Claims

1. An artificial nanopore comprising a multimeric assembly of subunits, wherein a subunit of the multimeric assembly of subunits comprises:

(i) a sequence of an engineered pore coupled to a sequence of a subunit of a ring-forming protein, wherein the engineered pore forming protein is a part and not an entirety of a ß-barrel pore forming protein or an α-helical pore forming protein, wherein the ring-forming protein is configured to effect translocation of a biopolymer through at least a portion of the artificial nanopore.

2. The artificial nanopore of claim 1, wherein the sequence of the engineered pore forming protein comprises a transmembrane (TM) sequence of an α-helical pore forming protein.

3. The artificial nanopore of claim 1, wherein the sequence of the engineered pore forming protein comprises a TM sequence of a ß-barrel pore forming protein.

4. The artificial nanopore of claim 3, wherein the TM sequence comprises the amino acid sequence VHGNAEVHASFFDIGGSVSAGF.

5. The artificial nanopore of any one of claims 1-4, wherein the sequence of the engineered pore forming protein is N-terminally or C-terminally fused to the sequence of the subunit of the ring-forming protein.

6. The artificial nanopore of any one of claims 1-4, wherein the sequence of the engineered pore forming protein is inserted within the sequence of the subunit of the ring-forming protein.

7. The artificial nanopore of any one of claims 1-5, wherein the sequence of the engineered pore forming protein is flanked on the N-

terminal side and/or C-terminal side by a flexible linker of at least 3 amino acids.

8. The artificial nanopore of any one of claims 1-7, wherein the ring-forming protein is a heptameric protein.

9. The artificial nanopore of claim 8, wherein the heptameric protein is configured to effect translocation of a polynucleotide or fragment thereof through the at least the portion of the artificial nanopore.

10. The artificial nanopore of claim 8, wherein the heptameric protein is configured to effect translocation of a polypeptide or fragment thereof through the at least the portion of the artificial nanopore.

11. The artificial nanopore of any one of claims 1-10, wherein a C-terminus of the sequence of the subunit of the ring-forming protein comprising the sequence of the engineered pore forming protein is coupled to an N-terminus of a sequence of proteasome α-subunit.

12. The artificial nanopore of any one of claims 1-11, wherein an N-terminus of the sequence of the subunit of the ring-forming protein comprising the sequence of the engineered pore forming protein is coupled to a C-terminus of a sequence of a Clp protease (ClpP) subunit.

13. A multi-protein nanopore sensor complex, comprising (i) the artificial nanopore of any one of claims 1-12, (ii) a proteasome activator, and (iii) one or two rings composed of proteasome α-subunits, or one or two rings composed of proteasome ß-subunits.

14. The multi-protein nanopore sensor complex of claim 13, wherein a proteasome ß-subunit of the one or two rings composed of proteasome ß-subunits is engineered to provide a distinct type of protease activity.

15. The multi-protein nanopore sensor complex of claim 13 or 14, further comprising a protein translocase which can bind, unfold, and

translocate the biopolymer through the multi-protein nanopore sensor complex in a sequential order.

16. The multi-protein nanopore sensor complex of claim 15, wherein the protein translocase is an NTP-driven unfoldase.

17. An analytical system comprising a hydrophobic membrane separating a fluid chamber into a *cis* side and a *trans* side, said hydrophobic membrane comprising the artificial nanopore of any one of claims 1-12, or the multiprotein nanopore sensor complex of any one of claims 13-16.

18. A method for single molecule analysis, comprising (a) adding the biopolymer to the fluid chamber of the analytical system of claim 17 and (b) contacting the biopolymer to the artificial nanopore.

19. A use of the analytical system of claim 17, for single molecule analysis.

20. A nucleic acid molecule encoding a subunit of the multimeric assembly of subunits of the artificial nanopore of any one of claims 1-12.

21. An expression vector comprising the nucleic acid molecule of claim 20.

22. A host cell comprising the expression vector of claim 21.

23. The artificial nanopore of any one of claims 1-12, wherein the ring-forming protein comprises a protein translocase.

24. The artificial nanopore of claim 23, wherein the protein translocase is selected from the group consisting of an AAA+ translocase, an AAA+ unfoldase, caseinolytic mitochondrial matrix peptidase chaperone subunit X (ClpX), VCP-like ATPase from Thermoplasma acidophilum (VAT), a proteasome-activating nucleotidase (PAN) from Methanococcus iannaschii (PAN), AAA protein from Archaeoglobus and methanogenic archaea

(AMA), open reading frame number 854 in the M. mazei genome (854), membrane-bound AAA (MBA) and small archaeal modifier protein (SAMP).

25. The artificial nanopore of any one of claims 1-12, wherein the ring-forming protein comprises a proteasome activator 28 (PA28) monomer, a proteasome activator 26 (PA26) monomer, an ATPase monomer, or a proteasome subunit, or any combination thereof.

26. The artificial nanopore of claim 2, wherein the sequence of the engineered pore forming protein is a sequence comprising a Fragaceatoxin C (FraC), Cytolysin A (ClyA), Aeromonas hydrophila B (AhlB), or Wza (translocon for E.coli capsular polysaccharides).

27. The artificial nanopore of claim 3, wherein the sequence of the engineered pore forming protein is a sequence comprising a α-hemolysin, aerolysin, or anthrax protective antigen.