Claims

1. An artificial nanopore comprising a multimeric assembly of subunits, each subunit comprising:

(i) the transmembrane (TM) sequence of a ß-barrel or α-helical pore forming protein fused to the amino acid sequence of (ii) a subunit of a ring-forming protein which controls the transport of a polypeptide or polynucleotide across the TM region of the assembly.

2. ~~A~~The artificial nanopore according to claim 1, comprising the TM sequence of an α-helical pore forming protein, preferably the TM sequence of FraC, ClyA, AhlB or Wza (translocon for *E. coli* capsular polysaccharides).

3. The a~~A~~rtificial nanopore according to claim 1, comprising the TM sequence of a ß-barrel pore forming protein, preferably the TM sequence of α-heamolysin, aerolysin or anthrax protective antigen (PA).

4. The a~~A~~rtificial nanopore according to claim 3, wherein the TM sequence comprises or consists of the amino acid sequence VHGNAEVHASFFDIGGSVSAGF.

5. The a~~A~~rtificial nanopore according to any one of claims 1-4, wherein the TM sequence is N- or C-terminally fused to the subunit of a ring-forming protein.

6. The a~~A~~rtificial nanopore according to any one of claims 1-4, wherein the TM sequence is inserted within the sequence of the subunit of a ring-forming protein.

~~7~~. The a~~A~~rtificial nanopore according to any one of claims 1-5, wherein the TM sequence is flanked on the N- and/or C-terminal side by a flexible linker of at least 3, preferably at least 5, amino acids, more preferably

wherein the N-terminal linker comprises or consists of the sequence GSS and/or wherein the C-terminal linker comprises or consists of the sequence SSG.

8. The a~~A~~rtificial nanopore according to any one of claims 1-7, wherein the ring-forming protein is a heptameric protein.

9. The a~~A~~rtificial nanopore according to claim 8, wherein the ring-forming heptameric protein controls the transport of a polynucleotide across the TM region, preferably ~~.~~

~~10. Artificial nanopore according to claim 9,~~ wherein the heptameric protein is an ATPase, preferably *A. aeolicus* ATPase or a homolog or functional equivalent thereof.

10~~11~~. ~~Artificial~~ The artificial nanopore according to claim 9~~8~~, wherein the ring-forming heptameric protein controls the transport of a polypeptide across the TM region~~.~~

~~12. Artificial nanopore according to claim 11,~~, preferably wherein the heptameric protein is proteasome activator PA28, PA26, or a homolog or functional equivalent thereof.

11~~13~~. The a~~A~~rtificial nanopore according to any one of claims 1-10~~12~~, wherein the C-terminus of the subunit of the ring-forming protein comprising the TM sequence is genetically fused to the N-terminus of a proteasome α-subunit.

12~~14~~. The a~~A~~rtificial nanopore according to any one of claims 1-11~~12~~, wherein the N-terminus of the subunit of the ring-forming protein comprising the TM sequence is genetically fused to the C-terminus of a Clp protease (ClpP) subunit.

13~~15~~. A multi-protein nanopore sensor complex, comprising (i) an artificial nanopore according to any one of claims 1-12~~14~~, (ii) one or two rings

composed of proteasome α-subunits, preferably wherein the proteasome α-subunit lacks at least 5 amino acids at its N-terminus, and optionally (iii) one or two rings composed of proteasome ß-subunits.

~~16. A multi-protein nanopore sensor complex according to claim 15, wherein the proteasome α-subunit lacks at least 5 amino acids at its N-terminus.~~

14~~17~~. The m~~M~~ulti-protein nanopore sensor complex according to claim 13~~15 or 16~~, wherein the ring composed of proteasome ß-subunits is engineered to provide a distinct type of protease activity.

15~~18~~. The m~~M~~ulti-protein nanopore sensor complex according to ~~any one of~~ claim~~s~~ 13 or 14~~15-17~~, further comprising a protein translocase which can bind, unfold, and translocate a polynucleotide or polypeptide through the nanopore sensor complex in a sequential order.

16~~19~~. The m~~M~~ulti-protein nanopore sensor complex according to claim 15~~18~~, wherein the protein translocase is an NTP-driven unfoldase, preferably an AAA+ unfoldase, more preferably wherein the protein translocase is selected from ClpX, VAT, PAN, AMA, 854, MBA and SAMP.

17~~20~~. An analytical system comprising a hydrophobic membrane separating a fluid chamber into a *cis* side and a *trans* side, said membrane comprising an artificial nanopore according to any one of claims 1-12~~14~~, or a multiprotein nanopore sensor complex according to any one of claims 13~~15~~-16~~19~~.

18~~21~~. A method for single molecule analysis, preferably for identification and/or sequencing of a biopolymer, more preferably for single molecule polypeptide or polynucleotide sequencing, comprising adding a biopolymer to be analyzed to the chamber of an analytical system according to claim 17~~20~~ and allowing the biopolymer to contact the pore.

19~~22~~. The use of an analytical system according to claim 17~~20~~, for single molecule analysis, preferably for identification and/or sequencing of a biopolymer, more preferably for single molecule polypeptide or polynucleotide sequencing.

20~~23~~. A nucleic acid molecule encoding a subunit of an artificial nanopore according to any one of claims 1-12~~14~~.

21~~24~~. An expression vector comprising a nucleic acid molecule according to claim 20~~23~~.

22~~25~~. A host cell comprising an expression vector according to claim 21~~24~~, optionally further comprising a distinct expression vector encoding a proteasome beta-subunit and/or a proteasome alpha-subunit.