CLAIMS

1. A nanopore, comprising:

   (i) at least a portion of an alpha helical pore forming protein or peptide, or (ii) at least a portion of a beta barrel pore forming protein or peptide, wherein the at least the portion of the beta barrel pore forming protein or peptide is not an alpha-hemolysin or is not an aerolysin, wherein the at least the portion of the alpha helical pore forming protein or peptide or the at least the portion of the beta barrel pore forming protein or peptide comprises (A) a first modification of one or more lumen facing amino acids into one or more natural or non-natural aromatic amino acids, and (B) a second modification of one or more amino acids configured to increase a net negative charge of the nanopore.
2. The nanopore of claim 1, wherein the nanopore comprises the at least the portion of the alpha helical pore forming protein or peptide.
3. The nanopore of claim 1 or claim 2, wherein the at least the portion of the alpha helical pore forming protein or peptide comprises an actinoporin.
4. The nanopore of claim 1, wherein the nanopore comprises the at least the portion of the beta barrel pore forming protein or peptide.
5. The nanopore of claim 1 or 4, wherein the at least the portion of the beta barrel pore forming protein or peptide comprises a cytolysin, leukocidin, bacterial outer membrane porin, or a de novo designed pore peptide.
6. The nanopore of any one of claims 1-5, wherein the first modification of the one or more lumen facing amino acids is within or adjacent to a constriction region of the nanopore.
7. The nanopore of claim 6, wherein the constriction region of the nanopore comprises an internal diameter of at most about 2 nanometers.
8. The nanopore of any one of claims 1-7, wherein the one or more lumen facing amino acids comprises an amino acid that is in contact with a central channel of the nanopore.
9. The nanopore of any one of claims 1-8, wherein the first modification comprises an amino acid sequence insertion, an amino acid sequence substitution, a chemical modification, a chemical ligation, a chemical functionalization, or a combination thereof.

10. The nanopore of any one of claims 1-9, wherein the nanopore comprises an increase in aromatic rings in the lumen of the nanopore, as compared to another nanopore without the first modification.
11. The nanopore of any one of claims 1-10, wherein the alpha helical pore forming protein comprises an amino acid sequence that is at least 80% identical to an amino acid sequence of Fragaceatoxin C.
12. The nanopore of any one of claims 1-11, wherein the at least the portion of the beta barrel pore forming protein or peptide comprises a Cytolysin K, lysenin, Anthrax toxin, Mycobacterium smegmatis porin A (MspA), Mycobacterium smegmatis porin B (MspB), Mycobacterium smegmatis porin C (MspC), Mycobacterium smegmatis porin D (MspD), outer membrane porin F (OmpF), outer membrane porin G (OmpG), outer membrane phospholipase A (OMPLA), ferric hydroxamate uptake component A (FhuA), Curli production transport component CsgG, or a Neisseria autotransporter lipoprotein (NalP).
13. The nanopore of any one of claims 1-12, wherein the first modification is at a first location and the second modification is at a second location different from the first location.
14. A method, comprising:
    (a) providing a system comprising (i) a fluidic chamber; (ii) a membrane that separates the fluidic chamber into a first side and a second side; and (iii) a nanopore disposed in the membrane,
    wherein the nanopore comprises (1) at least a portion of an alpha helical pore forming protein or peptide, or (2) at least a portion of a beta barrel pore forming protein or peptide, wherein the at least the portion of the beta barrel pore forming protein or peptide is not an alpha-hemolysin or is not an aerolysin, wherein the at least the portion of the alpha helical pore forming protein or peptide or the at least the portion of the beta barrel pore forming protein or peptide comprises a modification of one or more lumen facing amino acids into one or more natural or non-natural aromatic amino acids, wherein the system comprises a pH of less than 4.5; and
    (b) bringing the nanopore in contact with an analyte.

15. The method of claim 14, further comprising translocating the analyte through the nanopore.
16. The method of claim 15, further comprising measuring a signal generated by translocating the analyte through the nanopore.
17. The method of any one of claims 14-16, wherein the nanopore is brought in contact with the analyte using an electro-osmotic force.
18. The method of any one of claims 14-17, wherein the nanopore comprises the at least the portion of the alpha helical pore forming protein or peptide.
19. The method of any one of claims 14-18, wherein the at least the portion of the alpha helical pore forming protein or peptide comprises an actinoporin.
20. The method of any one of claims 14-19, wherein the nanopore comprises the at least the portion of the beta barrel pore forming protein or peptide.
21. The method of any one of claims 14-20, wherein the at least the portion of the beta barrel pore forming protein or peptide comprises a cytolysin, leukocidin, bacterial outer membrane porin, or de novo designed pore peptide.
22. The method of any one of claims 14-21, wherein the analyte comprises a non-nucleic acid analyte.
23. The method of any one of claims 14-22, wherein the analyte comprises a peptide, an oligopeptide, or a protein.
24. The method of any one of claims 14-23, wherein the at least the portion of the beta barrel pore forming protein or peptide comprises a Cytolysin K, lysenin, Anthrax toxin, Mycobacterium smegmatis porin A (MspA), Mycobacterium smegmatis porin B (MspB), Mycobacterium smegmatis porin C (MspC), Mycobacterium smegmatis porin D (MspD), outer membrane porin F (OmpF), outer membrane porin G (OmpG), outer membrane phospholipase A (OMPLA), ferric hydroxamate uptake component A (FhuA), Curli production transport component CsgG, or a Neisseria autotransporter lipoprotein (NalP).
25. The method of any one of claims 14-24, wherein the at least the portion of the alpha helical pore forming protein or peptide or the at least the portion of the beta barrel pore forming protein or peptide comprises a second modification of one or more amino acids configured to increase a net negative charge of the nanopore.