	GCACGGTGCGGATTGTAACGTAAAACTAGCATCTAT	Core staple	1021
29[39]	TCAGGACAGAATTCCCAATTCTGCCATG	Core staple	1022
29[53]	GACAACAAAGTAATTTCAAAATCTACGTTAAAGAT	Core staple	1023
29[88]	GGTTCAATATGATATCCGCCCAAAAACATTATGACCCTATCA	Core staple	1024
29[130]	AGCGATTCAATGAGAGATCTACAACGGT	Core staple	1025
28[58]	AGGTAGATTTAGTTTGAGAATATAGCGGATGGCTTAGACGAA	Core staple	1026
28[72]	TAACGTCACCCTCAGCAGCGAAAGTTAAACGCCAG	Core staple	1027
28[100]	GAATAACCTGTTTAGCTAAAGCCTTTTTGCGGGAGAAGAGAA	Core staple	1028
28[114]	GACCAACGGCACAGCGGATCAAACGATCGCAACGC	Core staple	1029
28[121]	GACCATTTGGGGCGCGAGAATTAGTTCAACGCAAGGATAGGT	Core staple	1030
30[37]	CGGACTTTGAAAACGAAAGAGGCACGCGGTT	Core staple	1031
30[48]	GCGGTATGATGGTTCTGCTCAGGGGTAAGCTTTAA	Core staple	1032
30[79]	GCAGTTGGGCGGTTATCATCATTGACCC	Core staple	1033
30[90]	ATTTGCCCGATTTTATGTGCTGCAAGCCCCAAAAAGTAGCCA	Core staple	1034
30[100]	ATTCGGAACGAGGGTAGTTTTTCACGTTGTACCGG	Core staple	1035
30[121]	GAATACAGAGGCGCCATGTTTACCCACGGAAAAAGAGACCG	Core staple	1036
32[69]	GGACGTTAACTAATCATAGTAAGAGCAAATGT	Core staple	1037
33[46]	TTAATAACCCTCGTTTAGCCAGAGTTCAGTGTTCA	Core staple	1038
33[98]	ATGTGAGCGACGACAGTATGAACTGGCTCCCATCAACATTAA	Core staple	1039
33[109]	TAACGTCTGGCCTTCCTCAGGAAGCTGGCGAGTCACGATGAG	Core staple	1040
33[130]	GTGAACGCCATCAAAAATATTTAAGCCTCTTGGCCAGTTGAG	Core staple	1041
35[132]	TAAAACACTCATCTTAGGCCGCTTTTGCGG	Core staple	1042
34[224]	TAGTTGCGCCGACAATAAATTGTGTCGAAA	Core staple	1043
37[53]	CACCGACCGTGTGATCAGACGACACAAG	Core staple	1044
37[84]	AATAGAAGCACCATTACCAGGAATACCCATTTTGTAAAT	Core staple	1045
36[44]	CTTAGTTACCAGAAGGAATAAGAGATAA	Core staple	1046
36[65]	GAAGAAACGCAATAATAAGAA	Core staple	1047
39[102]	AATCAAAATCACCAGTAAATTCATGTTAATTTGTAAATCGAGGTG	Core staple	1048
39[144]	ATCTATCACCGTCACCGTCAACCGGTGAGAATAGAAACGTTA	Core staple	1049
38[44]	AAAGAGGGTAATTGAGCCAGCCTTCAGCCATTTTT	Core staple	1050
38[65]	AAGTCAGAGAGATAACCTAACGTCTCCA	Core staple	1051
38[72]	TTGTGCAGACAGCCCTCCTGACCTCACAATC	Core staple	1052
38[93]	AAAGCGTAACCAAACTAACGTATCACCGTACTTGC	Core staple	1053
38[107]	TCTAGAGCCGCCACCCTAGACGATCGCAGTCACAG	Core staple	1054
38[114]	TTTTCGTCTTCACTGAGGTTTAGTTGATATAAGTATAGTCTG	Core staple	1055
38[135]	GTCAATGAATATAGGAAAACCGCCGATAAGTGCCGTCGGAGG	Core staple	1056
41[25]	CACCCTGAACCATAAAAATTT	Core staple	1057
41[60]	ATACCCAATAAACCGAGCTGGCATGATTAAGAAGA	Core staple	1058
41[123]	ACCCCTTATTCAGCACCCCATTTGGGAATTACCAAAGAAACT	Core staple	1059
40[41]	AGAATAAAAAGTCACAATGAACGAACAAATTACGC	Core staple	1060
40[97]	ACAAACAAATAATTTTTTGTTCAGAGCCACCACCGGAACCGC	Core staple	1061
40[135]	GGATCCAGTAACGGGGTAGACTCCTCAAGAGCCAG	Core staple	1062

5' — end	Sequence	Note	SEQ ID NO:
43[32]	GCCTATCCTGTTATCCGGTATTCTTACCGCGCAATCAAAGCC	Core staple	1063
43[60]	TTTCCTGTTTACATGTTGAAA	Core staple	1064
43[74]	AATTTAAATCCCGACTTGCGGGAGCGAGAACGTATTAATAAA	Core staple	1065
42[51]	GCACGAGGCGTTTTAGCTATTTTCTCCT	Core staple	1066
42[90]	CCTGCTTTGAAGCCAAGAAACTGTAGCATTCCACAAGAACGGAAGCAAG	Core staple	1067
42[114]	TGCCATGAAAGTATTAAAGAGGGTACCGCCATAAT	Core staple	1068
44[65]	GCGATCCCAAAAAAATGAAAATAGGCTA	Core staple	1069
44[107]	GTCTGGAAAGTGGCCTTGATATTCCTCCCTCTTTCATACACC	Core staple	1070
45[60]	TATGCGACCTAAATAAGAATACTTATGGTTTCAGCTAAAGTT	Core staple	1071
45[129]	TCAGCCCATGTTTACCGTGGTTGAGGCAGGTCCAGA	Core staple	1072
47[39]	GACGTAATAAATAAAAGAAACGCAACTC	Core staple	1073
47[53]	ACAATCAACACTGTCTTATCGTAGGAATCATAAGA	Core staple	1074
47[88]	TTATCACCGGAACCACAACTTAGCAAGGCCGGAAACGTATCA	Core staple	1075
47[130]	GTAATAGCCCGCCACCCTCAGAGCGACA	Core staple	1076
46[58]	TACCACGGAATAAGTTTAAAA	Core staple	1077
46[72]	TTAAGGTTGGGTTATATAACTATATCATCTTATAG	Core staple	1078
46[100]	TTAATGGTTTACCAGCGGAGCCAGGAAACCATCGATAGAGCG	Core staple	1079
46[114]	TTTAATCGCAATCGGTTTATCAGCTCAGGAGTTTC	Core staple	1080
46[121]	GAACAAAAGGGCGACATACTTGAGGTAATCAGTAGCGATTCG	Core staple	1081
48[37]	GGATTTTCGAGCAAATAAGGCGTTGCTCCAT	Core staple	1082
48[48]	GTTACTTTAATCGGATAGATAAAATAAATACAGAG	Core staple	1083
48[79]	CAGCTTGATACCGATCCCATTCCAGAAC	Core staple	1084
48[90]	AATTTCTACCAAGTCAACGCCGAATCCTCATTAAAAATGCCC	Core staple	1085
48[100]	TTTGCTGATGCAAATCCTCAAATAAGTTTTGGCCA	Core staple	1086
48[121]	TGTAGACAAAGAAGGAACAACTAACCAAAAGGAGCCTTCCC	Core staple	1087
50[69]	CCGTTTTGAACCTCAAGATTAGTTGCTAATTA	Core staple	1088
51[46]	ACGCCCAGCTACAATTTAGTTACAAGTCCTGTCCA	Core staple	1089
51[98]	CTATTATCCCGGAATAGGTCGCACTCATGTCTATTTCGGAAC	Core staple	1090
51[109]	AAACCGTATAAACAGTTGCCAGAAACCAGTAGATCTAATATT	Core staple	1091
51[130]	CTGCAGTGCCTTGAGTATCTGAATACCGTAATCCAGACGCGA	Core staple	1092
53[130]	AACACCGGAATCATAATACCTTTTTAACCTCCGG	Core staple	1093
52[167]	AAATCATAGGTCTGAGAGACTTACTAGAAAAAGCCTGTTTAG	Core staple	1094
52[188]	GAGTCAATAGTGAATTTATCATATCATATGCGTTATACAAAT	Core staple	1095
52[205]	GATTAAGACGCTGAGAATCTTACCAGTATAAAGC	Core staple	1096
34[167]	CTGAGGCTTGCAGGGAGTTAATGACCCCCAGCGATTATACCA	Core staple	1097
34[188]	CATAACCGATATATTCGGTCGAGCGCGAAACAAAGTACAACG	Core staple	1098
34[209]	TGACAACAACCATCGCCCACGGAGATTTGTATCATCGCCTGA	Core staple	1099
5[25]	GTGGTTCCGATCCACGCAGAG	Core staple	1100
23[25]	CTGACTATTAAGAAAACAAGT	Core staple	1101
41[25]	CACCCTGAACCATAAAAATTT	Core staple	1102
0[166]	CTGAGTAGAAGAACTCAAACACGACCAGTA	Core staple	1103
2[163]	ATTCTGGCCAACAGAGATAAAACAGAG	Core staple	1104
4[163]	AGTATTAACACCGCCTGCAACAGTCAGAAGATAGAACCCAGT	Core staple	1105
6[163]	TCTTTAGGAGCACTAACAACTAATAAGGAATGAAA	Core staple	1106
8[142]	TTGTTACCTGAAACAAATACTTCTTTGATTAGTAATA	Core staple	1107
8[166]	GCACGTAAAACAGAAATAAATGAGGAAGGT	Core staple	1108
10[160]	AACAAACATCAAGAAGCAAAA	Core staple	1109
12[163]	ACATAAATCAATATATGGAACCTACCATAT	Core staple	1110
14[142]	CAGAGGGTTATGAGTGATTGAATTACCTTTTTTA	Core staple	1111
14[160]	GCGGAACAAAGAAAGAGTAAC	Core staple	1112

5' — end	Sequence	Note	SEQ ID NO:
18[166]	ATTAACATCCAATAAATCATTTTAGAACCC	Core staple	1113
20[163]	AAATGCAATGCCTGAGTCAGGTCATTG	Core staple	1114
22[163]	GGAGCAAACAAGAGAATCGATGAAAGGCTATAATGTGTAAAA	Core staple	1115
24[163]	TGTTAAATCAGCTCATTTTTTAACTATTTTGTGGG	Core staple	1116
26[142]	AAGGGTGGAGAATCGGCAGGTGGCATCAATTCTACTA	Core staple	1117
26[166]	CATTCAGGCTGCGCAACTGTTTAAAATTCG	Core staple	1118
28[160]	ACCTCACCGGAAACCCGCCAC	Core staple	1119
30[163]	TCTCCGTGGTGAAGGGAGAAACCAGGCAAA	Core staple	1120
32[142]	GGGGGTGCCGTAGCTCTAGTCCCGGAATTTGTGA	Core staple	1121
32[160]	GGTCACGTTGGTGTATTGACC	Core staple	1122
36[166]	ATTATTCATTAAAGGTGAATAAGTTTGCCT	Core staple	1123
38[163]	CTGTAGCGCGTTTTCATCTCAGAGCCG	Core staple	1124
40[163]	ACCACCAGAGCCGCCGCCAGCATTCACCACCCGGCATTCAGA	Core staple	1125
42[163]	GGAGTGTACTGGTAATAAGTTTTAAGCGTCAAAGC	Core staple	1126
44[142]	CCATTTCTGTCAGCGGAATTGAGGGAGGGAAGGTAAA	Core staple	1127
44[166]	CCCTCATTTTCAGGGATAGCTACATGGCTT	Core staple	1128
46[160]	ACTTTCAACAGTTTATGGGAT	Core staple	1129
48[163]	TTGAAAATCTCCAAAAAGAACCGCCACCCT	Core staple	1130
50[142]	GCGACCCTCAAAAGGCTAGGAATTGCGAATAATA	Core staple	1131
50[160]	GGTTTTGCTCAGTAAAGGATT	Core staple	1132
9[160]	CAAAATTATGA	Connector staple	1133
27[160]	GCGCCATTCCA	Connector staple	1134
45[160]	CAGAGCCACTA	Connector staple	1135
11[154]	GAAGATGATTT	Connector staple	1136
29[154]	GGGAACGGACA	Connector staple	1137
47[154]	TTTGCTAAAGC	Connector staple	1138
7[157]	TATCTAAAAAC	Connector staple	1139
25[157]	CATTAAATTGA	Connector staple	1140
43[157]	TTGATGATATT	Connector staple	1141
1[160]	ACATCACTTTT	Connector staple	1142
19[160]	ATAGTAGTAGG	Connector staple	1143
37[160]	TATTGACGGTA	Connector staple	1144
13[157]	ATGGAAACAGT	Connector staple	1145
31[157]	GAGATAGACCG	Connector staple	1146
49[157]	ATTTTTTCATT	Connector staple	1147
3[157]	ATAAAAGGGTA	Connector staple	1148
5[157]	GTGAGGCGGTC	Connector staple	1149
15[154]	ATTATCATTGC	Connector staple	1150
21[157]	TCATATATTCA	Connector staple	1151
23[157]	CCTGAGAGTCC	Connector staple	1152
33[154]	GTAATGGGAAA	Connector staple	1153
39[157]	TTAGCGTCATT	Connector staple	1154
41[157]	CCACCAGAACT	Connector staple	1155
51[154]	AGGATTAGCGC	Connector staple	1156
1[12]	TTTTTAAACAGGAGGCCGATTAATCAGATCACGGTCACGCTGAACG	Vertex staple	1157
0[34]	TCGTTAGAAAGGGATTACACTTTTCTTTCGCCATATTTAACAACGCCAATTTTT	Vertex staple	1158
3[9]	TTTTTAAAAACCGTCTAGCGGGAGCTTTTTT	Vertex staple	1159
2[30]	TGGGCATCAGTGTGCACGTTTTCATTCCTGTGTGAAATTGTTATTTTT	Vertex staple	1160
9[12]	TTTTTCAGAATGCGGCGGGCCTCTGTGGCGC	Vertex staple	1161
13[14]	TTTTTGTAATGGGTAAAGGGGTGTGTTCAGCTTTTT	Vertex staple	1162

5' — end	Sequence	Note	SEQ ID NO:
15[16]	TTTTTTCCGCTCACAATCGTGCCAGCTGCATTAATGTTTTT	Vertex staple	1163
19[12]	TTTTTAGTTTCATTCCATATAAAGTACGGAGAGTACCTTTAAGAA	Vertex staple	1164
18[34]	GCAACTAACAGTTGTGAACGGCTGACCAGTCACTGTTGCCCTGCGGCTGTTTTT	Vertex staple	1165
21[9]	TTTTTAGGTCAGGATTAGTGTCTGGATTTTT	Vertex staple	1166
20[31]	CCAGGCTGACCAATAAGGTAAATTGAACTAACGGAACAACATTATTTTT	Vertex staple	1167
27[12]	TTTTTACACCAGAACGAGTAGCTTGCCCGCA	Vertex staple	1168
31[14]	TTTTTATAAGGGAACCGAATGTACAGACCAGTTTTT	Vertex staple	1169
33[16]	TTTTTTTACAGGTAGAAACGATAAAAACCAAAATAGTTTTT	Vertex staple	1170
37[12]	TTTTTTACATACATAAAGGTGTAGCAAAAGTAAGCAGATAGCATAG	Vertex staple	1171
36[34]	AGTATGTGCAACATGAGAATAAGAGGCAACGAGGCGCAGACGGTCAATCTTTTT	Vertex staple	1172
39[9]	TTTTTCTTTTTAAGAAACGTAGAAAATTTTT	Vertex staple	1173
38[30]	CAAAATTCTGAACAAGATAGAAACCCCAATAGCAAGCAAATCATTTTT	Vertex staple	1174
45[12]	TTTTTCTAATTTACGAGCATGAAAATAAGAG	Vertex staple	1175
49[14]	TTTTTCATGTAATTTAGGCTAAAGTACCGACTTTTT	Vertex staple	1176
51[16]	TTTTTGATATAGAAGGCAATCTTACCAACGCTAACGTTTTT	Vertex staple	1177
5[9]	TTTTTAAAATCCTGTTTCGTCAAAGGGCGTTTTT	Vertex staple	1178
7[24]	GGGGTGGTTTGCCCCAGCAGGCGTTTTT	Vertex staple	1179
23[9]	TTTTTAAATCAGGTCTTGCAAACTCCAACTTTTT	Vertex staple	1180
25[24]	AAAGGAGAATGACCATAAATCAATTTTT	Vertex staple	1181
41[9]	TTTTTGGGAGAATTAACCTTACCGAAGCCTTTTT	Vertex staple	1182
43[24]	CCTAACAGGGAAGCGCATTAGACTTTTT	Vertex staple	1183
7[9]	TTTTTAATCGGCCAACGTGCTGCGGCTTCACTAATCTGATGAAAAGGTAAAGTTAGCTATTGAA	Vertex bundle strand	1184
25[9]	TTTTTCGAGAGGCTTTTTGACGAGAAGCAAAATTCTCATTGAAATCGTTAACGACTCCAAGATG	Vertex bundle strand	1185
43[9]	TTTTTAGCGTCTTTCCATATCCCATCAGTGGCGATATCGCGCATAGGCTGACCGGAATACC	Vertex bundle strand	1186
	CATCAGATTAGTGAA	Vertex bundle strand (complementary)	1187
	CAATGAGAATTTTGC	Vertex bundle strand (complementary)	1188
	GATATCGCCACT	Vertex bundle strand (complementary)	1189

Table 9. Sequences of the hexagonal prism.

5' — end	Sequence	Note	SEQ ID NO:
1[53]	CCGAGCGTGGTGCTGAAGTTACCTGTCC	Core staple	1190
1[84]	GTACTATTCCATCACGCAAGACGGGGAACCGCTACGTGC	Core staple	1191
0[44]	AGGAATCGGAACCCTAAAACAAGAGCAG	Core staple	1192
3[102]	TTTAGTAAAAGAGTCTGGGTTGCTAGCACATGATGCTGAAACATC	Core staple	1193
3[144]	AACCCAGAATCCTGAGAATCAGAGCTTTTACATCGGTTAAAT	Core staple	1194
2[44]	ACTAAAATCCCTTATAATGAGAGACGCCAGGCTGC	Core staple	1195
2[65]	TCCGAATAGCCCGAGATTTGCCCTCACC	Core staple	1196
2[72]	GTGCCGAATAATGGAAGACGGAACAGGGCGC	Core staple	1197
2[93]	AATACCTACCATCCTGATCGACAACTCGTATATGA	Core staple	1198
2[107]	ACATCACACGACCAGTATCTTTAACCAGCAGTTGC	Core staple	1199
2[114]	AATTGCACGTTGATGGCTTTGCCCGAAGTATTAGACTTTCAA	Core staple	1200
2[135]	AACGAAATTGATCATATTTAAAAGGATAATACATTTGAGGAA	Core staple	1201
5[25]	GTGGTTCCGATCCACGCAGAGGCGAACCTGTTCCACACAACATACTAG	Core staple	1202
5[39]	GGCATTAAAGAGCACTAGAAGAAAGCGAAAGGTCACGCTTAC	Core staple	1203

5[60]	AAAAGTTTGGAGGGAGCGAACGTGGCGAGAAACAC	Core staple	1204
5[123]	AAGACGCTCATCACTTGTTATAATCAGTGAGTAACGTGTCGC	Core staple	1205
4[97]	GCCCTAAAACATAACAGCTGAAGATTATTTACATTGGCAGAT	Core staple	1206
4[135]	TTTGTGAGGCTGAAAAATATCTAAAATATCTGTCA	Core staple	1207
7[60]	TTTACGATCCGCGGTGCGAAC	Core staple	1208
7[74]	AGTACATTAAGGGTGCCTAATGAGGAGGATCCGCGTCCCAAA	Core staple	1209
7[109]	CCATGCGCGAACTGATATCACCAGTTTTGACCTTC	Core staple	1210
6[51]	CCGAAGCATAAAGTGTATCGAATTCCAG	Core staple	1211
6[90]	ATCAAAGCTAACTCGAGACGGGATTATACTTCTCTTGTTCTTCCCGGGT	Core staple	1212
6[114]	TGATTGAAAGGAATTGAGGATTTAGAACGTTTTAC	Core staple	1213
8[65]	CAGTTCTTTTTCACCGCCTGGCCCATCA	Core staple	1214
9[60]	CACTGATAAAGCAACCGCAAGTAGACTTGTACGGTGCCTTGT	Core staple	1215
9[130]	ATTTCCTGATAACAGAGTGAATGGCTATTAGATAA	Core staple	1216
11[39]	CGGACATCCCTGCGCGTAACCACCAGGA	Core staple	1217
11[53]	CCAAGCGCAGGTTTCTGCGTAATCATGGTCAGAGC	Core staple	1218
11[88]	AGACGTCTGAAATGGGGTTATTAACCGTTGTAGCAATAGCTC	Core staple	1219
11[130]	AAAAGGAAAAGGACATTCTGGCCAATAT	Core staple	1220
10[58]	GTCCCGCGCTTAATGCGAGCCGGCCCCCGATTTAGAGCTTGA	Core staple	1221
10[72]	CGGTGATGAAGGGTAAAGTTAAACCCTCATAGGTT	Core staple	1222
10[100]	CAGTTGACGAGCACGTAGCCACCGGATTAGTAATAACATGGA	Core staple	1223
10[114]	TGGAAACGCGAGCAAAAGAAGATGTAAATCCAATTCATCGAA	Core staple	1224
10[121]	TCGCTTTCCTCGTTAGAAGTGTTTCCTGAGTAGAAGAATTGC	Core staple	1225
12[48]	TTAAATAACCGGGGTGTCACTTATTGGGGTTGCAGCAAGCGGAATC	Core staple	1226
12[79]	ATTAATTACATTTAGTGGCGTGCCGCAT	Core staple	1227
12[90]	AAGAAAAGTGAGCCTTGTTTGGCCGCCATTAAAAAACCCTCA	Core staple	1228
12[100]	AACATTGCCGTTCCGGCCAGCCTCAATTATTACCT	Core staple	1229
12[121]	CTGGTCCGTTTTGAGAAACAATAAATTATTCATTTCAAATTA	Core staple	1230
14[38]	CTGTCGGTCATAGAATAAGCTCGTCATGTCTGGTCAGCATAAGGCG	Core staple	1231
14[69]	ACCGAGCAAGCCTGTTGCGTTGCGCTCAGTGG	Core staple	1232
15[46]	CGGCTTTCCAGTCGGGAGTTTGCGGCGCGCCATGC	Core staple	1233
15[98]	TGGCAAATACAAACAATTCCTCACAGTTTGTATCTGGTCAGT	Core staple	1234
15[109]	CAGACCTCAAATATCAATACCGAACAATATAATATCAACGGC	Core staple	1235
15[130]	GGTTCTAAAGCATCACCAAGATAATATCAGAAAAACAGCGTC	Core staple	1236
17[91]	AATGCCAACGGCAGGCACAGGCGGCCTT	Core staple	1237
17[105]	CACCGTCGGTGCATCCCAAAAATCCCGTAAAGCC	Core staple	1238
17[126]	ACGCAACCAGCTTACGGCTGGCGGTTGTGTACATCGACATAA	Core staple	1239
17[147]	AGGTGTCCAGCGCGGGGCATTTGCCGCCGTTGGG	Core staple	1240
16[181]	CTTAAATTTCTGCTTCATTGCAGGCGCT	Core staple	1241
19[53]	GTTCTTTGAGGACTAACGGTGTACTAAG	Core staple	1242
19[84]	TCTGCGAATTAGCAAAATTTCCTTTTGAAGTTGATGGGT	Core staple	1243
18[44]	TAGCTCCAACAGGTCAGAAAAGATAGAC	Core staple	1244
21[102]	AAGAGGCAAGGCAAAGAACGAGTACGAAAGAATATATTCGGAAAA	Core staple	1245
21[144]	CTTATTCTACTAATAGTGTCAATAGCCGCCACGGGACCAGGG	Core staple	1246
20[44]	AGGAAATCAAAAATCAGCCAATACCGAGAGGACAT	Core staple	1247
20[65]	GATCCCTGACTATTATAAATGTTTGTTT	Core staple	1248
20[72]	CAATGACGCCAGCTGGCGGAACGATCCCAAT	Core staple	1249
20[93]	AGAGGATGTGCGATCGGATTAACCGTGCATCGCTC	Core staple	1250
20[107]	TAACATCAATATGATATAAACAAGGTTGATAAATC	Core staple	1251
20[114]	GCCAGTTGGGCTGCGCATTGAGGGTCACGTTGGTGTAGGGCC	Core staple	1252
20[135]	CTCTCCCAGTAAGCGCCCGGCCTCGATTGACCGTAATGCATC	Core staple	1253
23[25]	AAAACGAGAAAAATATTCGACGATCGAGGCAAATAAAACGAACTATTA	Core staple	1254
23[39]	CATAAGCCCGAAGCAAAAGCTTAATTGCTGATGCAACTCATA	Core staple	1255

23[60]	TTATGCATCAGATTAGATCATTTTTGCGGATGGAA	Core staple	1256
23[123]	CCGTTAAATGCCAAAAATTAACATCCAATAAATTAGATCGGG	Core staple	1257
22[97]	GTAATCGTAAAATAATAGTAAGTAGAAAGGCCGGAGACAGTC	Core staple	1258
22[135]	GCCAAAAACAATTCGCAATTAAATGTGAGCGAACG	Core staple	1259
25[60]	TGCAAGAGTAGCGCATAACAG	Core staple	1260
25[74]	TGCCCACATTATTCATCAGTTGAGAATCATTCTTGAGACAGA	Core staple	1261
24[51]	AACAACATTATTACAGGGCGATTTCAGA	Core staple	1262
24[90]	CGCCATTAGGAATACAGAGGGCTCTTCGCTATTACAATTGGGGTGAATT	Core staple	1263
24[114]	AGCCTGTAGCCAGCTTTGGATAGGGACGACGTTTC	Core staple	1264
26[65]	ATCAAAAGAAAGACTGGATAGCGTGTCT	Core staple	1265
26[107]	TTGTACCCCGAGAATCGATGAACGAAATCACTGTGTAGCATA	Core staple	1266
27[60]	ACGGCACTCATGAGGAAGTTTACAAACGGCTGGCTGGCAGCG	Core staple	1267
27[129]	GTATATTCGCCAAGCCCCTGAGAGTCTGGAGCTCAA	Core staple	1268
29[39]	AACGGTCAATAAAGTACGGTGTCTGGCT	Core staple	1269
29[53]	CAGATCTTGAGAAACACTAAGAACTGGCTCAACGG	Core staple	1270
29[88]	GGGTTCAAAAGGGTGCAGCAAGCAATAAAGCCTCAGAGGTAA	Core staple	1271
29[130]	TTTATATATTTTCTAGCTGATAAACATT	Core staple	1272
28[58]	AGGTCATTCCATATAACTAAGAGGGAGTACCTTTAATTGAAG	Core staple	1273
28[72]	AGCACCATCGCCCACGCATAACCGCAGCATCGAAA	Core staple	1274
28[100]	CAGGATTTAGTTTGACCATCATACCTAAATCGGTTGTACAAT	Core staple	1275
28[114]	ATCTGCAGGGGTGGTGAAGGGATATGCCAGTACTG	Core staple	1276
28[121]	TTGACATTTCGCAAATGAGTAGCACATTATGACCCTGTAACC	Core staple	1277
30[48]	GGGCGCGCTGACGACAAGAACAAAATAGTGCGGAATCGTCATTGAC	Core staple	1278
30[79]	AACAGCGGATCAAATTCAGTAGTACTTC	Core staple	1279
30[90]	AGAGACGTGGTTTATGCGGGCGGCTAGCATGTCAAATAGGAA	Core staple	1280
30[100]	TCACGGTCGCTGAGGCTGTCACCCGCGATTATGAG	Core staple	1281
30[121]	TCCAGTTAAAGGACGGATAACCTCTGTGAGAGATAGACACA	Core staple	1282
32[38]	TACCGCTTGCCGTTGCGGGAGGCGCAGAAGACTTTTTCAATCCGCC	Core staple	1283
32[69]	ACCTTATTAGAAAGCAACTAATGCAGATCTTT	Core staple	1284
33[46]	AACGCCAAAAGGAATTAAAAAACCCGGATATGATG	Core staple	1285
33[98]	CGCGTCTATGGGCGCATCGTTCAACTTTATTCAAAAATAATT	Core staple	1286
33[109]	TTCTCATTTTTTAACCATCATATGGGAAGGGCTGCAAGTCAG	Core staple	1287
33[130]	AACTTAAATTTTTGTTAATCAGAAATTCAGGTAACGCCGCTT	Core staple	1288
35[131]	CCATTAAACGGGTAAATGCGCCGACAATGACA	Core staple	1289
35[147]	ATACGTAATGCCACTACGAAGAAACAGCTTGATACCGATAGT	Core staple	1290
35[168]	GCACCAACCTAAAACGAAAAAGAATACACTAAAAC	Core staple	1291
34[209]	AATTGTATCGGTTTATCTTTCGAGGTGAATTTCTT	Core staple	1292
34[230]	AAGGCTCCAAAAGGAGCCTTTACTCATCTTTGACCCCCAGCG	Core staple	1293
34[246]	GAAAATCTCCAAAAAAATTATACCAAGCGCGA	Core staple	1294
37[53]	AGATATATAACTATATATAACAACGAAT	Core staple	1295
37[84]	CAGTATGGAAGGTAAATATATAGCAATAGACTCCTAACC	Core staple	1296
36[44]	GAATGAGTTAAGCCCAAGACGGGAGCCA	Core staple	1297
36[65]	TCTAGCAAGAAACAATGTAAA	Core staple	1298
39[102]	TGACCGATTGAGGGAGGTTAGCAAGGTCTGATGAAAACAAAGGAA	Core staple	1299
39[144]	GCCCATATGGTTTACCAAAAAGAAAGCGTAACGATCAGAGTT	Core staple	1300
38[44]	TAATCAAAAATGAAAATAGAGCCTTAGTTGCTAGA	Core staple	1301
38[65]	AAGTTTACAGAGAGAATAACGCTACTAC	Core staple	1302
38[72]	AACAGACCCTCATTTTCCCTTTTTTATTACG	Core staple	1303
38[93]	GAAGCAAGCCTCAGAACAATCCTCAAGAGAAAACA	Core staple	1304
38[107]	AATATCGGCATTTTCGGCTCAGAAAGCCGCCTCTC	Core staple	1305
38[114]	GCAGTACCGTCCACCCTGATTAGCACATGAAAGTATTAGAGT	Core staple	1306
38[135]	CCATCACCAGTACTCAGTACCAGGTTCGGAACCTATTATAAC	Core staple	1307

41[25]	CGATTTTTGAAAATAATTTGAAGTAAGAACCAAGTACCGCACTCGCT	Core staple	1308
41[39]	ACGCTGAACACAAGAATAAGTAAGCAGATAGACGCAATAAAG	Core staple	1309
41[60]	GCCCGCATTATAATAAGTACCGAAGCCCTTTCAAA	Core staple	1310
41[123]	AGCCATCGATCGACTTGAGACAAAAGGGCGATACATAAAGTG	Core staple	1311
40[97]	GCCACCACCCTCAATCTTACCAATTAGCGTCAGACTGTAGCG	Core staple	1312
40[135]	CCCGAGGTTGAAGCCAGGTCAGTGCCTTGAGTGCC	Core staple	1313
43[60]	TTGAGCCAGTTGTAATTGTTG	Core staple	1314
43[74]	AATCAATAGCTCATCGTAGGAATCCCCATCCAAGTCCTTAAT	Core staple	1315
42[51]	AGGACAAGCAAGCCGTTGTAGAAAGCCT	Core staple	1316
42[90]	CATACTACCGCGCCTTTATCCCTCAGAGCCACCGCAATAGATTAATTTA	Core staple	1317
42[114]	TGACTGGTAATAAGTTTTTCTGAAGGGGTTTAGCG	Core staple	1318
44[65]	TCGCACCCAGACGAGCGTCTTTCCAGCA	Core staple	1319
44[107]	ACCCCACCAGCCGCCACCCTCAGACGTTTTCCAGTAGCAAGG	Core staple	1320
45[60]	GTTAAAGTACTGCAAATCCAATAAGGCTTAGTAGGCAGAGGG	Core staple	1321
45[129]	TCAGGAGGTTTTTGACAGTCAGAGCCGCCACCTCAT	Core staple	1322
47[39]	ATTCCAGTATAATAACGGAATACCTTAA	Core staple	1323
47[53]	ACAAATAAGAAGAACGCCCAATCAATAATCGATCG	Core staple	1324
47[88]	ATATCAAGTTTGCCTCAAATGACGGAAATTATTCATTAGACA	Core staple	1325
47[130]	TCGATGAAACCCCCTTATTAGCGTGCCT	Core staple	1326
46[58]	GGTACTGGCATGATTAAGCTA	Core staple	1327
46[72]	TCCTTAATTTTCCCTTAGAATCCTGAGACTAAGGG	Core staple	1328
46[100]	ATAACGTAGAAAATACACATTCAAATTATCACCGTCACAGCA	Core staple	1329
46[114]	AATGATTAAGTGAGAATAGAAAGGGGATTAGCAGA	Core staple	1330
46[121]	AATAGGTGGCAACATATGCGCCAAAGCCATTTGGGAATGTCA	Core staple	1331
48[48]	ATTTGTACTAATGCGAATATATCAAGATAATTTGCCAGTTACTTTA	Core staple	1332
48[79]	AATTTTTTCACGTTAACTATCAACATTT	Core staple	1333
48[90]	TTGCGAAGAACAAGCGCCACCTGAGAGCCGCCACCTAAGCGT	Core staple	1334
48[100]	ACTATAGCGATAGCTTATTATCAAAACCCATCCGT	Core staple	1335
48[121]	GAGACGCTGAGATAAAGTTTTGTCCTTTCAACAGTTTCTGC	Core staple	1336
50[38]	GTCTTGTTCAGTCATCGCACAAATTCTTGTAAATGCTGAAACGGAG	Core staple	1337
50[69]	CGAGCATTTTATTTAAGCAAATCAGATATATT	Core staple	1338
51[46]	AGACTTATCCGGTATTCCCTTAAAAAGTACCCCAT	Core staple	1339
51[98]	GATACAGAGAGGCTGAGACAAATAATATATATGGCTTTTGAT	Core staple	1340
51[109]	GTAATTTACCGTTCCAGAGAACCAGCCACCCCAATAGGAATC	Core staple	1341
51[130]	GGGAATGGAAAGCGCAGGCCAGCAAGTACCGAACACTGAGTC	Core staple	1342
53[91]	TCGCAAGACAAAGATAAATCGTCGCTAT	Core staple	1343
53[105]	ACGCGAGAAAATTCAAAGAGTGAATAACCTTCTG	Core staple	1344
53[126]	TATATTTTAGTTAATTTCATCAGTACATAAATCAATATATGT	Core staple	1345
53[147]	TTCTGACCTAAAATGGTATTACCTTTTTGGAAAC	Core staple	1346
52[181]	ACAATTTCATTTGATTGAAATACCGACC	Core staple	1347
0[166]	TTTTAGACAGGAACGGTACGTATCGGCCTT	Core staple	1348
2[163]	CCAGAACAATATTACCGTAGAACCCTT	Core staple	1349
4[163]	GCGTAAGAATACGTGGCACAGACAACAGAGACCAGCCACTCA	Core staple	1350
6[163]	GCCACGCTGAGAGCCAGCAGCAAAGGTCAGTAATT	Core staple	1351
8[142]	ATCCGTAGATACAGTACCGGGAGCTAAACAGGAGGCC	Core staple	1352
8[166]	GAAACCACCAGAAGGAGCGGATTAACACCG	Core staple	1353
10[160]	ATGAATATACAGTATTTCAGG	Core staple	1354
12[163]	AGTTACAAAATCGCGCAAACATTATCATTT	Core staple	1355
14[142]	ATATTTGAGTGAGGCGACGGATTCGCCTGATTGC	Core staple	1356
14[160]	AATAGATTAGAGCCTTAGGAG	Core staple	1357
18[166]	GAGCTGAAAAGGTGGCATCATTGCGGGAGA	Core staple	1358
20[163]	CAACGCAAGGATAAAAACGGAGAGGGT	Core staple	1359

22[163]	AGAGATCTACAAAGGCTATCAGGTTTAATGCTTTTTAGAATA	Core staple	1360
24[163]	TGTAAACGTTAATATTTTGTTAAAGGAAGATCCAG	Core staple	1361
26[142]	GCACACGACGAGGTGGAACCTGTTTAGCTATATTTTC	Core staple	1362
26[166]	ACCGCTTCTGGTGCCGGAAATGTATAAGCA	Core staple	1363
28[160]	TGCCAAGCTTTCAGTTGTAAA	Core staple	1364
30[163]	GCCATGTTTACCAGTCCTCGCACTCCAGCC	Core staple	1365
32[142]	GCGAGGAAGACGGAATTACCGGAAACAATCGGCG	Core staple	1366
32[160]	TCTCCGTGGGAACAAGTAACA	Core staple	1367
36[166]	GTCACAATCAATAGAAAATTAGCAAAATCA	Core staple	1368
38[163]	ATTACCATTAGCAAGGCCTTTTCATAA	Core staple	1369
40[163]	GGAACCAGAGCCACCACCGGAACCTTGCCATCGGAAACTAGA	Core staple	1370
42[163]	TCACAAACAAATAAATCCTCATTAAGGCAGGATCA	Core staple	1371
44[142]	CCGTACAAACCATAGTTACGCAAAGACACCACGGAAT	Core staple	1372
44[166]	GTATAGCCCGGAATAGGTGTTCAGACGATT	Core staple	1373
46[160]	CCACAGACAGCCCTTACAACG	Core staple	1374
48[163]	TCTGTATGGGATTTTGCGTGCCGTCGAGAG	Core staple	1375
50[142]	TATCGGATAATAAACAAGTCTTTCCAGACGTTAG	Core staple	1376
50[160]	CAGTTAATGCCCCCTAACAGT	Core staple	1377
13[157]	TTTGAATACCA	Connector staple	1378
31[157]	AAACGTACATT	Connector staple	1379
49[157]	TAAATGAATGC	Connector staple	1380
9[160]	TGCGGAACAAG	Connector staple	1381
27[160]	AGCTTTCCGTT	Connector staple	1382
45[160]	GGTTGATATAG	Connector staple	1383
11[154]	TTTAACGTCAA	Connector staple	1384
29[154]	ACGACGGCCAA	Connector staple	1385
47[154]	CCTGTAGCAGC	Connector staple	1386
1[160]	GATTAAAGGCT	Connector staple	1387
3[157]	GCTGGTAATGT	Connector staple	1388
5[157]	CTGACCTGAAA	Connector staple	1389
7[157]	CCTGCAACAAT	Connector staple	1390
15[154]	CACTAACAAGA	Connector staple	1391
19[160]	ATTTGGGGCAA	Connector staple	1392
21[157]	AGCCTTTATAT	Connector staple	1393
23[157]	AGCTATTTTCC	Connector staple	1394
25[157]	AATATTTAACC	Connector staple	1395
33[154]	ACCCGTCGGTT	Connector staple	1396
37[160]	AAGTTTATTAT	Connector staple	1397
39[157]	CCAGTAGCAAT	Connector staple	1398
41[157]	TCAAAATCATG	Connector staple	1399
43[157]	GGCCTTGATTT	Connector staple	1400
51[154]	GCCCGTATAGC	Connector staple	1401
1[12]	TTTTTGCTGGCAAGTGTAGCGGAGCGGGTCAAGGTGCCGTAAAACG	Vertex staple	1402
3[9]	TTTTTAAAAACCGTCTACGCTAGGGCTTTTT	Vertex staple	1403
2[30]	TGGGCATCAGTGTGCACGTTTTCATTCCTGTGTGAAATTGTTATTTTT	Vertex staple	1404
9[12]	TTTTTCAGAATGCGGCGGGCCTCTGTGGCGC	Vertex staple	1405
10[30]	ACTTTTCTTTACACCGGAATCATAATTACTAGAAAATTTTT	Vertex staple	1406
13[9]	TTTTTGGCTGGTAATGGGTAAAGGGGTGTGTTCAGCTTTTT	Vertex staple	1407
15[16]	TTTTTTCCGCTCACAATCGTGCCAGCTGCATTAATGTTTTT	Vertex staple	1408
19[12]	TTTTTCAACATGTTTTAAATAATATAATGCGAACCAGACCGGAAA	Vertex staple	1409
21[9]	TTTTTTCGAGCTTCAAAGCTGTAGCTTTTTT	Vertex staple	1410
20[31]	GACTGAGGACATCATTACGAATAAGAGTCAGGACGTTGGGAAGATTTTT	Vertex staple	1411

27[12]	TTTTTAAGCTGCTCATTCAGTCCAAATCTAC	Vertex staple	1412
28[30]	AGGCCGGAACTATGAGCCGGGTCACTGTTGCCCTGCTTTTT	Vertex staple	1413
31[9]	TTTTTCCTGCTCCATGTTACTTAGGAACCGAACTGATTTTT	Vertex staple	1414
33[16]	TTTTTAAAATCTACGTTTAGTAAGAGCAACACTATCTTTTT	Vertex staple	1415
37[12]	TTTTTGAAGGAAACCGAGGAACCGAACAAGAGAGATAACCCACCCT	Vertex staple	1416
39[9]	TTTTTAGCGCTAATATCAAGTTACCATTTTT	Vertex staple	1417
38[30]	GAAAGAATCGGACAAAAAACAACATTCCTTATCATTCCAAGAATTTTT	Vertex staple	1418
45[12]	TTTTTCCAGACGACGACAATAGGTAAAGGGG	Vertex staple	1419
46[30]	CCAGCGTTATCTGATAAATTGTGTCGAAATCCGCGATTTTT	Vertex staple	1420
49[9]	TTTTTAGCCTGTTTAGTATCATATACGCTCAACAGTTTTTT	Vertex staple	1421
51[16]	TTTTTCGGGTATTAAACGCGAGGCGTTTTAGCGAACTTTTT	Vertex staple	1422
7[24]	GGGGTGGTTTGCCCCAGCAGGCGACAGTTAAAATTCTCATTGCAATCCAAATAAAGAGGGTAATTGTTTTT	Vertex bundle strand	1423
25[24]	CAGACATTGAATCCCCCTCAAATAATAGTAGTCTAATCTATGAAAATCCTGTTTCGTCAAAGGGCGTTTTT	Vertex bundle strand	1424
43[24]	AGGTACAGCCATATTATTTATCCCACTAATCTTATGTAGCTTTAAACAGTTCGCGTTTTAATTTTTT	Vertex bundle strand	1425
7[9]	TTTTTAATCGGCCAACGTGCTGCGGCCACA AGTT AAAGAT TCGTC ATTGAAGGGCTTAATTGCAAAGTCGAAA	Vertex bundle strand	1426
25[9]	TTTTTATAACCCTCGTTAACGTAACAGTAA TAGT AGTCTA CATCT ATGGCAAATCGTTAACGACTCCAAGATG	Vertex bundle strand	1427
43[9]	TTTTTCTCCCGACTTGCTAATTCTGTTAA TCT TAT GTACCAACTTTGAAATCAAATATCAG	Vertex bundle strand	1428
	CAATGAGAATTTTAACTGT	Vertex bundle strand (complementary)	1429
	CATAGATTAGACTACTATT	Vertex bundle strand (complementary)	1430
	TACATAAGATTAGTG	Vertex bundle strand (complementary)	1431
	TCAAT GACGA ATCTTT AACT TGTG	Vertex bundle strand (complementary)	1432
	GCCAT AGATG TAGACT ACTA TTAC	Vertex bundle strand (complementary)	1433
	TAC ATA AGA TTA	Vertex bundle strand (complementary)	1434

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CLAIMS

What is claimed is:

1. A nucleic acid structure comprising

a first (x), a second (y), and a third (z) nucleic acid arm, each connected at one end to the other arms to form a vertex, and

a first, a second, and a third nucleic strut, wherein the first nucleic acid strut connects the first (x) nucleic arm to the second (y) nucleic arm, the second nucleic acid strut connects the second (y) nucleic arm to the third (z) nucleic arm, and the third nucleic acid strut connects the third (z) arm to the first (x) nucleic acid strut.

2. A nucleic acid structure comprising

three nucleic acid arms radiating from a vertex at fixed angles.

3. A nucleic acid structure comprising

N nucleic acid arms radiating from a vertex, wherein N is the number of nucleic acid arms and is 3 or more, and

M nucleic acid struts, each strut connecting two nucleic acid arms to each other, wherein M is the number of nucleic acid struts and is 3 or more.

4. The nucleic acid structure of claim 3, wherein N is equal to M.

5. The nucleic acid structure of claim 3, wherein N is less than M.

6. The nucleic acid structure of claim 1, wherein the nucleic acid structure comprises 4 nucleic acids and at least 4 nucleic acid struts, or 5 nucleic acid arms and at 5 nucleic acid struts.

7. The nucleic acid structure of claim 1, wherein the nucleic acid arms are equally spaced apart from each other (or the arms are separated from each other by the same angle).

8. The nucleic acid structure of claim 1, wherein the nucleic acid arms are not equally separated from each other (or the arms are separated from each other by different angles).

9. The nucleic acid structure of claim 1, further comprising a vertex nucleic acid.

10. The nucleic acid structure of claim 1, further comprising a connector nucleic acid.

11. The nucleic acid structure of claim 1, wherein the nucleic acid arms, nucleic acid struts, and/or vertex nucleic acid are comprised of parallel double helices.

12. The nucleic acid structure of claim 1, wherein nucleic acid arms are of identical length.

13. The nucleic acid structure of claim 1, wherein the nucleic acid struts are of identical length.

14. The nucleic acid structure of claim 1, wherein the nucleic acid struts are of different lengths.

15. The nucleic acid structure of claim 1, wherein at least one nucleic acid arm comprises a blunt end.

16. The nucleic acid structure of claim 1, wherein at least one nucleic acid arm comprises a connector nucleic acid at its free (non-vertex) end that is up to 16 nucleotides in length.

17. The nucleic acid structure of claim 1, wherein at least one nucleic acid arm comprises a connector nucleic acid at its free (non-vertex) end, thereby comprising a 1 or 2 nucleotide overhang.

18. The nucleic acid structure of claim 1, wherein the nucleic acid structure is up to 5 megadaltons (MD) in size.

19. The nucleic acid structure of claim 1, wherein the nucleic acid arms are 50 nm in length.

20. The nucleic acid structure of claim 1, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 60° - 60° - 60° (tetrahedron).

21. The nucleic acid structure of claim 1, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 60° - 90° - 90° (triangular prism).

22. The nucleic acid structure of claim 1, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 90° - 90° - 90° (cube).

23. The nucleic acid structure of claim 1, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 108° - 90° - 90° (pentagonal prism).

24. The nucleic acid structure of claim 1, wherein the nucleic acid structure comprises three nucleic acid arms separated from each other by 120° - 90° - 90° (hexagonal prism).

25. A composite nucleic acid structure comprising L nucleic acid structures selected from the nucleic acid structures of claim 1, wherein L is an even number of nucleic acid structures, and wherein the L nucleic acid structures are connected to each other at free (non-vertex) ends of the nucleic acid arms.

26. The composite nucleic acid structure of claim 25, wherein the two more nucleic acid structures are two, four, six, eight, ten, twelve or more nucleic acid structures.

27. The composite nucleic acid structure of claim 25, wherein the composite nucleic acid structure is a tetrahedron, a triangular prism, a cube, a pentagonal prism, or a hexagonal prism.

28. The composite nucleic acid structure of claim 25, wherein the composite nucleic acid structure is 20 megadaltons (MD), 30 MD, 40 MD, 50 MD, or 60 MD in size.

29. The composite nucleic acid structure of claim 25, wherein the composite nucleic acid structure has edge widths, comprised of two nucleic acid arms from adjacent nucleic acid structures, of 100 nm.

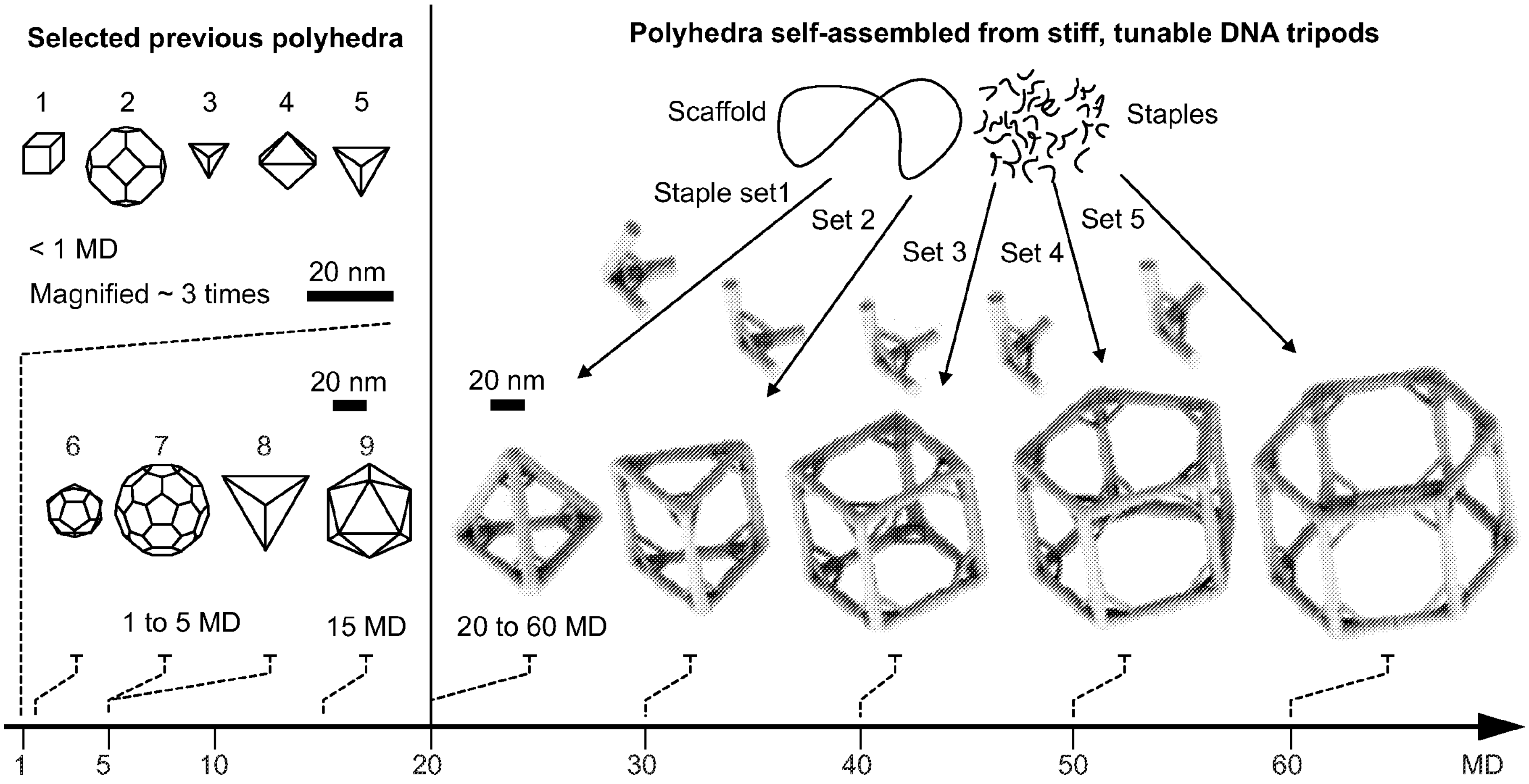

Selected previous polyhedra
1
2
3
4
5
< 1 MD
Magnified ~ 3 times
20 nm
20 nm
6
7
8
9
1 to 5 MD
15 MD
Polyhedra self-assembled from stiff, tunable DNA tripods
Scaffold
Staples
Staple set1
Set 2
Set 3
Set 4
Set 5
20 nm
20 to 60 MD
1
5
10
20
30
40
50
60
MD

FIG. 1A

FIG. 1B

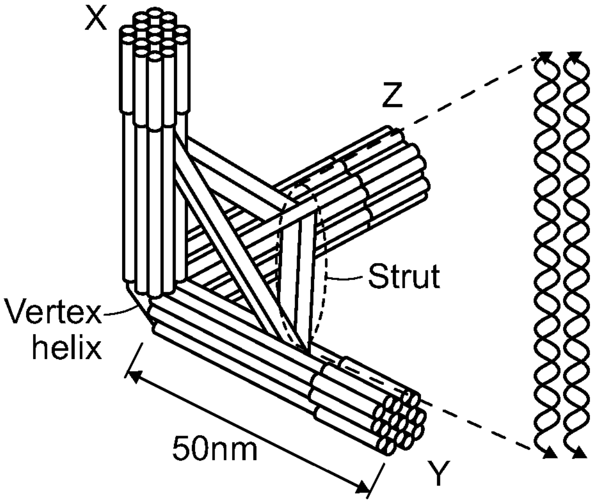


FIG. 1C

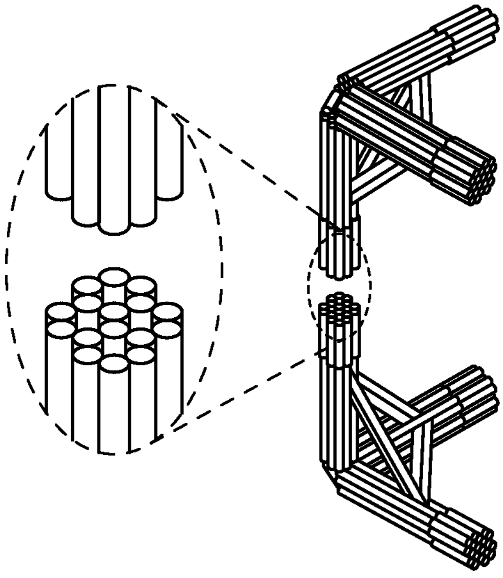


FIG. 1D

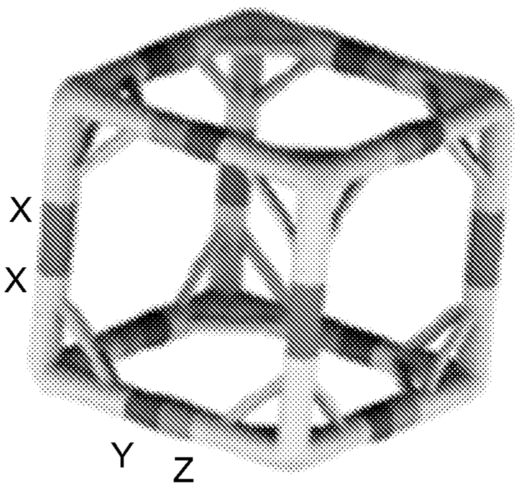
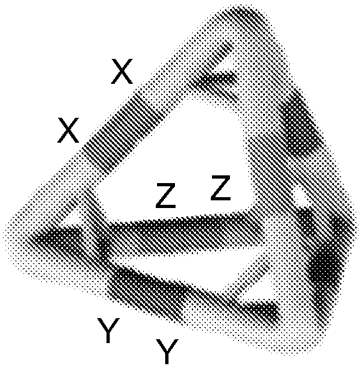


FIG. 1E



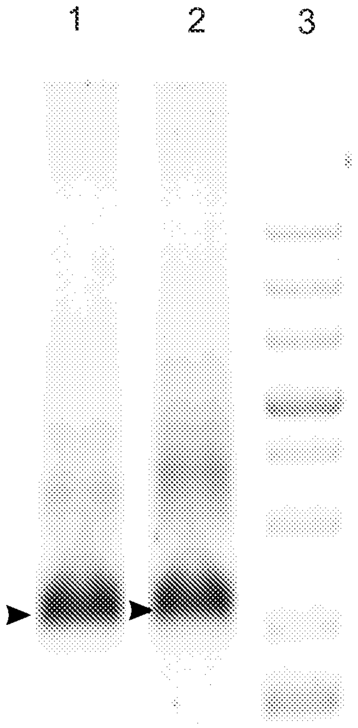
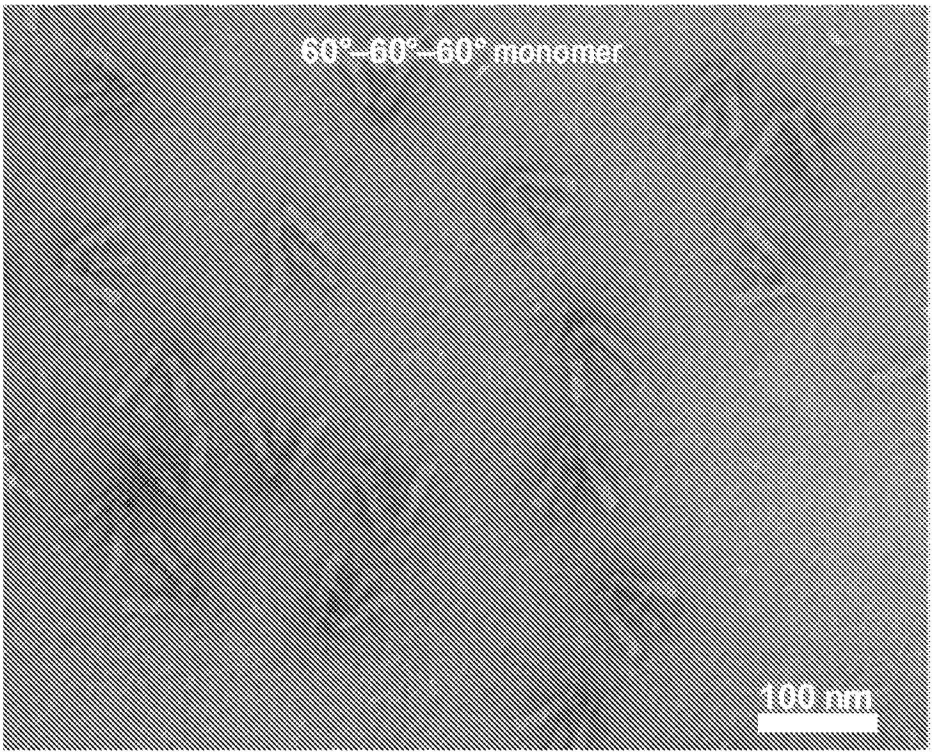


FIG. 2A

FIG. 2B



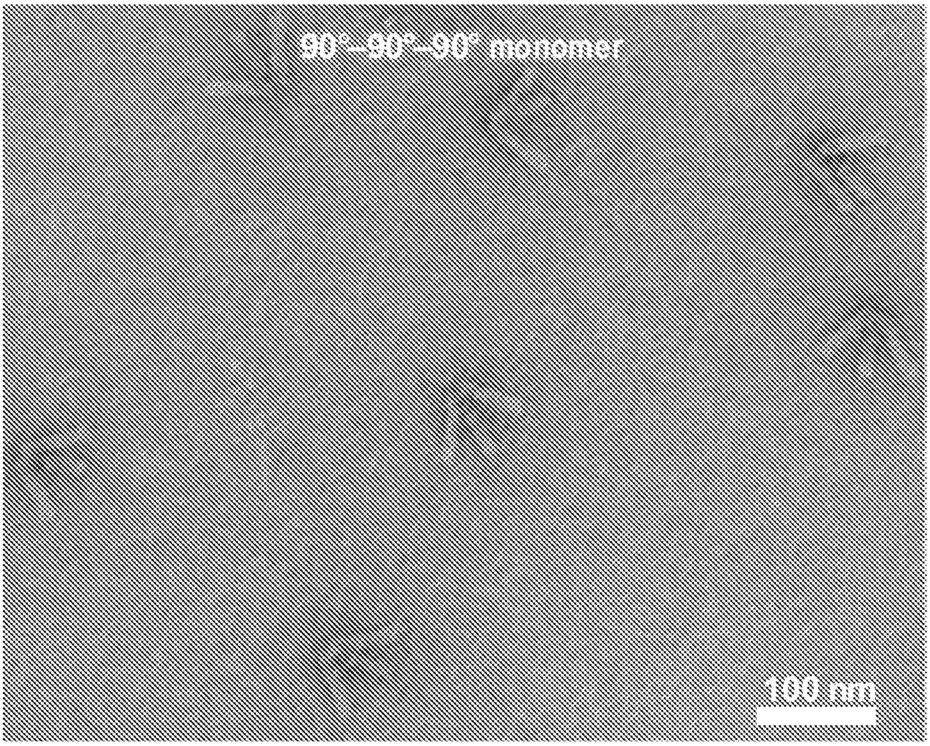


FIG. 2C

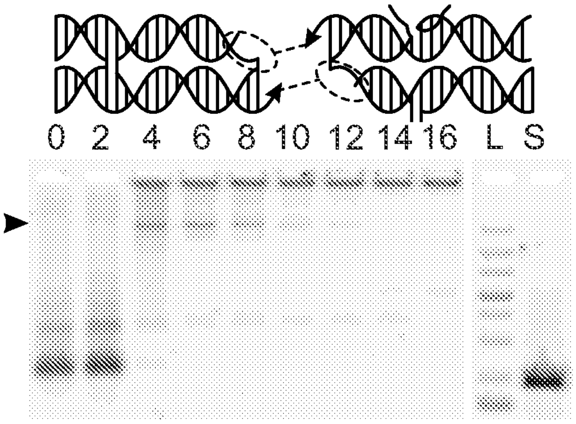


FIG. 2D

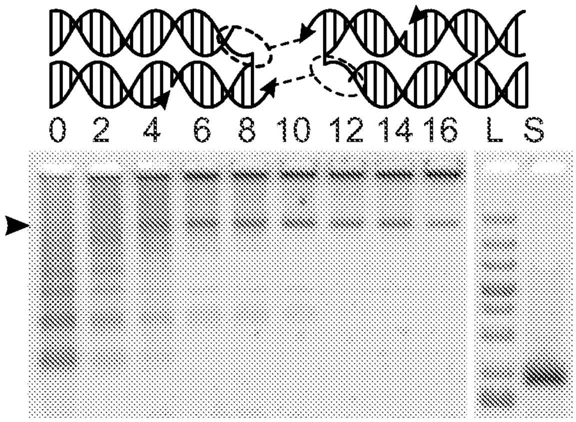
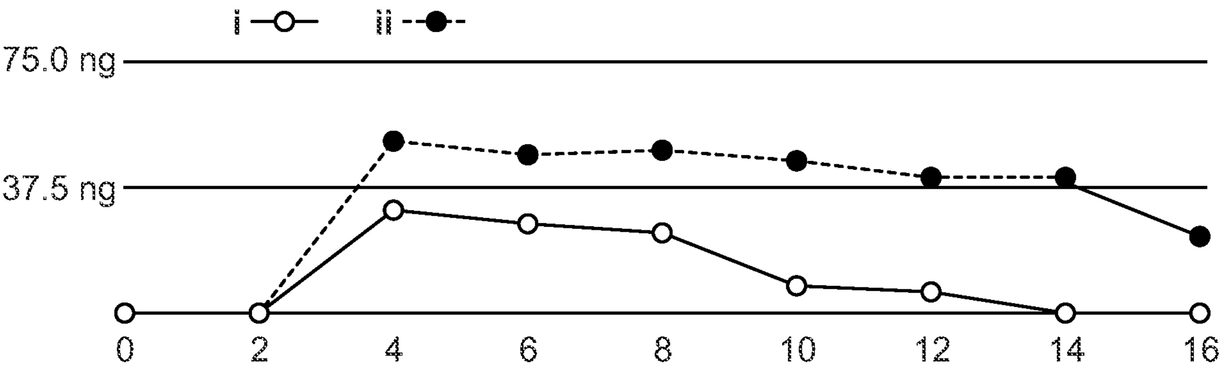


FIG. 2E



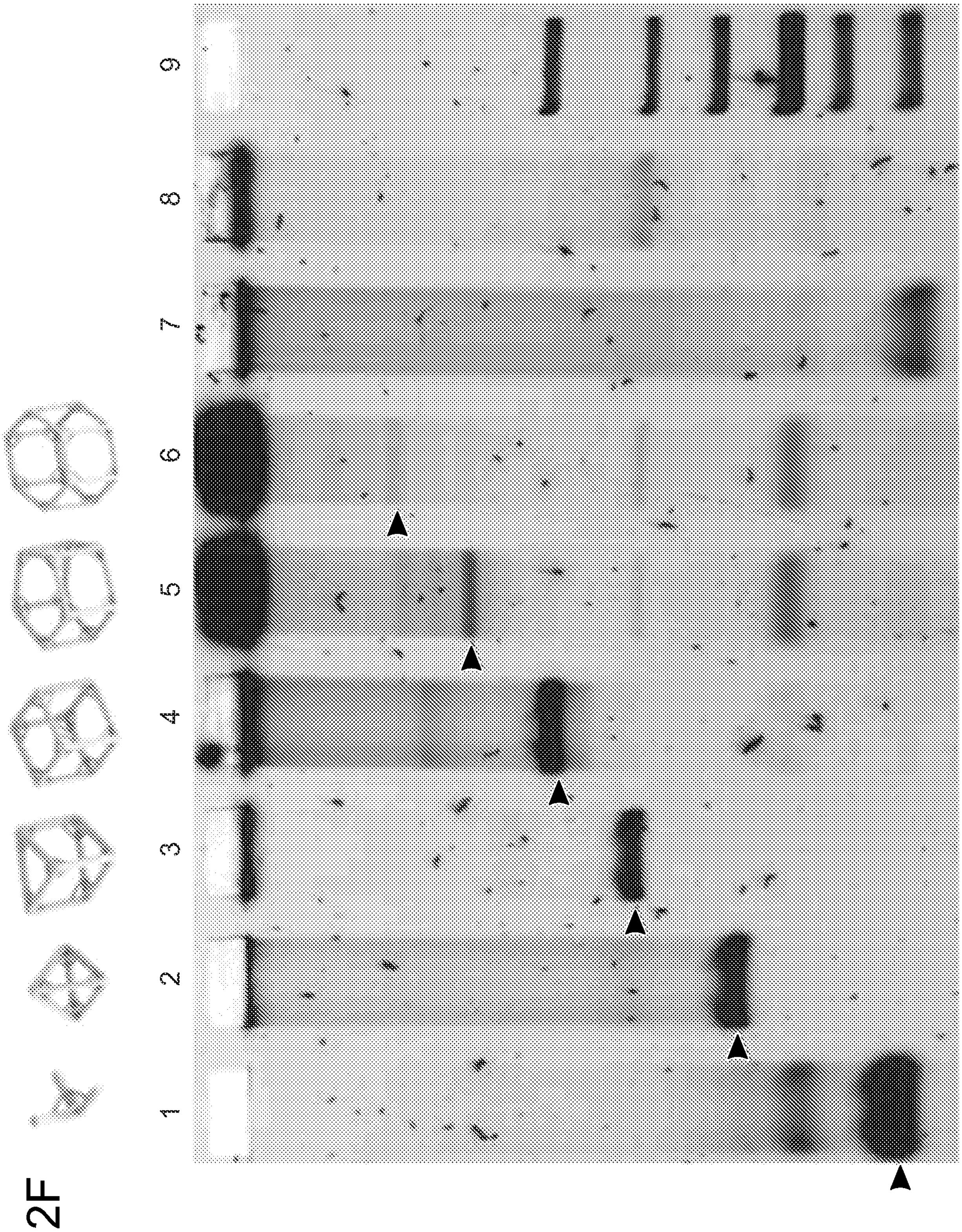


FIG. 2F

FIG. 3A

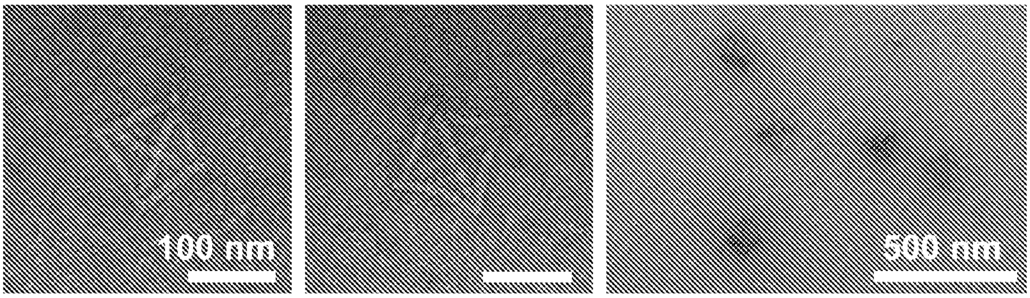


FIG. 3B

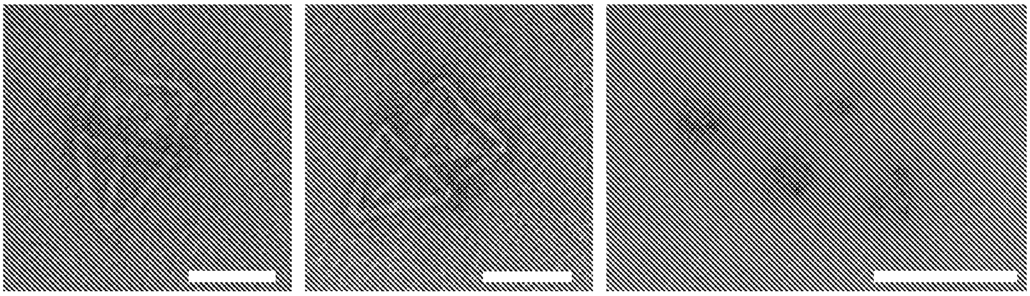


FIG. 3C

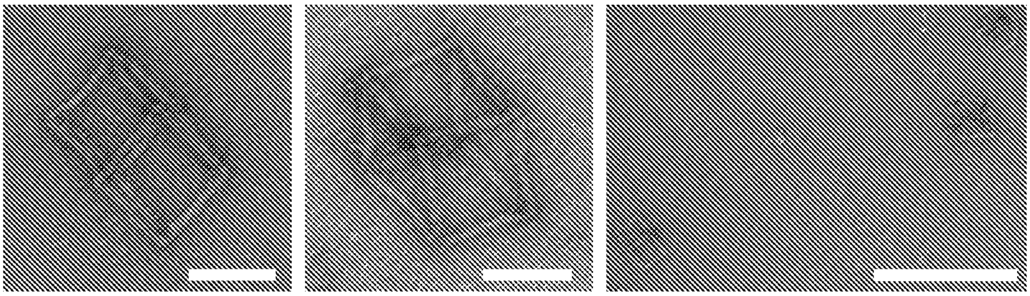


FIG. 3D

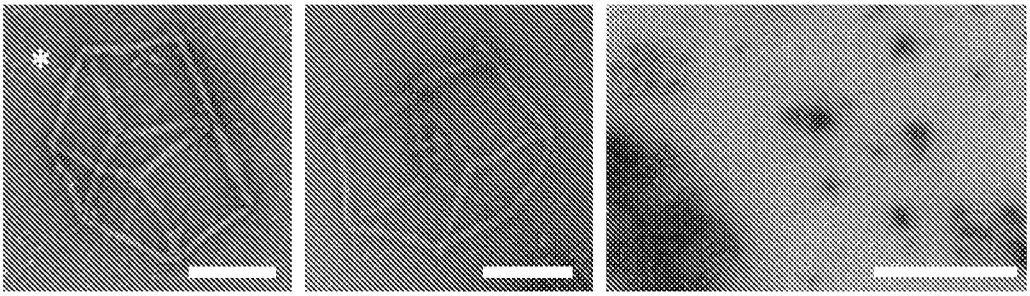
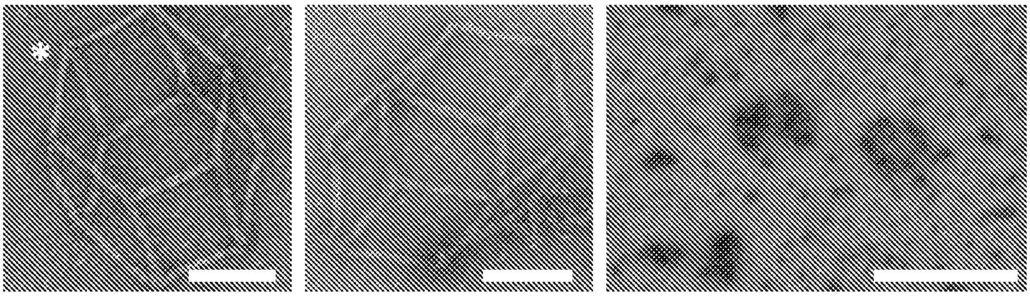


FIG. 3E



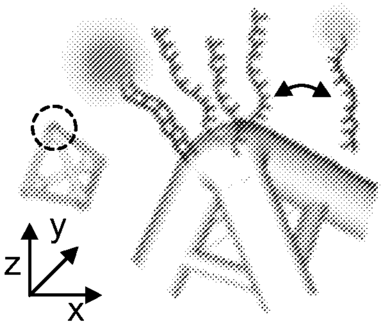


FIG. 4A1

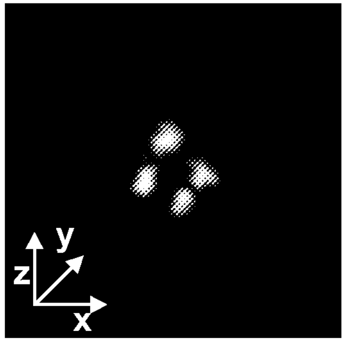


FIG. 4A2

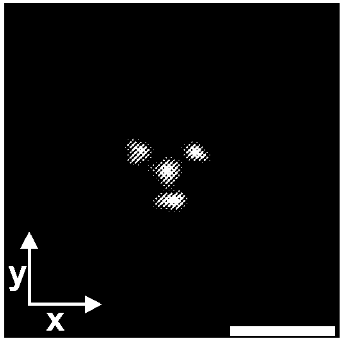


FIG. 4A3

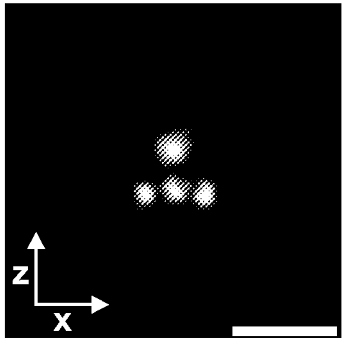


FIG. 4A4

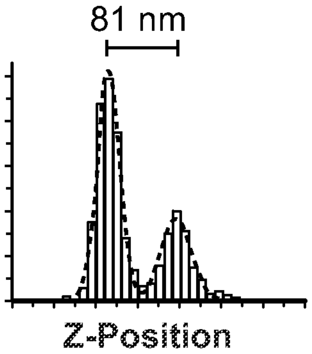


FIG. 4A5

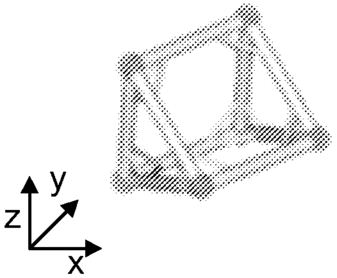


FIG. 4B1

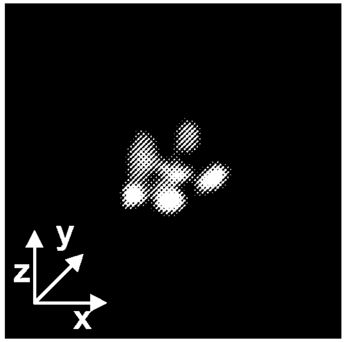


FIG. 4B2

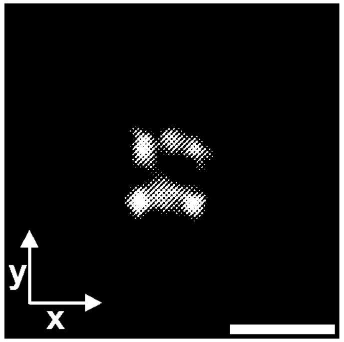


FIG. 4B3

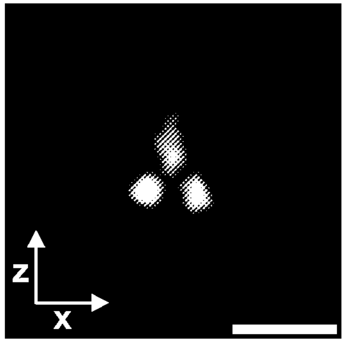


FIG. 4B4

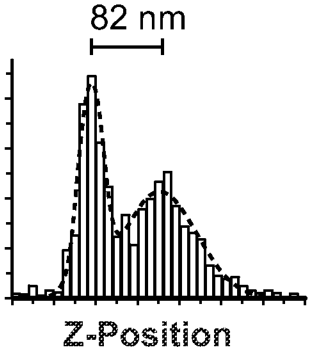


FIG. 4B5

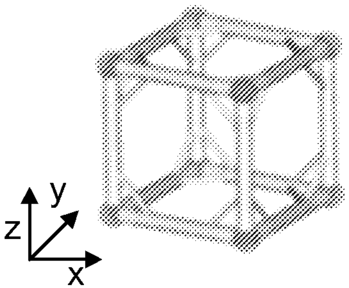


FIG. 4C1

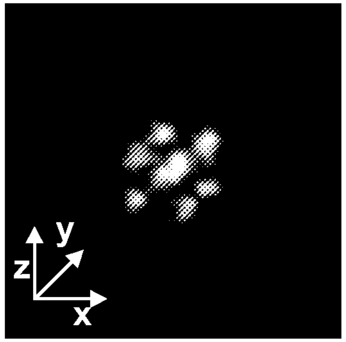


FIG. 4C2

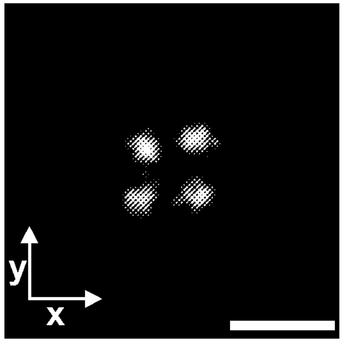


FIG. 4C3

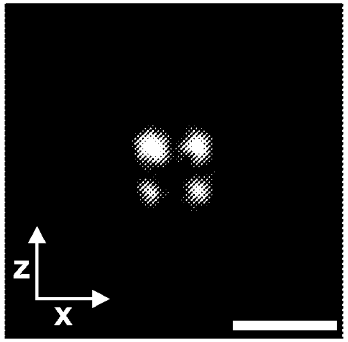


FIG. 4C4

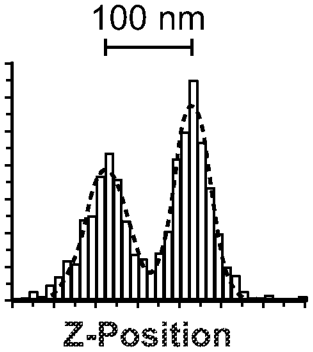


FIG. 4C5

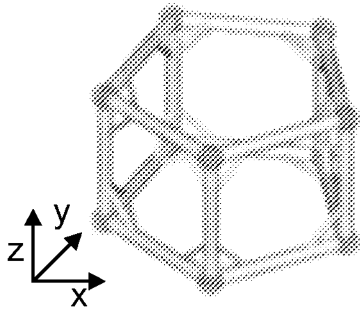


FIG. 4D1

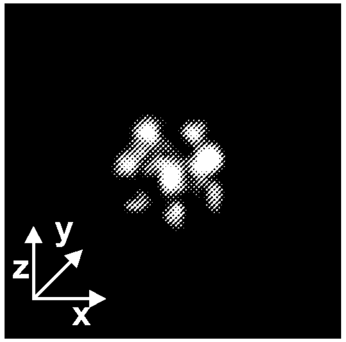


FIG. 4D2

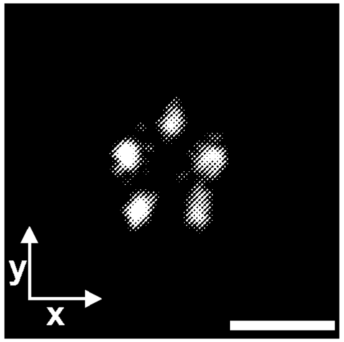


FIG. 4D3

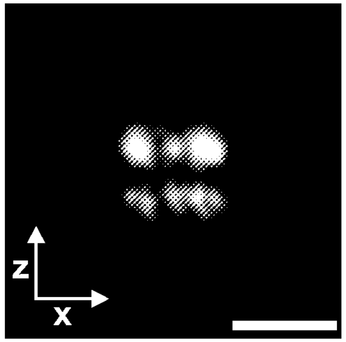


FIG. 4D4

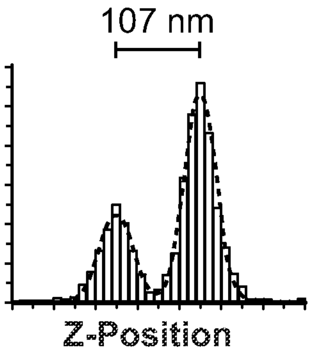


FIG. 4D5

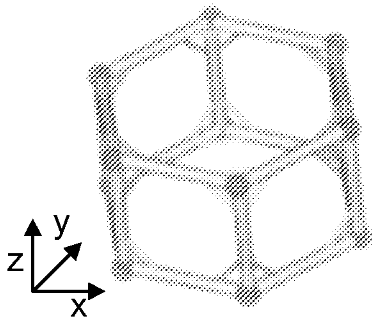


FIG. 4E1

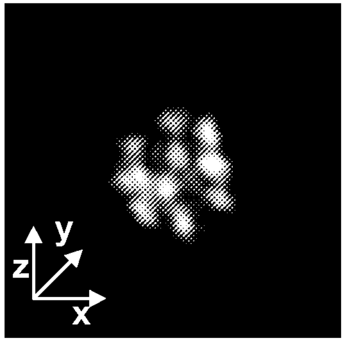


FIG. 4E2

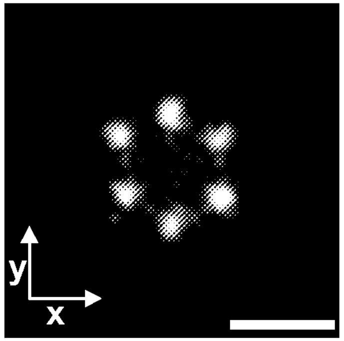


FIG. 4E3

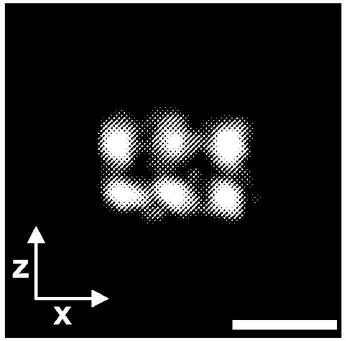


FIG. 4E4

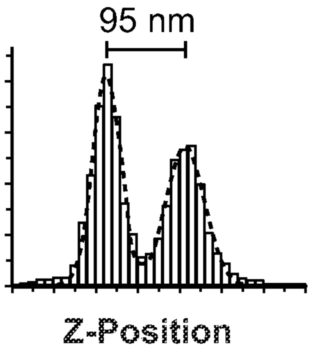


FIG. 4E5

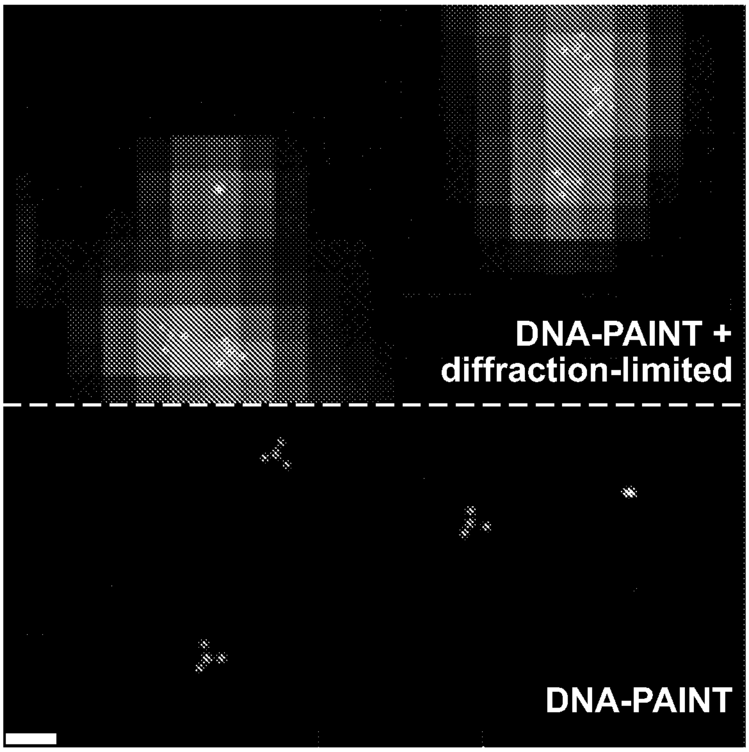


FIG. 4F

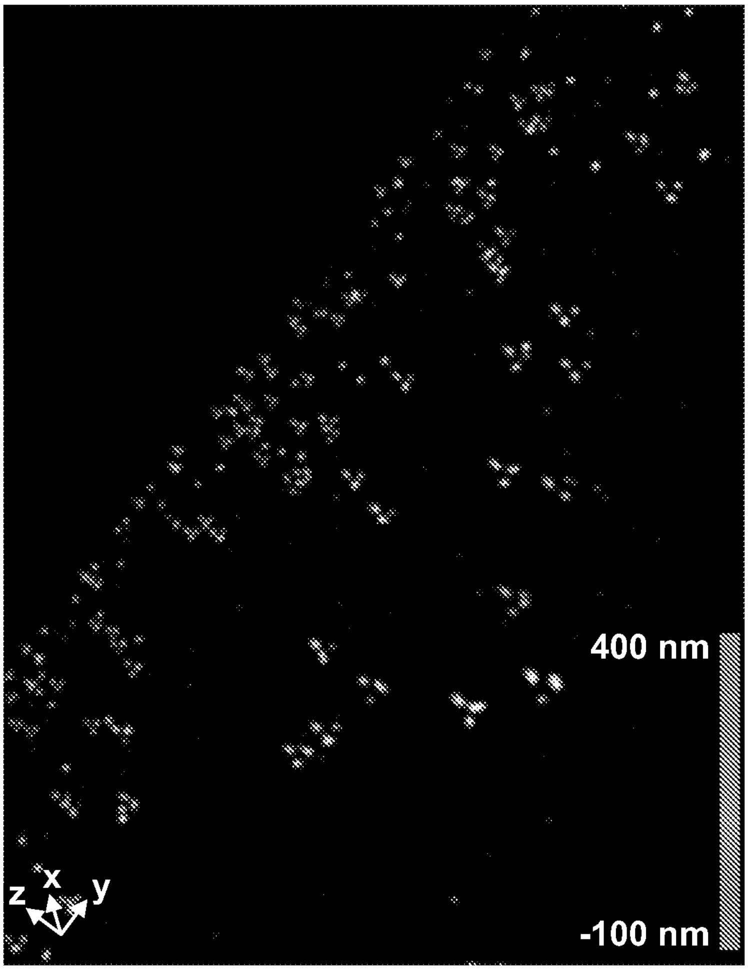
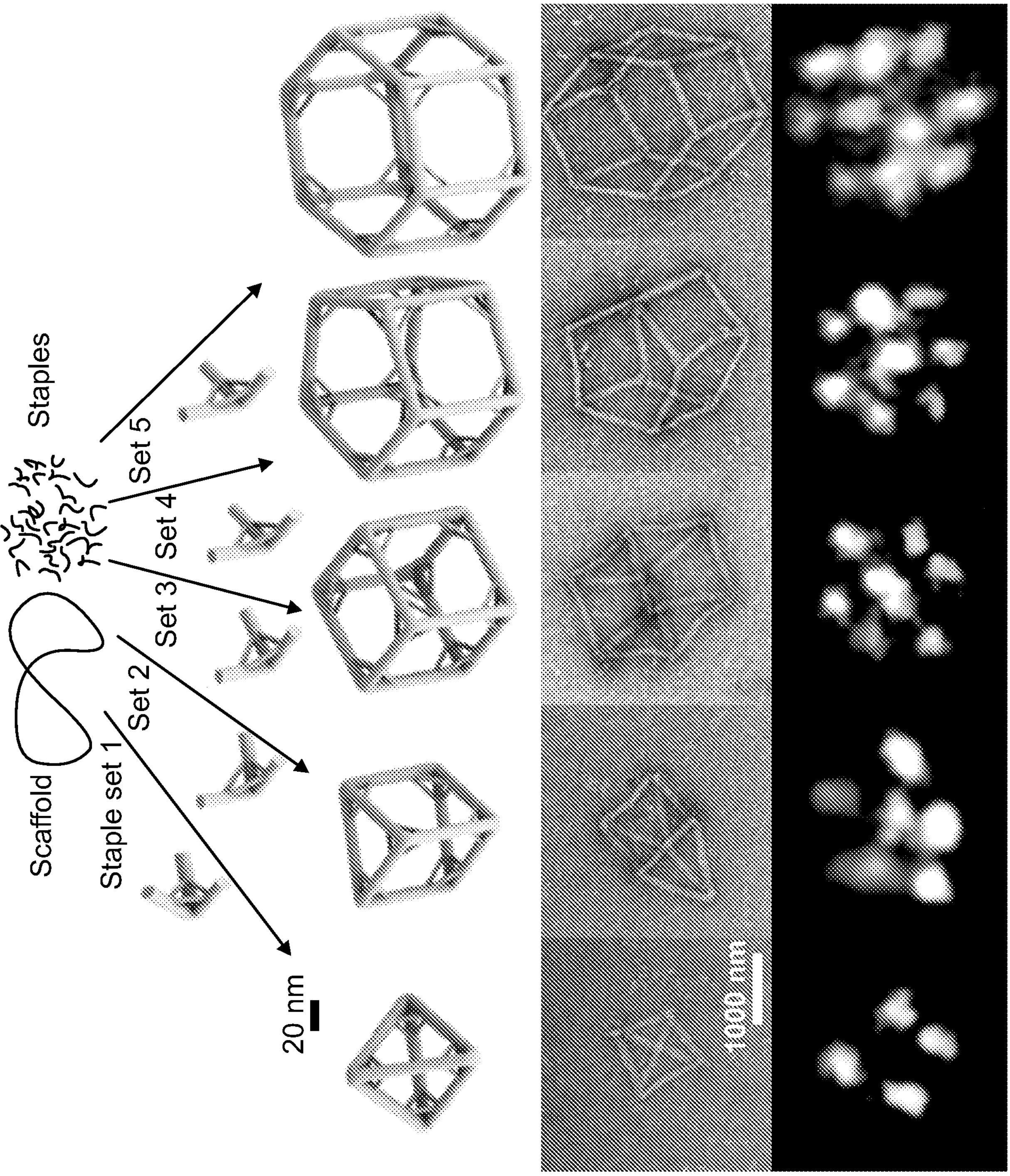


FIG. 4G

FIG. 5

Polyhedra self-assembled from stiff, tunable DNA tripods



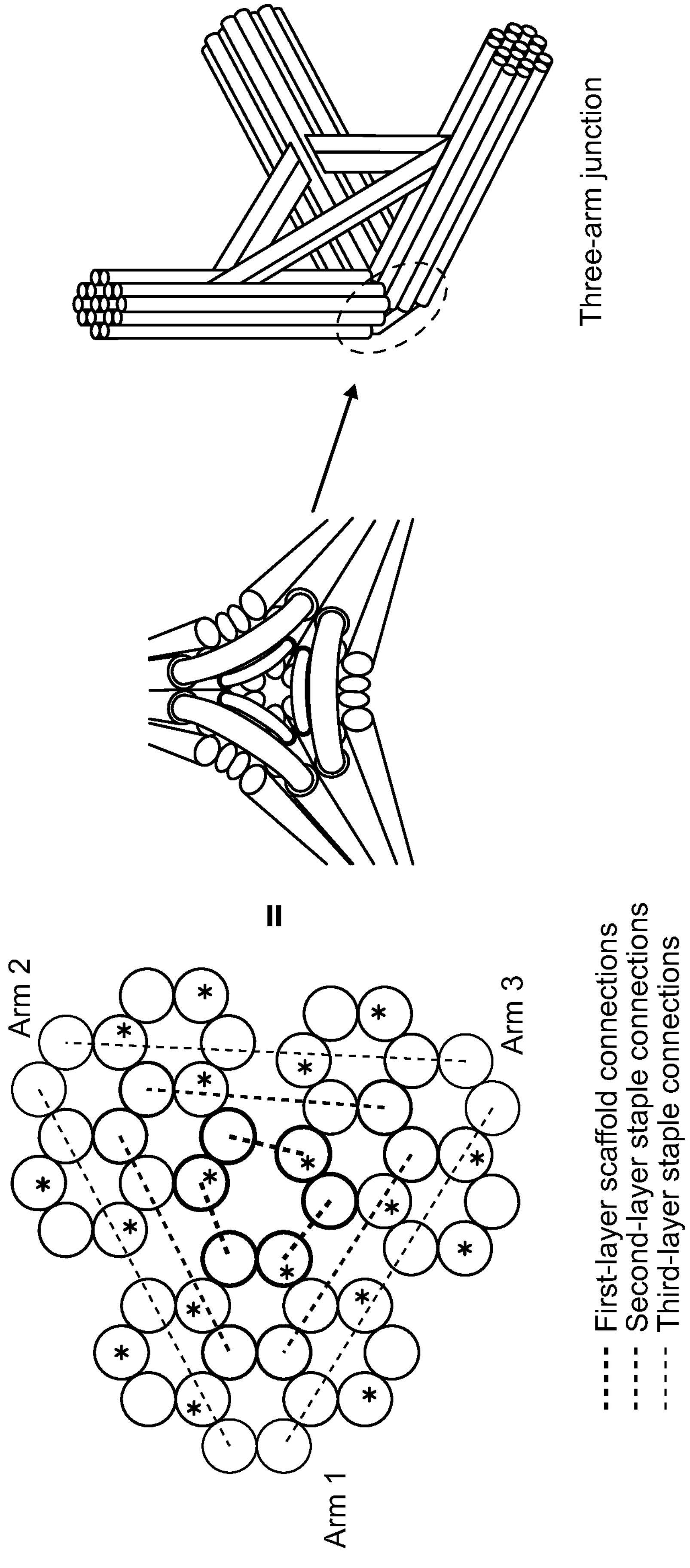

Arm 1
Arm 2
Arm 3
=
First-layer scaffold connections
Second-layer staple connections
Third-layer staple connections
Three-arm junction

FIG. 6

FIG. 7A

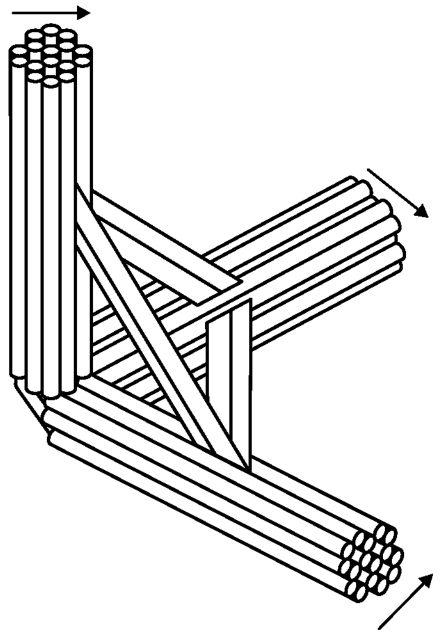


FIG. 7B

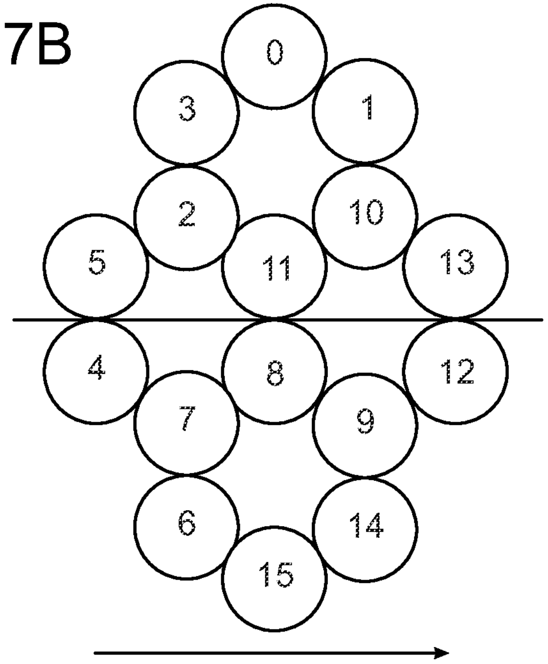


FIG. 7C

Number of connections	2	4	6	8	10	12	14	16
	12<--->13	12<--->13	12<--->13	12<--->13	12<--->13	12<--->13	12<--->13	12<--->13
		9<--->10	9<--->10	9<--->10	9<--->10	9<--->10	9<--->10	9<--->10
			8<--->11	8<--->11	8<--->11	8<--->11	8<--->11	8<--->11
				2<--->7	2<--->7	2<--->7	2<--->7	2<--->7
					4<--->5	4<--->5	4<--->5	4<--->5
						3<--->6	3<--->6	3<--->6
							0<--->15	0<--->15
								1<--->14

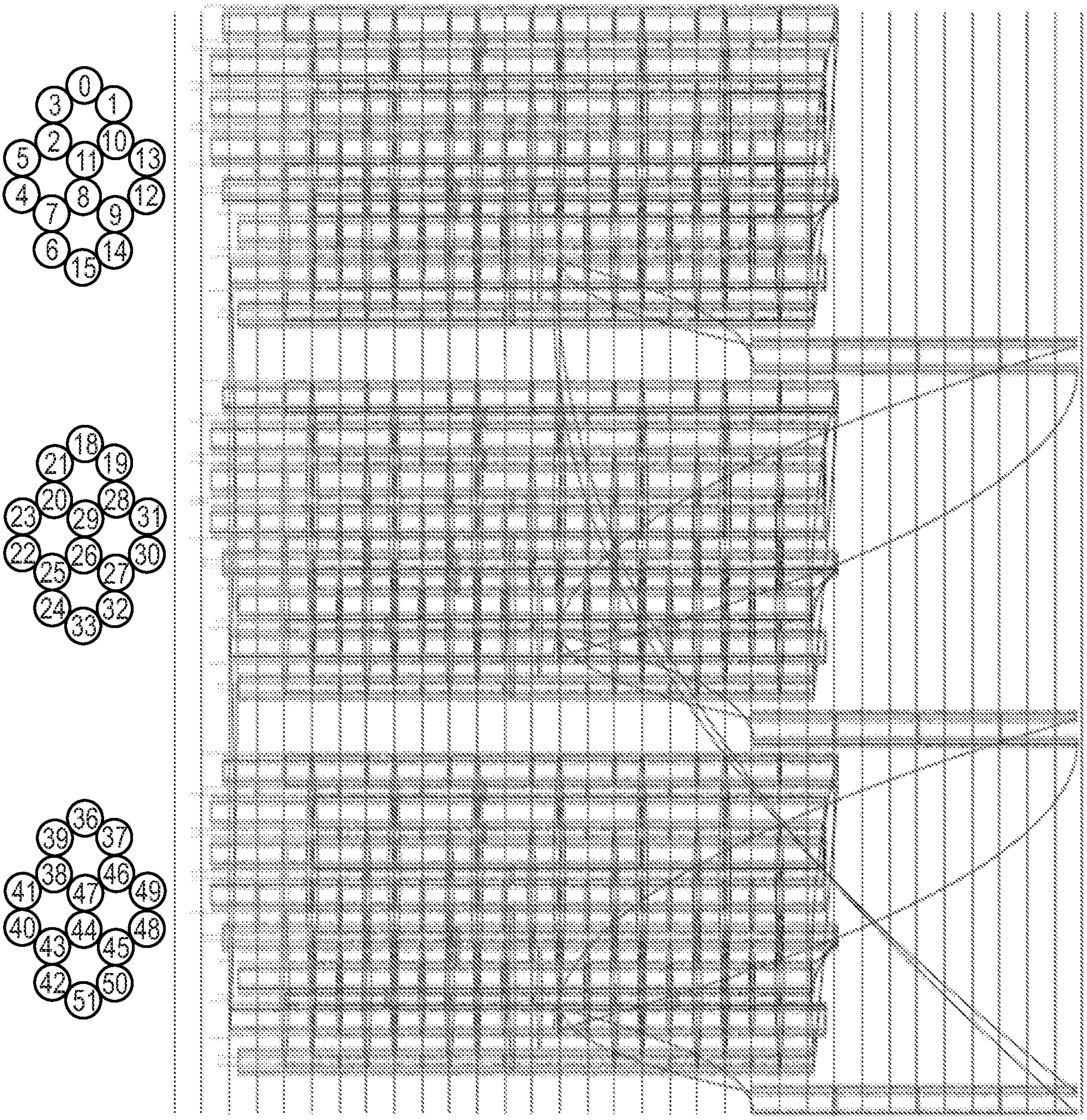

0
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FIG. 8

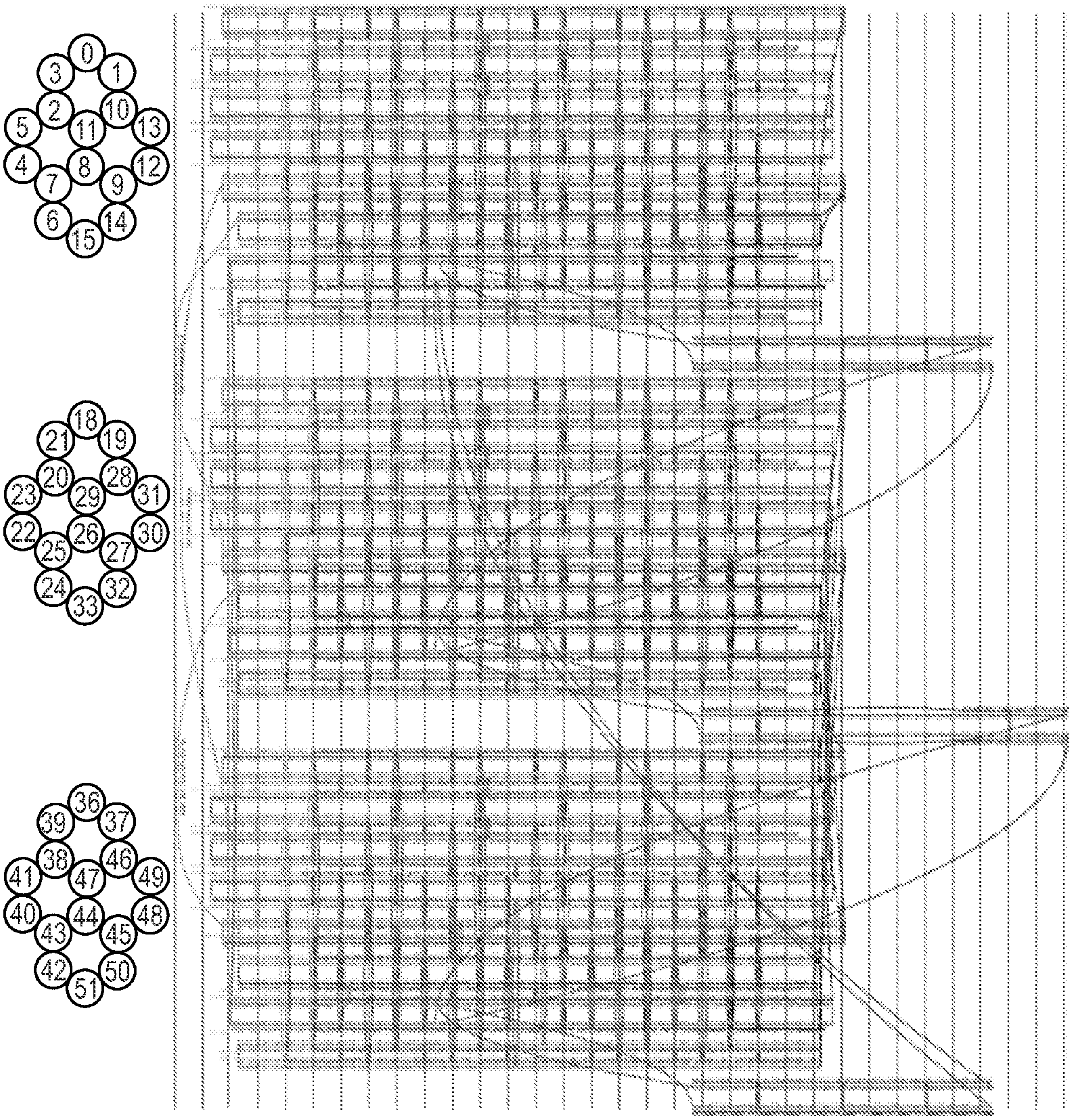
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FIG. 9

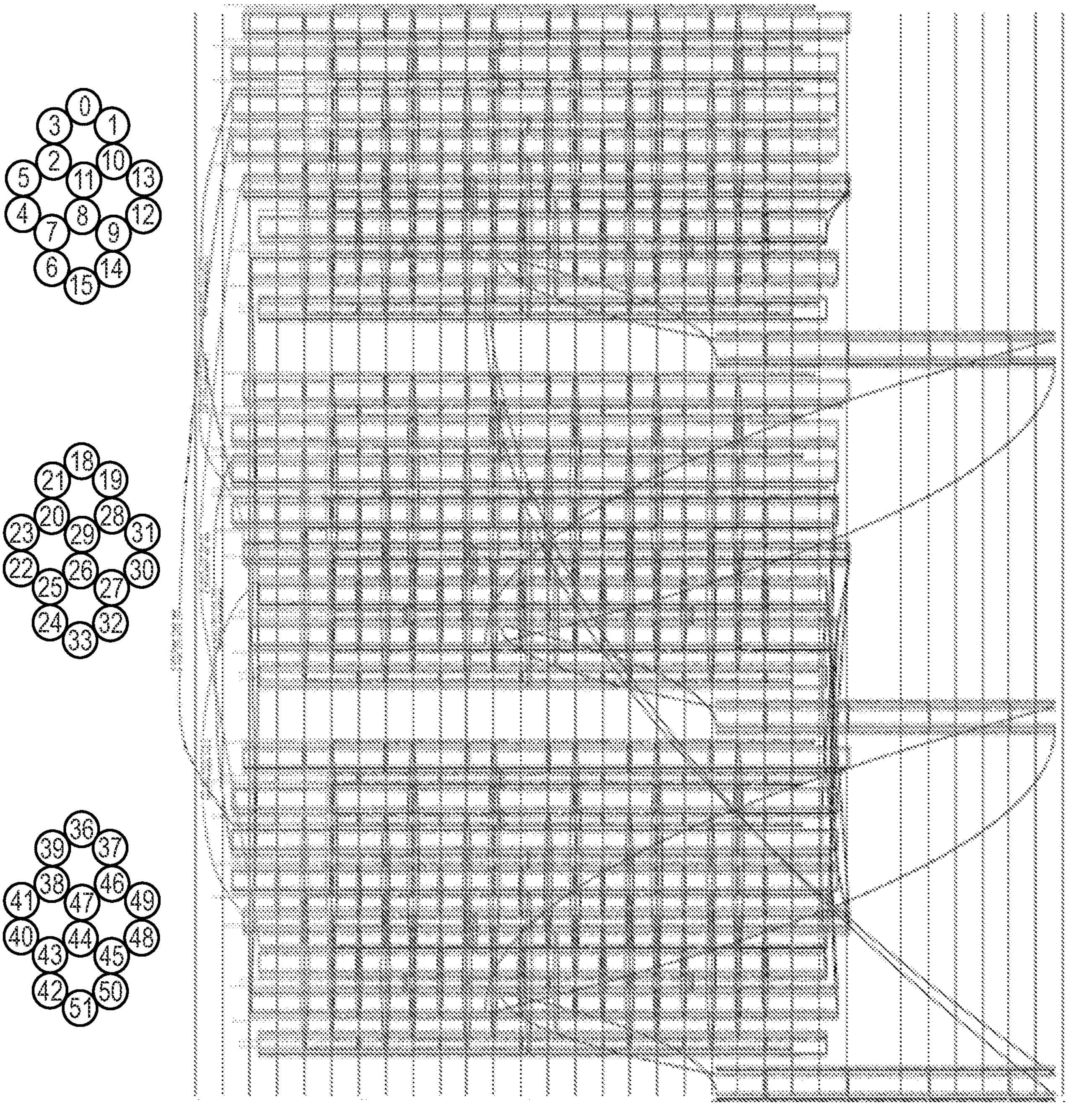
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FIG. 10

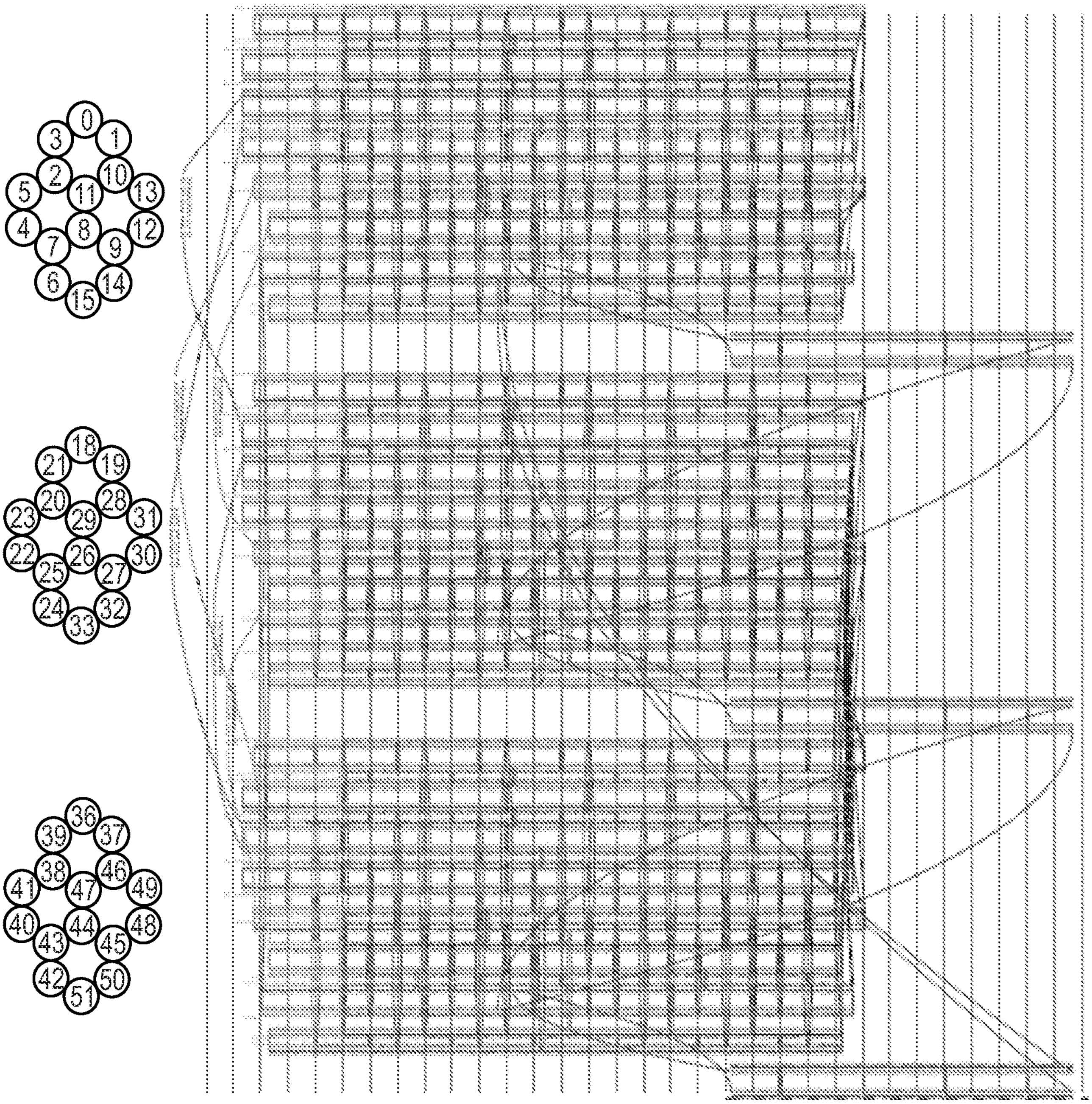
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FIG. 11

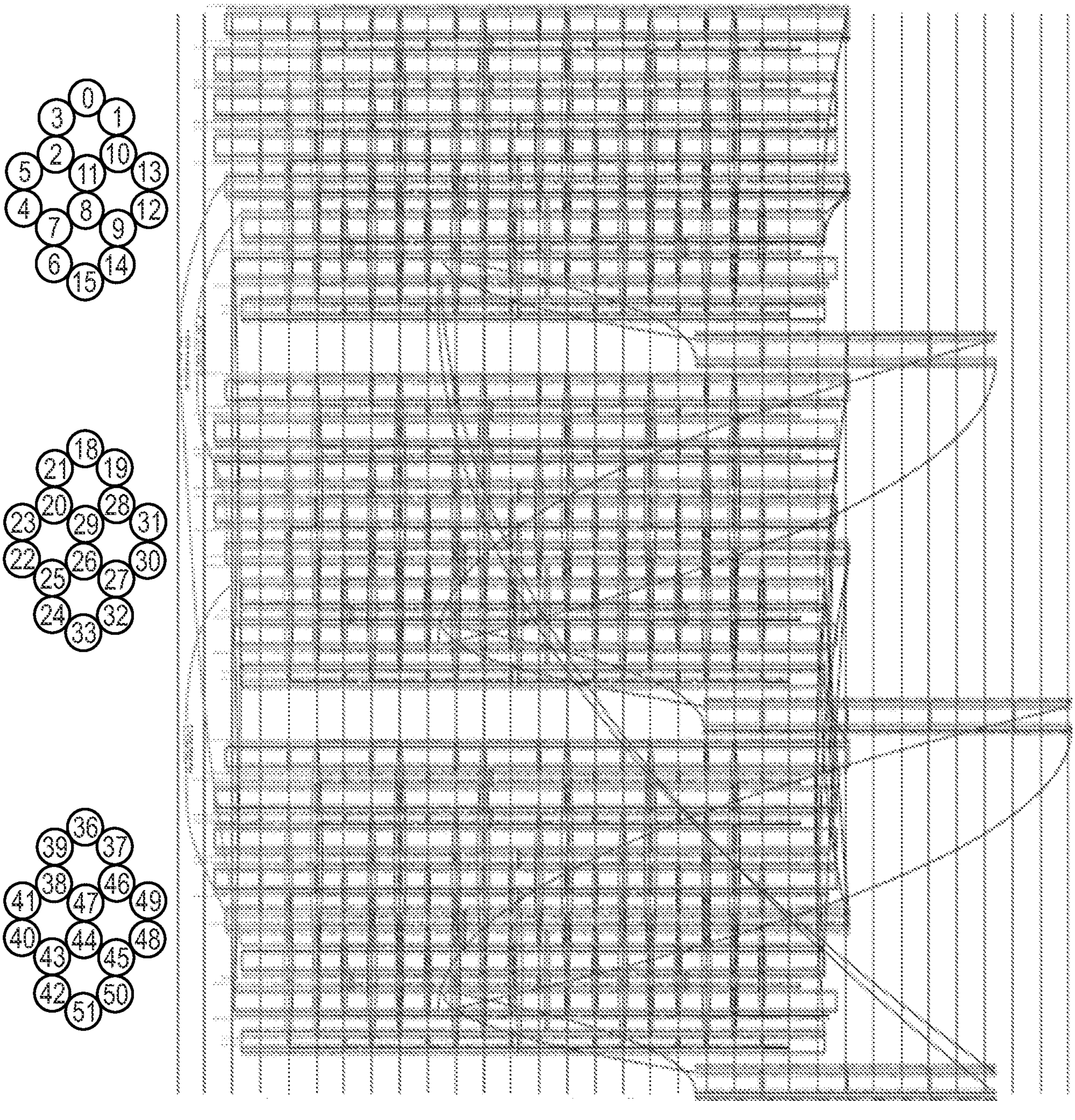
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FIG. 12

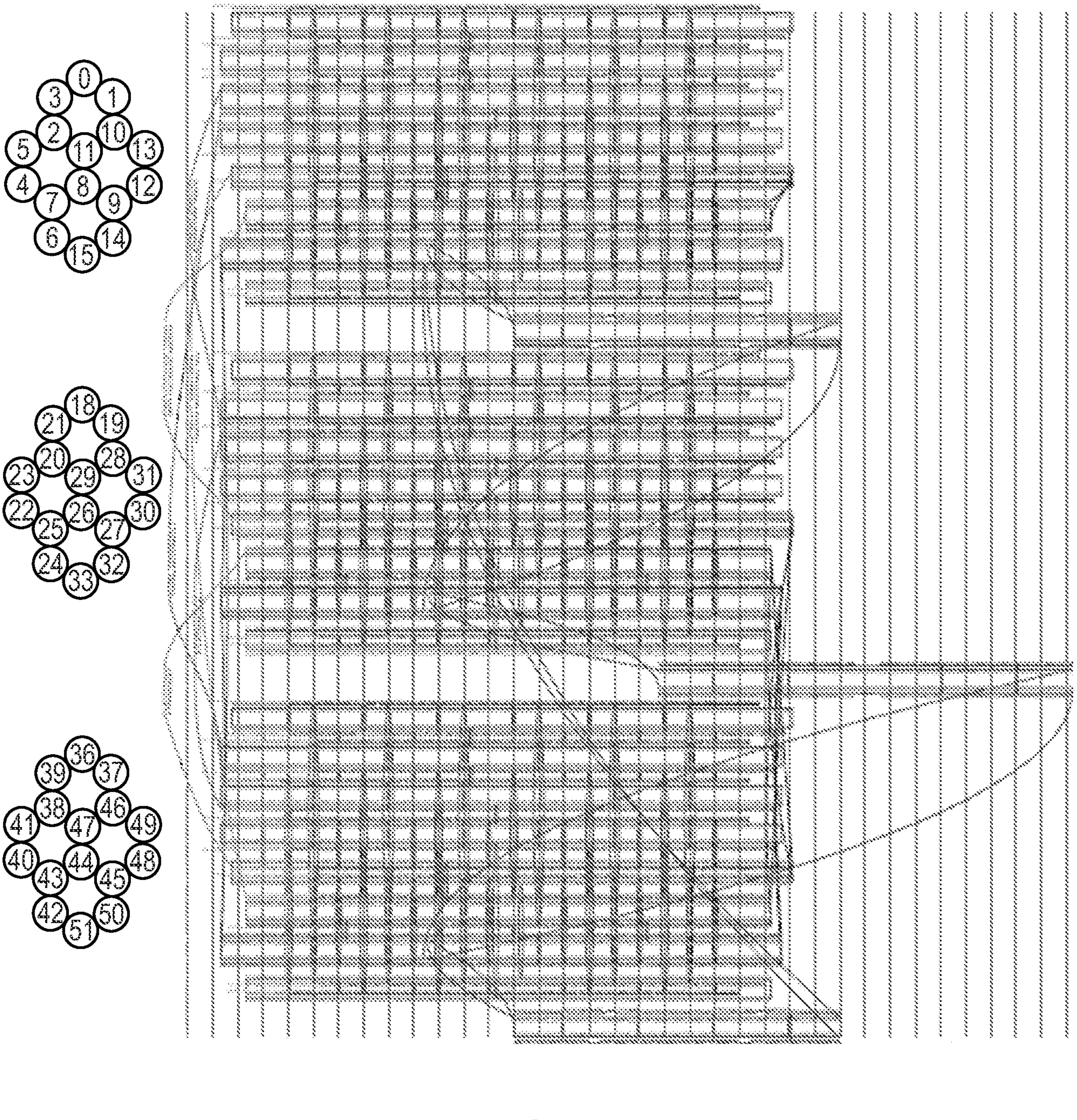
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FIG. 13

FIG. 14A

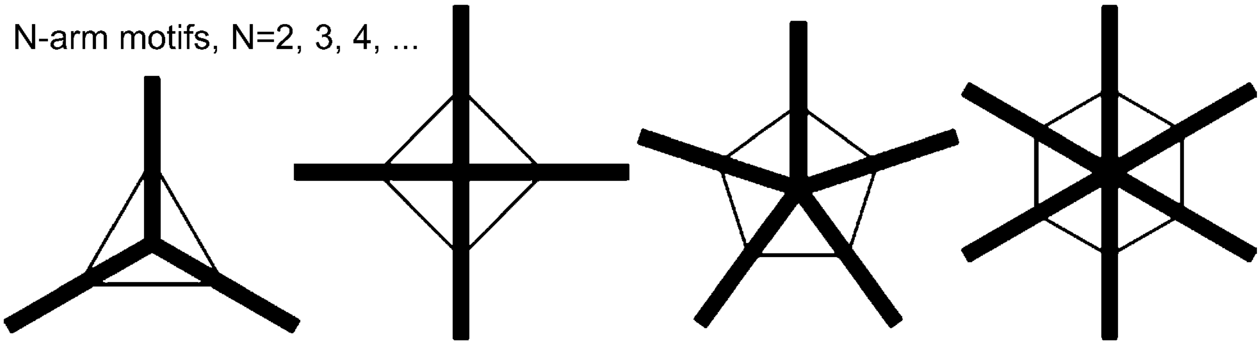


FIG. 14B

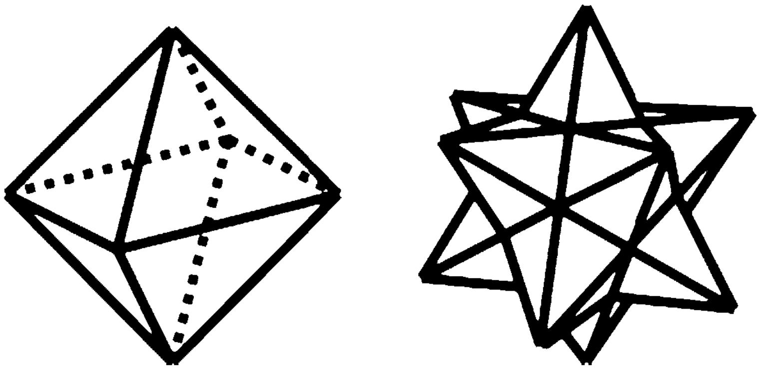
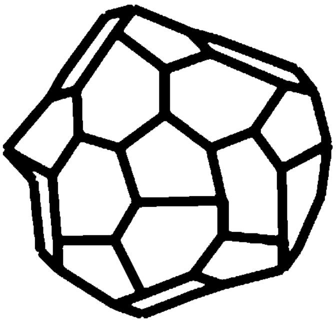


FIG. 14C



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 15/19135

Box No. I **Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)**

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

a. ☒ forming part of the international application as filed:

☒ in the form of an Annex C/ST.25 text file.

☐ on paper or in the form of an image file.

b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

c. ☒ furnished subsequent to the international filing date for the purposes of international search only:

☒ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 15/19135

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C07H 21/00, 21/04; C12Q 1/68 (2015.01)
CPC - C07H 21/00; C12Q 1/68
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
CPC: C07H 21/00; C12Q 1/68

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
CPC: C07H 21/00; C12Q 1/68 (text search)
USPC: 536/25.3, 23.1, 22.1; 435/6.1 (text search)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Electronic data bases: PatBase, Google Scholar; Google Patents
Search terms: nucleic acid arms, branched nucleic acid, 3 arm nucleic acid, strut, vertex, tripod, three dimension DNA nanostructure, nanoarchitecture, nucleic acid structure, polyhedron, tetrahedron, cube, self-assembly

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ---- Y	US 2009/0227774 A1 (TURBERFIELD et al.) 10 September 2009 (10.09.2009). Especially para [0040], [0048], [0057], [0060], [0130-131], [0149-0150]	1-8, 10, 12-20, 22, 25-29 ---- 9, 11, 21, 23, 24
Y	HE et al. Hierarchical self-assembly of DNA into symmetric supramolecular polyhedra. Nature 13 March 2008 Vol 452 No 7184 Pages 198-201. Especially pg 198 fig 1.	9
Y	FU et al. DNA double-crossover molecules. Biochemistry 06 April 1993 Vol 32 No 13 Pages 3211-3220. Especially pg 3212 fig 1.	11
Y	ALDAYE et al. Assembling materials with DNA as the guide. Science 26 September 2008 Vol 321 No 5897 Pages 1795-1799. Especially pg 1799 fig 3B.	21, 23, 24
X,P	Iinuma et al. Polyhedra self-assembled from DNA tripods and characterized with 3D DNA-PAINT. Science ePub 13 March 2014 Vol 344 No 6179 Pages 65-69. Especially entire article.	1-29
A,P	Ke. Designer three-dimensional DNA architectures. Curr Opin Struc Biol ePub 11 August 2014 Vol 27 Pages 122-128. Review of field.	1-29

☐ Further documents are listed in the continuation of Box C. ☐

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search 08 May 2015 (08.05.2015)	Date of mailing of the international search report 09 JUN 2015
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer: Lee W. Young PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774