CLAIMS

1. Use of a bacterial composition comprising at least one naturally occurring or engineered bacterial strain in the manufacture of a medicament for the treatment of a cancer, wherein said at least one bacterial strain expresses the protein of SEQ ID No: 1 or a fragment thereof of at least 9 amino acids comprising at least one epitope selected from the group consisting of SEQ ID Nos: 13, 14, 55, 56, 62, 63 and 66, with the proviso that said at least one bacterial strain is different from (i) the *Enterococcus hirae* strain 13144 deposited on November 7, 2013 at the CNCM under the number I-4815, (ii) the *Enterococcus hirae* strain IGR7 deposited on August 31, 2017 at the CNCM under the number I-5224, and (iii) the *Enterococcus hirae* strain IGR11 deposited on November 27, 2017, at the CNCM under the number I-5261, and wherein said bacterial composition is to be administered in combination with an antineoplastic drug.

2. The use of claim 1, wherein said composition comprises at least one bacterial strain containing a prophage genome encoding a protein with at least 80, preferably at least 90 and more preferably at least 95% identity with the protein of SEQ ID No: 1.

3. The use of claim 1, wherein said composition comprises at least one strain harbouring a prophage genome with at least 80 and preferably at least 95% identity with the prophage of SEQ ID No: 2, so that the phage encoded by this prophage can *in vivo* infect the other strains of the composition and/or commensal bacteria of the gut microbiota of a subject in need thereof.

4. The use of claim 1, wherein said composition comprises bacteria selected from the group consisting of:

(i) any bacterial strain other than *Enterococcus hirae* strains CNCM I-4815, CNCM I-5224 and CNCM I-5261, wherein said bacterial strain expresses a protein with a fragment of at least 20, preferably at least 30 and more preferably at least 40 amino acids from the protein of SEQ ID No: 1 comprising at least one epitope selected from the group consisting of SEQ ID Nos: 13, 14, 55, 56, 62, 63 and 66, and

(ii) mixtures of at least two strains selected from the group consisting of the strains recited in (i) and *Enterococcus hirae* strains CNCM I-4815, CNCM I-5224 and CNCM I-5261, preferably a mixture of the strain I-4815 and the strains recited in (i).

5. The use of claim 1, wherein said composition further comprises *Enterococcus hirae* strain IGR4 deposited on November 27, 2017, at the CNCM under the number I-5260.

6. A method of increasing the immunogenicity of a bacterial strain, comprising *in vitro* introducing, into said strain, a nucleotide sequence encoding the protein of SEQ ID No: 1 or a fragment thereof comprising at least the peptides of SEQ ID Nos: 13 and 14, or a sequence encoding a peptide of at least 9, preferably at least 20 amino acids comprising at least one epitope selected from the group consisting of SEQ ID No: 55, 56, 62, 63 and 66.

7. The method of claim 6, comprising *in vitro* infecting bacteria of said strain with a bacteriophage encoding a protein with at least 80, preferably at least 90 and more preferably at least 95% identity with the protein of SEQ ID No: 1.

8. The method of claim 7, wherein said bacteriophage has a genome comprising a nucleotide sequence of SEQ ID NOs: 2 or a sequence having at least 90% or at least 95% identity thereto.

9. Use of a bacterial composition comprising an engineered bacterial strain which has been obtained by the method according to any of claims 6 to 8 and which is different from (i) the *Enterococcus hirae* strain 13144 deposited on November 7, 2013 at the CNCM under the number I-4815, (ii) the *Enterococcus hirae* strain IGR7 deposited on August 31, 2017 at the CNCM under the number I-5224, and (iii) the *Enterococcus hirae* strain IGR11 deposited on November 27, 2017, at the CNCM under the number I-5261, in the manufacture of a medicament for the treatment of a cancer.

10. The use of claim 9, wherein said bacterial strain is selected from the group consisting of *Escherichia coli*, *Enterococcus gallinarum, Enterococcus faecalis* and *Enterococcus hirae*.

11. The use of claim 9, for the treatment of a cancer in a HLA-A*0201 patient.

12. Use of the bacterial composition as defined in claims 1 to 5 and 9 to 11, in the manufacture of a medicament for the treatment of a cancer, wherein said bacterial composition is to be administered in combination with an antineoplastic drug capable of triggering the lytic cycle of a phage encoded by a prophage present in at least some bacteria of the composition.

13. The use of claim 12, wherein said bacterial composition is to be administered in combination with a CDK4/6 inhibitor.

14. The use of claim 12 or 13, wherein said bacterial composition is to be administered in combination with an immune checkpoint blocker.

15. Use of an immunogenic composition comprising an isolated polypeptide comprising a sequence of at least 9 consecutive amino acids from the protein of SEQ ID No: 1 selected from the group consisting of SEQ ID No: 55, 56, 62, 63 and 66 or a polynucleotide encoding the same, in the manufacture of an anticancer vaccine.

16. The use of claim 15, wherein the immunogenic composition comprises a peptide comprising the sequence of SEQ ID No: 63 or a polynucleotide encoding the same, wherein said anticancer vaccine is to be administered to a HLA-A*0201 patient.

17. A cell composition comprising antigen presenting cells (APC) which have been pulsed *ex vivo* with a bacterial composition according to any of claims 1 to 5 and 9 to 11 or with an immunogenic composition according to any of claim 15 to 16.

18. Use of a cell composition according to claim 17, in the manufacture of a medicament for treating a cancer.

19. An MHC multimer for isolating T-cells with high affinity for the protein of SEQ ID No: 1, characterized in that MHC molecules are bound to an epitope selected from the group consisting of SEQ ID No: 55, 56, 62, 63 and 66.

20. The MHC multimer of claim 19, which is a HLA-A*0201 multimer loaded with an antigenic peptide comprising SEQ ID No: 63.

21. Use of a bacteriophage composition in the manufacture of a medicament for treating a cancer, wherein said bacteriophage expresses a protein comprising at least one epitope selected from the group consisting of SEQ ID Nos: 13, 14, 55, 56, 62, 63 and 66and having at least 80, preferably at least 90 and more preferably at least 95% identity with the protein of SEQ ID No: 1, wherein said medicament is to be used as an adjuvant to an antineoplastic treatment.

22. The use of claim 21, wherein the bacteriophage present in said bacteriophage composition has a genome comprising a nucleotide sequence of SEQ ID No: 2 or a sequence having at least 90% or at least 95% identity thereto.

23. The use of any of claims 15 to 16, wherein said vaccine is to be administered in combination with a drug blocking an immune checkpoint.

24. The use of any of claims 18, 21 and 22, wherein said medicament is to be administered in combination with a drug blocking an immune checkpoint.

25. The use of any of claims 1 to 5 and 9 to 12, or the use of any of claims 15 to 16, 18, 21 and 22, in the manufacture of a medicament or of an anticancer vaccine for treating a cancer that expresses mRNA levels of GPD1L superior to levels expressed in paired normal tissues.

26. A screening method for identifying antineoplastic drugs, comprising assessing the ability of drug candidates to trigger the lytic cycle of the phage comprising the protein of SEQ ID No: 1 by incubating different concentrations of the drug candidates with bacteria from the strain CNCM I-4815 and measuring the phage excision at several time points of incubation.

27. A method of determining if a patient having a cancer is likely to be a good responder to a treatment by chemotherapy or immune checkpoint blockade, comprising assessing the presence, in a biological sample from said patient, of a sequence having at least 80% identity with the protein of SEQ ID No: 1, wherein if such a sequence is present in the sample, the patient is likely to respond to the treatment.

28. The method of claim 27, comprising the steps of

(i) cultivating a stool sample from said patient in aerobic conditions in a permissive medium to allow isolation of enterococci colonies,

(ii) performing a PCR in several cultivable isolated colonies with a pair of primers specific for a fragment of SEQ ID No: 1, and

(iii) detecting the amplified fragment.

29. An *in vitro* method of determining if a patient is likely to be a good responder to a treatment by chemotherapy or immune checkpoint blockade, comprising *in vitro* using the MHC multimer as defined in claim 19 or claim 20 to measure the levels of circulating $CCR9^+$ $CXCR3^+$ $CD8^+$ T cells specific to the protein of SEQ ID No: 1 at diagnosis and/or during said treatment in a biological sample from the patient, wherein if said level is above a predetermined threshold, the patient is likely to respond to the treatment.

30. The method of claim 29, wherein the patient is HLA-A*0201 and the MHC multimer is as defined in claim 20.

31. The method of any of claims 27 to 30, further comprising assessing the level of GPD1L mRNA or the level of GPD1L protein in the tumor, wherein if said level is above a predetermined threshold, the patient is likely to respond to the treatment.

32. A method of determining if a patient having a tumor is likely to be a good responder to a treatment by immune checkpoint blockade, comprising assessing the level of GPD1L mRNA or the level of GPD1L protein in the tumor, wherein if said level is above a predetermined threshold, the patient is likely to respond to the treatment.

33. Use of a bacterial composition as defined in any of claims 1 to 5 and 9 to 12 or an immunogenic composition as defined in any of claims 15 to 16, for the manufacture of a medicament for increasing the response to a treatment by chemotherapy or immune checkpoint blockade in a patient who has not been identified,

by a method of any of claims 27 to 32, as likely to be a good responder to a treatment by chemotherapy or immune checkpoint blockade.