CLAIMS

1. A Mnep monomer variant, characterized in that the Mnep monomer variant comprises an amino acid sequence with amino acid mutations of G92K, D93F, G95L and A104K based on SEQ ID NO: 1.

2. The Mnep monomer variant according to claim 1, characterized in that the Mnep monomer variant comprises an amino acid sequence of SEQ ID NO:18.

3. The Mnep monomer variant according to any one of claims 1-2, the nucleotide sequence encoding the Mnep monomer variant is shown in SEQ ID NO: 11.

4. The Mnep monomer variant according to any one of claims 1-3, the Mnep monomer variant also include mutations introducing cysteine to link molecules for sequencing.

5. The Mnep monomer variant according to claim 4, the molecules for sequencing comprise the nucleic acid binding proteins.

6. A construct comprising at least one Mnep monomer variant of any one of claims 1-5.

7. The construct according to claim 6, characterized in that the construct also comprises wild-type Mnep monomers.

8. The construct according to claim 6 or 7, characterized in that the construct comprises 1-20 Mnep monomer variants, wherein the Mnep monomer variants are identical or different; or the construct comprises 1-20 wild-type Mnep monomers.

9. The construct according to claim 7 or 8, characterized in that the Mnep monomer variant and the Mnep monomer variant, the wild-type Mnep monomer and the wild-type Mnep monomer, as well as the Mnep monomer variant and the wild-type Mnep monomer are covalently attached.

10. The construct according to any one of claims 6-9, characterized in that the construct comprises 4-10 identical or different Mnep monomer variants.

11. A porin comprising at least one Mnep monomer variant, characterized in that the Mnep monomer variant comprises an amino acid sequence with any one or more amino acid mutations of G92K, D93F, G95L and A104K based on SEQ ID NO: 1.

12. The porin according to claim 11, characterized in that the Mnep monomer variant comprises an amino acid sequence of SEQ ID NO:18.

13. The porin according to any one of claims 11-12, the nucleotide sequence encoding the Mnep monomer variant is shown in SEQ ID NO: 11.

14. The porin according to any one of claims 11-13, the Mnep monomer variant also include mutations introducing cysteine to link molecules for sequencing.

15. The porin according to claim 14, the molecules for sequencing comprise the nucleic acid binding proteins.

16. The porin according to any one of claims 11-15, characterized in that the porin comprises 1-20 Mnep monomer variants, wherein the Mnep monomer variants are identical or different.

17. The porin according to any one of claims 11-16, characterized in that the porin comprises wild-type Mnep monomers.

18. The porin according to any one of claims 11-17, characterized in that the porin comprises 1-20 wild-type Mnep monomers.

19. The porin according to any one of claims 11-18, characterized in that the porin comprises 4-10 identical or different Mnep monomer variants.

20. The porin according to any one of claims 17-19, characterized in that the Mnep monomer variant and the Mnep monomer variant, the wild-type Mnep monomer and the wild-type Mnep monomer, as well as the Mnep monomer variant and the wild-type Mnep monomer are covalently attached.

21. The porin according to any one of claims 11-20, characterized in that a pore channel diameter of a narrow region of the porin is less than 18.7Å.

22. The porin according to claim 21, characterized in that the pore channel diameter of the narrow region of the porin is less than 17.2Å.

23. A nucleotide sequence encoding the Mnep monomer variant of any one of claims 1-5, the construct of any one of claims 6-10 or the porin of any one of claims 11-22.

24. A vector comprising the nucleotide sequence of claim 23.

25. The vector according to claim 24, characterized in that the vector comprises a promoter operably linked to the nucleotide sequence encoding the Mnep monomer variant of any one of claims 1-5 or the construct of any one of claims 6-10 or the porin of any one of claims 11-22.

26. The vector according to claim 25, characterized in that the promoter is an inducible promoter or constitutive promoter, wherein the inducible promoter is an acetamide-inducible promoter.

27. The vector according to any one of claims 24-26, characterized in that the nucleotide sequence encoding the porin comprises a nucleotide sequence encoding the Mnep monomer variant.

28. The vector according to claim 27, characterized in that the nucleotide sequence encoding the porin also comprises at least one nucleotide sequence encoding the Mnep monomer variant and/or a wild-type Mnep monomer.

29. The vector according to claim 28, characterized in that the nucleotide sequence encoding the Mnep monomer variant and the nucleotide sequence encoding the Mnep monomer variant, the nucleotide sequence encoding the Mnep monomer variant and the nucleotide sequence encoding the wild-type Mnep monomer, or the nucleotide sequence encoding the wild-type Mnep monomer and the nucleotide sequence encoding the wild-type Mnep monomer are linked by sequence encoding amino acid linker.

30. A mutant bacterium expressing the Mnep monomer variant of any one of claims 1-5, the construct of any one of claims 6-10 or the porin of any one of claims 11-22.

31. A method for producing a Mnep porin, characterized in that the method comprises transforming the mutant bacterium of claim 30 with the vector of any one of claims 24-29 to induce the mutant bacterium to express the Mnep porin.

32. A method for characterizing a target polynucleotide, characterized in that the method comprises the steps of:

(a) contacting the target polynucleotide with the porin of any one of claims 11-22, so that the target polynucleotide sequence passes through the porin; and

(b) obtaining one or more characteristics of an interaction between the nucleotide and the porin when the target polynucleotide passes through the porin to characterize the target polynucleotide.

33. The method according to claim 32, characterized in that the step (a) also comprises a step of contacting the target polynucleotide with one or a combination of two or more of nucleic acid binding protein, helicase, polymerase, reverse transcriptase, translocase, exonuclease, telomerase and/or topoisomerase, which makes the translocation speed of the target polynucleotide sequence passes through the porin less than the translocation speed in the absence of the nucleic acid binding protein, helicase, polymerase, reverse transcriptase, translocase, exonuclease, telomerase and/or topoisomerase.

34. The method according to claim 32 or 33, characterized in that the method also comprises a step of applying a potential difference across the porin contacted with the target polynucleotide.

35. An application in characterizing the target polynucleotide of the porin of any one of claims 11-22, the Mnep monomer variant of any one of claims 1-5, the construct of any one of claims 6-10, the nucleotide sequence of claim 23, the vector of any one of claims 24-29 or the mutant bacterium of claim 30.

36. A kit for characterizing a target polynucleotide, characterized in that the kit comprises the porin of any one of claims 11-22, the Mnep monomer variant of any one of claims 1-5, the construct of any one of claims 6-10, the nucleotide sequence of claim 23, the vector of any one of claims 24-29 or the mutant bacterium of claim 30.

37. An apparatus for characterizing a target polynucleotide, characterized in that the apparatus comprises the porin of any one of claims 11-22, the Mnep monomer variant of any one of claims 1-5, the construct of any one of claims 6-10, the nucleotide sequence of claim 23, the vector of any one of claims 24-29 or the mutant bacterium of claim 30.