

VACCINES AND THEIR USE

The present invention relates to vaccines and their use, and in particular to vaccines for meningococcal disease.

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The listing or discussion of a prior-published document in this specification should not necessarily be taken as an acknowledgement that the document is part of the state of the art or is common general knowledge. The documents listed in the specification are hereby incorporated by reference.

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Microbial infections remain a serious risk to human and animal health, particularly in light of the fact that many pathogenic microorganisms, particularly bacteria, are or may become resistant to anti-microbial agents such as antibiotics.

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Vaccination provides an alternative approach to combating microbial infections, but it is often difficult to identify suitable immunogens for use in vaccines which are safe and which are effective against a range of different isolates of a pathogenic microorganism, particular a genetically diverse microorganism.

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Although it is possible to develop vaccines which use as the immunogen substantially intact microorganisms, such as live attenuated bacteria which typically contain one or mutations in a virulence-determining gene, not all microorganisms are amenable to this approach, and it is not always desirable to adopt this approach for a particular microorganism where safety cannot always be guaranteed. Also, some microorganisms express molecules which mimic host

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proteins, and these are undesirable in a vaccine.

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A particular group of microorganisms for which it is important to develop further vaccines is *Neisseria meningitidis* which causes meningococcal disease, a life threatening infection which in the Europe, North America, developing countries and elsewhere remains an important cause of childhood mortality despite the introduction of the conjugate serogroup C polysaccharide vaccine. This is because infections caused by serogroup B strains (*NmB*), which express an α 2-8 linked

polysialic acid capsule, are still prevalent. The term “serogroup” in relation to *N. meningitidis* refers to the polysaccharide capsule expressed on the bacterium. The common serogroup in the UK causing disease is B, while in Africa it is A. Meningococcal septicaemia continues to carry a high case fatality rate; and survivors are often left with major psychological and/or physical disability. After a non-specific prodromal illness, meningococcal septicaemia can present as a fulminant disease that is refractory to appropriate anti-microbial therapy and full supportive measures. Therefore, the best approach to combating the public health menace of meningococcal disease is through prophylactic vaccination.

The non-specific early clinical signs and fulminant course of meningococcal infection mean that therapy is often ineffective. Therefore vaccination is considered the most effective strategy to diminish the global disease burden caused by this pathogen (Feavers (2000) ABC of meningococcal diversity. *Nature* **404**, 451-2). Existing vaccines to prevent serogroup A, C, W135, and Y *N. meningitidis* infections are based on the polysaccharide capsule located on the surface of bacterium (Anderson *et al* (1994) Safety and immunogenicity of meningococcal A and C polysaccharide conjugate vaccine in adults. *Infect Immun.* **62**, 3391-33955; Leach *et al* (1997) Induction of immunologic memory in Gambian children by vaccination in infancy with a group A plus group C meningococcal polysaccharide-protein conjugate vaccine. *J Infect Dis.* **175**, 200-4; Lieberman *et al* (1996). Safety and immunogenicity of a serogroups A/C *Neisseria meningitidis* oligosaccharide-protein conjugate vaccine in young children. A randomized controlled trial. *J. American Med. Assoc.* **275**, 1499-1503). Progress toward a vaccine against serogroup B infections has been more difficult as its capsule, a homopolymer of α 2-8 linked sialic acid, is a relatively poor immunogen in humans. This is because it shares epitopes expressed on a human cell adhesion molecule, N-CAM1 (Finne *et al* (1983) Antigenic similarities between brain components and bacteria causing meningitis. Implications for vaccine development and pathogenesis. *Lancet* **2**, 355-357). Indeed, generating immune responses against the serogroup B capsule might actually prove harmful. Thus,

there remains a need for new vaccines to prevent serogroup B *N. meningitidis* infections.

The most validated immunologic correlate of protection against meningococcal disease is the serum bactericidal assay (SBA). The SBA evaluates the ability of antibodies (usually IgG2a subclass) in serum to mediate complement deposition on the bacterial cell surface, assembly of the membrane attack complex, and bacterial lysis. In the SBA, a known number of bacteria are exposed serial dilutions of the sera with a defined complement source. The number of surviving bacteria is determined, and the SBA is defined as the reciprocal of the highest dilution of serum that mediates 50% killing. The SBA is predictive of protection against serogroup C infections, and has been widely used as a surrogate for immunity against *NmB* infections. Importantly the SBA is a ready marker of immunity for the pre-clinical assessment of vaccines, and provides a suitable endpoint in clinical trials.

Most efforts at *NmB* vaccine development are directed toward defining effective protein subunits. There has been a major investment in 'Reverse vaccinology', in which genome sequences are interrogated for potentially surface expressed proteins which are expressed as heterologous antigens and tested for their ability to generate meaningful responses in animals. However, this approach is limited by 1) the computer algorithms for predicting surface expressed antigens, 2) failure to express many of potential immunogens, and 3) the total reliance on murine immune responses.

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The key to a successful vaccine is to define antigen(s) that elicit protection against a broad range of disease isolates irrespective of serogroup or clonal group. A genetic screening method (which we have termed Genetic Screening for Immunogens or GSI) was used to isolate antigens that are conserved across the genetic diversity of microbial strains and this is exemplified in relation to meningococcal strains. This was done by identifying microbial antigens, such as *N. meningitidis* antigens, by GSI as described in more detail below; and validated

by assessing the function of the immune response elicited by the recombinant antigens and by evaluating the protective efficacy of antigens (see Examples and see PCT/GB2004/005441 (published as WO 2005/060995 on 7 July 2005) incorporated herein by reference). In essence, the GSI method relates to a method for identifying a polypeptide of a microorganism which polypeptide is associated with an immune response in an animal which has been subjected to the microorganism, the method comprising the steps of (1) providing a plurality of different mutants of the microorganism; (2) contacting the plurality of mutant microorganisms with antibodies from an animal which has raised an immune response to the microorganism or a part thereof, under conditions whereby if the antibodies bind to the mutant microorganism the mutant microorganism is killed; (3) selecting surviving mutant microorganisms from step (2); (4) identifying the gene containing the mutation in any surviving mutant microorganism; and (5) identifying the polypeptide encoded by the gene. It will be appreciated that by the way in which the polypeptides have been identified, they are highly relevant as antigenic polypeptides.

As described in more detail in the Examples, particular genes identified by the GSI method are the NBM0341 (TspA), NMB0338, NMB1345, NMB0738, NBM0792 (NadC family), NMB0279, NMB2050, NMB1335 (CreA), NMB2035, NMB1351 (Fmu and Fmv), NMB1574 (IivC), NMB1298 (rsuA), NMB1856 (LysR family), NMB0119, NMB1705 (rfak), NMB2065 (HemK), NMB0339, NMB0401 (putA), NMB1467 (PPX), NMB2056, NMB0808, NMB0774 (upp), NMA0078, NMB0337 (branched-chain amino acid transferase), NMB0191 (ParA family), NMB1710 (glutamate dehydrogenase (gdhA), NMB0062 (rfbA-1), NMB1583 (hisB), NMB0377, NMB0264, NMB1333, NMB1036, NMB1176, NMB1359 and NMB1138 genes of *Neisseria meningitidis*. The genome sequence for *N. meningitidis* is available, for example from The Institute of Genome Research (TIGR); www.tigr.org.

Although these genes form part of the genome that has been sequenced, as far as the inventors are aware, they have not been isolated, the polypeptides they encode

have not been produced (and have not been isolated), and there is no indication that the polypeptides they encode may be useful as a component of a vaccine.

Thus, the invention includes the isolated genes as above and in the Examples and
5 variants and fragments and fusions of such variants and fragments, and includes the polypeptides that the genes encode as described above, along with variants and fragment thereof, and fusions of such fragments and variants. Variants, fragments and fusions are described in more detail below. Preferably, the variants, fragments and fusions of the given genes above are ones which encode a
10 polypeptide which gives rise to neutralizing antibodies against *N. meningitidis*. Similarly, preferably, the variants, fragments and fusions of the polypeptide whose sequence is given above are ones which gives rise to neutralizing antibodies against *N. meningitidis*. The neutralising antibodies may be produced in any animal with an immune system, for example a rat, mouse or rabbit. The invention
15 also includes isolated polynucleotides encoding the polypeptides whose sequences are given in the Example (preferably the isolated coding region) or encoding the variants, fragments or fusions. The invention also includes expression vectors comprising such polynucleotides and host cells comprising such polynucleotides and vectors (as is described in more detail below). The polypeptides described in
20 the Examples are antigens identified by the method of the invention.

Molecular biological methods for use in the practice of the method of the invention are well known in the art, for example from Sambrook & Russell (2001) Molecular Cloning, a laboratory manual, third edition, Cold Spring Harbor
25 laboratory Press, Cold Spring Harbor, New York, incorporated herein by reference.

Variants of the gene may be made, for example by identifying related genes in other microorganisms or in other strains of the microorganism, and cloning,
30 isolating or synthesizing the gene. Typically, variants of the gene are ones which have at least 70% sequence identity, more preferably at least 85% sequence identity, most preferably at least 95% sequence identity with the genes as given

above. Of course, replacements, deletions and insertions may be tolerated. The degree of similarity between one nucleic acid sequence and another can be determined using the GAP program of the University of Wisconsin Computer Group.

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Variants of the gene are also ones which hybridise under stringent conditions to the gene. By "stringent" we mean that the gene hybridises to the probe when the gene is immobilised on a membrane and the probe (which, in this case is >200 nucleotides in length) is in solution and the immobilised gene/hybridised probe is
10 washed in 0.1 x SSC at 65°C for 10 min. SSC is 0.15 M NaCl/0.015 M Na citrate.

Fragments of the gene (or the variant gene) may be made which are, for example, 20% or 30% or 40% or 50% or 60% or 70% or 80% or 90% of the total of the
15 gene. Preferred fragments include all or part of the coding sequence. The variant and fragments may be fused to other, unrelated, polynucleotides.

The polynucleotide encodes a polypeptide which is immunogenic and is reactive with the antibodies from an animal which has been subjected to the
20 microorganism from which the gene was identified.

The antigen may be the polypeptide as encoded by the gene identified above, and the sequence of the polypeptide may readily be deduced from the gene sequence. In further embodiments, the antigen may be a fragment of the identified
25 polypeptide or may be a variant of the identified polypeptide or may be a fusion of the polypeptide or fragment or variant.

Thus, a particular aspect of the invention provides a polypeptide comprising the amino acid sequence selected from any one of SEQ ID Nos 2, 4, 6, 8, 10, 12, 14,
30 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68; or a fragment or variant thereof or a fusion of such a fragment or variant. Thus, the invention provides the following isolated proteins, or

fragments or variants thereof, or fusion of these: NMB0341, NMB1583, NMB1345, NMB0738, NMB0792, NMB0279, NMB2050, NMB1335, NMB2035, NMB1351, NMB1574, NMB1298, NMB1856, NMB0119, NMB1705, NMB2065, NMB0339, NMB0401, NMB1467, NMB2056,
5 NMB0808, NMB0774, NMA0078, NMB0337, NMB0191, NMB1710, NMB0062, NMB1333, NMB0377, NMB0264, NMB1036, NMB1176, NMB1359 and NMB1138 as described below.

Fragments of the identified polypeptide may be made which are, for example,
10 20% or 30% or 40 % or 50% or 60% or 70% or 80% or 90% of the total of the polypeptide. Typically, fragments are at least 10, 15, 20, 30, 40 , 50, 100 or more amino acids, but less than 500, 400, 300 or 200 amino acids. Variants of the polypeptide may be made. By "variants" we include insertions, deletions and substitutions, either conservative or non-conservative, where such changes do not
15 substantially alter the normal function of the protein. By "conservative substitutions" is intended combinations such as Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. Such variants may be made using the well known methods of protein engineering and site-directed mutagenesis.

20 A particular class of variants are those encoded by variant genes as discussed above, for example from related microorganisms or other strains of the microorganism. Typically the variant polypeptides have at least 70% sequence identity, more preferably at least 85% sequence identity, most preferably at least 95% sequence identity with the polypeptide identified using the method of the
25 invention.

The percent sequence identity between two polypeptides may be determined using suitable computer programs, for example the GAP program of the University of Wisconsin Genetic Computing Group and it will be appreciated that percent
30 identity is calculated in relation to polypeptides whose sequence has been aligned optimally.

The alignment may alternatively be carried out using the Clustal W program (Thompson *et al.*, (1994) *Nucleic Acids Res* **22**, 4673-80). The parameters used may be as follows:

Fast pairwise alignment parameters: K-tuple(word) size; 1, window size; 5, gap
5 penalty; 3, number of top diagonals; 5. Scoring method: x percent.

Multiple alignment parameters: gap open penalty; 10, gap extension penalty; 0.05.
Scoring matrix: BLOSUM.

The fusions may be fusions with any suitable polypeptide. Typically, the
10 polypeptide is one which is able to enhance the immune response to the
polypeptide it is fused to. The fusion partner may be a polypeptide that facilitates
purification, for example by constituting a binding site for a moiety that can be
immobilised in, for example, an affinity chromatography column. Thus, the
fusion partner may comprise oligo-histidine or other amino acids which bind to
15 cobalt or nickel ions. It may also be an epitope for a monoclonal antibody such as
a Myc epitope.

As discussed above, the variant polypeptides or polypeptide fragments, or fusions
of these, are typically ones which give rise to neutralizing antibodies against *N.*
20 *meningitidis*.

The invention also includes, therefore, a method of making an antigen as
described above, and antigens obtainable or obtained by the method.

25 The polynucleotides of the invention may be cloned into vectors, such as
expression vectors, as is well known on the art. Such vectors maybe present in
host cells, such as bacterial, yeast, mammalian and insect host cells. The antigens
of the invention may readily be expressed from polynucleotides in a suitable host
cell, and isolated therefrom for use in a vaccine.

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Typical expression systems include the commercially available pET expression
vector series and *E. coli* host cells such as BL21. The polypeptides expressed may

be purified by any method known in the art. Conveniently, the antigen is fused to a fusion partner that binds to an affinity column as discussed above, and the fusion is purified using the affinity column (eg such as a nickel or cobalt affinity column).

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It will be appreciated that the antigen or a polynucleotide encoding the antigen (such as a DNA molecule) is particularly suited for use as in a vaccine. In that case, the antigen is purified from the host cell it is produced in (or if produced by peptide synthesis purified from any contaminants of the synthesis). Typically the antigen contains less than 5% of contaminating material, preferably less than 2%, 1%, 0.5%, 0.1%, 0.01%, before it is formulated for use in a vaccine. The antigen desirably is substantially pyrogen free. Thus, the invention further includes a vaccine comprising the antigen, and method for making a vaccine comprising combining the antigen with a suitable carrier, such as phosphate buffered saline.

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Whilst it is possible for an antigen of the invention to be administered alone, it is preferable to present it as a pharmaceutical formulation, together with one or more acceptable carriers. The carrier(s) must be "acceptable" in the sense of being compatible with the antigen of the invention and not deleterious to the recipients thereof. Typically, the carriers will be water or saline which will be sterile and pyrogen free.

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The vaccine may also conveniently include an adjuvant. Active immunisation of the patient is preferred. In this approach, one or more antigens are prepared in an immunogenic formulation containing suitable adjuvants and carriers and administered to the patient in known ways. Suitable adjuvants include Freund's complete or incomplete adjuvant, muramyl dipeptide, the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminium hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic polyols or the Ribi adjuvant system (see, for example GB-A-2 189 141). "Pluronic" is a Registered Trade Mark. The patient to be immunised is a patient requiring to be protected from infection with the microorganism.

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The invention also includes a pharmaceutical composition comprising a polypeptide of the invention or variant or fragment thereof, or fusion of these, or a polynucleotide of the invention or a variant or fragment thereof or fusion of these, and a pharmaceutically acceptable carrier as discussed above.

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The aforementioned antigens of the invention (or polynucleotides encoding such antigens) or a formulation thereof may be administered by any conventional method including oral and parenteral (eg subcutaneous or intramuscular) injection. The treatment may consist of a single dose or a plurality of doses over a period of

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time.

It will be appreciated that the vaccine of the invention, depending on its antigen component (or polynucleotide), may be useful in the fields of human medicine and veterinary medicine.

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Diseases caused by microorganisms are known in many animals, such as domestic animals. The vaccines of the invention, when containing an appropriate antigen or polynucleotide encoding an antigen, are useful in man but also in, for example, cows, sheep, pigs, horses, dogs and cats, and in poultry such as chickens, turkeys,

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ducks and geese.

Thus, the invention also includes a method of vaccinating an individual against a microorganism, the method comprising administering to the individual an antigen (or polynucleotide encoding an antigen) or vaccine as described above. The

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invention also includes the use of the antigen (or polynucleotide encoding an antigen) as described above in the manufacture of a vaccine for vaccinating an individual.

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The antigen of the invention may be used as the sole antigen in a vaccine or it may be used in combination with other antigens whether directed at the same or different disease microorganisms. In relation to *N. meningitidis*, the antigen obtained which is reactive against NmB may be combined with components used

in vaccines for the A and/or C serogroups. It may also conveniently be combined antigenic components which provide protection against *Haemophilus* and/or *Streptococcus pneumoniae*. The additional antigenic components may be polypeptides or they may be other antigenic components such as a polysaccharide.
5 Polysaccharides may also be used to enhance the immune response (see, for example, Makela *et al* (2002) *Expert Rev. Vaccines* 1, 399-410).

It is particularly preferred in the above vaccines and methods of vaccination if the antigen is the polypeptide encoded by any of the genes as described above (and in
10 the Examples), or a variant or fragment or fusion as described above (or a polynucleotide encoding said antigen), and that the disease to be vaccinated against is *Neisseria meningitidis* infection (meningococcal disease).

The invention will now be described in greater detail by reference to the following
15 non-limiting Examples.

Example 1: Genetic screening for immunogens (GSI) in *N. meningitidis*

The application of GSI in this example involves screening libraries of insertional
20 mutants of *N. meningitidis* for strains which are less susceptible to killing by bactericidal antibodies. GSI is described in more detail in PCT/GB2005/005441 (published as WO 2005/060995 on 7 July 2005).

We have demonstrated the effectiveness of GSI by screening a library of mutants
25 of the sequenced NmB isolate, MC58, with sera raised in mice against a capsule minus of the same strain. A total of 40,000 mutants was analysed with sera raised in mice by intraperitoneal immunisation with the homologous strain; the SBA of this sera is around 2,000 against the wild-type strain. Surviving mutants were detected when the library was exposed to serum at a 1:560 dilution (which kills all
30 wild-type bacteria). To establish whether the transposon insertion in the surviving mutants was responsible for the ability to withstand killing, the mutations were backcrossed into the parental strain, and the backcrossed mutants were confirmed

as being more resistant to killing than the wild-type in the SBA. The sequence of the gene affected by the transposon was examined by isolating the transposon insertion site by marker rescue. We found that two of the genes affected were TspA and NMB0338. TspA is a surface antigen which elicits strong CD4+ T cell responses and is recognized by sera from patients (Kizil *et al* (1999) *Infect Immun.* 67, 3533-41). NMB0338 is a gene of previously unknown function which encodes a polypeptide that is predicted to contain two transmembrane domains, and is located at the cell surface. The amino acid sequence encoded by NMB0338 is:

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MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCGGVFIYGA
NMKLIYTVIKIIILLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFFVVGII
FGMFALFGRLLSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQP

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There are several practical advantages of using *NmB* for GSI aside from the public health imperative: a) the bacterium is genetically tractable; b) killing of the bacterium by effector immune mechanism is straightforward to assay; c) the genome sequences are available for three isolates of different serogroups and clonal lineages (IV-A, ET-5, and ET-37 for serogroups A, B, and C, respectively); and d) well-characterised clinical resources are available for this work.

GSI has two potential limitations. First, targets of bactericidal antibodies may be essential. This is unlikely as all known targets of bactericidal antibodies in *NmB* are non-essential, and no currently licensed bacterial vaccine targets an essential gene product. Second, sera will contain antibodies to multiple antigens, and, loss of a single antigen may not affect the survival of mutants. We have already shown that even during selection with sera raised against the homologous strain, relevant antigens were still identified using appropriate dilutions of sera.

The major advantages of GSI are that 1) the high throughput steps do not involve technically demanding or costly procedures (such as protein expression/purification and immunisation), and 2) human samples can be used in the assay rather than relying solely on animal data. GSI will rapidly pinpoint the

subset of surface proteins that elicit bactericidal activity, allowing more detailed analysis of a smaller number of candidates.

1. *Identification of targets of bactericidal antibodies using GSI*

5 Murine sera raised against heterologous strains, and human sera, are used to identify cross-reactive antigens. The sera are obtained from:

- i) mice immunised by the systemic route with heterologous strains: the strains will be selected and/or constructed to avoid isolates with the same immunotype and sub-serotype.
- 10 ii) acute and convalescent sera from patients infected with known isolates of *N. meningitidis* (provided by Dr R. Wall, Northwick Park)
- iii) pre- and post-immunisation samples (provided by the Meningococcal Reference Laboratory) from volunteers receiving defined outer membrane vesicle (OMVs) vaccines derived from the NmB isolate,
15 H44/76.

Each of these sources of sera has specific advantages and disadvantages.

Serum source	Advantages	Disadvantages
Murine	1) Defined antigenic exposure. 2) Use of genetically modified strains to generate immune response. 3) Naïve samples available 4) Examine individuals responses	1) Animal source of material
Patient sera	1) Human material 2) Known strain exposure 3) Acute and convalescent sera available	1) Background immunity 2) Limited material
Sera following immunisation with H4476 OMVs	1) Human material 2) Defined antigenic exposure 3) Pre and post immunisation sera available 4) Examine individuals responses	1) Background immunity 2) Limited material

a) Sera from animals immunised with heterologous strains (ie the sequenced serogroup A or C strains) are used in GSI to select the library of MC58 mutants. We have shown that immunisation with live, attenuated *NmB* elicits cross-reactive bactericidal antibody responses against serogroup A and C strains. The antigen absent in mutants with enhanced survival in the face of human sera are identified by marker rescue of the disrupted gene.

b) Mutations are identified that confer resistance against killing by heterologous sera, and it is determined whether the gene product is also a target for killing of the sequenced, serogroup A and C strains, Z2491 and FAM18 respectively. The genome databases are inspected for homologues of the genes. If a homologue is present, the transposon insertion is amplified from the MC58 mutant and introduced into the serogroup A and C strains by transformation. The relative survival of the mutant and wild-type strain of each serogroup are

compared. Thus, GSI can quickly give information whether the targets of bactericidal activity are conserved and accessible in diverse strains of *N. meningitidis*, irrespective of serogroup, immunotype and subserotype.

- 5 c) Mutants with enhanced survival against sera raised in mice are tested using human sera from either convalescent patients or vaccinees receiving heterologous OMV vaccines (derived from H44/76). This addresses the important question of whether the targets are capable of eliciting bactericidal antibodies in human. With other vaccine approaches, this information is only gained at the late, expensive
10 stage of clinical trials that requires GMP manufacture of vaccine candidates.

The advantages are that GSI is a high-throughput analysis performed using simple, available techniques. Antigens which elicit bactericidal antibodies in humans and which mediate killing of multiple strains can be identified rapidly as GSI is
15 flexible with respect to the bacterial strain and sera used. Mutants selected using human sera are analysed in the same way as those selected by murine sera.

2. *Assessment of the antibody response of recombinant GSI antigens*

- 20 Proteins which are targets of bactericidal antibodies that are recognised by sera from convalescent patients and vaccines are expressed in *E. coli* using commercially available vectors. The corresponding open reading frames are amplified by PCR from MC58, and ligated into vectors such as pCR Topo CT or pBAD/His, to allow protein expression under the control of a T7 or arabinose-
25 inducible promoter, respectively. Purification of the recombinant proteins from total cellular protein is performed via the His Tag fused to the C terminus of the protein on a Nickel or Cobalt column.

- Adult New Zealand White rabbits are immunized on two occasions separated by
30 four weeks by subcutaneous injection with 25 µg of purified protein with Freund's incomplete adjuvant. Sera from animals will be checked prior to immunisation for pre-existing anti-*Nm* antibodies by whole cell ELISA. Animals which have an

initial serum titre of <1:2 are used for immunisation experiments. Post-immunisation serum are obtained two weeks after the second immunisation. To confirm that specific antibodies have been raised, pre- and post-immunisation serum is tested by i) Western analysis against the purified protein and ii) ELISA using cells from the wild-type and the corresponding mutant (generated by GSI).

SBAs will be performed against MC58 (the homologous strain), and the sequenced serogroup A and C strains with the rabbit immune serum. The assay will be performed in triplicate on at least two occasions. SBAs of >8 will be considered significant. The results provide evidence of whether the protein candidates can elicit bactericidal antibodies as recombinant proteins.

3. *Establishing the protective efficacy of GSI antigens*

All the candidates are tested for their ability to protect animals against live bacterial challenge as this allows any aspect of immunity (cellular or humoral) to be assessed in a single assay. We have established a model of active immunisation and protection against live bacterial infection. In this model, adult mice are immunised on days 0 and 21, and on day 28 receive live bacterial challenge of 10^6 or 10^7 CFU of MC58 intraperitoneally in iron dextran (as the supplemental iron source). The model is similar to that described for evaluation of the protective efficacy of immunisation with Tbps Danve *et al* (1993) *Vaccine* **11**, 1214-1220. Non-immunised animals develop bacteraemia within 4 hours of infection, and show signs of systemic illness by 24 hours. We have already been able to demonstrate the protective efficacy of both attenuated *Nm* strains and a protein antigen against live meningococcal challenge; PorA is an outer membrane protein that elicits bactericidal antibodies, but which is not a lead vaccine candidate because of extensive antigenic variation (Bart *et al* (1999) *Infect Immun.* **67**, 3832-3846).

Six week old, BALB/c mice (group size, 35 animals) receive 25 µg of recombinant protein with Freund's incomplete adjuvant subcutaneously on days

day 0 and 21, then are challenged with 10^6 (15 animals) or 10^7 (15 animals) CFU of MC58 intraperitoneally on day 28. Two challenge doses are used to examine the vaccine efficacy at a high and low challenge dose; sera are obtained on day 28 from the remaining five animals in each group, and from five animals before the first immunisation and stored at -70°C for further immunological assays. Animals in control groups receive either i) adjuvant alone, ii) recombinant refolded PorA, and iii) a live, attenuated *Nm* strain. To reduce the overall number of animals in control groups, sets of five candidates will be tested at one time (number of groups = 5 candidates + 3 controls). Survival of animals in the groups is compared by Mann Whitney U Test. With group sizes of 15 mice/dose, the experiments are powered to show a 25% difference in survival between groups.

For vaccines which show significant protection against challenge, a repeat experiment is performed to confirm the finding. Furthermore, to establish that vaccination with a candidate also elicits protection against bacteraemia, levels of bacteraemia are determined during the second experiment; blood is sampled at 22 hr post-infection in immunised and un-immunised animals (bacteraemia is maximal at this time). The results are analysed using a two-tailed Student-T test to determine if there is a significant reduction in bacteraemia in vaccinated animals.

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Further materials and methods used

Mutagenesis of *Neisseria meningitidis*

For work with *Neisseria meningitidis*, mutants were constructed by *in vitro* mutagenesis. Genomic DNA from *N. meningitidis* was subjected to mutagenesis with a Tn5 derivative containing a marker encoding resistance to kanamycin, and an origin of replication which is functional in *E. coli*. These elements are bound by composite Tn5 ends. Transposition reactions were carried out with a hyperactive variant of Tn5 and the DNA repaired with T4 DNA polymerase and ligase in the presence of ATP and nucleotides. The repaired DNA was used to

transform *N. meningitidis* to kanamycin resistance. Southern analysis confirmed that each mutant contained a single insertion of the transposon only.

Serum bactericidal assays (SBAs)

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Bacteria were grown overnight on solid media (brain heart infusion media with Levantals supplement) and then re-streaked to solid media for four hours on the morning of experiments. After this time, bacteria were harvested into phosphate buffered saline and enumerated. SBAs were performed in a 1 ml volume, containing a complement source (baby rabbit or human) and approximately 10^5 colony forming units. The bacteria were collected at the end of the incubation and plated to solid media to recover surviving bacteria.

Isolating the transposon insertion sites

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Genomic DNA will be recovered from mutants of interest by standard methods and digested with *PvuII*, *EcoRV*, and *DraI* for three hours, then purified by phenol extraction. The DNA will then be self-ligated in a 100 microlitre volume overnight at 16°C in the presence of T4 DNA ligase, precipitated, then used to transform *E. coli* to kanamycin resistance by electroporation.

Example 2: Further screening and results thereof

GSI has been used to screen a library of approximately 40,000 insertional mutants of MC58. The library was constructed by *in vitro* Tn5 mutagenesis, using a transposon harbouring the origin of replication from pACYC184.

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MC58 was chosen as it is a serogroup B isolate of *N. meningitidis*, and the complete genome sequence of this strain is known.

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The library is always screened in parallel with the wild-type strain as a control, and the number of colonies recovered from the library and the wild-type is shown.

Selection with murine sera

Initially the library was analysed using sera from animals immunised with the
 5 attenuated strain YH102. Adult mice (Balb/C) received 108 colony forming units
 intra-peritoneally on three occasions, and sera was collected 10 days after the final
 immunisation,

The screen identified several mutants with enhanced resistance to serum killing:
 10 This was confirmed by isolating individual mutants, reconstructing the mutation in
 the original genetic background, and re-testing the individual mutants for their
 susceptibility to complement mediated lysis against the wild-type. The transposon
 insertions are in the following gene:

15 NMB0341 (TspA) DNA sequence

ATGCCCGCCGCGCGACTGCCCGCCGATGCCCGATGATGACGAAATTTACAGACTGTACG
 CGGTCAAACCGTATTTCAGCCGCCAACCCACAGGGGATACATCTTGAAAAACAACAGACAA
 ATCAAAGTATTGCCGCCTCCGTGCGAGTTGCCGCATCCTTTTCAGGCACATGCTGGACTG
 GGCGGACTGAATATCCAGTCCAACCTTGACGAACCCCTTTTCGGGCAGCATTACCGTAACC
 20 GGCGAAGAAGCCAAAGCCCTGCTAGGCGGGCGGCAGCGTTACCGTTTCCGAAAAAGGCCTG
 ACCGCCAAAGTCCACAAGTTGGGCGACAAAGCCGTCATTGCCGTTTCTTCCGAACAGGCA
 GTCCGCGATCCCGTCTGTTGTTCCGCATCGGCGCAGGCGCACAGGTACGCGAATACACC
 GCCATCCTCGATCCTGTGCGCTACTCGCCCAAAACCAATCTGCACTTTTCAGACGGCAAG
 ACACACCGCAAAACCGCTCCGACAGCAGAGTCCCAAGAAAAATCAAAACGCCAAAGCCCTC
 25 CGCAAAACCGATAAAAAAGACAGCGCGAAGCAGCCGTCAAACCGGCATACAAACGGCAAA
 ACCCATACCGTCCGCAAGGCGAAACGGTCAAACAGATTGCCGCCGCCATCCGCCCGAAA
 CACCTGACGCTCGAACAGGTTGCCGATGCGCTGCTGAAGGCAAACCCAAATGTTTCCGCA
 CACGGCAGACTGCGTGCGGGCAGCGTGCTTACATTCCGAATCTGAACAGGATCAAAGCG
 GAACAACCCAAACCGCAACCGGCGAAACCCAAAGCCGAAACCGCATCCATGCCGTCCGAA
 30 CCGTCCAAACAGGCAACGGTAGAGAAACCGGTTGAAAAACCTGAAGCAAAAGTTGCCGCG
 CCCGAAGCAAAAGCGGAAAAACCGGCCGTTGACCCGAACCTGTACCCGCTGCAAATACT
 GCCGCATCGGAAACCGCTGCCGAATCCGCCCCCCAAGAAGCCGCCGCTTCTGCCATCGAC
 ACGCCGACCGACGAAACCGGTAACGCCGTTTCCGAACCTGTGGAACAGGTTTCTGCCGAA
 GAAGAAACCGAAAGCGGACTGTTTGACGGTCTGTTTCGGCGGTTTCGTACACCTTGCTGCTT
 35 GCCGGCGGAGGCGCGGCATTAATCGCCCTGCTGCTGCTTTTGCGCCTTGCCCAATCCAAA
 CGCGCGCGCCGTACCGAAGAATCCGTCCCTGAGGAAGAGCCTGACCTTGACGACGCGGCA
 GACGACGGCATAGAAATCACCTTTGCCGAAGTCGAAACTCCGGCAACGCCCGAACCCGCT
 CCGAAAAACGATGTAAACGACACACTTGCCCTAGATGGGGAATCTGAAGAAGAGTTATCG
 40 GCAAAACAAACGTTTCGATGTGAAACCGATACGCCCTTCCAACCGCATCGACTTGATTTC
 GACAGCCTGGCAGCCGCGCAAAACGGCATTATATCCGGCGCACTTACGCAGGATGAAGAA
 ACCCAAAACGCGCGGATGCCGATTGGAACGCCATCGAATCCACAGACAGCGTGTACGAG
 CCCGAGACCTTCAACCCGTACAACCTGTGGAATCGTCATCGACACGCCCGAACCCGAA
 TCTGTGCCCCAACTGCCGAAAAACAAACCGGAAACCGTCGATACCGATTTCTCCGACAAC
 CTGCCCTCAAACAACCATATCGGCACAGAAGAAACAGCTTCCGCAAAACCTGCCTCACCC
 45 TCCGGACTGGCAGGCTTCTGAAAGGCTTCTCGCCCGAAACCATCTTGAAAAAACAGTT
 GCCGAAGTCCAAACACCGGAAGAGTTGCACGATTTCTGAAAGTGTACGAAACCGATGCC
 GTGCGGGAAACTGCGCCTGAAACGCCCGATTTCAACGCCCGCGCAGACGATTTGTCCGCA

TTGCTTCAACCTGCCGAAGCACCGTCCGTTGAGGAAAATATAACGGAAACCGTTGCCGAA
 ACACCCGACTTCAACGCCACCGCAGACGATTTGTCCGCATTACTTCAACCTTCTAAAGTA
 CCTGCCGTTGAGGAAAATGCAGCGGAAACCGTTGCCGATGATTTGTCCGCACTGTTGCAA
 CCTGCTGAAGCACCGGCCGTTGAGGAAAATGTAACGGAAACCGTTGCCGAAACACCCGAT
 5 TTCAACGCCACCGCAGACGATTTGTCCGCATTACTTCAACCTTCTGAAGCACCTGCCGTT
 GAGGAAAATGCAGCGGAAACCGTTGCCGATGATTTGTCCGCACTGTTGCAACCTGCTGAA
 GCACCGGCCGTTGAGGAAAATGCAGCGGAAATCACTTTGGAAACGCCTGATTCCAACACC
 TCTGAGGCAGACGCTTTGCCCGACTTCCTGAAAGACGGCGAGGAGGAAACGGTAGATTGG
 AGCATCTACCTCTCGGAAGAAAATATCCCAAATAATGCAGATACCAGTTCCCTTCGGAA
 10 TCTGTAGGTTCTGACGCGCCTTCCGAAGCGAAATACGACCTTGCCGAAATGTATCTCGAA
 ATCGGCGACCGCGATGCCGCTGCCGAGACAGTGCAGAAATTGCTGGAAGAAGCGGAAGGC
 GACGTACTCAAACGTGCCCAAGCATTGGCGCAGGAATTGGGTATTTGA

NBM0341 Protein sequence

15 MPAGRLPRRCPPMTKFTDCTRSNRIQPPTHRGIYILKNNRQIKLIAASVAVAASFQAHAGL
 GGLNIQSNLDEPFSGSITVTGEEAKALLGGGSVTVSEKGLTAKVHKLGDKAVIAVSSEQA
 VRDPVLVFRIGAGAQVREYTAILDPVGYSPKTKSALSDGKTHRKTAPTAESENQNAKAL
 RKTDKKDSANAAVKPAYNGKTHTVRKGETVKQIAAAIRPKHLTLEQVADALLKANPNVSA
 HGRLRAGSVLHIPNLNRIKAEQPKPQTAKPKAETASMPSEPSKQATVEKPVEKPEAKVAA
 20 PEAKAEKPAVRPEPVPAANTAASETAESAPOEAAAASIDTPTDETGNVSEPVEQVSAE
 EETESGLFDGLFGGSYTLALLAGGGAALIALLLLRLAQSKRARRTEESVPEEPPDLDDAA
 DDGIEITFAEVETPATPEPAPKNDVNDTLALDGESEEEELSAKQTFDVETDTPSNRIDLDF
 DSLAAQNGILSGALTQDEETQKRADADWNAIESTDSVYEPETFPNPNPVEIVIDTPEPE
 SVAQTAENKPEVTDFSDNLPSNNHIGTEETASAKPASPSGLAGFLKASSPETILEKTV
 25 AEVQTPEELHDFLKVYETDAVAETAPETPDFNAAADDLSALLQPAEAPSVENITETVAE
 TPDFNATADDLSALLQPSKVPVEENAAETVADDLSALLQPAEAPVEENVETETVAETPD
 FNATADDLSALLQPEAPAVEENAAETVADDLSALLQPAEAPAVEENAAETITLETDPDSNT
 SEADALPDFLKDGEETVDWSIYLSSENI PNNA DTSFPS SVGS DAPSEAKYDLAEMYLE
 IGDRDAAAETVQKLLEEAEGDVLKRAQALAQELGI

NMB0338 DNA sequence

ATGGAAAGGAACGGTGTATTTGGTAAAATTGTGCGCAATCGCATACTCCGTATGTCGTCC
 GAACACGCTGCCGCATCCTATCCGAAACCGTGCAAATCGTTTAAACTAGCGCAATCTTGG
 TTCAGAGTGCGAAGCTGTCTGGGCGGCGTTTTTTATTTACGGAGCAAACATGAAACTTATC
 35 TATACCGTCATCAAATCATTATCCTGCTGCTCTTCCTGCTGCTTGCCGTCATTAATACG
 GATGCCGTTACCTTTTCTACCTGCCGGGGCAAAAATTCGATTTGCCGCTGATTGTCGTA
 TTGTTCCGGCGCATTTGTAGTCGGTATTATTTTGGAAATGTTGCCTTGTTCCGACGGTTG
 TTGTCGTTACGTGGCGAGAACGGCAGGTTGCGTGCCGAAGTAAAGAAAAATGCGCGTTTG
 ACGGGGAAGGAGCTGACCGCACCCACGGCGCAAAATGCGCCCGAATCTACCAAACAGCCT
 40 TAA

NMB0338 Protein sequence

45 MERNGVFGKIVGNRI LRMSSEHAAASYPKPKSFKLAQSWFRVRSCLGGVFIYGANMKLI
 YTVIKII ILLFLLLAVINTDAVTF SYLPQGKFDLPLIVVLFGAFVVGII FGMFALFGRLL
 LSLRGENGR LRAEVKKNARLTGKELTAPPAQNAPESTKQP

Analysis of the polypeptide indicates that it is predicted to have two membrane
 spanning domains, from residues 54 to 70 and 88 to 107. Thus, fragments from
 the regions 1 to 53, and 108 to the end (C-terminal) may be particularly useful as
 50 immunogens.

NMB1345 DNA sequence

ATGAAAAAACCTTTGATTTCCGTTGCCGCAGCATTGCTCGGCGTTGCTTTGGGCACGCCT
 TATTATTTGGGTGTCAAAGCCGAAGAAAGCTTGACGCAGCAGCAAAAAATATTGCAGGAA

ACGGGCTTCTTGACCGTCGAATCGCACCAATATGAGCGCGGCTGGTTTACCTCTATGGAA
 ACGACGGTCATCCGTCTGAAACCCGAGTTGCTGAATAATGCCGAAAATACCTGCCGGAT
 AACCTGAAAACAGTGTGGAACAGCCGTTACGCTGGTTAACCATATCACGCACGGCCCT
 TTCGCCGGCGGATTTCGGCACGCAGGCGTACATTGAAACCGAGTTCAAATACGCGCCTGAA
 5 ACGGAAAAAGTTCTGGAACGCTTTTTTGGAAAACAAGTCCCGGCTTCCCTTGCCAATACC
 GTTTATTTTAAACGGCAGCGGTAAAATGGAAGTCAGTGTTCCCGCCTTCGATTATGAAGAG
 CTGTCCGGCATCAGGCTGCACTGGGAAGGCCTGACGGGAGAAACGGTTTATCAAAAAGGT
 TTCAAAGCTACCGGAACGGCTATGATGCCCCCTTGTTTAAAATCAAGCTGGCAGACAAA
 GGCGATGCCGCGTTTGA AAAAGTGCATTTTCGATTTCGAAACTTCAGACGGCATCAATCCG
 10 CTTGCTTTGGGCAGCAGCAATCTGACCTTGGAAAAATTCTCCCTAGAATGGAAAGAGGGT
 GTCGATTACAACGTCAAGTTAAACGAACTGGTCAATCTTGTTACCGATTTCAGATTGGC
 GCGTTTATCAATCCCAACGGCAGCATCGCACCTTCCAAAATCGAAGTCGGCAAACCTGGCT
 TTTTCAACCAAGACCGGGGAATCAGGCGCGTTTATCAACAGTGAAGGGCAGTTCCGTTTC
 GATACACTGGTGTACGGCGATGAAAAATACGGCCCCGCTGGACATCCATATCGCTGCCGAA
 15 CACCTCGATGCTTCTGCCTTAACCGTATTGAAACGCAAGTTTGACACAAATTTCCGCCAAA
 AAAATGACCGAGGAACAAATCCGCAATGATTTGATTGCCGCCGTCAAAGGAGAGGCTTCC
 GGACTGTTACCAACAATCCCGTATTGGACATTA AAACTTTCCGATTTCAGCTGCCATCG
 GGAAAAATCGATGTGGGCGGAAAAATCATGTTTAAAGACATGAAGAAGGAAGATTTGAAT
 CAATTGGGTTTGATGCTGAAGAAAACCGAAGCCGACATCAGAATGAGTATTTCCCAAAAA
 20 ATGCTGGAAGACTTGGCGGTCAAGCAGGCAATATTTTCAGCGTCAATGCCGAAGAT
 GAGGCGGAAGGCAGGGCAAGTCTTGACGACATCAACGAGACCTTGCGCCTGATGGTGGAC
 AGTACGGTTCAGAGTATGGCAAGGGAAAAATATCTGACTTTGAACGGCGACCAGATTGAT
 ACTGCCATTTCTCTGAAAAACAATCAGTTGAAATTGAACGGTAAAACGTTGCAAAACGAA
 CCGGAGCCGGATTTTGATGAAGGCGGTATGTTTCAGAGCCGCAGCAGTAA
 25

NMB1345 Protein sequence

MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQETGFLTVESHQYERGWFTSME
 TTVIRLKPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
 TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
 30 FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
 VDYNVKLNELVNLVTDLQIGAFINPNSIAPSKIEVGKLAFTSTKTGESGAFINSEGQFRF
 DTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEAS
 GLFTNNPVLDIKTRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
 MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQID
 35 TAISLKNQLKLNGKTLQNEPEPDFDEGGMVSEPOQ

Selection with vaccinees sera

40 Sera from the Meningococcal Reference Laboratory in Manchester has been made
 available to us. This sera has come from a clinical trial of OMV immunisation of
 volunteers.

Mutants selected by vaccinee C1 sera (screened once)

45

The following sequences were isolated

NMB0338 (as above)

NMB0738 DNA sequence

ATGAAGATCGTCCTGATTAGCGGCCTGTCCGGTTCGGGCAAGTCCGTGCGACTGCGCCAA
 ATGGAAGATTCGGGTTATTTCTGCGTGGACAATTTGCCTTTGGAAATGTTGCCCCGCGCTG
 GTGTCGTATCATATCGAACGTGCGGACGAAACCGAATTGGCGGTGAGCGTCGATGTGCGT
 5 TCCGGCATTGACATCGGACAGGCGCGGGAACAGATTGCCTCTCTGCGCAGACTGGGGCAC
 AGGGTTGAAGTTTGTGTTGTCGAGGCGGAAGAAAGCGTGTGGTCCGCCGGTTTTCCGAA
 ACCAGGCGAGGACATCCTCTGAGCAATCAGGATATGACCTTGTGGAAAGCTTAAAGAAA
 GAACGGGAATGGCTGTTCCCGCTTAAAGAAATCGCCTATTGTATCGACACTTCCAAGATG
 AATGCCCAACAGCTCCGCCATGCAGTCCGGCAGTGGCTGAAGGTCGAACGTACCGGGCTG
 10 CTGGTGATTTTGGAGTCCTTCGGGTTCAAATACGGTGTGCCGAACAACGCGGATTTTATG
 TTCGATATGCGCAGCCTGCCCAACCCGTATTACGATCCCGAGTTGAGGCCTTACACCGGT
 ATGGACAAGCCCGTTTGGGATTATTTGGACGGACAGCCGCTTGTGCAGGAAATGGTTGAC
 GACATCGAAAGGTTTGTACGCATTGGTTACCGCGTTTGGAGGATGAAAGCAGGAGCTAC
 GTTACCGTCGCCATCGGTTGCACGGGAGGACAGCACCCTTCGGTCTATATTGTGCAAAAA
 15 CTCGCCCCAAGGTTGAAAGGGCGTTATGAATTGCTGATACGGCACAGACAGGCGCAAAAC
 CTGTCAGACCGCTAA

NMB0738 Protein sequence

MKIVLISGLSGSGKSVALRQMEDSGYFCVDNLPLEMLPALVSYHIERADETELAVSVDVR
 20 SGIDIGQAREQIASLRRLGHRVEVLVFEAEESVLVRRFSETRRGHPLSNQDMTLLESLLK
 EREWLFPLKEIAYCIDTSKMNAQQLRHAVRWLKVVERTGLLVILESFQFKYGVNNADFM
 FDMRSLPNFYDPFLRPYTGMDKPVWDYLDGQPLVQEMVDDIERFVTHWLPRLEDESRSY
 VTVAIGCTGGQHRSVYIVEKLARRLKGRYELLIRHRQAQNLSDR

NMB0792 NadC family (transporter) DNA sequence

ATGAACCTGCATGCAAAGGACAAAACCCAGCATCCCGAAAACGTGAGCTGCTCAGTGCG
 CAGAAGCCGATTACCGACTTTAAGGGCCTGCTGACCACCATTTATTTCCGCCGTCGTCTGT
 TTCGGCATTACACATCCTGCCTTACAGCCCCGATGCCAATAAAGGTATCGCGCTGCTG
 ATTTTCGTTGCCGCACTTTGGTTTACCGAGGCCGTCCACATTACCGTAACCGCACTGATG
 30 GTGCCGATTCTCGCCGTGCTACTCGGTTTTCCCGACATGGACATCAAAAAGGCGATGGCT
 GATTTTTCCAACCCGATTATCTACATTTTTTTTCGGCGGCTTCGCGCTTGCCACCGCCCTG
 CATATGCAGCGGCTGGACCGTAAAATCGCCGTGAGCCTGTTGCGCCTGTCGCGCGGCAAT
 ATGAAAGTGGCGGTTTTGATGTTGTTCCCTCGTTACCGCCTTTCTGTCCATGTGGATCAGC
 AACACCGCCACCGCCGCGATGATGCTGCCTCTAGCAATGGGTATGCTGAGCCACCTCGAC
 35 CAGGAAAAAGAACACAAAACCTACGTCTTCTCTGCTCGGCATCGCCTATTGCGCCAGC
 ATCGGCGGCTTGGGCACGCTCGTCGGCTCGCCGCCAACCTGATTGCCGCCAAAGCCCTA
 AATCTGGACTTCGTCGGCTGGATGAAGCTCGGCCTGCCGATGATGCTGTTGATTCTGCC
 TTGATGCTGCTCTCCCTGTACGTCATCCTCAAACCTAATTTGAACGAACGCGTGGAATC
 AAAGCCGAATCCATCCCTTGGACGCTGCACCGCGTGATCGCGCTGTTGATTTTCTTGCC
 40 ACAGCCGCGCGCTGGATATTACGCTCCAAAATCAAAACCGCCTTCGGCATTTCGAATCCC
 GACACCGTTATCGCCCTGAGTGCCGCGCTCGCCGTGCTCGTCTTCGGCGTGCGCAATGG
 AAGGAAGTCGCCCGCAATACCGACTGGGGCGTGTGATGCTCTTCGGCGGCGGCATCAGC
 CTGAGCACGCTGTTGAAAACATCCGGCGCGTCCGAAGCCTTGGGACAGCAGGTTGCCGCC
 ACCTTTTCCGGCGCGCCCGCATTTTTTGGTGATACTCATCGTCGCCGCTTCATTATTTTT
 45 CTGACCGAGTTCACCAGCAACACCGCCTCCGCCGATTGCTTGTACCGATTTTCTCCGGC
 ATCGCTATGCAGATGGGGCTGCCCGAACAAGTCTTGGTATTTCGTATCGGCATCGGCGCA
 TCTTGTGCCTTCATGCTGCCGTTGCCACACCGCCTAACGCGATTGTGTTCCGGCACGGGC
 TTAATCAAGCAACGCGAAATGATGAATGTCGGCATACTGCTGAACATCCTCTGCGTAGTA
 TTGGTTGCTCTGTGGGCTTATGCTGTACTGATGTAA

NMB0792 Protein sequence

MNLHAKDKTQHPENVELLSAQKPITDFKLLTTIISAVVCFGIYHILPYSPDANKGIAL
 IFVAALWFTEAVHITVTALMPILAVVLGFPDMDIKKAMADFSNPITYIFFGGFALATAL
 HMQRDLDRKIAVSLRLSRGNMKVAVLMLFLVTAFLSMWISNTATAAMMLPLAMGMLSHLD
 55 QEKEHKTYVFLLLGIAYCASIGGLGTLVGSPNLI AAKALNLD FVGWMKLG LPMMLLILP
 LMLLSLYVILKPNLNERVEIKAESIPWTLHRVIALLI FLATAAAWIFSSKI KTAFGISNP
 DTVIALSAAVAVVFGVAQWKEVARNTDWGVLMFLGGGISLSTLLKTS GASEALGQQVAA
 TFSGAPAFVLIVLIVAAFIIFLTFEFTSNTASAALLVPIFSGIAMQMGLPEQVLVVFVIGIGA

SCAFMLPVATPPNAIVFGTGLIKQREMMNVGILLNILCVVLVALWAYAVLM

NMB0279 DNA sequence

ATGCAACGACAAATCAAACGAAAAATTGGCTTCAGACCGTTTATCCCGAACGGGACTTC
 5 GATCTGACTTTTGC GGCGGGCGGATGCTGATTTCCGCCGCTATTTCCGTGCAACGTTTTCA
 GACGGCAGCAGTGTCTGCTGATGGATGCACCGCCCGACAAGATGAGTGTGCGACCTTAT
 TTGAAAGTGCAGAACTGTTTGACATGGTCAATGTGCCGCAGGTATTGCACGCGGACACG
 GATCTGGGGTTTGTGGTATTGAACGACTTGGGCAATACGACGTTTTTGACCGCAATGCTT
 CAGGAACAGGGCGAAACGGCGCACAAAGCCCTGCTTTTGGAGGCAATCGGCGAGTTGGTC
 10 GAATTGCAGAAGGCGAGCCGTGAAGGGGTTTTGCCGAATATGACCGTGAAACGATGTTG
 CGCGAAATCAACCTGTTCCCGGAATGGTTTTGTCGAAAAGAATTGGGGCGCGAATTAACA
 TTCAAACAACGCCAACTTTGGCAGCAAACCGTCGATACGCTGCTGCCGCCCTGTTGGCG
 CAGCCCAAAGTCTATGTGCACCGCGACTTTATCGTCCGCAACCTGATGCTGACGCGCGGC
 AGGCCGGGCGTTTTAGACTTCCAAGACGCGCTTTACGGCCCGATTTCTACGATTTGGTG
 15 TCGCTGTTGCGCGATGCCTTTATCGAATGGGAAGAAGAATTTGTCTTGGACTTGGTTATC
 CGCTACTGGGAAAAGGCGCGGGCTGCCGGCTTCCCGTCCCGAAGCGTTTGACGAGTTT
 TACCGCTGGTTTCAATGGATGGGCGTGCAGCGGCACTTGAAGGTTGCAGGCATCTTCGCA
 CGCCTGTACTACCGCGACGGCAAAGACAAATACCGTCCGGAATCCCGCGTTTTCTTAAAC
 TATCTGCGCCGCGTATCGCGCCGTTATGCCGAACCTCGCCCCGCTCTACGCGCTCTTGGTC
 20 GAACTGGTCGGCGATGAAGAACTGGAACGGGCTTTACGTTTTAA

NMB0279 Protein sequence

MQRQIKLKNWLQTVYPERDFDLTFAAADADFRRYFRATFSDGSSVVCMDAPDPKMSVAPY
 LKVQKLFDMVNPQVLHADTDLGFVVLNDLGNNTTFLTAMLQEQGETAHKALLLEAIGELV
 25 ELQKASREGVLPEYDRETMREINLFPWFVAKELGRELTFKQRLWQQTVDTLPLPLLA
 QPKVYVHRDFIVRNLMLTRGRPGVLDFODALYGPISYDLVSLLRDAFIEWEEEFVLDLVI
 RYWEKARAAGLPVPEAFDEFYRWFWMGVQRHLKVAGIFARLYYRDGKDKYRPEIPRFLN
 YLRRVSRRYAELAPLYALLVELVGDEELETGFTF

30 NMB2050 DNA sequence

ATGGAAGTATGACTGTTTTGCTGCCTTTGGCGGCGTTGGTGTCGGGCGTGTTGTTTACA
 TGGTTGCTGATGAAGGGCCGTTTCAGGGCGAGTTTGCCGGTTTGAACGCGCACCTGGCG
 GAAAAGGCGGCAAGATGTGATTTTGTGAACAGGCACACGGCAAACCGTGTCGAATTG
 GCGGTGTTGGACGGGAAATACCGGCATTTGCAGGACGAAAATTATGCTTTGGGCAACCGT
 35 TTTTCCGCAGCCGAAAAGCAGATTGCCCATTTGCAGGAAAAGAGGCGGAGTCGGCGCGG
 CTGAAGCAGTCTATATCGAGTTGCAGGAAAAGGCACAGGGTTTGGCGGTTGAAAACGAA
 CGTTTTGGCAACGATCGGACAGGAACGGAAGGCGTTTGCCGACCAATATGCCTTGGA
 CGCCAAATCCGCCAAAGAATCGAAACCGATTTGGAAGAAAGCCGCAAACTGTCCGCGAC
 GTGCAAAACGACCTTTCCGATGTGCGCAACCGTTTTGCCGAGCCGAAAAACAGATTGCC
 40 CATTTGCAGGAAAAGAGGCGGAAGCGGAGCGGTTGAGGCAGTCGCATACCGAGTTGCAG
 GAAAAGGCACAGGGTTTGGCGGTTGAAAACGAACGTTTGGCAACGCAATCGAACAGGAA
 CGCCTTGCTTCTGAAGAGAAGCTGTCTTGTGCGGAGGCGCGCAAAAGTTTGAAGCAGT
 CAGTTTCAAATCTTGCCAACACGATTTTGAAGAAAAAAGCCCGCTTTTACCGAGCAG
 AACC GCGAGCAGCTCCATCAGGTTTTGAACCGCTAAACGAACGCATCCACGGTTTCGCG
 45 GAGTTGGTCAAGCAAACCTATGATAAAGAATCGCGCGAGCGGCTGACGTTGGAAAACGAA
 TTGAAACGGCTTCAGGGGTTGAACGCGCAGCTGCACAGCGAGGCAAAGGCCCTGACCAAC
 GCGCTGACCGGTACGCAGAATAAGGTTTCAAGGGGCGGAATATGTGGTTTCAAGCGGCATCCGTC
 GTTTTGGAAAATTCGGGCCCTTCAGAAAGGGCGGGAATATGTGGTTTCAAGCGGCATCCGTC
 CGAAAAGAGGAAGACGGCGGCACGCGCCGCTCCAGCCCGACGTTTTTGGTCAACCTGCCC
 50 GACAACAAGCAGATTGTGATTGATTCGAAGGTCTCGCTGACAGCTTATGTGCGCTACACG
 CAGGCGGCGGATGCGGATACGGCGGCACGCGAACTGGCGGCACACGTTGCCAGCATCCGT
 GCACACATGAAAGGCTTGTGCTGAAGGATTACACCGATTTGGAAGGTGTGAACACATTG
 GATTTTCGTCTTTATGTTTATCCCTGTGCAACCGGCCTACCTGTTGGCGTTGCAGAAATGAC
 GCGGGCTTGTTCGAAGAGTGTTCGACAAACGGATTATGCTGGTCGGCCCCAGTACGCTG
 55 CTGGCGACTTTGAGGACGGTGGCGAATATTTGGCGCAACGAACAGCAAAATCAGAACGCA
 CTGGCGAATTGCGGACGAAGGCGGCAAGCTGTACGACAAGTTTGTGCGGCTTCGTACAGACG
 CTCGAAAGCGTCCGCAAGGCATCGATCAGGCGCAAAGCAGTTTTTCAACGGCATTCAG
 CAACTTGCCGAAGGGCGCGGAATCTGGTCGGACGCGCCGAGAACTGCGTCTGTTGGGC

GTGAAGGCAGGCAAACAACCTTCAACGGGATTTGGTCGAGCGTTCCAATGAAACAACGGCG
TTGTCTGGAATCTTTGGAATACGCGGCAGAGATGAAGCAGTCTGA

NMB2050 Protein sequence

5 MELMTVLLPLAALVSGVLF¹TWLLMKGRFQGEFAGLNAHLAEKAARCDFVEQAHGKTVSEL
AVLDGKYRHLQDENYALGNRFSAAEKQIAHLQEKEAESARLKQSYIELQEKAQGLAVENE
RLATQLGQERKAFADQYALERQIRQRIETDLEESRQTVRDVQNDLSDVGNRFAAAEKQIA
HLQEKEAEAEERLRQSHTELQEKAQGLAVENERLATQIEQERLASEEKL¹⁰SLLGEARKSLSD
QFQNLANTILEEKSRRFTEQNREQLHQVLNPLNERIHGFGELVKQTYDKESRERL¹⁵TLNE
LKRLLQGLNAQLHSEAKALT²⁰NALTGTQNKVQGNWGE²⁵MIETVLENSGLQKGREYVVQAASV
RKEEDGGTRRLQPDVLVNL³⁰PDNKQIVIDSKVSLTAYVRYTQAADADTAARELA³⁵AHVASIR
AHMKGLSLKDYTDLEGVNTLDFVFMFIPVEPAYLLALQNDAGLFQECFDKRIMLVGPSTL
LATLRTVANIWRNEQQNQNALAIAD⁴⁰EGGKLYDKFVGFVQTLESV⁴⁵GKIDQAQSS⁵⁰FQTAFK
QLAEGRGNLVGRAEKLRL⁵⁵LGVKAGKQLQ⁶⁰RD⁶⁵LVERSNETTALSESLEYAAEDEAV

NMB1335 CreA protein DNA sequence

ATGAACAGACTGCTACTGCTGTCTGCCGCCGTCTCTGCTGACTGCCTGCGGCAGCGGCGAA
ACCGATAAAATCGGACGGGCAAGTACCGTTTTCAACATACTGGGCAAAAACGACCGTATC
GAAGTGGAAGGATTCCGACGATCCCGACGTTCAAGGGGTTGCCTGTTATATTTCTGATGCA
20 AAAAAAGCGGCTTGAAGGAAATGGTCAATTTGGAAGAGGACGCGTCCGACGCATCGGTT
TCGTGCGTTCCAGACGGCATCTTCGATTTCTTTT²⁵GACGAAACCGCGTGC³⁰GCAAACCGAAA
GAAGTTTTCAAACACGGTGC³⁵GAGCTTCGCGTTCAAGAGCCGGCAGATTGTCCGTTATTAC
GACCCCAAACGCAAAACCTTCGCCTATTTGGTGTACAGCGATAAAATCATCCAAGGCTCG
CCGAAAAATTCTTAAAGCGCGGTTTCTGTTT⁴⁰CGGCGCGCGCATACCGCAAACCGATGGG
25 GTGCAAGCCGATACTTCCGGCAACCTGCTTGCCGGCGCCTGCATGATTTCCAACCCGATA
GAAATCTCGACAAACGCTGA

NMB1335 Protein sequence

30 MNRLLLLSAAVLLTACSGGETDKIGRASTVFN³⁵ILGKNDRIEVEGFDDPDVQGVACYISYA
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA⁴⁰VRKPKVEVFKHGASFAFKSRQIVRY
DPKRKTFA⁴⁵LVYS⁵⁰DKIIQGS⁵⁵PKNSLSAVSCF⁶⁰GGGIPQTDGVQADTSGNLLAGACMISNPI
ENLDR

NMB2035 DNA sequence

35 ATGACCGCCTTTGTCCACACCCTTT⁴⁰CAGACGGCATGGA⁴⁵ACTGACCGTCGAAATCAAGCGC
CGTGCCAAGAAAAACCTGATTATCCGCCCGCGGCACACATAACCGTCCGCATCAGCGTC
CCACCTGCTTCTCCGTCTCCGCTCTAAACCGCTGGCTGTATGAAAACGAAGCCGTCCTG
CGGCAAACACTGGCGAAAACACCGCCGCGCGCAA⁵⁰ACTGCCGAAAACCGGCTGCCCGAATCC
ATCCTCTTCCACGGCAGACAGCTTGCCTCACC⁵⁵GCCATCAAGACACGCAAAATCCTGCTG
40 ATGCCGTCTGAAATCCGTGTTCCCGAAGGCGCAC⁶⁰CCGAAAACAGCTTGC⁶⁵GCTGCTGCGG
GACTTTTTTGGAAACGGCAGGCGCACAGTTACCTGATTCCCGCCTCGAACGCCACGCCCGC
ACCACACAAC⁷⁰TGTTCCCGCCTCCTCCTCGCTGACCTCTGCCAAAACCTTCTGGGGCGTG
TGCCGCAA⁷⁵AACACAGGCATACGCTTCAACTGGCGGCTGGT⁸⁰CGGCGCACCGGAATACGTT
GCCGACTATGTCTGCATACAGAACTCTGCCACCTCGCCCATCCCGACCACAGCCCCGCC
45 TTTTGGGAACTGACCGCGCGCTTCGCCCCCTACACGCCCAAAGCGAAACAGTGGCTCAAA
ATCCACGGCAGGGAAC⁹⁰TTTTCGCCTTAGGCTGA

NMB2035 Protein sequence

50 MTA⁵⁵FAVHTLS⁶⁰DMELTVEIKRRAKKNLIIRPAG⁶⁵HTTVRISVPPCFSVSALNRWLYENEAVL
RQTLAKTPPPQTAENRLPESILF⁷⁰HGRQLALTAHQDTQILLMPSEIRVPEGAPEKQLALLR
DFLERQ⁷⁵AHSYLI⁸⁰PRLERHARTTQLFPASSSLTAKTFWGVCRKTTGIRFNWRLVGAPEYV
ADYVCIHELCHLAHPDHSPAFWELTRRFAPYTPKAKQWLKI⁸⁵HGRELFALG

NMB1351 Fmu and Fmv protein DNA sequence

55 ATGAACGCCGCACAAC⁶⁰TCGACCATACCGCCAAAGTTTTGGCTGAAATGCTGACTTTCAA
CAGCCTGCCGATGCCGTCTCTCCGCTATTTCCGCGAACACAAAAAGCTCGGCAGTCAA
GATCGCCACGAAATCGCCGAAACCGCCTTTGCCGCGCTGCGCCACTATCAAAAAATCAGT

ACCGCCCTACGCCGTCCGCACGCGCAGCCGCGCAAAGCCGCTCTCGCCGCACTGGTTCTC
 GGCAGAAGCACCAACATCAGCCAAATCAAAGACCTGCTTGATGAAGAAGAAACAGCGTTC
 CTCGGCAATTTGAAAGCCCGTAAACCCGAGTTTTTCAGACAGCCTGAATACCGCCGCAGAA
 TTGCCGCAATGGCTGGTGGAACAACCTGAAACAGCATTGGCGCGAAGAAGAAATCCTCGCT
 5 TTCCGGCCGACGATCAACCAGCCTGCCCGCTGTTGCAAGCCGAAAGTGCCGATGCAGAGGCAACGCCT
 AAACGCGATAAAGTGCTGCCGCTGTTGCAAGCCGAAAGTGCCGATGCAGAGGCAACGCCT
 TATTCGCCTTGGGGCATCCGCCTGAAAAACAAAATCGCGCTTAACAAACACGAACTGTTT
 TTAGACGGCACACTGGAAGTCCAAGACGAAGGCAGCCAGCTGCTTGCCTTATTGGTGGGC
 GCAAAACGAGGCGAAATCATTGTGATTTCTGTGCCGGTGCCGGCGGTAAAACCTTGGCT
 10 GTCGGTGCGCAAATGGCGAACAAAGGCAGAATCTACGCCTTCGATATCGCCGAAAAACGC
 CTTGCCAACCTCAAACCGCGTATGACCCGCGCCGGACTGACCAATATCCACCCCGAACGC
 ATCGGCAGCGAACACGATGCCCGTATCGCCCGACTGGCAGGCAAAGCCGACCGTGTGTG
 GTGGACGCGCCCTGCTCCGTTTTGGGCACTTTACGCCGCAATCCCGACCTCAAATACCGC
 CAATCCGCCGAAACCGTCGCCAACCTTTTGGAACAGCAACACAGCATCCTCGATGCCGCC
 15 TCCAAACTGGTAAAACCGCAAGGACGTTTTGGTGTACGCCACTTGCAGCATCCTGCCCGAA
 GAAAACGAGCTGCAAGTCGAACGTTTTCTGTCCGAACATCCCGAATTTGAACCCGTCAAC
 TGCGCCGAACTGCTTGCCGGTTTTGAAAATCGATTTGGATACCGGCAAATACCTGCGCCTC
 AACTCCGCCCGACACCAAACCGACGGCTTCTTCGCCCGCGTATTGCAACGCAAATAA

20 NMB1351 Protein sequence

MNAAQLDHTAKVLAEMLTFKQPADAVLSAYFREHKKLGSQDRHEIAETAFAALRHYQKIS
 TALRRPHAQPRKAALALVLRSTNISQIKDLLDEEETAFLGNLKARKTEFSDSLNTAAE
 LPQWLVEQLKQHWREEEILAFGRSINQAPPLDIRVNTLKGKRDKVLPLLOAESADAEATP
 YSPWGIRLKNKIALNKHELFLDGTLEVQDEGSQLLALLVGAKRGEIIVDFCAGAGGKTLA
 25 VQAQMANKGRIYAFDIAEKRLANLKPMTTRAGLTNIHPERIGSEHDARIARLAGKADRVL
 VDAPCSGLGLTRRNPDLKYRQSAETVANLLEQQHSILDAASKLVKPOGRLVYATCSILPE
 ENELQVERFLSEHPEFEPVNCAELLAGLKIDLDTGKYLRLNSARHQTDFGFFAVALQRK

NMB1574 IlvC DNA sequence

30 ATGCAAGTCTATTACGATAAAGATGCCGATCTGTCCCTAATCAAAGGCAAAACCGTTGCC
 ATCATCGGTTACGGTTCGCAAGGTCATGCCCATGCCGCCAACCTGAAAGATTTCGGGTGTA
 AACGTGGTGATTGCTGCGCCAAGGTTCTTCTTGAAAAAAGCCGAAGCAGCCGGTCAT
 GTCGTCAAACCGTTGCTGAAGCGACCAAGAAGCCGATGTGCTTATGCTGCTGCTGCCT
 GACGAAACCATGCCTGCCGTCTATCACGCCGAAGTTACAGCCAATTTGAAAGAAGGCGCA
 35 ACGCTGGCATTGTCACACGGCTTCAACGTGCACTACAACCAAATCGTTCCGCGTGCCGAC
 TTGGACGTGATTATGGTTGCCCCCAAAGGTCCGGGCCATACCGTACGCAGTGAATACAAA
 CGCGGCGGCGGCGTGCTTCTCTGATTGCCGTTTACCAAGACAATCCGGCAAAGCCAAA
 GACATCGCCCTGTCTTATGCGGCTGCCAACGGCGGCACCAAAGGCGGTGTGATTGAAACC
 ACTTTCGCGGAAGAAACCGAAACCGATCTGTTTCGGCGAACAAGCCGTATTGTGCGGCGGC
 40 GTGGTCGAGTTGATCAAGGCGGGTTTTGAAACCCTGACCGAAGCCGGTTACGCGCCTGAA
 ATGGCTTACTTCAATGTCTGCACGAAATGAAACTGATCGTTGACCTGATTTTCGAAGGC
 GGTATTGCCAATATGAACTACTCCATTTCCAACAATGCGGAGTACGGCGAATACGTTACC
 GGCCCTGAAGTGGTCAATGCTTCCAGCAAAGAAGCCATGCGCAATGCCCTGAAACGCATT
 CAAACCGGCGAATACGCAAAAATGTTTATCCAAGAGGGTAATGTCAACTATGCGTCTATG
 45 ACTGCCCGCCGCGCTCTGAATGCCGACCACCAAGTTGAAAAAGTCGGCGCACAACTGCGT
 GCCATGATGCCTTGGATTACTGCCAACAAATTGGTTGACCAAGACAAAAACTGA

NMB1574 Protein sequence

50 MQVYYDKDADLSLIKGTVAIIIGYGSQGHAAANLKDSGVNVVIGLRQGSSWKKAEEAAGH
 VVKTVAEATKEADVMLLLPDETMPAVYHAEVTANLKEGATLAFAGHFNHYNQIVPRAD
 LDVIMVAPKGPGHVTRSEYKRGGGVPSLIAVYQDN SGKAKDIALSYAAANGGTKGGVIET
 TFREETETDLFGEQAVLCGGVVELIKAGFETLLEAGYAPEMAYFECLHEMKLIVDLIFEG
 GIANMNYSISNNAEYGEYVTGPEVVNASSKEAMRNALKRIQTGEYAKMFIQEGNVNYASM
 TARRRLNADHQVEKVGQQLRAMMPWITANKLVDQDN

NMB1298 rsuA DNA sequence

ATGAACTTATCAAATACCTGCAATATCAAGGCATAGGAAGCCGCAAGCAGTGCCAAATGG
 CTGATTGCCGGCGGTTATGTTTTTCATCAACGGAACCTGCATGGACGACACCGATGCAGAC

ATCGATTCCCTCATCCGTCGAAACGTTGGATATTGACGGGGAAGCAGTAACCGTCGTTCCC
GAACCCATATTTCTACATCATGCTCAACAAGCCTGAAGATTACGAACTTCGCACAAACCC
AAGCACTACCGCAGCGTATTGAGCCTGTTCCCCGACAATATGCGGAACATCGATATGCAG
GCGGTCGGCAGGCTGGATGCAGATACGACCGGCGTATTGCTGATTACCAACGACGGCAAA
5 C TGAACCACAGCCTGACTTCGCCGAGCAGAAAAATTCCCAAGCTGTACGAAGTAACGCTC
AAACACCCACAGGAGAAACGCTCTGCGAAACCTTGAAAAACGGCGTGCTGCTCCACGAC
GAAAACGAAACCGTTTGTGCCGCCGATGCCGTTTTGAAAAACCCGACCACCCTGCTGCTG
ACCATTACCGAAGGAAAATACCACCAAGTCAAACGCATGATCGCCGCCGCCGGCAACCGC
GTGCAACACCTTCATCGCCGGCGATTTCGCACATCTGGAAACAGAAACCTCAAACCCGGG
10 GAATGGAAATTTATCGAATGTCCAAATTCTGA

NMB1298 Protein sequence

MKLIKYLQYQGIGSRKQCQWLIAGGYVFINGTCMDDTDADIDSSSVETLDIDGEAVTVVP
EPYFYIMLNKPEDYETSHKPKHYRSVSLFPDNMRNIDMQAVGRLDADTTGVLLITNDGK
15 LNHSLTSPSRKIPKLYEVLKHPTGETLCELTNGVLLHDENETVCAADAVLKNPTTLLL
TITEGYHQVKRMIAAAGNRVQHLHRRRFAHLETENLKPGEWKFIKCPKF

NMB1856 Lys R family (transcription regulator) DNA sequence

ATGAAAACCAATTCAGAAGAACTGACCGTATTTGTTCAAGTGGTGAAAGCGGCAGCTTC
20 AGCCGTGCGGCGGAGCAGTTGGCGATGGCAAATTCTGCCGTAAGCCGCATCGTCAAACGG
CTGGAGGAAAAGTTGGGTGTGAACCTGCTCAACCGCACCACGCGGCAACTCAGTCTGACG
GAAGAAGGCGCGCAATATTTCCGCCGCGCGCAGAGAATCCTGCAAGAAATGGCAGCGGCG
GAAACCGAAATGCTGGCAGTGCACGAAATACCGCAAGGCGTGTTGAGCGTGGAATCCGCG
ATGCCGATGGTGCTGCATCTGCTGGCGCCGCTGGCAGCAAAATTCAACGAACGCTATCCG
25 CATATCCGACTTTTCGCTCGTTTCTTCCGAAGGCTATATCAATCTGATTGAACGCAAAGTC
GATATTGCCTTACGGGCCGAGAAATTGGACGATTCCGGGCTGCGTGACGCCATCTGTTT
GACAGCCGCTTCCGCGTAATCGCCAGTCTGAATACCTGGCAAAACACGGCACGCCGCAA
TCTACAGAAGAGCTTGCCGGCCACCAATGTTTAGGCTTCACCGAACCCGGTTCTCTAAAT
ACATGGGCGGTTTTAGATGCGCAGGGAAATCCCTATAAGATTTACCGCACTTTACCGCC
30 AGCAGCGGTGAAATCTTACGCTCGTTGTGCCTTTAGGTTGCGGTATTGTTTGCTTATCA
GATTTTTTGGTTGACAACGACATCGTGAAGGAAAGTTAATTTCCCTGCTCGCCGAACAA
ACCTCCGATAAAACACACCCCTTTAATGCTGTTTATTACAGCGATAAAGCCGTCAATCTC
CGCTTACGCGTATTTTTTGATTTTTTAGTGGAGGAAGTGGGAAACAATCTCTGTGGATAA

NMB1856 Protein sequence

MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT
EEGAQYFRRAQRILQEMAAAETEMLAVHEIPQGVLSVDSAMPMLVHLLAPLAAKFNERYP
HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ
STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS
40 DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNLCLG

NMB0119 DNA sequence

ATGATGAAGGATTTGAATTTGAGCAACAGCCTGTTCAAAGGCTACAACGACAAACATGGC
TTAATGATTTGTGGCTATGAATGGGGTTGGAGTAAAGCCGATGAGGCTGCTTATGTAGCA
45 GGTGAATACAACTCCCTGAAAACAAAATCGACCATAACATTTGCAAACAAATCCCTCTAT
TTCGGAGAGCAGGCAAAAAAGTGGCGTTACGACAATACGATAAAAAATTGGTTTGAAATG
TGGGGACACCCCTTAGACGAAAATGGATTGGGCGGTGCATTTGAAAAATCCCTGGTTCAA
ACCAACTGGGCTGCTACACAGGGCAACACTATCGACAATCCCGACAAGTTCACACAACCC
GAGCACATCGATAATTTTCTCTACCACATCGAAAACTGCGTCCGAAAGTCATCTCTTC
50 ATGGGCAGCAGGTTGGCGGATTTTCTGAACAACCAAATGTACTGCCACGCTTCGAGCAG
TTGGTCGGTAAGCAGACCAAACCGCTGGAGACGGTGCAAAAAGAATTTGACGGTACACGT
TTCAATGTCAAATCCAATCGTTTGAAGATTGCGAAGTCGTCTGCTTTCCCATCCCAGT
GCCAGTCGCGGTCTATCTTACGATTACATCGCCTTGTTTGCGCCTGAAATGAACCGGATT
TTATCGGACTTTAAAACAACACGCGGATTCAAATAA
55

NMB0119 Protein sequence

MMKDLNLSNSLFGYNDKHGLMICGYEWGWSKADEAAYVAGEYKLPENKIDHTFANKSLY

FGEQAKKWRYDNTIKNWFEMWGHPLDENLGGAFEKSLVQTNWAATQGNITIDNPKFTQP
EHIDNFLYHIEKLRPKVILFMGSRDLADFLNNQNVLPREFQLVGKQTKPLETVQKEFDGTR
FNVKFQSFEDCEVVCFFPHPSASRGLSYDYIALFAPEMNRILSDFKTTTRGFK

5 NMB1705 rfaK DNA sequence

ATGGAAAAAGAATTTCAGGATATTAAATATCGTATCGGCCAAGATTGGGGTGGAGGCGAA
CAATATGTCTATGATGTTTCAAAGCATTGGGGCTTCGGGGCTGCACAATGTTTACCGCC
GTCAATAAAAAATAATGAATTGATGCACAGGCGATTTTCCGAAGTTTCTTCCGTTTTTACA
ACGCGCCTTTCACACGCTCAACGGGCTGTTTTCGCTCTACGCACTTACCGCTTTATCCGG
10 AAAAACCGCATTTCACACCTGATGATACACACCGGCAAAATTGCCGCCTTATCCATACTT
TTGAAAAAACTGACCGGGGTGCGCCTGATATTTGTCAAACATAATGTCGTCGCCAACAAA
ACCGATTTTTTACCACCGCCTGATACAGAAAAACACAGACCGCTTTATTTGCGTTTCCCGT
CTGGTTTACGATGTGCAACCGCCGACAATCCCTTTAAAGAAAAATACCGGATTGTTTAT
AACGGTATCGATACCGGCCGTTTCCCTCCCTCTCAAGAAAAACCGACAGCCGTTTTTTT
15 ACCGTCGCCTACGCCGGCAGGATCAGTCCAGAAAAAGGATTGGAAAACCTGATTGAAGCC
TGTGTGATACTGCATCGGAAATATCCTCAAATCAGGCTCAAATTGGCAGGGGACGGACAT
CCGGATTATATGTGCCGCTGAAGCGGGACGTATCTGCTTCAGGAGCAGAACCATTGTGTT
TCTTTTGAAGGGTTTACCGAAAACTTGCTTCGTTTTACCGCCAAAGCGATGTCGTGGTT
TTGCCCAGCCTCGTCCCGGAGGCATTTCGGTTTGTGATTATGCGAGGCGATGTACTGCCGA
20 ACGGCGGTGATTTCCAATACTTTGGGGGCGCAAAAGGAAATTGTGGAACATCATCAATCG
GGGATTCTGCTGGACAGGCTGACACCTGAATCTTTGGCGGACGAAATCGAACGCCCTCGTC
TTGAACCCTGAAACGAAAAACGCACTGGCAACGGCAGCTCATCAATGCGTCGCCGCCCGT
TTTACCATCAACCATAACCGCCGACAAATTATTGGATGCAATATAA

25 NMB1705 Protein sequence

MEKEFRILNIVSAKIWGGGEQYVYDVSKALGLRGCTMFTAVNKNNELMHRRFSEVSSVFT
TRLHTLNLGLFSLYALTRFIRKNRISHLMIHTGKIAALSILLKKLTGVRLIFVKHNVVANK
TDFYHRLIQKNTDRFICVSRVLVDVQADNPFKEKYRIVHNGIDTGRFPPSQEKPDSRFF
TVAYAGRISPEKGLENLIEACVILHRKYPQIRLKLADGHPDYMCRCLKRDVSASGAEPFV
30 SFEGFTEKLASFYRQSDVVLPVSLVPEAFGLSLCEAMYCRTAVISNTLGAQKEIVEHHQS
GILLDLRLTPESLADEIERLVLNPETKNALATAAHQCVAARFTINHTADKLLDAI

NMB2065 Hemk protein DNA sequence

ATGCAGGAACAGAATCGGAAACCAAGTTTTCCCATAGTGATGTTGCTGGTGTGCGTTGCC
35 CTGTGGATAGCGTCTTTATCCAATGTTGCATTTTATTGGCAATCATGGAAGCATGGAG
GGTTTGACCGTTTTGATTTTGGGGTCGATATTGCTTCTTTGGATATCAGGTATTGTGCG
GTCTATGCGAATTATTGTTGGTTGGCGGCCATTGTTTTGCTGGCGTTGCGGAAGAAGGTC
GTCCCTGTCCATCGCGCACTTTGGGGCTTGCGGTTGGTGGCTTTCAGTGTGAAAGCCGTA
TACGTCGATGAAGCAGGGAATACATCGGATATTGTGCGCTACGGTGCAGGATTTTATTTG
40 TGGTATGCCGCATTTGCGGTTGCCACCATCGGTACGTTTGCCGGAAGAATAAGGAAAGA
AAAGCCGCATCAGCGGCAGACGGGATAAAAATGACGTTTGATAAATGGTTGGGCTTGTC
AAACTGCCTAAAAATGAAGCAAGAATGCTGCTACAATATGTTTCGGAATATACGCGCGTG
CAGTTGTTGACGCGGGGCGGGGAAGAAATGCCGGACGAAGTCCGACAGCGGGCGGACAGG
CTGGCGCAACGCCGCTCTGAACGGCGAGCCGTTGCCTATATTTAGGTGTGCGCGAATTT
45 TATGGCAGACGCTTTACAGTCAATCCGAGCGTGCTGATTCCGCGCCCCGAAACCGAACAT
TTGGTTCGAAGCCGATTGGCGCGCCTGCCCGAAAACGGGCGCGTGTGGGATTGGGGACG
GGCAGCGGCGCGGTTGCCGTAACCGTCGCGCTCGAACGCCCCGATGCGTTTGTGCGCGCA
TCCGACATCAGCCCGCCCGCCCTTGAAACGGCGCGGAAAAATGCGGCGGATTGGGGCGG
CGGGTCGAATTTGCACACGGTTTCGTGGTTCGACACCGATATGCCGTCTGAAGGGAAATGG
50 GACATCATCGTGTCCAACCCGCCCTATATCGAAAACGGCGATAAACATTTGTTGCAAGGC
GATTTGCGGTTTGAGCCGCAATCGCGCTGACCGACTTTTACAGACGGCCTAAGCTGCATC
CGCACCTTGCGCAAGGCGCGCCCGACCGTTTGGCGGAAGGCGGTTTTTTATTGCTGGAA
CACGGTTTCGATCAGGGCGCGCGGTGCGCGCGTGTGGCGGAGAATGGTTTTTCAGGA
GTGGAAACCCTGCCGATTGGCGGGTTTGACAGGGTTACGCTGGGGAAGTATATGAAG
55 CATTGAAATAA

NMB2065 Protein sequence

MQEQNRKPSFPIVMLLVSVLWIASLSNVAFYLGNHGSMGLTVLILGSIFASLDIRYCA
 VYANYVWLAIAIVLLALRKVVVPVHAALWGLALVAFSVKAVYVDEAGNTSDIVRYGAGFYL
 WYAAFAVATIGTFAGKNKERKAASAADGIKMTFDKWLGLSKLPKNEARMLLQYVSEYTRV
 5 QLLTRGGEEMPDEVRQRADRLAQRRNLNGEPVAYILGVREFYGRFRFTVNPSVLI PRPETEH
 LVEAVLARLPENGRVWDLGTGSGAVAVTVALERPDADFVRASDISPPALETARKNAADLGA
 RVEFAHGSWFDTDMPSEGKWDIIIVSNPPYIENGDKHLLQGDRLRFEPQIALTDFSDGLSCI
 RTLAQGAPDRLAEGGFLILLEHGFDDQGAAVRGVLAENGFSGVETLPDLAGLDRVTLGKYMK
 10 HLK

Mutants selected by vacinee's 17 D sera (Screened once only)

NMB0339 DNA sequence

ATGGACAACGAATTGTGGATTATCCTGCTGCCGATTATCCTTTTGCCCGTCTTCTTCGCG
 15 ATGGGCTGGTTTGCCGCCCCGCTGGATATGAAAACCGTATTGAAGCAGGCAAAAAGCATC
 CCTTCGGGATTTTATAAAAGCTTGGACGCTTTGGTCGACCGCAACAGCGGGCGCGCGCA
 AGGGAGTTGGCGGAAGTCGTCGACGGCCGGCCGCAATCGTATGATTTGAACCTCACCTC
 GGCAAACTTTACCGCCAGCGTGGCGAAAAACGACAAAAGCCATCAACATACACCGGACAATG
 CTCGATTCTCCCGATACGGTTCGGCGAAAAGCGCGCGCGCTCCTGTTTGAATTGGCGCAA
 20 AACTACCAAAGTGGCGGGTGGTCGATCGTGCCGAACAGATTTTTTTGGGGCTGCAAGAC
 GGTAAAATGGCGCGTGAAGCCAGACAGCACCTGCTCAATATCTACCAACAGGACAGGGAT
 TGGGAAAAAGCGTTGAAACCGCCCGGCTGCTCAGCCATGACGATCAGACCTATCAGTTT
 GAAATCGCCAGTTTATTGCGAACTTGCCCAAGCCGCGCTGTTCAAGTCCAATTTTCGAT
 GTCGCGCGTTTCAATGTCGGCAAGGCATCGAAGCCAAACAAAAATGCACCCGCGCCAAC
 25 ATGATTTTGGGCGACATCGAACACCGACAAAGGCAATTTCCCTGCCGCGCTCGAAGCCTAT
 GCCGCCATCGAGCAGCAAAAACCATGCATACTTGAGCATGGTCGGCGAGAAGCTTTACGAA
 GCCTATGCCGCGCAGGGAAAAACCTGAAGAAGGCTTGAACCGTCTGACAGGATATATGCAG
 ACGTTTCCCGAACTTGACCTGATCAATGTCGTGTACGAGAAATCCCTGCTGCTTAAGTGC
 GAGAAAGAAGCCGCGCAAAACCGCCGTCGAGCTTGTCCGCCGCAAGCCCGACCTTAACGGC
 30 GTGTACCGCTGCTCGGTTTGAAGTCAAGCATATGAATCCGGCTTGGAAAGCCGATGCC
 GACATGATGCGTTTCGGTTATCGGACGGCAGCTACAGCGCAGCGTGTGTACCGTTGCCGC
 AACTGCCACTTCAAATCCCAAGTCTTTTTCTGGCACTGCCCCGCTGCAACAAATGGCAG
 ACGTTTACCCCGAATAAAATCGAAGTTTAA

NMB0339 Protein sequence

MDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKSLDALVDRNSGRAA
 RELAEVVDGRPQSYDLNLTLGKLYRQRGENDKAINIHRTMLDSPDTVGEKRARVLFELAQ
 NYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQODRDWEKAVETARLLSHDDQTYQF
 EIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIEHRQGNFPAAVEAY
 40 AAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGYMQTFPELDLINVVYEKSLLLKC
 EKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAWKADADMMSVIGRQLQRSVMYRCR
 NCHFQSQVFFWHCPACNKWQTFTPNKIEV

Selection with patient's sera

We have a collection of acute and convalescent sera available to us for screening.

This is from individuals infected with different serogroup of *N. meningitidis*.

Screens have been performed with acute (A) or convalescent (C) sera. The period between the acute infection and collection of sera was from 2 weeks to 3 months.

NMB0401 putA DNA sequence

ATGTTTCATTTTGCATTTCCGGCACAACTGCCCTGCGCCAAGCGATAACCGATGCCTAC
 CGCCGTAATGAAATCGAAGCCGTACAGGATATGTTGCAACGTGCACAGATGAGCGACGAA

GAGCGCAACGCCGCTCCGAGCTTGCCCGCCGTTTGGTTACCCAAGTCCGCGCCGGCCGC
ACCAAGGCCGGCGGTGGATGCGCTGATGCACGAGTTTTCTACTCTCCAGCGAAGAAGGC
ATCGCGCTGATGTGTCTGGCAGAAGCCCTGCTGCGTATCCCCGACAACGCCACGCGCGAC
CGCTGATTGCCGACAAGATTTAGACGGCAACTGGAAAAGCCATTTGAACAACAGCCCT
5 TCCCTCTTCTGTCATGCTGCCGCTGGGGCCTGCTGATTACCGGCAAACTGACCGCCACA
AACGACAAACAAATGAGTTCCGCACTCAGCCGCTGATCAGCAAAGGCGGCGCACCCTC
ATCCGCCAAGGCGTAAATTACGCCATGCGGCTTCTGGGCAAACAGTTCGTAACCGGACAG
ACCATTTGAAGAAGCCCTGCAAAACGGCAAAGAACGCGAAAAAATGGGCTACCGCTTCTCC
TTCGATATGTTGGGCGAAGCCGCTTACCCCAAGCCGATGCCGACCGCTACTACCGCGAC
10 TATGTGCGAAGCCATCCACGCCATCGGCAAAGATGCGGCAGGACAAGGCGTTTACGAAGGT
AACGGTATTTCCGTCAAACCTTCCGCCATCCATCCGCGCTACTCGCGCACCCAAACACGGC
CGCGTGATGGGCGAACTGTTGCCGCGCCTGAAAGAGCTGTTCTTTTGGGTAAAAAATAC
GATATCGGTATCAACATCGATGCCGAAGAAGCCAACCGTCTGGAGCTGTCTTTGGATTG
ATGGAGGCTTTGGTTTTCAGACCCTGACTTGGCTGGCTACAAAGGTATCGGTTTCTGTTGTC
15 CAAGCCTACCAAAAACGTTGTCCGTTTCTGTTATCGACTACCTGATCGACCTTGCCCGCCGC
AACAACCAAAAACCTAATGATCCGCTCGTCAAAGGCGCGTATTGGGACAGCGAAATCAAA
TGGGCGCAAGTGGACGGCTTGAACGGCTATCCGACCTACACCGCAAAGTCCACACCGAC
ATCTCTTACCTCGCCTGCGCGCGCAAACCTGCTTCCGCGCAAGACGCGGTATTTCCCGCAA
TTTGCCACCCACAACGCCCTACACTTTGGGCGCAATCTACCAAATGGGTAAAGGCAAAGAT
20 TTTGAACACCAATGCCTGCACGGTATGGGCGAAACCCTGTACGACCAAGTCGTCCGCCCG
CAAACTTAGGCCGCCGCGTGCAGCGGTGTACGCCCCAGTCGGCACACACGAAACCCTGCTC
GCCTACTTGGTGCGCCGCTGTTGAAAACGGCGCGAACTCGTCTTTCTGTCACCAAAATC
GTCGATGAAAACATCAGCATCGACACGCTCATCCGACGCCGTTTCGACACCATCGCCGAA
CAAGGCATCCACCTGCACAACGCCCTGCCGCTGCCGCGCGATTTGTACGGCAAATGCCGT
25 CTGAACTCGCAAGGCGTGGACTTGAGCAAACGAAAACGTATTGCAGCAGCTTCAAGAACAG
ATGAACAAAGCCCGCGCGCAAGACTTCCACGCGCATCCATCGTCAACGGCAAAGCCCGC
GATGTCGCGGAAGCGCAACCGATTAAAAACCCTGCCGACCACGACGACATCGTCGGCACA
GTCAGCTTTGCCGATGCCGCGCTTGCCCAAGAAGCGGTTGGCGCAGCCGTTGCCGCGTTC
CCCGAATGGAGTGCGACACCTGCCGCCGAACGCGCCGCTGCCTGCGCCGTTTTGCCGAT
30 TTGCTGGAGCAGCACACCCAGCACTGATGATGCTTGCCGTGCGCGAAGCAGGCAAAACG
CTGAACAACGCCATTGCCGAAGTGCGCGAAGCCGTGATTTCTGCCGCTACTACGCAAAC
GAAGCCGAACATACCCTGCCTCAAGACGCAAAAGCCGTGCGCGCGATTGTGCCATCAGC
CCGTGGAACTTCCCGCTCGCCATCTTTACCGGCGAAGTCGTTTCCGCATTGGCGGCAGGC
AACACCGTCATCGCAAACCCGCCGAACAAACCAGCCTGATTGCCGGTTATGCCGTTTCC
35 CTCATGCACGAAGCCGGCATCCCGACTTCCGCCCTGCAACTCGTCTCGGCGCAGGCGAC
GTGGGTGCGGCATTGACCAACGATGCCCGCATCGGCGGCGTGATTTTACCGGCTCGACC
GAAAGTGGCGCGCTGATCAACAAAGCCCTTGCCAAACGCGGCGACAATCCCGTCTTGATT
GCCGAAACCGGCGGACAAAACGCCATGATTGTGATTCACCGCACTTGCCGAGCAAGTC
TGCGCCGACGTATTGAACTCCGCCCTTCGACAGCGCGGGACAACGCTGCTCCGCCCTGCGC
40 ATTTTGTGCGTCCAAGAAGACGTTGCCGACCGTATGCTCGACATGATCAAAGGCGCTATG
GACGAACTCGTCGTGGCAAACCGATTGAGCTCACTACCGATGTGCGCCCGCTCATCGAT
GCCGAAGCACAGCAAAACCTGTTGAACCACATCAACAAAATGAAAGGTGTTGCCAAGTCC
TACCACGAAGTCAAAACCGCGCCGATGTCGATTCAAAAAATCCACGTTGTTGCGCCCG
ATCCTGTTTGAATTGAACAACCTCAACGACTGCAACGCGAAGTCTTCGGTCCCGTCTTG
45 CACGTGCTCCGCTACCCGCGCCGACGAACTCGACAACGTATCGACCAAATCAACAGCAAA
GGCTACGCCCTGACCCACGGCGTACACAGCCGCATCGAAGGCACGGTACGCCACATCCGC
AGCCGCTCGAAGCCGGCAACGTTTACGTCAACCGCAACATCGTCGGCGCAGTCGTCCGC
GTACAGCCCTTCGGCGGACACGGTCTGTCCGGCACAGGCCCAAGCAGGCGGTTCTGTT
TACCTGCAAAAACCTGACCCGCGCCGGCGAATGGGTTGCCCGACCCCTGAGCCAAATCGGA
50 CAGGCGGACGAAGCCGCACTCAAACGCCTCGAAGCACTGGTTACAAAACCTACCGTTCAAC
GCCGAAGAGAAAAAAGCCGCGAGCGGCCGCTTTGGGACACGCCCGCATCCGCACCCTGCGC
CGTGCCGAAACCGTCTTACCGGACCGACCGGCGAGCGCAACAGCATCTCATGGCACGCG
CCCAACGCGCTTTGGATACAGGCGGCGAGCACGGTTCAAGCCTTTGCCGCACTGACCGAA
CTTGCCGCTTCCGGCATACAGGCGAGTGGTCAACCCGACAGCCCTTGGCTTCTTACACT
55 GCCGACTTGGAAGGTCTGCTGCTGGTCAACGGCAAACCCGAAACCGCCGGCATCAGCCAC
GTTGCCGCCCTGTGCTTTTGGACAGCGCGCGCAAACAGGAACCTTGCCGCCACGACGGC
GCACTCATCCGCATCTCTCCCTTCGGAAAACGGACTCGACATCCTGCAAGTGTGTTGAAGAA
ATCTCTTGACGCGTCAACACCACAGCCGCCGCGGCAACGCCAGCCTGATGGCGGTGCGC

GACTGA

NMB0401 Protein sequence

MFHFAFPAQTALRQAITDAYRNEIEAVQDMLQRAQMSDEERNAASELARRLVTQVRAGR
 5 TKAGGVDALMHEFSLSSEEGIALMCLAEALLRIPDNATRDRLIADKISDGNWKSHLNNSP
 SLFVNAAWGLLITGKLTATNDKQMSSALSRLISKGGAPLIRQGVNYAMRLLGKQFVTGQ
 TIEEALQNGKEREKMGYRFSFDMLGEAAQTQADADRYRDYVEAIHAIGKDAAGQGVYEG
 NGISVKLSAIHPRYSRTQHGRVMGELLPRLKEFLLGKKYDIGINIDAEENRLELSLDL
 MEALVSDPDLAGYKIGFVVQAYQKRCPFVIDYLDLARRNNQKLMIRLVKGAYWDSEIK
 10 WAQVDGLNGYPTYTRKVHTDISYLACARKLLSAQDAVFPQFATHNAYTLGAIYQMGKGKD
 FEHQCLHGMGETLYDQVVGPNLGRVRVYAPVGTHETLLAYLVRRLLENGANSSFVNQI
 VDENISIDTLIRSPFDTIAEQGIHLHNALPLPRDLYGKCRSNSQGVDLSENENVLQQLQEQ
 MNKAAAQDFHAASIVNGKARDVGEAQPIKNPADHDDIVGTVSFADAALAEAVGAAVAFAF
 PEWSATPAAERAACLRRFADLLEQHTPALMMLAVREAGKTLNNAIAEVREAVDFCRYAN
 15 EAEHTLPQDAKAVGAIVAI SPWNFPLAIFTGEVVSALAAGNTVIAKPAEQTSIAGYAVS
 LMHEAGIPTSALQLVLGAGDVGAALTNDARIGGVIFTGSTEVARLINKALAKRGDNPVLI
 AETGGQNAMIVDSTALAEQVCADVLNSAFDSAGQRCSALRILCVQEDVADRMLDMIKGAM
 DELVVGKPIQLTTDVGPIVDAEAQQNLLNHINKMKGVAKSHEVKTAADVDSKKSTFVRP
 ILFELNNLNELQREVFGPVLHVVRRADELNDVIDQINSKGYALTHGVHSRIEGTVRHIR
 20 SRIEAGNVYVNRNIVGAVVGVQPFGGHGLSGTGPKAGGSFYLLQKLTRAGEWVAPTLSQIG
 QADEAALKRLEALVHKLPFNAEEKKAAAAALGHARITLRRRAETVLTGPTGERNSISWHA
 PKRVWIHGGSTVQAFALTELAASGIQAVVEPDSPLASYTADLEGLLLVNGKPETAGISH
 VAALSPLDSARKQELAAHDGALIRILPSENGLDILOVFEEISCSVNTTAAGGNASLMAVA
 D
 25 NMB1335 CreA

DNA and Protein sequences given above

30 NMB1467 PPX DNA sequence
 ATGACCACCACCCCGCAAACGTCTCGCCTCCGTCGATTTGGGTTCCAACAGTTTCCGC
 CTCCAGATTTGCGAAAACAACAACGGACAATTAAAAGTCATCGATTCGTTCAAACAGATG
 GTGCGCTTCGCCGCCGGACTGGACGAACAGAAAAATCTGAGTGCCGCTTCCCAAGAACAG
 GCTTTGGACTGTCTGGCAAATTCGGCGAACGCCTGCGCGGCTTCCGCCCTGAACAGGTA
 35 CGCGCCGTGGCAACCAACACATTCGCGGTTGCCAAAAACATCGCAGATTTCTTCCCAAA
 GCCGAAGCGGCATTGGGTTTCCCCATCGAAATCATCGCCGGGCGCGGAAGAGGCGCGGCTG
 ATTTATACCGGCGTGATCCACACCCTCCCCCGGGCGGCGGCAAAATGCTGGTTATCGAC
 ATCGGCGGCGGTTTCGACAGAATTTGTTCATCGGCTCGACGCTGAATCCCGACATTACCGAA
 AGCCTGCCCTTGGGCTGCGTAACCTACAGCCTGCGCTTCTTCCAAAACAAAATCACCGCC
 40 AAAGACTTCCAATCTGCCATTTCCGCCGCCGCAACGAAATCCAGCGTATCAGCAAAAAT
 ATGAGGCGCGAAGGTTGGGATTTCCGCCGTCGGCACATCGGTTTCGGCAAAATCCATCCGC
 GACGTGCTTGCCGCCGAAATGCCCAAGAGCGGACATTACCTACAAAGGCATGCGCGCC
 CTCGCCGAACGCATCATCGAAGCCGGTTCGGTCAAAAAAGCCAAATTTGAAAACCTGAAA
 CCGGAACGCATCGAAGTTTTTGGCGGCGGACTTGCCGTGATGATGGCGGCGTTTGGAGGAA
 45 ATGAAACTCGACAGGATGACCGTAACCGAAGCCGCCCTGCGCGACGGCGTGTTTTACGAT
 TTGATCGGGCGCGGTTTAAACGAAGATATGCGCGGACAAACGGTTGCCGAGTTCCAACAC
 CGCTACCACGTGAGCCTCAATCAGGCGAAACGCACCGCCGAGACCGCGCAAACTTTATG
 GACAGCCTCTGCCACGCTAAAAACGTTACAGTTCAAGAGCTTGCTTGTGGCAACAGTAT
 CTCGGACGCGCGCGCGCTGCACGAAATCGGTTTGGACATCGCCACACCGGCTATCAC
 50 AAGCATTCGCGCTACATCCTCGAAAACGCCGATATGCCGGGTTTCTACGCAAGAAGACAG
 ACCATACTTGCCCAACTGGTCATCGGTTCATCGCGCGATATGAAAAAATGAGCGGCATC
 ATCGGCACCAACGAAATGTTGTGGTATGCCGTTTTGTCCCTGCGCCTTGCCGCACTGTTT
 TGCCGTTTCGCGCAAGACCTGTCTTTCCCGAAAAATATGCAGTTGCGCACGGATACGGAA
 AGCTGCGGCTTCATCCTGCGTATTGACAGGGAATGGCTGGAACGCCATCCCCTGATTGCC
 55 GACGCATTGGAATATGAAAGCGTCCAATGGCAAAAAATCAATATGCCGTTCAAAGTCGAG

GCCGTCTGA

NMB1467 Protein sequence

MTTTPANVLASVDLGSNSFRLQICENNNGQLKVIDSFKQMVRFAGLDEQKNLSAASQEQ
 5 ALDCLAKFGERLRGFRPEQVRVATNTFRVAKNIADFLPKAEALGFPIEIIAGREEEARL
 IYTGVIHTLPPGGGKMLVIDIGGGSTEFVIGSTLNPDITESLPLGCVTYSLRFFQNKITA
 KDFQSAISAAARNEIQRISKNNMRREGWDFAVGTSGSAKSIRDVLAEMPQEADITYKGMRA
 LAERII EAGSVKKAKFENLKPERIEVFAGGLAVMMAAFEEMKLDGMTVTEAALRDGVFYD
 10 LIGRGLNEDMRGQTVAEFQHRYHVSLNQAARTAEATAQTFMDSLCHAKNVTVQELALWQQY
 LGRAAALHEIGLDIAHTGYHKHSAYILENADMPGFSRKEQTLAQLVIGHRGDMKKMSGI
 IGTNEMLWYAVLSRLAALFCRSRQDLSFPKNMQLRTDTESCGFILRIDREWLERHPLIA
 DALEYESVQWQKINMPFKVEAV

15 NMB2056 HemK

ATGAACGGTAAATACTACTACGGCACAGGCCGCCGCAAAAGTTCAGTGGCTCGTGATTC
 CTGATTAAAGGTACAGGTCAAATCATCGTAAACGGTCGTCCCGTTGACGAATTCCTCGCA
 CGGGAAACCAGCCGAATGGTTGTTTCGCCAACCCCTTGGTTCTGACTGAAAACGCCGAATCT
 TTCGACATCAAAGTCAATGTTGTTGGCGGCGCGCAAACCGGCCAGTCCGGCGCAATCCGC
 20 CACGGCATTACCCGTGCCCTGATCGACTTCGATGCCGCGTTGAAACCCGCCCTGTCTCAA
 GCTGGTTTTGTTACCCGCGATGCCGCGAAGTGAACGTAAAAAACCGGGTCTGCGCAAA
 GCACGCCGTGCAAAACAATTCTCCAACGTTAA

NMB2056 Protein sequence

25 MNGKYYYGTGRRKSSVARVFLIKGTGQIIVNGRPVDEFFARETSRMVVRQPLVLTENAES
 FDIKVVNVGGGETGQSGAIRHGITRALIDFDAALKPALSQAGFVTRDAREVERKKPGLRK
 ARRAKQFSKR

NMB0808 DNA sequence

30 ATGTCCGCCCTCCTCCCATCATCAACCGCTGATTCTGCAAAGCCCGGACAGCCGCTCG
 GAACTTGCCGCCTTTGCAGGCAAAACACTGACCCTGAACATTGCCGGGCTGAAACTGGCG
 GGACGCATCACGGAAGACGGTTTTGCTCTCGGCGGGAAACGGCTTTGCAGACACCGAAATT
 ACCTTCCGCAACAGCGCGGTACAGAAAATCCTCCAAGGAGGCGAACCCGGGGCGGGCGAC
 ATCGGGCTCGAAGGCGACCTCATCTCGGCATCGCGGTACTGTCCCTGCTCGGCAGCCTG
 35 CGTTCCCGCGCATCGGACGAATTGGCACGGATTTTCGGCACGCAGGCAGACATCGGCAGC
 CGTGCCGCGGACATCGGACACGGCATCAAACAAATCGGCAGGAACATCGCCGAACAAATC
 GGCGGATTTTCCCGCGAATCCGAGTCCGCAAACATCGGCAACGAAGCCCTTGCCGACTGC
 CTCGACGAAATAAGCAGACTGCGCGACGGCGTGGAACGCCTCAACGAACGCCTCGACCGG
 CTCGAACGCGACATTTGGATAGACTAA
 40

NMB0808 Protein sequence

MSALLPIINRLILQSPDSRSELAFAAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
 TFRNSAVQKILQGEPGAGDIGLEGLDILGIAVLSSLGSLRSRASDELARIFGTQADIGS
 45 RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRRLRDGVERLNERLDR
 LERDIWID

NMB0774 upp DNA sequence

ATGAACGTTAATGTTATCAACCATCCGCTCGTCCGCCACAAATTAACCCTGATGAGGGAG
 GCGGATTGCAGACCTACAAATTCGGGACGCTTGCCACCGAGCTGGCGCGCCTGATGGCA
 50 TACGAGGCAAGCCGTGATTTTGAAATCGAAAAATACCTTATCGACGGATGGTGCGGTGAG
 ATTGAAGGCGACCGCATCAAGGGCAAAACATTGACCGTCGTTCCTACTGCGTGCAGGT
 TTGGGTATGCTTGACGGTGTGCTCGACCTGATTCCGACTGCCAAAATCAGTGTAGTCGGA
 CTGCAGCGCGACGAAGAAACGCTGAAGCCTATTTCTATTTGAGAAATTTGTGGACAGT
 ATGGACGAACGTCCGGCTTTGATTATCGATCCTATGCTGGCGACAGGCGGTTGATGGTT
 55 GCCACCATCGACCTTTTGAAAGCCAAGGGCTGCAAAAATATCAAGGCACTGGTGTGGTT
 GCCGCGCCCCGAGGGTGTGAAGGCGGTCAACGACGCGCACCCCTGACGTTACGATTTACACC
 GCCGCGCTCGACAGCCACTTGAACGAGAACGGCTACATCATCCCCGGCTTGGGCGATGCG

GGCGACAAGATTTTCGGCACGCGCTAA

NMB0774 Protein sequence

MNVNVINHPLVRHKLTLMREADCSTYKFRTLATELARLMAYEASRDFEIEKYLIDGWCGQ
 5 IEGDRIKGTLLTVVPILRAGLGLMDGVLDLIPTAKISVVGLQRDEETLKPISYFEKFDVDS
 MDERPALIIDPMLATGGSMVATIDLLKAKGCKNIKALVLVAAPGKAVNDAHDPDVTIYT
 AALDSHLNENGYIIPGLGDAGDKIFGTR

NMA0078 putative integral membrane protein DNA sequence

10 TTGGCGTTTACTTTAATGCGTCGCGCCATGATACGTAAAATGCCCTATACGGAAGATATG
 CGCCCAGGCGATACCGCTAATCCTTATGGTGCCTCCAAAGCGATGGTGGAACGGATGTTA
 ACCGACATCCAAAAGCCGATCCGCGCTGGAGCATGATTTTGTTCGCTTATTTCAATCCG
 ATTGGCGCGCATGAAAGCGGCTTGATTGGCGAGCAGCCAAACGGCATCCCGAATAATTTG
 TTGCCTTATATCTGCCAAGTGGCGGCAGGCAAACCTGCCGCAATTGGCGGTATTTGGCGAT
 15 GACTACCCTACCCCCGACGGCACGGGGATGCGTGACTATATTCATGTGATGGATTTGGCA
 GAAGGCCATGTCGCGGCTATGCAGGCAAAAAGTAATGTAGCAGGCACGCATTTGCTGAAC
 TTAGGCTCCGGCCGCGCTTCTTCGGTGTGGAAATCATCCGCGCATTTGAAGCAGCTTCG
 GGTTTGACGATTCCGTATGAAGTCAAACCGCGCCGTGCCGGTGATTGGCGTGCTTCTAT
 GCCGACCCTTCCTATACAAAGGCGCAAATCGGCTGGCAAACCCAGCGTGATTAAACCCAA
 20 ATGATGGAAGACTCATGGCGCTGGGTGAGTAATAATCCGAATGGCTACGACGATTAA

NMA0078 Protein sequence

MAFTLMRRAMIRKMPYTEDMRPGDTANPYGASKAMVERMLTDIQKADPRWSMILLRYFNP
 IGAHESGLIGEOPNGIPNNLLPYICQVAAGKLPQLAVFGDDYPTPDGTGMRDYIHVMDLA
 25 EGHVAAMQAKSNVAGTHLLNLGSGRASSVLEIIRAFEAAAGSLTIPYEVKPRRAGDLACFY
 ADPSYTKAQIGWQTQDRLTQMMEDSWRWVSNPNNGYDD

NMB0337 Branched-chain amino acid aminotransferase DNA sequence

ATGAGCAGACCCGTACCCGCCGTATTCGGCAGCGTTTTTCACAGTCAAATGCCCGTCCTC
 30 GCCTACCGCGAAGGCAAATGGCAGCCGACCGAATGGCAATCTTCCAAGACCTCTCCCTC
 GCACCGGGCGCGCACGCCCTGCACTACGGCAGCGAATGTTTCGAGGGACTGAAAGCCTTC
 CGTCAGGCAGACGGCAAAATCGTGCTGTTCCGTCCGACTGCCAATATCGCGCGTATGCGG
 CAAAGTGCGGACATTTTGCACCTGCCGCGCCCCGAAACCGAAGCTTATCTTGACGCGCTA
 ATCAAATTGGTCAAACGTGCCGCCGATGAAATTCGCGATGCGCCTGCCGCCCTGTACCTG
 35 CGTCCGACCTTAATCGGTACCGATCCCGTTATCGGCAAGGCCGGTTCTCCTTCCGAAACC
 GCCCTGCTGTATATTTGGCTTCCCCCGTCGGCGACTATTTCAAAGTCGGATCGCCCGTC
 AAAATTTTGGTGGAACCGAACACATCCGCTGCGCCCCGCATATGGGCCGCGTCAAATGC
 GGCGGCAACTACGCTTCCGCCATGCACTGGGTGCTGAAGGCGAAAGCCGAATATGGCGCA
 AATCAAGTCCTGTTCTGCCGAACGGCGACGTGCAGGAAACGGCGCGTCCAACCTTTATC
 40 CTGATTAACGGCGATGAAATCATTACCAAACCGCTGACCGACGAGTTTTTGCACGGCGTA
 ACCCGCGATTCCGTACTGACGGTTGCCAAAGATTTGGGCTATACCGTCAGCGAACGCAAT
 TTCACGGTTGACGAACTCAAAGCTGCGGTGGAAAACGGTGCGGAAGCCATTTTGACCGGT
 ACGGCAGCCGTATCTCGCCCGTTACTTCCTTCGTATCGGCGGCAAAGAAATCGAAGTG
 AAAAGCCAAGAACGGGCTATGCCATCCGTAAGGCGATTACCGACATCCAGTATGGTTTG
 45 GCGGAAGACAAATACGGCTGGCTGGTTGAAGTGTGCTGA

NMB0337 Protein sequence

MSRPVPAVFGSVFHSQMPVLAYREGKWQPTWQSSQDLAPGAHALHYGSECFEGLKAF
 RQADGKIVLFRPTANIARMQASADILHLPRPETEAYLDALIKLVKRAADEIPDAPAAALYL
 50 RPTLIGTDPVIGKAGSPSETALLYILASPVGDYFKVGSFVKILVETEHIRCAPHMGRVKC
 GGNYSAMHWWLKAKEYGANQVLFPCPNGDVQETGASNFILINGDEIITKPLTDEFLHGV
 TRDSVLTVAKDLGYTVSERNFTVDELKAAVENGAFAAILTGTAAVISPVTSFVIGGKEIEV
 KSQERGYAIRKAITDIQYGLAEDKYGWLVEVC

NMB0191 ParA family protein DNA sequence

ATGAGTGCGAACATCCTTGCCATCGCCAATCAGAAGGGCGGTGTGGGCAAAACGACGACG

ACGGTAAATTTGGCGGCTTCGCTGGCATCGCGCGGCAAACGCGTGCTGGTGGTCGATTTG
GATCCGCAGGGCAATGCGACGACGGGCAGCGGCATCGACAAGGCGGGTTTGCAGTCCGGC
GTTTATCAGGTCTTATTGGGCGATGCGGACGTGCAGTCGGCGGCGGTACGCAGCAAAGAG
GGCGGATACGCTGTGTTGGGTGCGAACC CGCGCTGGCCGGCGCGGAAATCGAACTGGTG
5 CAGGAAATCGCCCGGGAAGTGCSTTTGAAAAACGCGCTCAAGGCAGTGGAAGAAGATTAC
GACTTTTATCCTGATCGACTGCCCCGCTTCGCTGACGCTGTTGACGCTTAACGGGCTGGTG
GCGGCGGGCGGCGTGATTGTGCCGATGTTGTGCGAATATTACGCGCTGGAAGGGATTTC
GATTTGATTGCGACCGTGCGCAAAATCCGTCAGGCGGTCAATCCCGATTGACATCACG
GGCATCGTGCGACGATGTACGACAGCCGAGCAGGCTGGTTGCCGAAGTCAGCGAACAG
10 TTGCGCAGCCATTTGGGGATTGCTTTTTGAAACCGTCATCCCGCGCAATATCCGCCTT
GCGGAAGCGCCGAGCCACGGTATGCCGGTGATGGCTTACGACGCGCAGGCAAAGGGTACC
AAGGCGTATCTTGCTTGGCGGACGAGCTGGCGGCGAGGGTGTCGGGGAAATAG

NMB0191 Protein sequence

15 MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLPQGNATTGSGIDKAGLQSG
VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
GIVRTMYDSRSLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQKGT
KAYLALADELAARVSGK

NMB1710 Glutamate dehydrogenase(gdhA) DNA sequence

ATGACTGACCTGAACACCCTGTTTGCCAACCTCAAACAACGCAATCCCAATCAGGAGCCG
TTCCATCAGGCGGTTGAAGAAGTCTTCATGAGTCTCGATCCGTTTTTGGCAAAAAATCCG
AAATACACCCAGCAAAGCCTGCTGGAACGCATCGTCGAACCCGAACGCGTCGTGATGTTT
25 CGCGTAACCTGGCAGGACGATAAAGGGCAAGTCCAAGTCAACCGGGGCTACCGCGTGCAA
ATGAGTTCGCCCATCGGTCTTACAAAGGCGGCCTGCGCTTCCATCCGACCGTCGATTTG
GGCGTATTGAAATTCCTCGCTTTTGAACAAGTGTTCAAAAACGCCTTGACCACCCTGCCT
ATGGGCGGCGGCAAAGGCGGTTCCGACTTCGACCCCAAAGGCAAATCCGATGCCGAAGTA
ATGCGCTTCTGCCAAGCCTTTATGACCGAACTCTACCGCCACATCGGCGCGGACACCGAT
30 GTTCCGGCCGGCGACATCGGCGTAGGCGGGCGCGAAATCGGCTACCTGTTCCGACAATAC
AAAAAATCCGCAACGAGTTTTCTTCGCTCCTGACCGGCAAAGGTTTGAATGGGGCGGC
AGCCTCATCCGTCCCGAAGCGACCGGCTACGGCTGCGTCTATTTGCCCCAAGCGATGCTG
CAAACCCGCAACGATAGTTTTGAAGGCAAACGCGTCTGATTTCCGGCTCCGGCAATGTG
GCGCAATACGCGCCGCCGAAAAAGCCATCCAACCTGGGTGCGAAAGTACTGACCGTTTCCGAC
35 TCCAACGGCTTCGTCTCTTCCCCGACAGCGGTATGACCGAAGCGCAACTCGCCGCCTTG
ATCGAATTGAAAGAAGTCCGCCGCGAACGCGTTGCCACCTACGCCAAAGAGCAAGGTCTG
CAATACTTTGAAAAACAAAAACCGTGGGGCGTCGCCGCCGAAATCGCCCTGCCCTGCGCG
ACCCAGAACGAATTGGACGAAGAAGCGCCAAAACCTGTTGGCAAACGGCTGCTACGTC
GTTGCCGAAGGTGCGAATATGCCGTCGACTTTGGGCGCGGTGAGCAATTTATCAAAGCC
40 GGCATCTCTACGCCCCGGGAAAAGCCTCCAATGCCGGCGGCGTGCAACTTCAGGTTTG
GAAATGAGCCAAAACGCCATCCGCCTGTCTTGGACTCGTGAAGAAGTCGACCAACGCCTG
TTCGGCATCATGCAAAGCATCCACGAATCCTGTCTGAAATACGGCAAAGTCGGCGACACA
GTAAACTACGTCAATGGTGCGAACATTGCCGTTTCGTCAAAGTTGCCGATGCGATGCTG
GCGCAAGGCTTCTAA

NMB1710 Protein sequence

55 MTDLNTLFANLKQRNPQNQEPFHQAVEEVFMSLDPFLAKNPKYTQQSLLERIVEPERVVMF
RVTWQDDKGQVQVNRGVRVQMSSAIGPYKGGLRFHPTVDLGVLFKFLAFEQVFKNALTTLP
MGGGKGGSDFDPKGKSDAEVMRFCQAFMTELYRHIGADTDVPAGDIGVGGREIGYLFQGY
KKIRNEFSSVLTGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNV
AQYAAEKAIQLGAKVLTVSDSNGFVLFPSGDMTEAQLAALIELKEVRRERVATYAKEQGL
QYFEKQKWPVGVAEIALPCATQNELDEEAAKTLLANGCYVVAEGANMPSTLGAVEQFIKA
GILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEDVQRLFGIMQSIHESCLKYKVGDT
VNYVNGANIAGFVKVADAMLAQGF

NMB0062 Glucose-1-phosphate thymidylyltransferase(rfbA-1) DNA sequence

ATGAAAGGCATCATACTGGCAGGCGGCAGCGGCACGCGCCTCTACCCCATCACGCGCGGC
GTATCCAAACAGCTCCTGCCCCGTGTACGACAAACCGATGATTTATTACCCCTTGTCGGTT

TTGATGCTGGCGGGAATCCGCGATATTTTGGTGATTACCGCGCCTGAAGACAACGCCTCT
 TTCAAACGCCGTGCTTGGCGACGGCAGCGATTTCGGCATTTCATCAGTTATGCCGTGCAA
 CCCAGTCCGGACGGCTTGGCACAGGCATTTATCATCGGCGAAGAATTTATCGGCAACGAC
 AATGTTTGGCTTGGTTTTTGGGCGACAATATTTTTTACGGTCAGTCGTTTACGCAACATTG
 5 AAACAGGCGCGCAGCGCAAACGCACGGCGCAACCGTGTTTGTATCAGGTCAAAAACCC
 GAACGTTTTCGGCGTGTTGAATTTAACGAAAACCTCCGCGCCGTTTCCATCGAAGAAAA
 CCGCAACGGCCCAAATCCGATTGGGCGGTAACCGGCTTGTATTTCTACGACAACCGCGCC
 GTCGAGTTCGCCAAACAGCTCAAACCGTCCGCACGCGCGAATTGGAAATTACCGACCTC
 AACC GGATGTATTTGGAAGACGGCTCGCTCTCCGTTCAAATATTGGGACGCGGTTTCGCG
 10 TGGCTGGACACCGGCACCCACGAGAGCCTGCACGAAGCCGCTTCATTCTGTCGAAACCGTG
 CAAAATATCCAAACCTGCACATCGCCTGCCTCGAAGAAATCGCTTGGCGCAACGGTTGG
 CTTTCCGATGAAAACTGGAAGAATTGGCGCGCCCGATGGCGAAAAACCAATACGGCCAA
 TATTTGCTGCGCCTGTTGAAAAAATAA

15 NMB0062 Protein sequence

MKGIILAGSGTRLYPITRGVSKQLLPVYDKPMIYYPLSVLMLAGIRDILVITAPEDNAS
 FKRLLDGSDFGISISYAVQSPDGLAQAFIIGEEFIGNDNVCLVLGDNIIFYGQSFTQTL
 KQAAAQTHGATVFAYQVKNPERFGVVEFNENFRAVSIIEKPQRPKSDWAVTGLYFYDNRA
 VEFKQLKPSARGELEITDLNRMYLEDGSLSVQILGRGFAWLDTGTHESLHEAASFVQTV
 20 QNIQNLHIACLEEIAWRNGWLSDEKLEELARPMKNQYGYLLRLLKK

NMB1583 Imidazoleglycerol-phosphate dehydratase(hisB) DNA sequence

ATGAATTTGACTAAAACACAACGCCAACTGCACAACCTTCTGACCCTCGCCCAAGAAGCA
 GGTTTCGCTGTCCAAGCTCGCCAACTCTGCGGCTACCGTACCCCGTCGCACTCTACAAA
 25 CTCAAACAACGCCTTGAAAAGCAGGCAGAAGACCCAGATGCACGCGGCATCCGTCCCAGC
 CTGATGGCAAACTCGAAAAACACACCGGCAAACCCAAAGGCTGGCTCGACAGAAAAACAC
 CGCGAACGCACTGTCCCCGAAACCGCCGCAGAAAGCACCGGAACCTGCCGAAACCCAAAT
 GCCGAAACCGCATCTGCTGCCGGCTGCCGCAGCGTTACCGTCAACCGCAATACCTGCGAA
 ACCCAAATCACCGTCTCCATCAACCTCGACGGCAGCGGCAAAAGCAGGCTGGATACCGGC
 30 GTACCTTCTCCTCGAACACATGATCGATCAAATCGCCCGCCACGGCATGATTGACATCGAC
 ATCAGCTGCAAAGGCGACCTGCACATCGACGACCACACACCGCCGAAGACATCGGCATC
 ACACTCGGACAAGCAATCCGGCAGGCACTCGGCGACAAAAAAGGCATCCGCCGTTACGGA
 CATTCCTACGTCCCGCTCGACGAAGCCCTCAGCCGCGTCTCATCGACCTTTCCGGCCGC
 CCCGGACTCGTGTACAACATCGAATTTACCGCGCACTAATCGGACGTTTCGATGTCGAT
 35 TTGTTTGAAGAATTTTTCCACGGCATCGTCAACCACAGTATGATGACCTGCACATCGAC
 AACCTCAGCGGCAAAAACGCCACCATCAGGCGGAAACCGTATTCAAAGCCTTCGGGCGC
 GCCCTGCGTATGGCAGTCGAACACGACCCGCGCATGGCAGGACAGACCCCTCGACCAAA
 GGCACGCTGACCGCATAA

40 NMB1583 Protein sequence

MNLTKTQRQLHNFLTLAQEAGSLSKLAKLCGYRTPVALYKLKQRLKQAEKQEDPDARGIRPS
 LMAKLEKHTGKPKGWLDKRRERTVPETAESTGTAETQIAETASAAGCRSVTVNRNTCE
 TQITVSINLDGSGKSRLDTGVFFLEHMIDQIARHGMIDIDISCKGDLHIDDHHTAEDIGI
 TLGQAIRQALGDKKIRRYGHSYVPLDEALSRRVIDLSGRPGLVYNIEFTRALIGRFVD
 45 LFEEFFHGIVNHSMMTLHIDNLSGKNAHQAEVFKAFGRALRMAVEHDPDMAGQTPSTK
 GTLTA

The following additional antigens were identified using essentially the
 50 methodology described above:

NMB1333 Nucleic acid sequence

ATGCGCTACAAACCCCTTCTGCTTGCCCTGATGCTCGTTTTTCCACGCCCCCGGTTGCC
 GCCCACGACGCGGCACACAACCGTTCCGCCGAAGTGAAAAACAGACGAAGAACAAAAA
 55 GAACAGCCCGAAGCGGCGGAAGGCAAAAAGAAAAAGGCAAAAATGGCGCAGTGAAAGAT

AAAAAAACAGGCGGCAAGAGGCGGCAAAAGAGGGCAAAAGAGTCCAAAAAACCGCCAAA
 AACCGCAAGAAGCAGAGAAGGAGGCGACATCCAGGCAGTCTGCGCGCAAAGGACGCGAA
 GGGGATAAGAAATCGAAGGCGGAACACAAAAAGGCACATGGCAAGCCCGTGTCCGGATCC
 AAAGAAAAAACGCAAAACACAGCCTGAAAAACAAAGGCAAAAAAGAGGCAAAAGGA
 5 CAGGGCAATCCGCGCAAGGGCGGCAAGGCGGAAAAAGACACTGTTTCTGCAAATAAAAA
 GTCCGTTCCGACAAGAACGGCAAGCAGTGAAACAGGACAAAAATACAGGGAAGAGAAA
 AATGCCAAAACCGATTCCGACGAATTGAAAGCCGCCGTTGCCGCTGCCACCAATGATGTC
 GAAAAACAAAAAGCCCTGCTCAAAACAAAGCGAAGGAATGCTGCTTCATGTCAGCAATTCC
 10 CTCAAACAGCTTCAGGAAGAGCGTATCCGCCAAGAGCGTATCCGTGAGGCGCGCGGCAAC
 GAGCTGAACCGTTTGA AAAACGGAAGTCGCCGCTACGAAAGCGCAGATTTCCCGTTTCGTA
 TCGGGGAACTATAAAAAACAGCCAGCCGAATGCGGTTGCCCTGTTCTGAAAAACGCCGAA
 CCGGGTCAGAAAAACCGCTTTTTCGCTTATACGCGTTATGTAAACGCCTCCAATCGGGAA
 GTTGTCAAGGATTTGGAAAAACAGCAGAAGGCTTTGGCGGTACAAGAGCAGAAAAATCAAC
 15 AATGAGCTTGCCCGTTTGAAGAAAATTCAGGCAAACGTGCAATCTCTGCTGAAAAACAG
 GGTGTAACCGATGCGGCGGAACAGACGGAAAGCCGCGAGCAGAATGCCAAAATCGCCAAA
 GATGCCCGAAAACCTGCTGGAACAGAAAGGGAACGAGCAGCAGCTGAACAAGCTCTTGAGC
 AATTTGGAGAAGAAAAAGGCCGAACACCGCATTCAGGATGCGGAAGCAAAAAGAAAATTG
 GCTGAAGCCAGACTGGCGGCAGCCGAAAAAGCCAGAAAAGAAGCGGCGCAGCAGAAGGCT
 20 GAAGCAGCAGCTGCGGGAATGTCCAACCTGACCGCCGAAGACAGGAACATCCAAGCGCCT
 TCGGTTATGGGTATCGGCAGTGCCGACGGTTTCAGCCGCATGCAAGGACGTTTGAAAAAA
 CCGGTTGACGGTGTGCCGACCGGACTTTTCGGGCAGAACCGGAGCGGCGGCGATATTGG
 AAAGGCGTGTCTATTCCACTGCACCGGCAACGGTTGAAAGCATTGCGCCGGAACGGTA
 AGCTATGCGGACGAGTTGGACGGCTACGGCAAGTGGTGGTTCGATCACGGCGAGAAC
 25 TACATCAGCATCTATGCCGTTTGGAGCGAAATTTCCGTGCGCAAGGGTTATATGGTCGCG
 GCAGGAAGCAAAATCGGCTCGAGCGGGTCTGCCGACGGGGAAGAGGGGCTTTACCTG
 CAAATACGTTATCAAGGTCAGGTATTGAACCTTCGAGCTGGATACGTTGA

NMB1333 Amino acid sequence

30 MRYKPLLLALMLVFSTPAVAAHDAAHNRSAEVKKQTKNKKEQPEAAEGKKEKGKNGAVKD
 KKTGGKEAAKEGKESKKTAKNRKEAEKEATSRSARKGREGDKSKAEHKKAHGKPVSGS
 KEKNAKTQPENKQKKEAKGQGNPRKGGKAEDTVSANKKVRSDKNGKAVKQDKKYREEK
 NAKTDSDELKAAVAAATNDVENKKALLKQSEGMLLHVSNSLKLQLEERIRQERIRQARGN
 LASVNRKQREAWDKFQKLNTELNRKTEVAATKAQISRFVSGNYKNSQPNVALFLKNAE
 35 PGQKNRFLRYTRYVNASNREVVKDLEKQKALAVQEQKINNELARLKKIQANVQSLKKQ
 GVTDAEQTESRRONAKIAKDARKLLEQKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKL
 AEARLAAAEKARKEAAQKAEARRAEMSNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLK
 PVDGVPTGLFGQNRSGDIWKGVFYSTAPATVESIAPGTVSYADELDGYGKVVVDHGEN
 YISIIYAGLSEISVGKGYMVAAGSKIGSSGSLPDGEEGLYLQIRYQGQVLNPSSWIR
 40

NMB0377 Nucleic acid sequence

ATGGCGTTTTGCACCAAGTTTGGGAGTGATGATGGAAACACAGCTTTACATCGGCATCATG
 TCGGGAACCAGCATGGACGGGGCGGATGCCGTACTGATACGGATGGACGGCGGCAATGG
 CTGGGCGCGGAAGGGCACGCCTTTACCCCTACCCCGGCAGGTTACGCCGCCAATTGCTG
 45 GATTTGCAGGACACAGGCGCAGACGAACTGCACCGCAGCAGGATTTTGTGCAAGAACTC
 AGCCGCCTATATGCGCAAACCGCCGCCGAACTGCTGTGCAGTCAAAACCTCGCACCGTCC
 GACATTACCGCCCTCGGCTGCCACGGGCAAACCGTCCGACACGCGCCGGAACACGGTTAC
 AGCATAACAGCTTGCCGATTGCGGCTGCTGGCGGAACGGACGCGGATTTTACCGTCGGC
 GACTTCCGCAGCCGCGACCTTGCGGCGCGGACAAGGCGCGCCACTCGTCCCCGCCTTT
 50 CACGAAGCCCTGTTCCGCGACAACAGGGAAACACGCGCGGTACTGAACATCGGCGGGATT
 GCCAACATCAGCGTACTCCCCCGACGCACCCGCCTTCGGCTTCGACACAGGGCCGGGC
 AATATGCTGATGGACGCGTGGACGCAGGCACACTGGCAGCTTCCTTACGACAAAAACGGT
 GCAAAGGCGGCACAAGGCAACATATTGCCGCAACTGCTCGACAGGCTGCTCGCCACCCG
 TATTTTCGCACAACCCACCCCTAAAAGCACGGGGCGCGAACTGTTTGCCTAAATTGGCTC
 55 GAAACCTACCTTGACGGCGGCGAAAACCGATACGACGTATTGCGGACGCTTTCCCGTTTT
 ACCGCGCAAACCGTTTGCACGCGCTCTCACACGACGCGGAGATGCCCGTCAAATGTAC
 ATTTGCGGCGGCGGCATCCGCAATCCTGTTTTAATGGCGGATTTGGCAGAAATGTTTCGGC

ACACGCGTTTCCCTGCACAGCACCGCCGACCTGAACCTCGATCCGCAATGGGTGGAAGCC
 GCCGCATTTGCGTGTTGGCGGCGTGTGGATTAATCGCATTCCCGGTAGTCCGCACAAA
 GCAACCGCGCATCCAAACCGTGTATTCTGGGCGCGGATATTATTATTGA

5 NMB0377 Amino acid sequence

MAFCTSLGVMMETQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTYPYGRRLRRQLL
 DLQDTGADELHRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHGY
 SIQLADLPLLAERTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDNRETRAVLNIGGI
 ANISVLPPDAPAFGFDTPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHP
 10 YFAQPHPKSTGRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMY
 ICGGGIRNPVLMADLAECFGTRVSLHSTADLNLDPOWVEAAFAWLAACWINRIPGSPHK
 ATGASKPCILGAGYYY

NMB0264 Nucleic acid sequence

15 ATGTTGAACAAAATATTTTCCCTGGTTCGAGTCCCGAATCGACCCTTATCCCGAAGCCGCC
 CCGAAAACGCCAGAAAAAGGCTTGTGGCGGTTTGTCTGGAGCAGCATGGCCGGCGTGCGG
 AAATGGATAGCCGCCCTGGCTGCGCTGACCGCCGCATCGGCATTATGGAAGCCCTGGTT
 TTTCAATTTATGGGCAAATCGTGGAGTGGCTCGGCAAATACGCGCCCGCCGAAGTGT
 GCCGAAAAAAGTTGGGAAGTGGCGGCAATGGCGGCGATGATGGTATTTTCGGTTGCGTGG
 20 GCGTTTGGCGCGTCCAACGTGCGCCTGCAAAACCCTTCAGGGCGTGTTCGCCATGCGCCTG
 CGCTGGAACTTCCACCGCTGATGCTGAACCAAAGCCTCGGTTTTTATCAGGACGAATTT
 GCCGGACGCGTGTCCGCCAAAGTCATGCAGACCGCGCTGGCGTTGCGCGACGCGGTGATG
 ACGGTTGCCGATATGGTCGTTTATGTGTGCGGTGATTTTCATTACCTCCGGCGTGATTCTC
 GCCTCGCTCGACTCATGGCTGCTGCTGCCCTTTATCGGCTGGATTGTGCGTTTCGCTTCG
 25 GTGATGCGCCTGCTGATTCCCAAATTGGGGCAAACCGCCGCATGGCAGGCGGATGCCCGC
 TCGCTGATGACCGGCCGATTACCGATGCCTATTCCAATATCGCCACCGTCAAACCTCTTC
 TCCCACGGCGCGCGTGAAGCCGCCTATGCCAAGCAGTCGATGGAAGAATTTATGGTTACG
 GTGCGCGCCCAAATGCGGCTGGCGACGCTGCTGCATTCTGTGAGCTTCATCGTCAACACC
 TCCCTGACCCTCTCCACCGCCGCACTGGGCATCTGGCTCTGGCACAACGGGCAGGTCCGGC
 30 GTGGGCGCGGTTGCTACAGCCACCGCCATGGCGTTGCGCGTCAACGGTTTGTGCAATAC
 ATTATGTGGGAATCCGCGCGGCTGTTTGAAAACATCGGCACCGTCCGGCAGCGCATGGCA
 ACCCTGTCCAAACCGCACACCATCCTCGACAAGCCCGGGCACTGCCGCTGAACGTGCCG
 CAAGGCGCAATCAAATTTGAACACGTGATTTCTCCTACGAAGCGGGCAAACCGCTGCTC
 AACGGCTTCAACCTCACCATCCGCCCCGGGCGAAAAAGTCGGCTTGATCGGACGCGAGCGGC
 35 GCGGGCAAATCCACCATCGTCAACCTGCTTTTGGCGTTCTACGAACCGCAAAGCGGCACG
 GTTTCGATCGACGGGCAGGACATAAGCGGCGTTACCCAAGAATCTTTACGCGCCCAAATC
 GGTTTGGTCACGCAAGATACCTCGCTGCTGCACCGTTCCGTGCGCGACAACATTATTTAC
 GGCCGCCCCGACGCGACCGATGCCGAAATGGTTTCTGCCGCCGAACGCGCCGAAGCCGCC
 GGCTTCATCCCCGACCTTTCCGATGCCAAAGGGCGGCGGGCTACGACGCACACGTCCGGC
 40 GAACGCGGCGTGAAACTCTCCGGCGGGCAACGCCAGCGCATCGCCATCGCCCGCGTGATG
 CTCAAAGACGCACCGATTCTTCTTTTGGACGAAGCCACCAGCGCGCTCGATTCCGAAGTC
 GAAGCCGCCATCCAAGAAAGCCTCGACAAAATGATGGACGGCAAACCGTCATCGCCATC
 GCCCACCGCCTCTCCACCATCGCCGCAATGGACAGGCTCGTCTGCTCGACAAAGGCCGC
 ATCATCGAAGAAGGCACACACGCCGAACCTCTCGAAAAACGCGGGCTTTACGCCAAACTC
 45 TGGGCGCACAGAGCGGCGGCTTCTCAACGAACACGTGAGTGGCAGCACGACTGA

NMB0264 Amino acid sequence

MLNKIFSWFESRIDPYPEAAPKTPEKGLWRFWSSMAGVRKWIAALAALTAGIGIMEALV
 FQFMGKIVEWLKGYAPAELEFAEKSWELAAMAAMMVFSVAWAFASNVRLQTLQGVFPMRL
 50 RWNFHRLMLNQSLGFYQDEFAGRVSQVMQALALRDVMTVADMVVVSVYFITSVIL
 ASLDSWLLLLPFIGWIVGFASVMRLLIPLKLGQTAAWQADARSMTGRITDAYSNIATVKLF
 SHGAREAAAYAKQSMEEFMVTVRAQMRLATLLHSCSFIVNTSLTLSTAALGIWLWHNGQVG
 VGAVATATAMALRVNGLSQYIMWESARLFENIGTVGDGMATLSKPHTILDKPRALPLNVP
 QGAIKFEHVDFS YEAGKPLNNGFNLTIRPGEKVGLIGRSGAGKSTIVNLLLRFYEPQSGT
 55 VSDIGQDISGVTQESLRAQIGLVTDTSLLHRSVRDNIYGRPDATDAEMVSAERAEEA
 GFIPDLSDAKGRRGYDAHVGERGVKLSGGQQRQRIARVMLKDAPILLLDEATSALDSEV
 EAAIQESLDKMMDGKTVIAIAHRLSTIAAMDRLVVLDKGRIIEEGTHAEELLEKRGLYAKL
 WAHQSGGFLNEHVEWQHD

NMB1036 Nucleic acid sequence

ATGACAGCACAAACCCCTCTACGACAAACTTTGGAACAGCCACGTCGTCCGCGAAGAAGAA
 GACGGCACCGTCTCTGCTCTACATCGACCGCCATTTGGTGACGAAGTTACCAGCCCTCAG
 5 GCATTTGAAGGCTTGAAAATGGCGGGGCGCAAGCTGTGGCGCATCGACAGCGTCGTCTCC
 ACCGCCGACCACAACACCCCGACCGGCGATTGGGACAAAGGCATCCAAGACCCGATTTC
 AAGCTGCAAGTCGATACTTTGGACAAAAACATTAAAGAGTTTGGCGCACTCGCCTATTTT
 CCGTTTATGGACAAAGGTCAGGGCATCGTACACGTTATGGGCCCCGAACAAGGCGCGACC
 CTGCCCCGTATGACCGTCGTCTGCGGCGACTCGCACACTTCCACCCACGGCGCATTCGGC
 10 GCACTGGCGCACGGCATCGGCACCTTCCGAAGTCGAGCACACCATGGCGACCCAATGTATT
 ACCGCGAAAAAATCCAAATCCATGCTGATTTCCGTTGACGGCAAATTAAAAGCGGGCGTT
 ACCGCCAAAGACGTGGCGCTCTACATCATCGGGCAAATCGGCACGGCAGGCGGTACAGGC
 TACGCCATCGAGTTTGGCGGCGAAGCCATCCGCAGCCTTTCTATGGAAAGCCGCATGACT
 TTATGCAATATGGCGATTGAGGCAGGCGCGCGCTCAGGCATGGTTGCCGTCGACCAAACC
 15 ACCATCGACTACGTAAAAGATAAACCTTCGCACCCGAAGGCGAAGCGTGGGACAAAGCC
 GTCGAGTACTGGCGTACGCTGGTGTCTGACGAAGGTGCGGTATTCGACAAAGAATACCGT
 TTCAACGCCGAAGACATCGAACC GCAAGTCACTTGGGGTACCTCGCCTGAAATGGTTTTA
 GACATCAGCAGCAAAGTGCCGAATCCTGCCGAAGAAACCGATCCGGTCAAACGCAGCGGT
 ATGGAACGCGCCCTTGAATACATGGGCTTGGAAAGCCGTACGCCATTAAACGAAATCCCC
 20 GTCGACATCGTATTCATCGGCTCTTGACCAACAGCCGCATCGAAGACTTGCGCGAAGCC
 GCCGCCATCGCCAAAGACCGCAAAAAAGCCGCCAACGTACAGCGCGTGTAAATCGTCCCC
 GGCTCCGGTTTGGTTAAAGAACAAGCCGAAAAAGAGGCTTGGACAAAATTTTCATCGAA
 GCCGGTTTGAATGGCGCGAACC GGCTGTTCGATGTGTCTCGCCATGAACGCCGACCGC
 CTGACCCCGGGCAACGCTGCGCCTCCACCTCCAACCGTAACCTTTGAAGGCCGTCAAGGC
 25 AACGGCGGACGTACCCACCTCGTCAGCCCCGCTATGGCAGCAGCCCGCCCGTTACCGGC
 CGCTTTACCGACATCCGCATGATGGCGTAA

NMB1036 Amino acid sequence

30 MTAQTLYDKLWNSHVVEEDGTVLLYIDRHLVHEVTSPOAFEGCLKMAGRKLWRIDSVVS
 TADHNTPTGDWDKGIQDPI SKLQVDTL DKNIKEFGALAYFPFMDKGQGI VHVMP EQGAT
 LPGMTVVCGDSHTSTHGAFGALAHGIGTSEVEHTMATQCITAKKSKSMLISVDGKLKAGV
 TAKDVALYIIIGQIGTAGGTGYAIEFGGEAIRSLMESRMTLCNMAIEAGARSGMVAVDQT
 TIDYVKDKPFAPEGEAWDKAVEYWR TLVSDEGAVFDKEYRFNAEDIEPQVTWGTSP E MVL
 35 DISSKVPNP AEETDPVKRSGMERALEYMGLEAGTPLNEIPVDIVFIGSCTNSRIEDLREA
 AAIAKDRKKAANVQVRVLIVPGSLVKEQAEKEGLDKIFIEAGFEWREPGCSMCLAMNADR
 LTPGQRCASTSNRNFEGRQNGGRTHLVSPAMAAAAAVTGRFTDIRMMA

NMB1176 Nucleic acid sequence

40 ATGAAAGACAAGCACGATTCTTCCGCCATGCGGCTGGACAAATGGCTTTGGGCGGCACGT
 TTTTTCAAGACCCGTTCCCTTGCGCAAAAGCACATCGAACTGGGTAGGGTTCAAGTAAAC
 GGCTCGAAGGTCAAAAACAGTAAAACCATAGACATCGGCGATATTATCGACCTGACGCTC
 AATTCCCTTCCCTATAAAATCAAGGTTAAAGGTTTGAACCACCAACGCCGCCCGGCATCC
 GAGGCGCGGCTTCTGTATGAAGAGGACGCGAAAACGGCAACATTGAGGGAAGAGCGCAAA
 45 CAGCTCGACCAATTAGCCGCATCACTTCCGCCTATCCCGACGGCAGACCGACCAAGCGC
 GACCGCCGCAACTGGACAGGCTGAAAAAGGAGACTGGTAA

NMB1176 Amino acid sequence

50 MKDKHDSSAMRLDKWLWAARFFKTRSLAQKHIELGRVQVNGSKVKNSKTIDIGDIIDLTL
 NSLPYKIKVKGLNHQRRPASEARLLYEEDAKTATLREERKQLDQFSRITSAYPDGRPTKR
 DRRQLDRLKKGDW

NMB1359 Nucleic acid sequence

55 ATGAACCACACCGTTACCCTGCCCGACCAAACCACCTTTGCCGCCAACGACGGCGAAACC
 GTTTTGACCGCTGCCGCGCGTCAAAACCTCAACCTGCCCATTCCTGCAAAAGCGGTGTC
 TGGCGACAATGCAAAAGCCGAAGTGGTCAGCGGCGATATTCAAATGGGCGGACACTCGGAA
 CAGGCTTTATCCGAAGCAGAAAAAGCGCAAGGCAAGATTTTGATGTGCTGCACCACTGCG

CAAAGCGATATCAACATCAACATCCCCGGCTACAAAGCCGATGCCCTACCCGTCCGCACC
 CTGCCCCGACGCATCGAAAAGTATTATTTTCAAACACGATGTCGCCCTCCTGAAACTTGCC
 CTGCCCCAAAGCCCCGCCGTTTGCCTTCTACGCCGGGCAATACATTGATTTACTGCTGCCG
 5 GGCAACGTCAGCCGAGCTACTCCATCGCCAATTTACCCGACCAAGAAGGCATTTTGGAA
 CTGCACATCCGCAGGCACGAAAACGGTGTCTGCTCGGAAATGATTTTCGGCAGCGAAGCC
 AAAGTCAAAGAAAAAGGCATCGTCCGCGTTAAAGGCCCGCTCGGTTTCGTTTACCTTGCAG
 GAAGACAGCGGCAAAACCCGTCATCCTGCTGGCAACCGGCACAGGCTACGCCCCCATCCGC
 AGCATCCTGCTCGACCTTATCCGCCAAGGCAGCAACCGCGCCGTCATTTCTACTGGGGC
 GCGCGTCATCAGGATGATTTGTATGCCCTCGAAGAAGCACAAGGGTTGGCATGCCGTCTG
 10 AAAAAACGCTGCTTCACCCCCGTATTGTCCCGCCCCGGAGAGGGCTGGCAGGGAAGAAAT
 GGTACAGTACAAGACATCGCGGCACAAGACCACCCCGACCTGTCCGAATACGAAGTATTT
 GCCTGCGGTTCTCCGGCCATGACCGAACAAACAAAGAATCTGTTTGTGCAACAGCATAAG
 CTGCCGGAAGAACTTGTTTTCTCCGACGCATTACGCCGTCCGCATCATAA

15

NMB1359 Amino acid sequence

MNHVTLPDQTTFEAANDGETVLTAAARQNLNLPHSCKSGVCGQCKAELVSGDIQMGGHSE
 QALSEAEKAQGKILMCCTTAQSDININIPGYKADALPVRTLPAIESIIFKHDVALLKLA
 LPKAPFFAFYAGQYIDLLLPGNVSRSYSIANLPDQEGILELHIRRHENGVCSEMI F GSEP
 20 KVKEKGIVRVKGPLSFTLQEDSGKPVILLATGTGYAPIRSILLDLIRQGSNRAVHFYWG
 ARHQDDLIALYALEEAQGLACRLKNACFTPVLSRPGEGWQGRNGHVQDIAAQDHPDLSEYEVF
 ACGSPAMTEQTKNLFVQQHKL PENLFFSDAFTPSAS

25

NMB1138 Nucleic acid sequence

ATGAAAGACAAGCACGATTCTTCGCCCATGCGGCTGGACAAATGGCTTTGGGCGGCACGT
 TTTTTCAAGACCCGTTCCCTTGCGCAAAAGCACATCGAACTGGGTAGGGTTCAAGTAAAC
 GGCTCGAAGGTCAAAAACAGTAAAACCATAGACATCGGCGATATTATCGACCTGACGCTC
 AATTCCCTTCCCTATAAAAAATCAAGGTTAAAGGTTTGAACCACCAACGCCGCCCGGCATCC
 30 GAGGCGCGGCTTCTGTATGAAGAGGACGCGAAAACGGCAACATTGAGGGAAGAGCGCAAA
 CAGCTCGACCAATTGAGCCGCATCACTTCCGCCATCCCGACGGCAGACCGACCAAGCGC
 GACCGCCGCCAACTGGACAGGCTGAAAAAAGGAGACTGGTAA

35

NMB1138 Amino acid sequence

MKDKHDSSAMRLDKWLWAARFFKTRSLAQKHIELGRVQVNGSKVKNSKTIDIGDIIDLTL
 NSLPYKIKVKGILNHQRRPASEARLLYEEDAKTATLREERKQLDQFSRITSAYPDGRPTKR
 DRRQLDRLKKGDW

40

Schedule of SEQ ID Nos

SEQ ID No	Sequence
1	NMB0341 DNA
2	NMB0341 Protein
3	NMB1583 DNA
4	NMB1583 Protein
5	NMB1345 DNA
6	NMB1345 Protein

7	NMB0738 DNA
8	NMB0738 Protein
9	NMB0792 DNA
10	NMB0792 Protein
11	NMB0279 DNA
12	NMB0279 Protein
13	NMB2050 DNA
14	NMB2050 Protein
15	NMB1335 DNA
16	NMB1335 Protein
17	NMB2035 DNA
18	NMB2035 Protein
19	NMB1351 DNA
20	NMB1351 Protein
21	NMB1574 DNA
22	NMB1574 Protein
23	NMB1298 DNA
24	NMB1298 Protein
25	NMB1856 DNA
26	NMB1856 Protein
27	NMB0119 DNA
28	NMB0119 Protein
29	NMB1705 DNA
30	NMB1705 Protein
31	NMB2065 DNA
32	NMB2065 Protein
33	NMB0339 DNA
34	NMB0339 Protein
35	NMB0401 DNA
36	NMB0401 Protein
37	NMB1467 DNA
38	NMB1467 Protein

39	NMB2056 DNA
40	NMB2056 Protein
41	NMB0808 DNA
42	NMB0808 Protein
43	NMB0774 DNA
44	NMB0774 Protein
45	NMA0078 DNA
46	NMA0078 Protein
47	NMB0337 DNA
48	NMB0337 Protein
49	NMB0191 DNA
50	NMB0191 Protein
51	NMB1710 DNA
52	NMB1710 Protein
53	NMB0062 DNA
54	NMB0062 Protein
55	NMB1333 DNA
56	NMB1333 Protein
57	NMB0377 DNA
58	NMB0377 Protein
59	NMB0264 DNA
60	NMB0264 Protein
61	NMB1036 DNA
62	NMB1036 Protein
63	NMB1176 DNA
64	NMB1176 Protein
65	NMB1359 DNA
66	NMB1359 Protein
67	NMB1138 DNA
68	NMB1138 Protein

CLAIMS

1. A polypeptide comprising the amino acid sequence selected from any one of SEQ ID Nos 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34,
5 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68;

or a fragment or variant thereof or a fusion of such a fragment or variant.
2. A polynucleotide encoding a polypeptide according to Claim 1.
- 10 3. A polypeptide according to Claim 1 or polynucleotide according to Claim 2 for use in medicine.
4. A polypeptide according to Claim 1 or polynucleotide according to
15 Claim 2 for use in a vaccine.
5. A method for making a polypeptide according to Claim 1, the method comprising expressing the polynucleotide of Claim 2 in a host cell and isolating said polypeptide.
- 20 6. A method for making a polypeptide according to Claim 1 comprising chemically synthesising said polypeptide.
7. A method of vaccinating an individual against *Neisseria meningitidis*, the
25 method comprising administering to the individual a polypeptide according to Claim 1 or a polynucleotide according to Claim 2.
8. Use of a polypeptide according to Claim 1 or a polynucleotide according to Claim 2 in the manufacture of a vaccine for vaccinating an individual
30 against *Neisseria meningitidis*.

9. A pharmaceutical composition comprising a polypeptide according to Claim 1 or a polynucleotide according to Claim 2 and a pharmaceutically acceptable carrier.