Claims

1. A mutant porin monomer comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1, wherein the amino acid sequence comprises amino acid mutations at one or more positions corresponding to 69-76, 64-79, 62, 63, 68, 69, 71, 75, 76, 104 or 68-76 of SEQ ID NO: 1, wherein the amino acid mutations are selected from the group consisting of:

(a) mutations in an amino acid sequence KPTPASSF corresponding to positions 69-76 of SEQ ID NO: 1 to $M_1M_2M_3M_4M_5M_6M_7M_8$, wherein M_1 is selected from 0 to 3 of R, K, and H; M_2 is selected from 0 to 1 of P; M_3 is selected from 0 to 10 of S, G, C, U, T, M, A, V, L, and I; M_4 is selected from 0 to 1 of P; M_5 is selected from 0 to 5 of A, G, V, L, and I; M_6 is selected from 0 to 5 of S, C, U, T, and M; M_7 is selected from 0 to 10 of A, T, G, V, L, I, S, C, U, and M; M_8 is selected from 0 to 7 of Q, D, E, N, K, H, and R;

(b) mutations in an amino acid sequence QTGQYKPTPASSFSTS corresponding to positions 64-79 of SEQ ID NO: 1 to $M_9M_{10}M_{11}M_{12}M_{13}M_{14}M_{15}M_{16}$ $M_{17}M_{18}M_{19}M_{20}M_{21}M_{22}M_{23}M_{24}$, wherein M_9 is selected from 0 to 5 of L, G, A, V, and I; M_{10} is selected from 0 to 5 of T, S, C, U, and M; M_{11} is selected from 0 to 5 of G, A, V, L, and I; M_{12} is selected from 0 to 4 of Q, D, E, and N; M_{13} is selected from 0 to 3 of Y, F, and W; M_{14} is selected from 0 to 3 of R, H, and K; M_{15} is selected from 0 to 1 of P; M_{16} is selected from 0 to 5 of S, C, U, T, and M; M_{17} is selected from 0 to 1 of P; M_{18} is selected from 0 to 5 of A, G, V, L, and I; M_{19} is selected from 0 to 5 of S, C, U, T, and M; M_{20} is selected from 0 to 5 of A, G, V, L, and I; M_{21} is selected from 0 to 9 of N, D, E, Q, L, G, A, V, and I; M_{22} is selected from 0 to 5 of S, C, U, T, and M; M_{23} is selected from 0 to 5 of T, S, C, U, and M; M_{24} is selected from 0 to 5 of A, G, V, L, and I;

(c) a mutation at an amino acid residue corresponding to position 62 of SEQ ID NO: 1 being 0 to 5 of S, C, U, T, and M; a mutation at an amino

acid residue corresponding to position 63 being 0 to 5 of V, G, A, L, and I; a mutation at an amino acid residue corresponding to position 68 being 0 to 2 of F and W; a mutation at an amino acid residue corresponding to position 69 being 0 to 2 of R and H; a mutation at an amino acid residue corresponding to position 71 being 0 to 4 of S, C, U, and M; a mutation at an amino acid residue corresponding to position 75 being 0 to 5 of A, G, V, L, and I; a mutation at an amino acid residue corresponding to position 76 being 0 to 4 of Q, D, E, and N; a mutation at an amino acid residue corresponding to position 104 being 0 to 5 of V, G, A, L, and I; and

(d) mutations in an amino acid sequence YKPTPASSF corresponding to positions 68-76 of SEQ ID NO: 1 to $M_{25}M_{26}M_{27}M_{28}M_{29}M_{30}M_{31}M_{32}M_{33}$, a mutation at position 171 being 0 to 3 of N, D, and Q, and a mutation at position 175 being 0 to 3 of N, E, and Q, wherein M_{25} is selected from 0 to 3 of F, Y, and W; M_{26} is selected from 0 to 3 of R, H, and K; M_{27} is selected from 0 to 1 of P; M_{28} is selected from 0 to 5 of S, C, U, T, and M; M_{29} is selected from 0 to 1 of P; M_{30} is selected from 0 to 5 of A, G, V, L, and I; M_{31} is selected from 0 to 5 of S, C, U, T, and M; M_{32} is selected from 0 to 5 of A, G, V, L, and I; M_{33} is selected from 0 to 4 of Q, D, E, and N.

2. The mutant porin monomer according to claim 1, wherein the amino acid mutations are selected from the group consisting of:

(a) mutations at positions 69-76 of SEQ ID NO: 1, wherein KPTPASSF is replaced with RPSPASAQ;

(b) mutations at positions 69-76 of SEQ ID NO: 1, wherein KPTPASSF is replaced with KPGPASTK;

(c) mutations at positions 64-79 of SEQ ID NO: 1, wherein QTGQYKPTPASSFSTS is replaced with LTGQYRPSPASANSTA;

(d) mutations at positions 64-79 of SEQ ID NO: 1, wherein QTGQYKPTPASSFSTS is replaced with LTGQYRPSPASALSTA;

(e) R62S, D63V, Y68F, K69R, T71S, S75A, F76Q, and E104V corresponding to SEQ ID NO: 1; and

(f) mutations at positions 68-76 of SEQ ID NO: 1, wherein YKPTPASSF is replaced with FRPSPASAQ, and E171N and D175N corresponding to SEQ ID NO: 1.

3. The mutant porin monomer according to claim 2, wherein the mutant porin monomer having the mutations of group (a) comprises an amino acid sequence set forth in SEQ ID NO: 24.

4. The mutant porin monomer according to claim 2, wherein the mutant porin monomer having the mutations of group (b) comprises an amino acid sequence set forth in SEQ ID NO: 26.

5. The mutant porin monomer according to claim 2, wherein the mutant porin monomer having the mutations of group (c) comprises an amino acid sequence set forth in SEQ ID NO: 27.

6. The mutant porin monomer according to claim 2, wherein the mutant porin monomer having the mutations of group (d) comprises an amino acid sequence set forth inSEQ ID NO: 28.

7. The mutant porin monomer according to claim 2, wherein the mutant porin monomer having the mutations of group (e) comprises an amino acid sequence set forth in SEQ ID NO: 29.

8. The mutant porin monomer according to claim 2, wherein the mutant porin monomer having the mutations of group (f) comprises an amino acid sequence set forth in SEQ ID NO: 30.

9. A protein pore comprising at least one mutant porin monomer according to any one of the preceding claims.

10. The protein pore according to claim 9, wherein the protein pore comprises at least two mutant porin monomers.

11. The protein pore according to any one of claims 9-10, wherein the protein pore has a pore channel diameter of a constriction zone of 0.7 nm to 2.2 nm, 0.9 nm to 1.6 nm, 1.4 nm to 1.6 nm, or 15.9 Å to 20.1 Å.

12. A complex for characterizing a target analyte, comprising the protein pore according to any one of claims 9-11 and a rate-controlling protein bound thereto.

13. A nucleic acid encoding the mutant porin monomer according to any one of claims 1-8, the protein pore according to any one of claims 9-11, or the complex according to claim 12, wherein the nucleic acid comprises a nucleotide sequence set forth in SEQ ID NO: 2.

14. A vector or a genetically engineered host cell comprising the nucleic acid according claim 13.

15. Use of the mutant porin monomer according to any one of claims 1-8, the protein pore according to any one of claims 9-11, the complex according to claim 12, the nucleic acid according to claim 13, or the vector or the genetically engineered host cell according to claim 14 in the detection of the presence, absence, or one or more characteristics of a target analyte or in the preparation of a product for detecting the presence, absence, or one or more characteristics of a target analyte.

16. A method for producing a protein pore or a polypeptide thereof, comprising transforming the host cell with the vector according to claim 14, and inducing the host cell to express the protein pore according to any one of claims 9-11 or the polypeptide thereof.

17. A method for determining the presence, absence, or one or more characteristics of a target analyte, comprising:

a. contacting the target analyte with the protein pore according to any one of claims 9-11, the complex according to claim 12, such that the target analyte moves relative to the protein pore; and

b. acquiring one or more measurements when the target analyte moves relative to the protein pore, thereby determining the presence, absence, or one or more characteristics of the target analyte.

18. The method according to claim 17, wherein the target analyte interacts with the protein pore present in a membrane, such that the target analyte moves relative to the protein pore.

19. A kit for determining the presence, absence, or one or more characteristics of a target analyte, comprising the mutant porin monomer according to any one of claims 1-8, the protein pore according to any one of claims 9-11, the complex according to claim 12, the nucleic acid according to claim 13, or the vector or the genetically engineered host cell according to claim 14.

20. A device for determining the presence, absence, or one or more characteristics of a target analyte, comprising the protein pore according to any one of claims 9-11 or the complex according to claim 12.

21. The use according to claim 15, the method according to claims 16-18,

the kit according to claim 19, or the device according to claim20, wherein the target analyte comprises a polysaccharide, a metal ion, an inorganic salt, a polymer, an amino acid, a peptide, a protein, a nucleotide, an oligonucleotide, a polynucleotide, a dye, a drug, a diagnostic agent, an explosive, or an environmental contaminant;

wherein the polynucleotide comprises DNA or RNA; and/or, the one or more characteristics are selected from (i) a length of the polynucleotide; (ii) an identity of the polynucleotide; (iii) a sequence of the polynucleotide; (iv) a secondary structure of the polynucleotide; and (v) whether the polynucleotide is modified; and/or, the rate-controlling protein in the complex comprises a polynucleotide binding protein.