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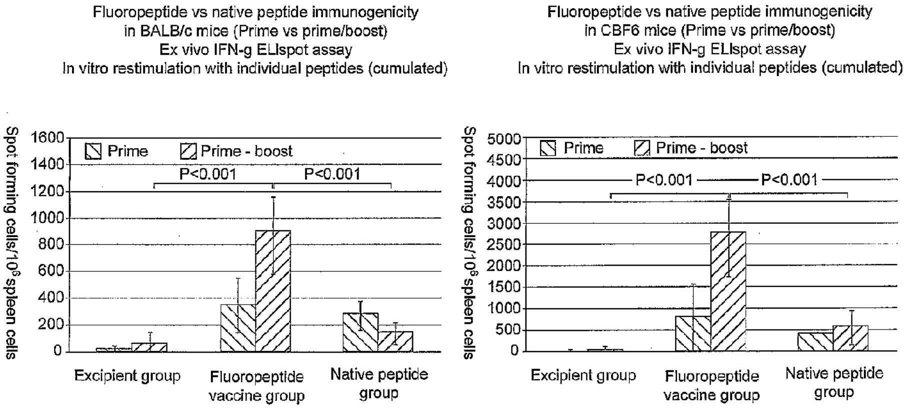

Fluoropeptide vs native peptide immunogenicity
in BALB/c mice (Prime vs prime/boost)
Ex vivo IFN-g ELIspot assay
In vitro restimulation with individual peptides (cumulated)

Fluoropeptide vs native peptide immunogenicity
in CBF6 mice (Prime vs prime/boost)
Ex vivo IFN-g ELIspot assay
In vitro restimulation with individual peptides (cumulated)

FIG. 1

(57) Abstract: The present invention relates to fluorocarbon vectors for the delivery of influenza antigens to immunoresponsive target cells. It further relates to fluorocarbon vector-influenza antigen constructs and the use of such vectors associated with antigens as vaccines and immunotherapeutics in animals, including humans.

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Influenza antigen delivery vectors and constructs

Background of the invention

Influenza is the generic term for diseases or infections caused by the influenza virus. Influenza viruses are members of the *Orthomyxoviridae* family of viruses and comprise two genera: influenza A and B viruses, and influenza C virus. Influenza A, B and C viruses are distinguished on the basis of their internal nucleoprotein and matrix proteins which are specific for each viral type. Influenza A viruses are naturally able to infect a range of animal species, including humans, swine, birds, seals and horses. Influenza B viruses, however, infect only humans, whilst influenza C virus infects humans and swine. Influenza A viruses are further categorised into subtypes that are determined by the antigenicity of the surface glycoproteins, the haemagglutinin (H) and neuraminidase (N).

Historically, influenza A human infections have been caused by three subtypes of haemagglutinin (H1, H2 and H3) and two neuraminidase subtypes (N1 and N2); more recently human infections by the previously avian-restricted subtypes H5, H7 and H9 have also been reported. A total of 16 distinct haemagglutinin and 9 neuraminidase influenza A subtypes have been identified to date; these are all prevalent in birds. Swine and horses, like humans, are limited to a much narrower range of subtypes.

Influenza A and B virions are pleiomorphic in structure, spherical examples being 80 - 120nm in diameter, whilst filamentous forms may be up to 300nm in length. There are approximately 500 surface spike glycoproteins per particle (usually in the ratio of four to five haemagglutinin proteins to one neuraminidase) that are embedded in a host-derived lipid bilayer membrane. Within the membrane is the transmembrane ion channel protein M2, whilst the structural protein M1 underlies the bilayer. Within the core of the virus, the single stranded negative sense RNA is associated with the six other viral proteins expressed from its genome: the nucleoprotein (NP), three transcriptases (PB2, PB1, and PA) and two nonstructural proteins (NS1 and NS2). The influenza virus genome comprises eight segments; a feature that enables "gene swapping" reassortment. The haemagglutinin enables the virus to bind to host cell receptors and facilitates the entry of the virus into the cell where it will replicate. The neuraminidase protein enzymatically cleaves terminal sialic acid residues, and is believed to assist in the transport of the virus through the mucin layer of the respiratory tract as well as facilitating the budding of the progeny virus away from the host cell. Influenza C viruses, which present much less of a health-risk to humans possess a single surface protein which combines the haemagglutinin, fusion activity and receptor destroying activity.

As a result of the error prone RNA polymerase enzyme, both the haemagglutinin and neuraminidase proteins of the influenza virus are liable to point mutations which need not necessarily affect the ability of the virus to replicate. Such a mutation (or coincident mutations) at one of the sites recognised by the host antibody response may result in the host antibody, induced by vaccination or a previous infection, being unable to bind effectively to the "new" virus strain thereby allowing an infection to persist. As the human influenza strains are continually evolving via these point mutations, the virus is able to escape from the limited antibody repertoire of the human immune response and cause epidemics. The regular "seasonal" bouts of influenza infections are therefore caused by the circulating strains in the population undergoing antigenic drift.

During seasonal epidemics influenza can spread around the world quickly and inflicts a significant economic burden in terms of hospital and other healthcare costs and lost productivity. The virus is transmitted in droplets in the air from human-to-human and targets epithelial cells in the trachea and bronchi of the upper respiratory tract. Influenza virus may also be picked up from contaminated surfaces and passed to the mouth. Disease spreads very quickly especially in crowded circumstances through coughing and sneezing. The stability of the virus is favoured by low relative humidity and low temperatures and, as a consequence, seasonal epidemics in temperate areas tend to appear in winter. Greater morbidity and mortality is observed with influenza A strains, with influenza B usually associated with lower attack rates and a milder disease. Occasionally, however, influenza B can cause epidemics of the same severity as type A viruses. Influenza B is primarily a childhood pathogen and does not usually exhibit the same degree of antigenic variation as type A.

The typical uncomplicated influenza infection is characterised by a rapid onset of illness (headache, cough, chills) followed by fever, sore throat, significant myalgias, malaise and loss of appetite. Further symptoms may include rhinorrhoea, substernal tightness and ocular symptoms. The most prominent sign of infection is the fever that is usually in the 38-40°C temperature range. Whilst the majority of people will recover from influenza infection within one to two weeks without requiring any medical treatment, for certain members of the population the disease may present a serious risk. Such individuals include the very young, the elderly and people suffering from medical conditions such as lung diseases, diabetes, cancer, kidney or heart problems. In this “at risk” population, the infection may lead to severe complications of underlying diseases, bacterial pneumonia, (caused by respiratory pathogens such as *Streptococcus pneumoniae, Haemophilus influenzae and Staphylococcus aureus)* and death. The clinical features of influenza infection are similar in children, although their fever may be higher and febrile convulsions can occur. In addition, children have a higher incidence of vomiting and abdominal pain as well as otitis media complications, croup and myositis.

The World Health Organization estimates that in annual influenza epidemics 5-15% of the population is affected with upper respiratory tract infections. Hospitalization and deaths mainly occur in high-risk groups (elderly and the chronically ill). Although difficult to assess, these annual epidemics are thought to result in between three and five million cases of severe illness and approximately 250 000 and 500 000 deaths every year around the world. Over 90% of the deaths currently associated with influenza in industrialized countries occur among the elderly over 65 years of age. In the U.S.A., the CDC estimate that more than 200,000 people are hospitalized every year on average following complications arising from seasonal influenza infection, with around 36,000 excess mortalities being recorded.

The host immune response that controls the recovery from influenza infection is conferred through a combination of serum antibodies directed to the surface proteins, mucosal secretory IgA antibodies and cell-mediated immune responses. About one to two weeks after a primary infection, neutralizing haemagglutination inhibiting (HAI) antibodies as well as antibodies to neuraminidase are detectable in the serum, peaking at approximately three to four weeks. After re-infection, the antibody response is more rapid. Influenza antibodies may persist for months or years, although in some high-risk groups antibody levels can begin to decline within a few months after vaccination. Secretory IgA antibodies peak approximately 14 days after infection and can be detected in saliva, nasal secretions, sputum and in tracheal washings. Preceding the occurrence of antibody-producing cells, cytotoxic T lymphocytes with specificity for influenza appear, and serve to limit the infection by reducing the maximal viral load whilst mediating more rapid viral clearance through the induction of antiviral cytokines and lysing infected cells. In addition, mononuclear cells infiltrate infected airways providing antibody dependent cell-mediated cytotoxicity against influenza-infected cells.

To date, vaccine approaches against respiratory virus infections such as influenza essentially rely upon the induction of antibodies that protect against viral infection by neutralizing virions or blocking the virus's entry into cells. These humoral immune responses target external viral surface proteins that are conserved for a given strain. Antibody-mediated protection is therefore effective against homologous viral strains but inadequate against heterologous strains with serologically distinct surface proteins. This distinction is of consequence since the surface proteins of many viruses are capable of rapid mutation; for example an effective humoral response–based vaccine against a form of the influenza virus may be ineffective against next season's variant.

There are currently two main types of licensed influenza vaccines. One group of vaccines contains the haemagglutinin and neuraminidase surface proteins of the virus as the active immunogens. These include whole inactivated virus vaccines, split virus vaccines consisting of inactivated virus particles disrupted by detergent treatment, subunit vaccines consisting essentially purified surface proteins from which other virus components have been removed and virosomes where the surface proteins are presented on a liposomal surface. The second group comprises the live attenuated, cold-adapted, strains of virus. For all these vaccines a blend of surface antigens from usually three or four virus strains are required; current commercial influenza vaccines contain antigens from two A subtypes, H3N2 and H1N1, and one type B virus. Each year in September and February respectively, the WHO Global Influenza Program recommends the composition of the influenza vaccine for the next season that normally begins in May–June in the southern hemisphere and in November–December in the northern hemisphere. The composition is based on surveillance data from the worldwide network of national influenza centres and WHO collaborating centres and attempts to cover the likely strains to be circulating nine months later. For this reason, manufacturers are obliged to change the composition of the influenza vaccine on an annual basis in order to ensure an accurate match is achieved with the circulating viral strains.

Most inactivated influenza vaccines are given via the intramuscular route in the deltoid muscle, except in infants where the recommended site is the antero-lateral aspect of the thigh. A single dose of inactivated vaccine annually is appropriate, except for previously unvaccinated preschool children with pre-existing medical conditions who should receive two doses at least one month apart. The live attenuated influenza vaccine (LAIV) is delivered intra-nasally. These have been available in Russia for a number of years and recently licensed for use in the USA in paediatric populations.

Such vaccines are able to elicit local antibody and cell-mediated immune responses at the nasal epithelial surface. The live attenuated influenza vaccine is not, however, licensed for use in the USA in elderly populations (over 50 years old).

To enhance the breadth and intensity of the immune response mounted to the influenza virus surface proteins, various adjuvants and alternative immuno-potentiating agents have been evaluated for inclusion in the vaccine formulation. An adjuvant in this context is an agent that is able to modulate the immune response directed to a co-administered antigen while having few if any direct effects when given on its own. Recent licensed developments in the influenza vaccine field include MF-59, a submicron oil-in water emulsion. Aluminium-containing adjuvants are also used by some manufacturers. The intention of these adjuvants is to amplify the resulting serum antibody response to the administered antigens.

Provided there is a good antigenic match between the vaccine strains and those circulating in the general population, inactivated influenza vaccines prevent laboratory-confirmed illness in approximately 70% – 90% of healthy adults. However, the CDC highlights that vaccine efficacy in the elderly (over 65 years old) can be as low as 30-40%. Of relevance in this regard is the observation that ageing in humans creates defects in memory T-cell responses that reduce vaccine efficacy and increases the risk to natural infection. Furthermore, a clinical study in a community based setting demonstrated that cell mediated immunity, and not humoral immunity, was correlated with influenza disease protection in a group of over 60 year olds.

In addition, efficacy rates decline significantly if the vaccine strain is antigenically different to the circulating strains. Antigenic variation studies have indicated that four or more amino acid substitutions over at least two antigenic sites of the influenza A haemagglutinin results in a drift variant sufficiently discrete to undermine a vaccine's efficacy (Jin H, Zhou H, Liu H, Chan W, Adhikary L, Mahmood K, et al. "Two residues in the hemagglutinin of A/Fujian/411/02-like influenza viruses are responsible for antigenic drift from A/Panama/2007/99." Virology. 2005;336:113–9).

In a case controlled study of adults aged 50-64 years with laboratory confirmed influenza during the 2003-04 season when the vaccine and circulating A/H3N2 strains were not well matched, vaccine effectiveness was estimated to be 52% among healthy individuals and 38% among those with one or more high-risk conditions, according to the CDC. The likelihood of mismatching is raised by the limited manufacturing window of opportunity; the time from strain confirmation, through seed production, antigen manufacture and purification, and the trivalent blending and product filling must all occur in typically less than six months.

Occasionally, a new influenza strain emerges in the population with high pathogenicity and antigenic novelty which results in a worldwide pandemic. Pandemic influenza is the result of an antigenic shift in the surface proteins and represents a serious threat to global health as no pre-existing immunity has been developed by individuals. Pandemic strains are characterised by their sudden emergence in the population and their antigenic novelty. During the twentieth century, four pandemics occurred; in 1918 the causative strain was H1N1, in 1957 H2N2, in 1968 H3N2 and in 1977 H1N1.

There are three alternative explanations for the occurrence of antigenic shift. Firstly, as the influenza virus genome is segmented, it is possible for two influenza strains to exchange their genes upon co-infection of a single host, for example swine, leading to the construction of a replication-competent progeny carrying genetic information of different parental viruses. This process, known as genetic reassortment, is believed to have been the cause of the 1957 and 1968 pandemics. The 1968 pandemic arose when the H3 haemagglutinin gene and one other internal gene from an avian donor reassorted with the N2 neuraminidase and five other genes from the H2N2 human strain that had been in circulation. Secondly, a non-human influenza strain acquires the ability to infect humans. The 1918 pandemic arose when an avian H1N1 strain mutated to enable its rapid and efficient transfer from human-to-human. Thirdly, a strain that had previously caused an epidemic may remain sequestered and unaltered within the human population. The 1977 H1N1 pandemic strain, for example, was essentially identical to a strain that had caused an epidemic 27 years previously and was undetected in the human and animal reservoir over the intervening years.

An influenza pandemic is threatened once three principal criteria have been met:

1. An influenza virus HA subtype, unseen in the human population for at least one generation, emerges (or re-emerges).
2. The virus infects and replicates efficiently in humans, causing significant illness.
3. The virus is transmitted readily and sustainably between humans.

Global pandemics can afflict between 20% and 40% of the world's population in a single year. The pandemic of 1918-19, for example, affected 200 million people, killing over 30 million worldwide. In the United States, more than half a million individuals died, which represented 0.5% of the population. Although healthcare has dramatically improved since that time, with vaccines and antiviral therapies being developed, the CDC estimate that a pandemic today would result in two to seven million deaths globally.

Since 1999, three different influenza subtype strains (H5N1, H7N7 and H9N2) have crossed from avian species to humans, all causing human mortality. As of August 14th 2007 a total of 320 human cases of H5N1 Highly Pathogenic Avian Influenza Virus (HPAIV) infection had been recorded worldwide, with 193 deaths.

Unlike normal seasonal influenza, where infection causes only mild respiratory symptoms in most healthy people, the disease caused by H5N1 follows an unusually aggressive clinical course, with rapid deterioration and high fatality. Primary viral pneumonia and multi-organ failure are common. It is significant that most cases have occurred in previously healthy children and young adults. H5N1 HPAIV incubates longer than other human influenza viruses before causing symptoms, up to eight days in some cases. In household clusters of cases, the time between cases has generally ranged from two to five days but has been reported to take as long as 17 days.

Initial symptoms of H5N1 HPAIV infection are more likely to include diarrhoea and can appear up to a week before any respiratory symptoms. This feature, combined with the detection of viral RNA in stool samples, suggests that the virus can multiply in the gastrointestinal tract. Lower respiratory tract symptoms such as shortness of breath appear early in the course of the illness, whereas upper respiratory symptoms such as rhinorrheoa are less common.

H5N1 HPAIV presently meets two of the conditions required for a pandemic; the H5 haemagglutinin represents a new antigen for humans. No one will have immunity should an H5N1-like pandemic virus emerge. In addition, the virus has infected more than 300 humans, with an apparent mortality rate of over 60%.

All prerequisites for the start of a pandemic have therefore been met save one: the establishment of efficient and sustained human-to-human transmission of the virus. The risk that the H5N1 virus will acquire this ability will persist as long as opportunities for human infections occur. This is believed to be a realistic probability, either through step-wise mutation or through reassortment with a human-adapted strain.

At the scientific level, one or more changes to the virus phenotype are necessary before the virus strain could achieve ready human-to-human transmission and begin a pandemic. However, a number of recent observations including specific mutations detected in recent human isolates from Turkey, the increasing pathogenicity to mammals of the circulating virus, the expansion of the H5N1 HPAIV host range to include other mammals, such as tigers and cats that were previously considered to be resistant to infection with avian influenza viruses, all indicate that the H5N1 virus is continuing to evolve capabilities that may ultimately facilitate human-to-human transmission.

Other influenza viruses with possibly even greater pandemic potential may yet emerge. These include a number of H9 and H7 virus strains, which in recent years have also been transmitted to humans. H9 viruses are now endemic in poultry in Asia and also have crossed efficiently into pig populations in South Eastern and Eastern China. Of concern is the fact that the H9N2 strains possess typical human-like receptor specificity and have a broad host range.

In early 2003, an H7N7 HPAIV outbreak occurred in poultry in the Netherlands. Bird-to-human transmission of the H7N7 virus occurred in at least 82 cases. Conjunctivitis was the most common disease symptom in people infected with the H7 strain, with only seven cases displaying typical influenza-like illness. The virus did not prove highly pathogenic for humans and only one fatal case was observed. Other viruses with pandemic potential are those of the H2 subtype, because of its past history as a pandemic virus, and H6 because of its high incidence in poultry species in Asia and North America.

This indicates that a threat of a new human influenza pandemic is not uniquely linked to the emergence of HPAI H5N1.

In preparation for an influenza pandemic a number of clinical trials with candidate H5N1 influenza vaccines have been conducted. These have consistently shown that in order to generate a serum antibody response predicted to be protective, multiple doses of either a much higher amount of haemagglutinin antigen than is normally used in a seasonal vaccine or the inclusion of an adjuvant is required. This is a direct reflection of the immunological naivety of the population to the H5 haemagglutinin. At the present, the only options available for a pandemic influenza vaccine are therefore either one with a very high HA content, which would severely limit the number of doses that could be produced, or the use of an adjuvant that is not currently licensed in the majority of countries. It should also be appreciated that a vaccine that matches the pandemic strain will take many months to manufacture from the time that it is first isolated in humans; a stockpiled vaccine produced in advance of the emergence of a pandemic will most probably not be antigenically identical and therefore provide only limited protection, if any at all. Evidence of antigenic drift is already evident in the most recent outbreaks of H5N1.

In summary, there is a clear requirement for both seasonal and pandemic influenza vaccines to be improved:

1. There are obvious limitations in their efficacy, in particular in unprimed individuals. This is of specific concern with regard to the prospects of an influenza pandemic arising from antigenic shift.
2. The dependence on being able to predict accurately the influenza strains likely to be circulating in the following fall/winter seasons. A mismatch between the vaccine strains and those actually causing infections will render a significant proportion of the population vulnerable to influenza.
3. The need to re-vaccinate at risk groups on a yearly basis as the virus undergoes antigenic drift.
4. Capacity constraints, as there are only a limited number of potential biological manufacturing plants worldwide.
5. The protection afforded to the elderly age group is limited by conventional vaccines.

An improved class of influenza vaccine would therefore preferably be synthetic, stable, effective against all influenza A strains (including potential pandemic strains) with enhanced efficacy in the elderly (at risk) groups.

Role of T cells in protection against influenza disease

Whilst conventional influenza vaccine technologies have focused primarily on the antibody responses to the viral surface proteins, these are subject to antigenic shift and drift which undermines efficacy and creates the logistical vulnerabilities described. In contrast, T cells, which mediate cellular immune responses, can target proteins more highly conserved across heterologous viral strains and clades. This property gives vaccines that induce protective cellular immune responses the potential to protect against heterologous viral strains and clades (heterosubtypic immunity). For the influenza virus, conservation of the PB1, PB2, PA, NP, M1, M2, NS1 and NS2 proteins and persistence of the corresponding antigen-specific CD4+ and CD8+ T cells makes these proteins attractive vaccine targets.

Protective antiviral cell-mediated immunity consists of the induction of a Type 1 response supported by Type 1 CD4+ T-helper lymphocytes (Th1) leading to the activation of immune effector mechanisms including the induction and maintenance of cytotoxic T lymphocytes (CTLs) as well as immunostimulatory cytokines such as IFN-γ and IL-2. The CD4+ T helper cells are primarily responsible for helping other immune cells through direct cell-cell interactions or by secreting cytokines after recognizing antigenic T cell peptide epitopes bound to major histocompatibility complex (MHC) class II molecules. The cytotoxic T lymphocytes (CTLs) typically express CD8 and induce lysis or apoptosis of cells on which they recognize foreign antigens presented by MHC class I molecules, providing a defense against intracellular pathogens such as viruses. This association of phenotype and function is not absolute, since CD4+ cells may exhibit cytolytic activity, while CD8+ cells secrete antiviral cytokines, notably interferon-γ (IFN-γ) and tumor necrosis factor. Indeed, $CD4^+$ CTL activity has been proposed as another immune mechanism to control acute and chronic viral infection in humans. $CD4^+$ CTL may control viral spread by direct antiviral cytolytic effect and may play a direct antiviral activity by the production of antiviral cytokines such as IFN-γ. IFN-γ is known to have a direct inhibitory and non-cytolytic effect on virus production. CD4+ T helper cells are also essential in determining B cell antibody response and class switching, and in maximizing bactericidal activity of phagocytes such as macrophages.

Cellular immune responses are believed to play an important role in controlling influenza infection, ameliorating signs of disease and promoting disease recovery. Influenza-specific cellular immunity is elicited following natural infection and several viral proteins have been identified as targets for human memory heterosubtypic T cell responses, including nucleoprotein (NP), polymerase (PB1, PB2, & PA), M1 and M2 proteins, and non-structural protein-1 (NS1). NS2 may also be implicated. These internal proteins contain highly conserved and immunodominant regions making them ideal T cell targets. In particular, experimental studies have shown that influenza-A NP represents an important target antigen for both subtype-specific and cross-reactive CTLs in mice and humans. This contrasts with haemagglutinin (HA) and neuraminidase (NA), which are unsuitable targets due to their high sequence variability within and between influenza subtypes.

More specifically, cell-mediated immunity is strongly implicated in the protection against influenza disease including highly pathogenic strains. Memory CD4+ and CD8+ T cells are present in the lung airways and evidence is mounting that these cells play a role in pulmonary immunity to influenza challenge by mediating engagement of the pathogen at the site of infection when pathogen loads are low. Depletion of CD8+ T cells reduces the capacity of primed mice to respond to influenza infection, which signifies a role for CD8+ T cells in the protective secondary response. Because viral replication is confined to cells in the respiratory epithelium, CD8+ T cells exert their effector functions at this site, producing antiviral cytokines and lysing target cells presenting viral determinants for which they bear a specific T-cell receptor. Lysis of infected epithelial cells is mediated by exocytosis granules containing perforin and granzyme, as well as Fas mechanisms. (Thomas PG, Keating R, Hulse-Post DJ, Doherty PC. “Cell-mediated protection in influenza infection.” Emerg Infect Dis. 2006 Jan;12(1):48-54).

Vigorous CD4+ T cell responses to influenza are initiated in the draining lymph node followed by the spleen and they peak in the lung and bronchoalveolar secretions at day 6-7 post infection. This primary CD4 T-cell response to influenza infection, albeit smaller in magnitude than the CD8 response, has been shown to involve robust CD4+ expansion, Th-1 differentiation and their migration to the site of infection. CD4+ T-helper cells are also necessary for long lasting and effective CD8 memory to influenza infection. CD4 effector T-cell and memory responses contribute to immunity against influenza via multiple mechanisms including their classic contribution as helpers during the generation of influenza specific CD8+ CTL responses, their ability to drive IgG2a to neutralize infective viral particles, and via their direct antiviral activity through the secretion of IFN-gamma. Both CD4+ and CD8+ T-cell epitopes have been shown to promote viral clearance and confer protection in mice against an influenza challenge.

Mouse models for influenza-A virus provide an experimental system to analyze T-cell mediated immunity. In particular, the T-cell immune response to influenza infection has been well characterized in C57BL/6 ($H2^b$) and Balb/C ($H2^d$) mice and their hybrids. Plotnicky *et al.* (Plotnicky H, Cyblat-Chanal D, Aubry JP, Derouet F, Klinguer-Hamour C, Beck A, Bonnefoy JY, Corva A "The immunodominant influenza matrix T cell epitope recognized in human induces influenza protection in HLA-A2/K(b) transgenic mice." Virology. 2003 May 10;309(2):320-9.) demonstrated the protective efficacy of the influenza matrix protein (M1) epitope 58-66 to lethal transgenic murine challenge. Protection was mediated by T-cells since protection was abolished following *in vivo* depletion of CD8+ and/or CD4+ T-cells. Mouse survival correlated with M1-specific T-cells in the lungs, which were directly cytotoxic to influenza-infected cells following influenza challenge. Woodland *et al.* (Crowe SR, Miller SC, Woodland DL. "Identification of protective and non-protective T cell epitopes in influenza." Vaccine. 2006 Jan 23;24(4):452-6) also demonstrated that a single CD4+ T cell epitope HA (211-225) could confer partial control of viral infection in vaccinated mice.

Whilst T cell targets tend to be prone to less frequent mutation than the influenza virus surface protein B cell epitopes, CD8+ and CD4+ T cell epitopes will also mutate under protective immune pressure over time (Berkhoff EG, de Wit E, Geelhoed-Mieras MM, Boon AC, Symons J, Fouchier RA,Osterhaus AD, Rimmelzwaan GF. "Fitness costs limit escape from cytotoxic T lymphocytes by influenza A viruses." Vaccine. 2006 Nov 10;24(44-46):6594-6.). This escape likely results from the confrontation between the virus and the highly polymorphic human leukocyte antigen (HLA) class I and II proteins which determines antigen processing and epitope presentation to host $CD8^+$ and $CD4^+$ T-cells respectively. This viral escape mechanism has been more clearly established for HIV and HCV and is known to shape the evolution of the virus. Therefore the selection of highly conserved peptide sequences with low inherent variability (entropy) is an important factor to be considered in the design of T-cell vaccines which can specifically counter antigenic shift and drift. Such methods have been described by Berkhoff *et al.* (Berkhoff EG, de Wit E, Geelhoed-Mieras MM, Boon AC, Symons J, Fouchier RA, Osterhaus AD, Rimmelzwaan GF "Functional constraints of influenza A virus epitopes limit escape from cytotoxic T lymphocytes" J Virol. 2005 Sep;79(17):11239-46.)

Adults over 65 years of age currently account for approximately 90% of all influenza-related mortality. This is also the target group where current vaccines are least effective. In humans, ageing appears to be associated with a decline in the ability to generate T-cell effectors from memory sub-populations. An increased frequency of central memory CD4+ T-cells and decreased frequency of effector memory CD4+ T cells in the elderly post-vaccination has been observed, which may be related to decreased levels of serum IL-7. Elderly subjects also demonstrate a blunted type-1 T-cell response to influenza vaccination which correlates directly with IgG1 responses. Furthermore, mice also exhibit an age related impairment of epitope-specific CD8+ CTL activity during primary influenza-A infection. This is associated with a defect in expansion of CD8+ CTL rather than effector activity of influenza-specific CD8+ T cells. (Mbawuike IN, Acuna C, Caballero D, Pham-Nguyen K, Gilbert B, Petribon P, Harmon M. "Reversal of age-related deficient influenza virus-specific CTL responses and IFN-gamma production by monophosphoryl lipid A." Cell Immunol. 1996 Oct 10;173(1):64-78.)

As an important element of the T cell response is directed at the clearance of infected cells, a T-cell vaccine may be used in a prophylactic manner to generate memory recall as well as in a therapeutic mode, post-infection, to enhance the host's natural cell-mediated immunity. The T-cell vaccine may also be used in combination with a conventional antibody-generating (humoral response-based) influenza vaccine, either through co-administration or by separate administration.

T-cell vaccine approaches

A review of the T-cell and Influenza vaccine fields highlights a number of critical challenges faced in the design of a broadly cross protective T-cell vaccine. A T-cell vaccine must first be capable of priming and boosting CD4+ HTL and CD8+ CTL T-cell memory and effector functions in a high percentage of vaccine recipients. Such a vaccine must also address viral genetic diversity, and ongoing mutation, as well as human genetic diversity manifest at the level of MHC allele polymorphism. The proposed invention seeks to address these design issues by combining a novel fluoropeptide vaccine delivery system together with highly conserved influenza peptides. The peptides are preferably antigens known to contain one or more epitopes, in particular T-cell epitopes.

Traditional peptide-based T-cell vaccine approaches have been epitope-based and focussed on minimal CTL (8-11aa) or T-helper (13aa) epitopes delivered as single epitopes or reconstituted artificial strings. Non-natural sequences may face inefficient antigen processing constraints as well as giving rise to the potential formation of unrelated neo-epitopes. Long, natural conserved peptide sequences containing overlapping T-cell epitopes, clustered T-cell epitopes or promiscuous T-cell epitopes in a single peptide sequence permit natural antigen processing while achieving broad population coverage. Moreover, the use of multiples of these long natural peptides in the one vaccine formulation is likely to offer even greater population coverage.

Precedent shows long peptides (30-35aa) comprising CD4+ & CD8+ T-cell epitopes have the ability to induce multi-epitopic responses in animals and humans (Coutsinos Z, Villefroy P, Gras-Masse H, Guillet JG, Bourgault-Villada I. Gahery-Segard H, Pialoux G, Figueiredo S, Igea C, Surenaud M, Gaston J,Gras-Masse H, Levy JP, Guillet JG. "Long-term specific immune responses induced in humans by a human immunodeficiency virus type 1 lipopeptide vaccine: characterization of CD8+-T-cell epitopes recognized".J Virol. 2003 Oct;77(20):11220-31.). For an effective anti-viral CTL response (CD8 T cell driven), an appropriate Th-1 cytokine environment is required (ensured by CD4 cells), thus the concomitant delivery of CD4 and CD8 epitopes is predicted to enhance cellular responses (Krowka, JF., Singh, B., Fotedar, A., Mosmann, T., Giedlin, MA., Pilarski, LM. "A requirement for physical linkage between determinants recognized by helper molecules and cytotoxic T cell precursors in the induction of cytotoxic T cell responses" J. Immunol 1986, May 15;136(10):3561-6.).

CD4+ and CD8+ T cells recognize short peptides resulting from the extracellular and intracellular processing of foreign and self proteins, presented bound to specific cell surface molecules encoded by the MHC system. There are two discrete classes of MHC molecules: (i) MHC class I presents endogenous peptides; and (ii) MHC class II presents exogenous peptides. The process of MHC class I antigen presentation involves protein degradation, peptide transport to the endoplasmic reticulum, peptide–MHC binding and export of peptide–MHC complexes to the cell surface for recognition by CD8+ T cells. Peptides are bound within a specific MHC binding groove, the shape and characteristics of which results in the binding of specific subsets of peptides sharing a common binding motif. T cells are activated when the T-cell receptor recognizes a specific peptide–MHC complex, and in this way identify cells infected by intracellular parasites or viruses or cells containing abnormal proteins (e.g. tumour cells) and mount appropriate immune responses against them. The peptides involved in specific peptide–MHC complexes triggering T-cell recognition (T-cell epitopes) are important tools for the diagnosis and treatment of infectious, autoimmune, allergic and neoplastic diseases. Because T-cell epitopes are subsets of MHC-binding peptides, precise identification of portions of proteins that can bind MHC molecules is important for the design of vaccines and immunotherapeutics. The MHC polymorphism is very high in the human population with 580 HLA-A, 921 HLA-B, 312 HLA-C, 527 HLA-DR(beta), 127 HLA-DRQ(beta) and 86 HLA-DQ(beta) alleles known to date. This situation is challenging when having to design a T-cell based vaccine with broad population coverage. MHC-binding peptides contain position-specific amino acids that interact with the groove of the MHC molecule(s), contributing to peptide binding. The preferred amino acids at each position of the binding motif may vary between allelic variants of MHC molecules. Computational models facilitate identification of peptides that bind various MHC molecules. A variety of computational methods, MHC binding assays, X-ray crystallography study and numerous other methods known in the art permit the identification of peptides that bind to MHC molecules. Novel *in silico* antigen identification methodologies offer the ability to rapidly process the large amounts of data involved in screening peptide sequences for HLA binding motifs necessary to delineate viral sequences useful for a T cell vaccine. HLA based bioinformatics approaches have been successfully applied in many fields of immunology and make it possible to address human genetic diversity concerns, for example: Depil S, Morales O, Castelli FA, Delhem N, Francois V, Georges B, Dufosse F, Morschhauser F, Hammer J, Maillere B, Auriault C, Pancre V. "Determination of a HLA II promiscuous peptide cocktail as potential vaccine against EBV latency II malignancies.", J Immunother (1997). 2007 Feb-Mar;30(2):215-26; Frahm N, Yusim K, Suscovich TJ, Adams S, Sidney J, Hraber P, Hewitt HS, Linde CH, Kavanagh DG, Woodberry T, Henry LM, Faircloth K, Listgarten J, Kadie C, JojicN, Sango K, Brown NV, Pae E, Zaman MT, Bihl F, Khatri A, John M, Mallal S,Marincola FM, Walker BD, Sette A, Heckerman D, Korber BT, Brander C. "Extensive HLA class I allele promiscuity among viral CTL epitopes." Eur J Immunol. 2007 Aug 17;37(9):2419-2433; Schulze zur Wiesch J, Lauer GM, Day CL, Kim AY, Ouchi K, Duncan JE, Wurcel AG,Timm J, Jones AM, Mothe B, Allen TM, McGovern B, Lewis-Ximenez L, Sidney J, SetteA, Chung RT, Walker BD. "Broad repertoire of the CD4+ Th cell response in spontaneously controlled Hepatitis C virus infection includes dominant and highly promiscuous epitopes." J Immunol. 2005 Sep 15;175(6):3603-13; Doolan DL, Southwood S, Chesnut R, Appella E, Gomez E, Richards A, HigashimotoYI, Maewal A, Sidney J, Gramzinski RA, Mason C, Koech D, Hoffman SL, Sette A. "HLA-DR-promiscuous T cell epitopes from Plasmodium falciparum pre-erythrocytic-stage antigens restricted by multiple HLA class II alleles." J Immunol. 2000 Jul 15;165(2):1123-37.).

Peptides that bind more than one MHC allelic variant ('promiscuous peptides') are prime targets for vaccine and immunotherapy development because they are relevant to a greater proportion of the human population. Promiscuous CD4+ T cell epitopes were also reported to bind multiple MHC class II molecules. (Panina-Bordignon P, Tan A, Termijtelen A, Demotz S, Corradin G, Lanzavecchia A. Universally immunogenic T cell epitopes: promiscuous binding to human MHC class II and promiscuous recognition by T cells. Eur J Immunol. 1989 Dec;19(12):2237-42.) On the other hand, some promiscuous CD8+ T cell epitopes were previously described having the ability to bind multiples MHC class I molecules sharing binding characteristics and forming a so-called supertype (Frahm N, Yusim K, Suscovich TJ, Adams S, Sidney J, Hraber P, Hewitt HS, Linde CH, Kavanagh DG, Woodberry T, Henry LM, Faircloth K, Listgarten J, Kadie C, JojicN, Sango K, Brown NV, Pae E, Zaman MT, Bihl F, Khatri A, John M, Mallal S,Marincola FM, Walker BD, Sette A, Heckerman D, Korber BT, Brander C. "Extensive HLA class I allele promiscuity among viral CTL epitopes." Eur J Immunol. 2007 Aug 17;37(9):2419-2433 ; Sette A, Sidney J. 'HLA supertypes and supermotifs: a functional perspective on HLA polymorphism.' Curr Opin Immunol. 1998 Aug;10(4):478-82). The identification of promiscuous CD4+ and CD8+ T cell epitopes represent an important strategy in vaccine design in order to achieve broad population coverage. MHC polymorphism is also addressed by selecting peptides known or predicted to contain an MHC binding motif related to highly frequent MHC alleles in a specific ethnic group or across multiple ethnic groups.

By selecting a combination of sequences that provide broad population coverage and are conserved across a range of influenza strains (identified by using, for example, the National Center for Biotechnology Information (NCBI) or Los Alamos National Laboratory (LANL) influenza sequence databases) one is able to address viral genetic diversity and achieve protection against the majority, if not all, relevant influenza strains.

Historically, the key failings of T-cell vaccine technologies (DNA and viral vector vaccines) have been the low percentage of vaccine subjects responding to the vaccines, often low levels of immunogenicity and their ability to achieve a booster amplification of memory and effector T-cell responses. The principal goal for an effective influenza T-cell vaccine is to promote robust T-cell memory responses such that on re-exposure to antigen there is rapid expansion of effector functions which control viral load and promote viral clearance from the lungs. To achieve this, robust virus specific Th-1 directed CD4+ & CD8+ T-cell central and effector memory responses are required. For a viable, commercial product this response must be elicited in a high percentage of vaccine recipients (>90%) and be capable of generating long term memory responses which will be required for memory recall and subsequent disease protection post-infection. However, to generate this type of durable immunity a vaccine must also achieve a robust booster amplifying effect with repeat vaccine exposure.

Current immunological strategies to improve the cellular immunity induced by vaccines and immunotherapeutics include the development of live attenuated versions of the pathogen and the use of live vectors to deliver appropriate antigens or DNA coding for such antigens. Such approaches, which invariably fail to generate a meaningful booster response in unselected populations, have led to convoluted prime-boost combinations and are also limited by safety considerations within an increasingly stringent regulatory environment. In addition, issues arising from the scalability of manufacturing processes and prohibitive costs often limit the commercial viability of products of biological origin. In this context, synthetic peptides are very attractive antigens as they are chemically well-defined, highly stable and can be designed to contain T and/or B cell epitopes.

In order to stimulate T lymphocyte responses *in vivo*, synthetic peptides contained in a vaccine or an immunotherapeutic product should preferably be internalized by antigen presenting cells and especially dendritic cells. Dendritic cells (DCs) play a crucial role in the initiation of primary T-cell mediated immune responses. These cells exist in two major stages of maturation associated with different functions. Immature dendritic cells (iDCs) are located in most tissues or in the circulation and are recruited into inflamed sites in the body. They are highly specialised antigen-capturing cells, expressing large amounts of receptors involved in antigen uptake and phagocytosis. Following antigen capture and processing, iDCs move to local T-cell locations in the lymph nodes or spleen. During this process, DCs lose their antigen-capturing capacity turning into immunostimulatory mature DCs (mDCs).

Dendritic cells are efficient presenting cells that initiate the host's immune response to peptide antigen associated with class I and class II MHC molecules. They are able to prime naïve CD4 and CD8 T-cells. According to current models of antigen processing and presentation pathways, exogeneous antigens are internalised into the endocytic compartments of antigen presenting cells where they are degraded into peptides, some of which bind to MHC class II molecules. The mature MHC class II/peptide complexes are then transported to the cell surface for presentation to CD4 T-lymphocytes. In contrast, endogenous antigen is degraded in the cytoplasm by the action of the proteosome before being transported into the cytoplasm where they bind to nascent MHC class I molecules. Stable MHC class I molecules complexed to peptides are then transported to the cell surface to stimulate CD8 CTL. Exogenous antigen may also be presented on MHC class I molecules by professional APCs in a process called cross-presentation. Phagosomes containing extracellular antigen may fuse with reticulum endoplasmic and antigen may gain the machinery necessary to load peptide onto MHC class I molecules

Over the decades numerous delivery methods have been evaluated, including vectors such as Penetratin, TAT and its derivatives, DNA, viral vectors, virosomes and liposomes. However, these systems either elicit very weak CTL responses, fail to generate a booster amplification on memory responses, have associated toxicity issues or are complicated and expensive to manufacture at the commercial scale.

There is therefore a recognised need for improved vectors to direct the intracellular delivery of antigens in the development of vaccines and drugs intended to elicit a cellular immune response. A vector in the context of immunotherapeutics or vaccines is any agent capable of transporting or directing an antigen to immune responsive cells in a host.

Fluorinated surfactants have been shown to have low critical micelle concentrations and thus self-organise into multimolecular micelle structures at a low concentrations. This physicochemical property is related to the strong hydrophobic interactions and low Van der Waal's interactions associated with fluorinated chains which dramatically increase the tendency of fluorinated amphiphiles to self-assemble in water and to collect at interfaces. The formation of such structures facilitates their endocytic uptake by cells, for example antigen-presenting cells (Reichel F. et al. J. Am. Chem. Soc. 1999, 121, 7989-7997). Furthermore haemolytic activity is strongly reduced and often suppressed when fluorinated chains are introduced into a surfactant (Riess, J.G.; Pace, S.; Zarif, L. Adv. Mater. 1991, 3, 249-251) thereby leading to a reduction in cellular toxicity.

This invention seeks to overcome the problem of delivering influenza antigens to immune responsive cells by using a fluorocarbon vector in order to enhance their immunogenicity. The fluorocarbon vector may comprise one or more chains derived from perfluorocarbon or mixed fluorocarbon/hydrocarbon radicals, and may be saturated or unsaturated, each chain having from 3 to 30 carbon atoms.

In order to link the vector to the antigen through a covalent linkage, a reactive group, or ligand, is incorporated as a component of the vector, for example –CO-, -NH-, S, O or any other suitable group is included; the use of such ligands for achieving covalent linkages are well-known in the art. The reactive group may be located at any position on the fluorocarbon molecule.

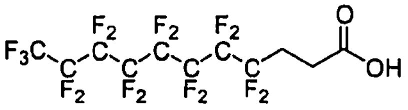
Coupling of the fluorocarbon vector to the antigen may be achieved through functional groups such as –OH, -SH, -COOH, $-NH_2$ naturally present or introduced onto any site of the antigen. Suitable links may contain a nitrogen, oxygen or sulphur atom, in either linear or cyclic form. Examples of the bonds formed by ligation may include oxime, hydrazone, disulphide or triazole or any suitable covalent bond. In particular, the fluorocarbon moiety could be introduced through a thioester bond to increase the immunogenicity of the peptide (Beekman, N.J.C.M. *et al.* "Synthetic peptide vaccines: palmitoylation of peptide antigens by a thioester bond increases immunogenicity." J. Peptide Res. 1997, 50, 357-364). Optionally, a spacer element (peptidic, pseudopeptidic or non-peptidic) may be incorporated to permit cleavage of the antigen from the fluorocarbon element for processing within the antigen-presenting cell and to optimise antigen presentation, as previously shown for lipopeptides (Verheul, A. F.M.; Udhayakumar, V.; Jue, D. L.; Wohlhueter, R.M.; Lal, A. L. Monopalmitic acid-peptide conjugates induce cytotoxic T cell responses against malarial epitopes: importance of spacer amino acids. Journal of Immunological Methods 1995, volume 182, pp219-226).

Thus, in a first aspect, the present invention provides a fluorocarbon vector-antigen construct having a chemical structure C_mF_n-C_yH_x-**(Sp)-R** or derivatives thereof, where $m = 3$ to 30, $n <= 2m + 1$, $y = 0$ to 15, $x <= 2y$, $(m + y) = 3 - 30$ and **Sp** is an optional chemical spacer moiety and R is an immunogenic influenza virus peptide selected

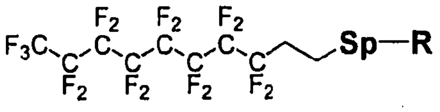
from:
HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK (SEQ ID NO: 1)
VAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQG (SEQ ID NO: 4)
YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE (SEQ ID NO: 17)
APIMFSNKMARLGKGYMFESKRMKLRTQIPAEMLA (SEQ ID NO: 18)
SPGMMMGMFNMLSTVLGVSILNLGQKKYTKTTY (SEQ ID NO: 19)
KKKSYINKTGTFEFTSFFYRYGFVANFSMELPSFG (SEQ ID NO: 20)
DQVRESRNPGNAEIEDLIFLARSALILRGSVAHKS (SEQ ID NO: 32)
DLEALMEWLKTRPILSPLTKGILGFVFTLTVPSER (SEQ ID NO: 35)
and homologues and combinations thereof, wherein said homologues have at least 50% identity to SEQ ID NO: 1, 4, 17, 18 or 20, 80 % identity to SEQ ID NO: 19 or 32 or 95% identity to SEQ ID NO: 35.

In the context of the present invention "derivatives" refers to relatively minor modifications of the fluorocarbon compound such that the compound is still capable of delivering the antigen as described herein. Thus, for example, a number of the fluorine moieties can be replaced with other halogen moieties such as chlorine (Cl), bromine (Br) or iodine (I). In addition it is possible to replace a number of the fluorine moieties with methyl groups and still retain the properties of the molecule as discussed herein.

In a particular example of the above formula the vector may be 2H, 2H, 3H, 3H-perfluoroundecanoic acid of the following formula:



Thus in a second aspect the invention provides a fluorocarbon vector-antigen construct of structure



where **Sp** is an optional chemical spacer moiety and **R** is an antigen derived from the influenza virus.

As used herein the term “antigen” refers to a molecule having the ability to be recognized by immunological receptors such as T cell receptor (TCR) or B cell receptor (BCR or antibody). In the fluorocarbon vector-antigen constructs of the invention, the antigens are peptides that present at least one epitope, for example a T cell and / or a B cell epitope.

Such antigens may be derived by purification from the native protein or produced by recombinant technology or by chemical synthesis. Methods for the preparation of antigens are well-known in the art.

The antigen associated with the vector is capable of inducing an immune response in an animal, including humans. Preferably the immune response will have a beneficial effect in the host.

The influenza antigen may contain one or more T cell epitopes or one or more B cell epitopes or combinations of T and B cell epitopes.

The T cell epitopes may be MHC class I or class II restricted.

As used herein the term “epitope” includes:

(i) CD4+ T cell epitopes which are peptidic sequences containing an MHC class II binding motif and having the ability to be presented at the surface of antigen presenting cells by MHC class II molecules, and

(ii) CD8+ T cell epitopes which are peptidic sequences containing an MHC class I binding motif and having the ability to be presented by MHC class I molecules at the cell surface, and

(iii)B cell epitopes which are peptidic sequences having a binding affinity for a B cell receptor.

The antigen comprises one or more epitopes from an influenza type A protein selected from matrix (M1) protein, nucleoprotein (NP), PB1 or PB2 in any such combination.

For the vector-antigen construct to be immunologically active the antigen must comprise one or more epitopes. The antigen is a peptide sequence derived from the influenza virus. Peptides in constructs of the invention preferably contain a sequence of at least seven, more preferably between 9 and 100 amino-acids and most preferably between around 15 to 40 amino acids. Preferably, the amino acid sequence of the epitope(s) bearing peptide is selected to enhance the solubility of the molecule in aqueous solvents. Furthermore, the terminus of the peptide which does not conjugate to the vector may be altered to promote solubility of the construct via the formation of multi-molecular structures such as micelles, lamellae, tubules or liposomes. For example, a positively charged amino acid could be added to the peptide in order to promote the spontaneous assembly of micelles. Either the N-terminus or the C-terminus of the peptide can be coupled to the vector to create the construct. To facilitate large scale synthesis of the construct, the N- or C-terminal amino acid residues of the peptide can be modified. When the desired peptide is particularly sensitive to cleavage by peptidases, the normal peptide bond can be replaced by a non-cleavable peptide mimetic; such bonds and methods of synthesis are well known in the art.

Non-standard, non-natural amino-acids can also be incorporated in peptide sequences provided that they do not interfere with the ability of the peptide to interact with MHC molecules and remain cross-reactive with T cells recognising the natural sequences.

Non-natural amino-acids can be used to improve peptide resistance to protease or chemical stability. Examples of non-natural amino acids include the D-amino-acids and cysteine modifications.

More than one antigen may be linked together prior to attachment to the fluorocarbon vector. One such example is the use of fusion peptides where a promiscuous T helper epitope can be covalently linked to one or multiple CTL epitopes or one or multiple B cell epitope which can be a peptide, a carbohydrate, or a nucleic acid. As an example, the promiscuous T helper epitope could be the PADRE peptide, tetanus toxoid peptide (830-843) or influenza haemagglutinin, HA (307-319). Alternatively, the peptide sequence may contain two or more epitopes, which may be overlapping thereby creating a cluster of densely packed multi-specific epitopes, or contiguous, or separated by a stretch of amino acids.

Thus in a further aspect, the present invention provides a vector-antigen construct where **R** is more than one epitope or antigen linked together. Epitopes may also be linear overlapping thereby creating a cluster of densely packed multi-specific epitopes.

Antigens bearing one or more B-cell epitopes may also be attached to the fluorocarbon vector, either with or without one or more T-cell epitopes. B cell epitopes can be predicted using *in silico* approaches (Bublil EM, Freund NT, Mayrose I, Penn O, Roitburd-Berman A, Rubinstein ND,Pupko T, Gershoni JM. "Stepwise prediction of conformational discontinuous B-cell epitopes using the Mapitope algorithm." Proteins. 2007 Jul 1;68(1):294-304.Greenbaum JA, Andersen PH, Blythe M, Bui HH, Cachau RE, Crowe J, Davies M,Kolaskar AS, Lund O, Morrison S, Mumey B, Ofran Y, Pellequer JL, Pinilla C, Ponomarenko JV, Raghava GP, van Regenmortel MH, Roggen EL, Sette A, Schlessinger A, Sollner J, Zand M, Peters B. "Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools" J Mol Recognit. 2007 Mar-Apr;20(2):75-82).

The present invention also provides vaccines and immunotherapeutics comprising one or more fluorocarbon vector-antigen constructs. Multi-component products of this type are desirable since they are likely to be more effective in eliciting appropriate immune responses in a greater number of individuals. Due to extreme HLA polymorphism in humans, it is unlikely that a single fluoropeptide will induce a multiepitopic immune response in a high percentage of a given population. Therefore, in order for a vaccine product to be effective across a population a number of fluoropeptides may be necessary in the vaccine formulation in order to provide broad coverage. Moreover, the optimal formulation of an influenza vaccine or immunotherapeutic may comprise a number of different peptide sequences derived from different influenza virus antigens. In this case the peptides may be linked together attached to a single fluorocarbon vector or each peptide antigen could be bound to a dedicated vector.

A multi-component product may contain one or more vector-antigen constructs, more preferably 2 to about 20, more preferably 3 to about 10. In particular embodiments the multi component vaccine may contain 5, 6, 7 or 8 eight constructs. This ensures that a multi-epitopic T-cell response is generated with a broad population coverage (ie addresses HLA diversity). For example, a formulation of multiple fluoropeptides may be composed of influenza A derived peptides alone, influenza B derived peptides alone or influenza C derived peptides alone or combinations of influenza types, most preferably influenza A and B.

In one embodiment the product comprises at least two vector-antigen constructs, the first construct comprising the influenza peptide sequence:

HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK

and the second construct comprising the influenza peptide sequence:

YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE

In a further embodiment the product comprises 8 vector-antigen constructs which comprise the following influenza peptide sequences:

Construct 1 HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK

Construct 2 VAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQG

Construct 3 YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE

Construct 4 APIMFSNKMARLGKGYMFESKRMKLRTQIPAEMLA

Construct 5 SPGMMMGMFNMLSTVLGVSILNLGQKKYTKTTY

Construct 6 KKKSYINKTGTFEFTSFFYRYGFVANFSMELPSFG

Construct 7 DQVRESRNPGNAEIEDLIFLARSALILRGSVAHKS

Construct 8 DLEALMEWLKTRPILSPLTKGILGFVFTLTVPSER

Alternatively, multiple epitopes may be incorporated into a formulation in order to confer immunity against a range of pathogens, one of which is the influenza virus. For example a respiratory infection vaccine may contain antigens from influenza virus and respiratory syncytial virus.

Compositions of the invention comprise fluorocarbon vectors associated to antigens optionally together with one or more pharmaceutically acceptable carriers and/or adjuvants. Such adjuvants and/or pharmaceutically acceptable carriers, would be capable of further potentiating the immune response both in terms of magnitude and/or cytokine profile, and may include, but are not limited to;

(1) natural or synthetically derived refinements of natural components of bacteria such as Freund's adjuvant & its derivatives, muramyldipeptide (MDP) derivatives, CpG, monophosphoryl lipid A;

(2) other known adjuvant or potentiating agents such as saponins, aluminium salts and cytokines;

(3) methods of formulating antigens with or without extraneous adjuvants (see 1 & 2 above) such as oil in water adjuvants, water-in-oil adjuvants, immunostimulating complex (ISCOMs), liposomes, formulated nano and micro-particles;
(4) bacterial toxins and toxoids; and
(5) Other useful adjuvants well-known to one skilled in the art.

The choice of carrier if required is frequently a function of the route of delivery of the composition. Within this invention, compositions may be formulated for any suitable route and means of administration. Pharmaceutically acceptable carriers or diluents include those used in formulations suitable for oral, ocular, rectal, nasal, topical (including buccal and sublingual), vaginal or parenteral (including subcutaneous, intramuscular, intravenous, intradermal, transdermal) administration.

The formulation may be administered in any suitable form, for example as a liquid, solid, aerosol, or gas. For example, oral formulations may take the form of emulsions, syrups or solutions or tablets or capsules, which may be enterically coated to protect the active component from degradation in the stomach. Nasal formulations may be sprays or solutions. Transdermal formulations may be adapted for their particular delivery system and may comprise patches. Formulations for injection may be solutions or suspensions in distilled water or another pharmaceutically acceptable solvent or suspending agent.

Thus in a further aspect, the present invention provides a prophylactic or therapeutic formulation comprising the vector-antigen construct(s) with or without a suitable carrier and/or adjuvant.

The appropriate dosage of the vaccine or immunotherapeutic to be administered to a patient will be determined in the clinic. However, as a guide, a suitable human dose, which may be dependent upon the preferred route of administration, may be from 1 to 1000μg. Multiple doses may be required to achieve an immunological or clinical effect, which, if required, will be typically administered between 2 to 12 weeks apart. Where boosting of the immune response over longer periods is required, repeat doses 1 month to 5 years apart may be applied.

The formulation may combine the vector-antigen construct with another active component to effect the administration of more than one vaccine or drug. A synergistic effect may also be observed through the co-administration of the two or more actives.

A vaccine formulation of the invention, comprising one or more fluoropeptides, may be used in combination with a humoral response-based influenza vaccine, such as Fluzone®, Agrippal™, Begrivac™, Fluvax®, Enzira®, Fluarix™, Flulaval™, FluAd®, Influvac®, Fluvirin®, FluBlok® or any influenza vaccine comprising haemagglutinin as the active component, or a live attenuated influenza virus, including the cold-adapted strains such as Flumist®. Administration may be as a combined mixture or as separate vaccine agents administered contemporaneously or separated by time.

The influenza vaccine formulation of the invention may be administered in combination with an anti-viral therapeutic composition, including neuraminidase inhibitor treatments such as amanidine, rimantidine, zanamivir or oseltamivir. Administration may be contemporaneous or separated by time.

In other aspects the invention provides:

i) Use of the immunogenic construct as described herein in the preparation of a medicament for treatment or prevention of a disease or symptoms thereof.

ii) The formulation described herein for use in a method of treatment or immunisation through the induction of an immune response.

The invention will now be described with reference to the following examples. These examples highlight the differential T-cell immune response obtained by the attachment of a fluorocarbon vector to antigens compared to the corresponding non-fluorinated antigens. The eight (8) antigens exemplified were selected from the list of Influenza sequences herein defined. This provisional selection utilized a proprietary selection algorithm encompassing a combination of parameters including; immunoinformatics selection, in-vitro binding assays, ex-vivo restimulation assays using human PBMC previously infected with influenza, manufacturing and formulation parameters. Finally the assessment in mice confirmed that fluoropeptides thus selected either individually or in combination were immunogenic and the responses obtained were superior to the native peptide antigens. The antigen selection focus and desire to utilize a combination of antigens for this vaccine prototype is such that both viral genetic and human HLA diversity are addressed in this rational vaccine design. This has been one of the key failings in the peptide vaccine field. Whilst it is possible to utilize a single antigen in the fluoropeptide vaccine it would limit the vaccine's immunogenicity potential in an outbred human (or other) population and therefore the selection of multiple peptides is essential for a broadly effective vaccine.

As used herein the term "fluoropepetides" refers to fluorocarbon vectors (chains) conjugated to peptide based antigens. The examples refer to the figures in which:

Figure 1: Shows a comparison of the immunogenicity of a multivalent fluoropeptide vaccine versus its native peptide equivalent in BALB/c and CBF6 mice, after prime or prime-boost, assessed by ex vivo IFN-γ ELIspot assay. Seven or eight mice per group were immunized subcutaneously with the fluoropeptide vaccine (composed of 8 formulated fluoropeptides at a dose of 1nmol per fluoropeptide in 100μl) or the equivalent native peptides (composed of 8 formulated native peptides at a dose of 1nmol per peptide in100μl). The control group received a formulation containing excipient only. Ten days after the final injection mice were sacrificed by cervical dislocation. Spleens were removed and single spleen cell suspensions were prepared

from individual mice. Murine IFN-γ ELISpot assays (Mabtech, Sweden) were performed according to manufacturer's instructions. Spleen cells ($5x10^5$) were stimulated, in duplicate, with 8 individual native peptides at a concentration of 10μg/ml per peptide in complete culture medium (RPMI supplemented with 10% Foetal Calf Serum) in a total volume of 200μl for 18 hours at 37°C and 5% CO_2.. The spots were counted using a CTL-immunospot reader unit. For each mouse, the total number of spots was cumulated for all 8 peptides and the value of the control wells (media only) was subtracted 8 times. The results correspond to mean ± standard deviation of spot forming cells (SFC) per million input spleen cells.

Figure 2: Shows a comparison of the immunogenicity of a multivalent fluoropeptide vaccine versus its native peptide equivalent in BALB/c and CBF6 mice, after prime or prime-boost, assessed by ex vivo IFN-γ ELIspot assay. Seven or eight mice per group were immunized subcutaneously with the fluoropeptide vaccine (composed of 8 formulated fluoropeptides at a dose of 1nmol per fluoropeptide in 100μl) or the equivalent native peptides (composed of 8 formulated native peptides at a dose of 1nmol per peptide in 100μl). The control group received a formulation containing excipient only. Ten days after the final injection mice were sacrificed by cervical dislocation. Spleens were removed and single spleen cell suspensions were prepared from individual mice. Murine IFN-γ ELISpot assays (Mabtech, Sweden) were performed according to manufacturer's instructions. Spleen cells ($5x10^5$) were stimulated, in duplicate, with a mixture of 8 peptides at a concentration of 1μg/ml per peptide in complete culture medium (RPMI supplemented with 10% Foetal Calf Serum) in a total volume of 200μl for 18 hours at 37°C and 5% CO_2. The spots were counted using a CTL-immunospot reader unit. For each mouse, the total number of spots was cumulated for all 8 peptides and the value of the control wells (media only) was subtracted 8 times. The results correspond to mean ± standard deviation of spot forming cells (SFC) per million input spleen cells.

Figure 3: Shows a comparison of individual peptide immunogenicity of fluoropeptides verses native peptides in BALB/c and CBF6 mice after prime or prime-boost assessed by ex vivo IFN-γ ELISpot. Seven or eight mice per group were immunized subcutaneously with the fluoropeptide vaccine (composed of 8 formulated fluoropeptides at a dose of 1nmol per fluoropeptide in 100µl) or the equivalent native peptides (composed of 8 formulated native peptides at a dose of 1nmol per peptide in 100µl). The control group received a formulation containing excipient only. Ten days after the last injection mice were sacrificed by cervical dislocation. Spleens were removed and single spleen cell suspensions were prepared from individual mice. Murine IFN-γ ELISpot assays (Mabtech, Sweden) were performed according to manufacturer's instructions. Spleen cells ($5x10^5$) were stimulated, in duplicate, with 8 individual native peptides at a concentration of 10µg/ml per peptide in complete culture medium (RPMI supplemented with 10% Foetal Calf Serum) in a total volume of 200µl for 18 hours at 37°C under 5% CO_2 atmosphere. The spots were counted using a CTL-immunospot reader unit. The results correspond to mean ± standard deviation of spot forming cells (SFC) per million input spleen cells.

Figure 4: Shows a comparison of the immunogenicity of a multivalent fluoropeptide vaccine versus its native peptide equivalent in BALB/c and CBF6 mice after prime-boost immunisation; assessment of cytokine profiles. Eight mice per group were immunized subcutaneously with the fluoropeptide vaccine (composed of 8 formulated fluoropeptides at a dose of 1nmol per fluoropeptide in 100µl) or the equivalent native peptides (composed of 8 formulated native peptides at a dose of 1nmol per peptide in 100µl). The control groups of mice were injected with a formulation containing excipient only. Mice were immunised at a 15 day interval. Ten days after the last injection mice were sacrificed by cervical dislocation. Spleens were removed and single spleen cell suspensions were prepared fromindividual mice. Splenocytes were stimulated with a mixture of 8 native peptides at a concentration of 1µg/ml per peptide in complete culture medium (RPMI supplemented with 10% Foetal Calf Serum) in a total volume of 200µl for 48 hours at 37°C under 5% CO_2 atmosphere. Analysis of

cytokine concentrations (interleukin-2 (IL-2), interleukin-4 (IL-4), interleukin-5 (IL-5), interferon-γ (IFN-γ), and Tumor Necrosis Factor (TNF)) from the culture supernatants of stimulated cells was conducted using a murine cytometric bead array kit (CBA; BD Biosciences, UK) according to manufacturer's instructions and was analyzed using a FacsCanto™ II flow cytometer. Standard curves were determined for each cytokine from a range of 210–2500 pg/ml. The lower limit of detection for the CBA, according to the manufacturer, is 2.5–3.2 pg/ml, depending on the analyte. The results correspond to mean values and standard deviation calculated for each group of mice for each cytokine. Results are expressed as cytokine concentration in pg/ml.

Figure 5: Both CD4+ T cells and CD8+ T cells are stimulated by the fluoropeptide vaccine in BALB/c mice. Four mice per group were immunized subcutaneously with the fluoropeptide vaccine (composed of 8 formulated fluoropeptides at a dose of 1nmol per fluoropeptide in 100μl). Mice received 2 injections (prime-boost) at a 15 day interval. Ten days after the last injection, mice were sacrificed by cervical dislocation. Spleens were removed and single spleen cell suspensions were prepared from individual mice. Cells were resuspended at $0.5x10^6$/well and stimulated with media only or a mixture of 8 native peptides (vaccine) for 72 hours at 37°C and 5% CO_2. Positive control cultures (PMA/I) received 50ng/ml PMA and 0.5μg/ml ionomycin for the final 5 hours of culture. All cultures received 10μl/ml Brefeldin A for the final 5 hours of culture. Cells were stained extracellularly for CD4 and CD8, and intracellularly for IFN-γ, and analysed by flow cytometry using a BD FACSCanto™ II cytometer. Results for individual mice are shown as percentage of CD4+ or CD8+ T cells expressing intracellular IFN-γ.

Figure 6: Shows a comparison of the immunogenicity of a multivalent fluoropeptide vaccine versus vaccine emulsified in CFA in BALB/c mice after a single immunisation; assessment of cytokine profiles. Ten mice per group were immunized subcutaneously with the fluoropeptide vaccine (composed of 8 formulated fluoropeptides at a dose of 1nmol per fluoropeptide in 100μl) or fluoropeptide vaccine

emulsified in complete Freund's adjuvant (CFA). The control group of mice was injected with a formulation containing excipient only. Ten days later mice were sacrificed by cervical dislocation. Spleens were removed and single spleen cell suspensions were prepared from individual mice. Splenocytes were stimulated with a mixture of 8 native peptides at a concentration of 1µg/ml per peptide in complete culture medium (RPMI supplemented with 10% Foetal Calf Serum) in a total volume of 200µl for 48 hours at 37°C under 5% CO_2 atmosphere. Analysis of cytokine concentrations (interleukin-2 (IL-2), interleukin-4 (IL-4), interleukin-5 (IL-5), interferon-γ (IFN-γ), and Tumor Necrosis Factor (TNF)) from the culture supernatants of stimulated cells was conducted using a murine cytometric bead array kit (CBA; BD Biosciences, UK) according to manufacturer's instructions and was analyzed using a FacsCanto™ II flow cytometer. Standard curves were determined for each cytokine from a range of 2.5–2500 pg/ml. The lower limit of detection for the CBA, according to the manufacturer, is 2.5–3.2 pg/ml, depending on the analyte. The results correspond to mean values ± standard error calculated for each group of mice for each cytokine. Results are expressed as mean cytokine concentration in pg/ml.

Figure 7: Shows a comparison of subcutaneous versus intradermal routes of fluoropeptide vaccine administration in BALB/c mice after a single immunisation: ex vivo IFN-γ ELISpot assay. Ten mice per group were immunized subcutaneously (s.c.) or intradermally (i.d.) with the fluoropeptide vaccine (composed of 8 formulated fluoropeptides at a dose of 1nmol per fluoropeptide in 100µl). The control group received a formulation containing excipient only administered subcutaneously. Ten days later mice were sacrificed by cervical dislocation. Spleens were removed and single spleen cell suspensions were prepared from individual mice. Murine IFN-γ ELISpot assays (Mabtech, Sweden) were performed according to manufacturer's instructions. Spleen cells ($5x10^5$) were stimulated, in duplicate, with 8 individual native peptides at a concentration of 10µg/ml per peptide in complete culture medium (RPMI supplemented with 10% Foetal Calf Serum) in a total volume of 200µl for 18 hours at 37°C under 5% CO_2 atmosphere. The spots were counted using a CTL-

immunospot reader unit. For each mouse, the total number of spots was cumulated for all 8 peptides and the value of the control wells (media only) was subtracted 8 times. The results correspond to mean ± standard error of spot forming cells (SFC) per million input spleen cells.

Example 1

Example peptides

Candidates for conjugating to a fluorocarbon vector for inclusion into a prophylactic or therapeutic vaccine for influenza may include the following one or more peptides or fragments thereof, or homologues (including the corresponding consensus, ancestral or central tree sequences as referred to in the Los Alamos National Laboratory influenza sequence database (Macken, C., Lu, H., Goodman, J., & Boykin, L., "The value of a database in surveillance and vaccine selection." in *Options for the Control of Influenza IV.* A.D.M.E. Osterhaus, N. Cox & A.W. Hampson (Eds.) 2001, 103-106.) or Influenza virus resources at NCBI) or natural and non-natural variants thereof, but not necessarily exclusively. Specific examples of appropriate peptides are given below where the standard one letter code has been utilised. Homologues have at least a 50% identity compared to a reference sequence. Preferably a homologue has 80, 85, 90, 95, 98 or 99% identity to a naturally occurring sequence. The use of non-natural amino acids must not interfere with the ability of the peptide to bind to MHC class I or II receptors. Fragments of these sequences that contain one or more epitopes are also candidate peptides for attachment to the fluorocarbon vector.

These sequences were selected from Influenza A consensus sequences. The influenza virus protein and the position of the peptide within that protein are specified. Protein sequences were collected from the Influenza virus resource. http://www.ncbi.nlm.nih.gov/genomes/FLU/

SEQ ID N°1
PB2 **Position 027 to 061**

HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK

SEQ ID N°2
PB2 **Position 123 to 157**
ERLKHGTFGPVHFRNQVKIRRRVDINPGHADLSAK

SEQ ID N°3
PB2 **Position 155 to 189**
SAKEAQDVIMEVVFPNEVGARILTSESQLTITKEK

SEQ ID N°4
PB2 **Position 203 to 237**
VAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQG

SEQ ID N°5
PB2 **Position 249 to 283**
EVRNDDVDQSLIIAARNIVRRAAVSADPLASLLEM

SEQ ID N°6
PB2 **Position 358 to 392**
EGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQ

SEQ ID N°7
PB2 **Position 370 to 404**
ATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVF

SEQ ID N°8
PB2 **Position 415 to 449**
RGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNW

SEQ ID N°9
PB2 **Position 532 to 566**
SSSMMWEINGPESVLVNTYQWIIRNWETVKIQWSQ

SEQ ID N°10
PB2 **Position 592 to 626**
YSGFVRTLFQQMRDVLGTFDTVQIIKLLPFAAAPP

SEQ ID N°11
PB2 **Position 607 to 641**
LGTFDTVQIIKLLPFAAAPPEQSRMQFSSLTVNVR

SEQ ID N°12
PB2 **Position 627 to 659**
QSRMQFSSLTVNVRGSGMRILVRGNSPVFNYNK

SEQ ID N°13
PB1 **Position 012 to 046**
VPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRT

SEQ ID N°14
PB1 **Position 114 to 148**
VQQTRVDKLTQGRQTYDWTLNRNQPAATALANTIE

SEQ ID N°15
PB1 **Position 216 to 250**
SYLIRALTLNTMTKDAERGKLKRRAIATPGMQIRG

SEQ ID N°16
PB1 **Position 267 to 301**
EQSGLPVGGNEKKAKLANVVRKMMTNSQDTELSFT

SEQ ID N°17
PB1 **Position 324 to 358**
YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE

SEQ ID N°18
PB1 **Position 340 to 374**
APIMFSNKMARLGKGYMFESKSMKLRTQIPAEMLA

SEQ ID N°19
PB1 **Position 404 to 436**
SPGMMMGMFNMLSTVLGVSILNLGQKKYTKTTY

SEQ ID N°20
PB1 **Position 479 to 513**
KKKSYINKTGTFEFTSFFYRYGFVANFSMELPSFG

SEQ ID N°21
PB1 **Position 486 to 520**
KTGTFEFTSFFYRYGFVANFSMELPSFGVSGINES

SEQ ID N°22
PB1 **Position 526 to 560**
GVTVIKNNMINNDLGPATAQMALQLFIKDYRYTYR

SEQ ID N°23
PB1 **Position 656 to 690**
EYDAVATTHSWIPKRNRSILNTSQRGILEDEQMYQ

SEQ ID N°24
PB1 **Position 700 to 734**
FPSSSYRRPVGISSMVEAMVSRARIDARIDFESGR

SEQ ID N°25
PA **Position 107 to 141**
PDLYDYKENRFIEIGVTRREVHIYYLEKANKIKSE

SEQ ID N°26
PA **Position 122 to 156**
VTRREVHIYYLEKANKIKSEKTHIHIFSFTGEEMA

SEQ ID N°27

PA **Position 145 to 179**
IHIFSFTGEEMATKADYTLDEESRARIKTRLFTIR

SEQ ID N°28
PA **Position 166 to 200**
ESRARIKTRLFTIRQEMASRGLWDSFRQSERGEET

SEQ ID N°29
PA **Position 495 to 529**
RRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTD

SEQ ID N°30
PA **Position 642 to 676**
AKSVFNSLYASPQLEGFSAESRKLLLIVQALRDNL

SEQ ID N°31
PA **Position 173 to 207**
PRRSGAAGAAVKGVGTMVMELIRMIKRGINDRNFW

SEQ ID N°32
NP **Position 240 to 274**
DQVRESRNPGNAEIEDLIFLARSALILRGSVAHKS

SEQ ID N°33
M1 **Position 002 to 026**
SLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKN

SEQ ID N°34
M1 **Position 023 to 057**
EIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTK

SEQ ID N°35
M1 **Position 038 to 072**
DLEALMEWLKTRPILSPLTKGILGFVFTLTVPSER

SEQ ID N°36
M1 **Position 055 to 089**
LTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGD

SEQ ID N°37
M1 **Position 166 to 200**
ATTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAA

SEQ ID N°38
NS1 **Position 128 to 162**
IILKANFSVIFDRLETLILLRAFTEEGAIVGEISP

SEQ ID N°39
NS2 **Position 026 to 060**
EDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQN

The following sequences were selected from Influenza B consensus sequences. The influenza virus protein and the position of the peptide within that protein are specified. Protein sequences were collected from the Influenza virus resource http://www.ncbi.nlm.nih.gov/genomes/FLU/

SEQ ID N°40
PB2 **Position 016 to 050**
NEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMK

SEQ ID N°41
PB2 **Position 117 to 151**
YESFFLRKMRLDNATWGRITFGPVERVRKRVLLNP

SEQ ID N°42
PB2 **Position 141 to 175**
ERVRKRVLLNPLTKEMPPDEASNVIMEILFPKEAG

SEQ ID N°43
PB2 **Position 197 to 231**
GTMITPIVLAYMLERELVARRRFLPVAGATSAEFI

SEQ ID N°44
PB2 **Position 311 to 345**

DIIRAALGLKIRQRQRFGRLELKRISGRGFKNDEE

SEQ ID N°45
PB2 **Position 404 to 438**
MVFSQDTRMFQGVRGEINFLNRAGQLLSPMYQLQR

SEQ ID N°46
PB2 **Position 519 to 553**
VSELESQAQLMITYDTPKMWEMGTTKELVQNTYQW

SEQ ID N°47
PB2 **Position 537 to 571**
MWEMGTTKELVQNTYQWVLKNLVTLKAQFLLGKED

SEQ ID N°48
PB2 **Position 572 to 606**
MFQWDAFEAFESIIPQKMAGQYSGFARAVLKQMRD

SEQ ID N°49
PB2 **Position 717 to 751**
LEKLKPGEKANILLYQGKPVKVVKRKRYSALSNDI

SEQ ID N°50
PB1 **Position 001 to 035**
MNINPYFLFIDVPIQAAISTTFPYTGVPPYSHGTG

SEQ ID N°51
PB1 **Position 097 to 131**
EEHPGLFQAASQNAMEALMVTTVDKLTQGRQTFDW

SEQ ID N°52
PB1 **Position 227 to 261**
MTKDAERGKLKRRAIATAGIQIRGFVLVVENLAKN

SEQ ID N°53
PB1 **Position 393 to 427**
KPFFNEEGTASLSPGMMMGMFNMLSTVLGVAALGI

SEQ ID N°54
PB1 **Position 616 to 650**
DPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGP

SEQ ID N°55

PB1 **Position 701 to 735**
SASYRKPVGQHSMLEAMAHRLRMDARLDYESGRMS

SEQ ID N°56
PA **Position 160 to 194**
SSLDEEGKGRVLSRLTELQAELSLKNLWQVLIGEE

SEQ ID N°57
PA **Position 491 to 525**
ESFDMLYGLAVKGQSHLRGDTDVVTVVTFEFSSTD

SEQ ID N°58
PA **Position 696 to 723**
VIQSAYWFNEWLGFEKEGSKVLESVDEIMDE

SEQ ID N°59
NP **Position 173 to 207**
FLKEEVKTMYKTTMGSDGFSGLNHIMIGHSQMNDV

SEQ ID N°60
NP **Position 253 to 287**
EAIRFIGRAMADRGLLRDIKAKTAYEKILLNLKNK

SEQ ID N°61
NP **Position 308 to 342**
IADIEDLTLLARSMVVVRPSVASKVVLPISIYAKI

SEQ ID N°62
NP **Position 338 to 372**
IYAKIPQLGFNVEEYSMVGYEAMALYNMATPVSIL

SEQ ID N°63
NP **Position 418 to 452**
GFHVPAKEQVEGMGAALMSIKLQFWAPMTRSGGNE

SEQ ID N°64
M1 **Position 166 to 300**
ARSSVPGVRREMQMVSAMNTAKTMNGMGKGEDVQK

SEQ ID N°65
M1 **Position 209 to 237**

IGVLRSLGASQKNGEGIAKDVMEVLKQSS

Candidate peptides for inclusion into a prophylactic or therapeutic vaccine for influenza may be peptides from any of the viral proteins haemagglutinin, neuraminidase, matrix (M1) protein, M2, nucleoprotein (NP), PA, PB1, PB2, NS1 or NS2 in any such combination.

Synthesis of Fluoropeptides and native peptides (unmodified peptides)

Eight native peptides and 8 fluoropeptides (selected from the peptide list contained herein; SEQ ID N°1 through 65) were obtained by solid phase peptide synthesis (SPPS). All peptides were synthesized on Rink amide PEG resin by using standard 9-fluorenyhnethoxycarbonyl (Fmoc) chemistry. The peptide chain was assembled on resin by repetitive removal of the Fmoc protecting group by treating with 20% piperidine/ N,N-Dimethylformamide for 30 minutes and coupling of protected amino acid by using 1,3-diisopropylcarbodiimide / 1-hydroxy-benzotriazole / N-methylmorpholine for 120 minutes. Ninhydrin test was performed after each coupling to check the coupling efficiency. After the addition of the N-terminal Lysinyl residue, the resin blocks were split to allow (1) on the first half of the resin, the incorporation of the 2H,2H,3H,3H-Perfluoroundecanoic acid fluorocarbon chain ($C_8F_{17}(CH_2)_2COOH$) on the Epsilon-chain of the N-terminal lysine to derive the fluoropeptide and (2) on the second half of the resin, the acetylation of the Epsilon-chain of the N-terminal lysine to derive the native peptide. Resins were washed and dried, then treated with reagent K for cleavage and removal of the side chain protecting groups. Crude peptides were precipitated from cold ether and collected by filtration. Purity was assessed by RP-HPLC and was superior to 92% for all peptides. Freeze-dried fluoropeptides were prepared under nitrogen and stored at -20°C. Stability of the fluoropeptides under storage conditions have been confirmed by RP-HPLC and LC-MS over 6 months.

Vaccine dose preparation

Eight freeze-dried fluoropeptides (fluoropeptide 1, fluoropeptide 2, fluoropeptide 3, fluoropeptide 4, fluoropeptide 5, fluoropeptide 6, fluoropeptide 7 & fluoropeptide 8) or eight freeze-dried equivalent native peptides (peptide 1, peptide 2, peptide 3, peptide 4, peptide 5, peptide 6, peptide 7 & peptide 8) were formulated to create an isomolar formulation yielding a broadly neutral pH for parenteral delivery.

The sequences of the influenza peptide portions of the constructs were as follows:

Fluoropeptide 1	HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK-NH2
Fluoropeptide 2	VAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQG-NH2
Fluoropeptide 3	YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE-NH2
Fluoropeptide 4	APIMFSNKMARLGKGYMFESKRMKLRTQIPAEMLA-NH2
Fluoropeptide 5	SPGMMMGMFNMLSTVLGVSILNLGQKKYTKTTY-NH2
Fluoropeptide 6	KKKSYINKTGTFEFTSFFYRYGFVANFSMELPSFG-NH2
Fluoropeptide 7	DQVRESRNPGNAEIEDLIFLARSALILRGSVAHKS-NH2
Fluoropeptide 8	DLEALMEWLKTRPILSPLTKGILGFVFTLTVPSER-NH2

Animals and immunization

Female, 6-8 weeks of age, BALB/c or CB6F1 (BALB/c x C57BL/6J) mice were purchased from Charles River (UK) &/or Harlan (UK). Injections were performed subcutaneously using 1ml syringe and 22-G needle. Immunisations were performed so that mice received either a single immunization (prime) or two immunizations (prime/boost). Immunisations were performed with a 14 day interval between each injection.

Fluoropeptide vaccine is strongly immunogenic and is superior to native peptides in both BALB/c and CB6F1 mice

The immunogenicity of the fluoropeptide vaccine (mixture of 8 fluoropeptides as above) was compared to the native peptide equivalent (mixture of 8 unmodified peptides – called native peptides as above) in BALB/c and CB6F1 mice. The study also compared the immunogenicity of both formulations using a prime or prime-boost regimen. Both formulations were injected subcutaneously without adjuvant in BALB/c and CBF6 mice. Mice were immunized with a fluoropeptide vaccine dose containing 1nmol/fluoropeptide (8 nmol total for eight fluoropeptides) or the native peptide vaccine equivalent at 1nmol/peptide (8 nmol total for eight native peptides). Neither vaccine preparation contained any adjuvant. 10 days after the final immunization, spleen cells were restimulated with each individual native peptide at 10 μg/ml and assessed using an IFN-γ ELISpot assay. According to ex vivo IFN-γ ELISpot assays (Figures 1 & 2), the immunogenicity of the fluoropeptide vaccine was superior to both the excipient alone and the native peptide vaccine equivalent after a prime-boost immunisation regimen ($P<0.001$). The results also demonstrated a strong increase in the number of spot forming cells using a prime-boost regimen compared to a single immunisation for the fluoropeptide vaccine group only (Figure 1 & 2). These results demonstrate the self-adjuvanticity property of the fluorocarbon chain linked to a peptide sequences.

Fluoropeptide vaccine induces a robust multiepitopic T cell response in both BALB/c and CB6F1 mice

The immunogenicity of the fluoropeptide vaccine (mixture of 8 fluoropeptides as above) was compared to its native peptide equivalent (mixture of 8 unmodified peptides – referred to as 'native peptides' as above) in BALB/c and CB6F1 mice. The study also compared the immunogenicity of both formulations on a prime and prime-boost regimen. Both formulations were injected subcutaneously without adjuvant in

BALB/c and CB6F1 mice. Mice were immunized with a fluoropeptide vaccine dose containing 1nmol/fluoropeptide (8 nmol total for eight fluoropeptides), the native peptide vaccine equivalent at 1nmol/peptide (8 nmol total for eight native peptides). Neither vaccine preparation contained any adjuvant. The control group consisted of mice immunized with excipient alone. 10 days after immunization, spleen cells were restimulated by each individual native peptide at 10 μg/ml and assessed using IFN-γ ELISpot assay. The fluoropeptide vaccine induce peptide-specific responses directed against 5 out of 8 peptides in BALB/c mice and 7 out of 8 peptides in CB6F1 mice which is superior to the response induced by the vaccine equivalent (unmodified peptides). This demonstrates that vaccination with fluoropetides can induce an immunological response that is both qualitatively and quantitatively superior to that of its native peptide equivalent.

The fluoropeptide vaccine induces a Th1 cytokine profile depending upon the murine strain tested

The immunogenicity of the fluoropeptide vaccine (mixture of 8 fluoropeptides as above) was compared to the native peptide equivalent (mixture of 8 unmodified peptides as above) in BALB/c and CB6F1 mice. Formulations were injected subcutaneously without adjuvant in BALB/c and CB6F1 mice. Mice were immunized with a fluoropeptide vaccine dose containing 1nmol/fluoropeptide (8 nmol total for eight fluoropeptides), the native peptide vaccine equivalent at 1nmol/peptide (8 nmol total for eight native peptides). Neither vaccine preparation contained any adjuvant. 10 days after the last immunization, spleen cells were restimulated with a mixture of 8 native peptides at 1 μg/ml per peptide. After 48 hours stimulation culture supernatants were assessed for cytokines by means of a multiplexed bead assay (CBA). Results demonstrate the cytokine profile in CBF6 mice is dominated by the production of IFN-γ and significant production of TNF-α highlighting a Th1 profile (Figure 4). This Th1-dominated cytokine profile was more pronounced compared to BALB/c mice due to a lower intensity of these Th1 responses compared to CB6F1 mice (as also observed by IFN-γ ELISpot - refer to Figures 1 & 2) and increases in Th2 cytokines. Nevertheless, an enhanced Th1 response was observed in BALB/c mice immunized with fluoropeptides compared to its native peptide equivalent.

The fluoropeptide vaccine stimulates both peptide-specific CD4+ and CD8+ T cells producing IFN-γ

Intracellular cytokine staining for IFN-γ was used to provide information about the frequency of peptide-specific CD4+ and CD8+ T cells producing IFN-γ.Mice were immunised with the fluoropeptide vaccine (mixture of 8 fluoropeptides as above) and CD4+ or CD8+ splenocytes were assessed for intracellular cytokine staining by flow cytometry after a short stimulation period with a mixture of 8 native peptides (vaccine). The results demonstrate that immunization of mice with the fluoropeptide vaccine was able to elicit both peptide-specific CD4+ and CD8+ T cells producing IFN-γ at a frequency of 0.5-2.6% (Figure 5). This validates that fluoropeptides engage both MHC class I & II antigen processing peptides if the peptides contain relevant MHC class I & II epitopes.

Example 2 Immune responses elicited by fluoropeptide vaccination are boosted by combination with adjuvant

Immunogenicity of the fluoropeptide vaccine (mixture of 8 fluoropeptides as above) was compared with immunogenicity of the fluoropeptide vaccine in the presence of an adjuvant, Freund's complete adjuvant (FCA). Fluoropeptide vaccine (1 nmol/peptide) or fluoropeptide vaccine (1 nmol/peptide) emulsified in CFA was used to immunize BALB/c mice. 10 days after the immunization, splenocytes were stimulated with individual peptides at 10μg/ml. 48 hours later culture supernatants were collected and tested for cytokines using a multiplex cytokine assay (CBA). Results show that using an CFA as an additional adjuvant can significantly boost Th1 cytokine production (IFN-γ and IL-2) without effecting the production of Th2 cytokines (IL-4, IL-5) (Figure 6). Therefore Th1 responses induced by fluoropeptide vaccination are preferentially boosted by combination with adjuvant during immunisation.

Both subcutaneous and intradermal routes of fluoropeptide vaccine administration can induce immune responses

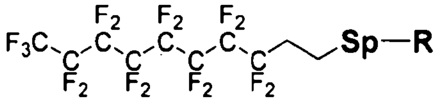
Immunogenicity of the fluoropeptide vaccine (mixture of 8 fluoropeptides as above) was compared using either intradermal or subcutaneous routes of administration in BALB/c mice. 10 days after the immunisation, splenocytes were stimulated with individual peptides at 10μg/ml and assessed for ex vivo IFN-γ production by means of ELISPOT. Results show that both subcutaneous and intradermal routes of fluoropeptide administration are suitable to induce robust antigen-specific responses (Figure 7).

CLAIMS

1. A fluorocarbon vector-antigen construct of structure C_mF_{n}-C_yH_x-(Sp)-R or derivatives thereof, where m = 3 to 30, n <= 2m +1, y = 0 to 15, x <= 2y, (m + y) = 3 – 30, Sp is an optional chemical spacer moiety and R is an immunogenic influenza virus peptide selected from:
HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK (SEQ ID NO: 1)
VAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQG (SEQ ID NO: 4)
YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE (SEQ ID NO: 17)
APIMFSNKMARLGKGYMFESKRMKLRTQIPAEMLA (SEQ ID NO: 18)
SPGMMMGMFNMLSTVLGVSILNLGQKKYTKTTY (SEQ ID NO: 19)
KKKSYINKTGTFEFTSFFYRYGFVANFSMELPSFG (SEQ ID NO: 20)
DQVRESRNPGNAEIEDLIFLARSALILRGSVAHKS (SEQ ID NO: 32)
DLEALMEWLKTRPILSPLTKGILGFVFTLTVPSER (SEQ ID NO: 35)
and homologues and combinations thereof, wherein said homologues have at least 50% identity to SEQ ID NO: 1, 4, 17, 18 or 20, 80 % identity to SEQ ID NO: 19 or 32 or 95% identity to SEQ ID NO: 35.

2. The fluorocarbon vector-antigen construct of claim 1, wherein R is an immunogenic influenza virus peptide selected from:
HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK (SEQ ID NO: 1)
VAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQG (SEQ ID NO: 4)
YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE (SEQ ID NO: 17)
APIMFSNKMARLGKGYMFESKRMKLRTQIPAEMLA (SEQ ID NO: 18)
SPGMMMGMFNMLSTVLGVSILNLGQKKYTKTTY (SEQ ID NO: 19)
KKKSYINKTGTFEFTSFFYRYGFVANFSMELPSFG (SEQ ID NO: 20)
DQVRESRNPGNAEIEDLIFLARSALILRGSVAHKS (SEQ ID NO: 32)
DLEALMEWLKTRPILSPLTKGILGFVFTLTVPSER (SEQ ID NO: 35)
and combinations thereof.

3. The fluorocarbon vector-antigen construct of claim 1 or 2 having the structure



$F_3C-(CF_2)_7-CH_2CH_2-\mathbf{Sp}-\mathbf{R}$

4. The fluorocarbon vector-antigen construct of claim 1 or 2 where **R** comprises multiple epitopes from an influenza virus protein and/or fusion peptides.

5. A pharmaceutical composition comprising the fluorocarbon vector-antigen construct of any one of claims 1 to 4 optionally together with one or more pharmaceutically acceptable carriers, excipients, diluents or adjuvants.

6. The pharmaceutical composition of claim 5 formulated for parenteral, oral, ocular, rectal, nasal, transdermal, topical or vaginal administration.

7. The pharmaceutical composition of claim 5 taking the form of a liquid, emulsion, solid, aerosol or gas.

8. The pharmaceutical composition of claim 5 comprising an adjuvant wherein said adjuvant is selected from:
(1) natural or synthetically derived refinements of natural components of bacteria;
(2) adjuvant or potentiating agents;
(3) oil in water adjuvants, water-in-oil adjuvants, immunostimulating complex (ISCOMs), liposomes, formulated nano and micro-particles; and
(4) bacterial toxins and toxoids.

9. The pharmaceutical composition of claim 8, wherein (1) is selected from Freund's adjuvant and its derivatives, muramyldipeptide (MDP) derivatives, CpG and monophosphoryl lipid A.

10. The pharmaceutical composition of claim 8, wherein (2) is selected from saponins, aluminium salts and cytokines.

11. The pharmaceutical composition of any one of claims 5 to 10 comprising from 2 to 20 vector-antigen constructs according to any one of claims 1 to 4.

12. The pharmaceutical composition of any one of claims 5 to 11 which comprises at least two vector-antigen constructs, the first construct comprising the influenza peptide sequence:

HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK (SEQ ID NO: 1)

and the second construct comprising the influenza peptide sequence:

YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE (SEQ ID NO: 17).

13. The pharmaceutical composition of claim 11 or 12, comprising 5, 6, 7 or 8 vector-antigen constructs according to any one of claims 1 to 4.

14. The pharmaceutical composition of claim 13 comprising 5, 6, 7 or 8 of the vector-antigen constructs which comprise the following influenza peptide sequences:

Construct 1 HMAIIKKYTSGRQEKNPSLRMKWMMAMKYPITADK (SEQ ID NO: 1)
Construct 2 VAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQG (SEQ ID NO: 4)
Construct 3 YITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFE (SEQ ID NO: 17)
Construct 4 APIMFSNKMARLGKGYMFESKRMKLRTQIPAEMLA (SEQ ID NO: 18)
Construct 5 SPGMMMGMFNMLSTVLGVSILNLGQKKYTKTTY (SEQ ID NO: 19)
Construct 6 KKKSYINKTGTFEFTSFFYRYGFVANFSMELPSFG (SEQ ID NO: 20)

Construct 7 DQVRESRNPGNAEIEDLIFLARSALILRGSVAHKS (SEQ ID NO: 32)

Construct 8 DLEALMEWLKTRPILSPLTKGILGFVFTLTVPSER (SEQ ID NO: 35).

15. The use of the fluorocarbon vector-antigen construct of any one of claims 1 to 4 in the preparation of a prophylactic vaccine or immunotherapeutic pharmaceutical product.

16. The use of the fluorocarbon vector-antigen construct of any one of claims 1 to 4 in the preparation of a prophylactic vaccine or immunotherapeutic pharmaceutical product for parenteral, mucosal, oral, nasal, topical, ocular, rectal, transdermal, or vaginal administration.

17. The pharmaceutical composition of any one of claims 5 to 14 for use in a method of treatment or immunisation.

18. The pharmaceutical composition of any one of claims 5 to 14 for use in a method of stimulating an immune response in a human or animal.

19. The pharmaceutical composition of claim 18 wherein the animal is a bird.

20. The pharmaceutical composition of claim 18 wherein the animal is a mammal.

21. The pharmaceutical composition of any one of claims 17 to 20 for use in combination with anti-influenza therapy.

22. The pharmaceutical composition of claim 21 wherein the anti-influenza therapy is a neuraminidase inhibitor.

23. The pharmaceutical composition of any one of claims 18 to 22 for use in combination with a haemagglutinin containing influenza vaccine by contemporaneous or separate administration.

24. A method of preparing a prophylactic or therapeutic pharmaceutical product comprising combining the fluorocarbon construct of any one of claims 1 to 4 with one or more pharmaceutically acceptable carriers, excipients, diluents, or adjuvants.

25. The method of claim 24 wherein the vaccine or product is for parenteral, mucosal, oral, nasal, topical, ocular, rectal, transdermal, or vaginal administration.

26. A fluorocarbon vector-antigen construct according to claim 1 substantially as described herein with reference to the Examples.

27. A pharmaceutical composition according to claim 5 substantially as described herein with reference to the Examples.

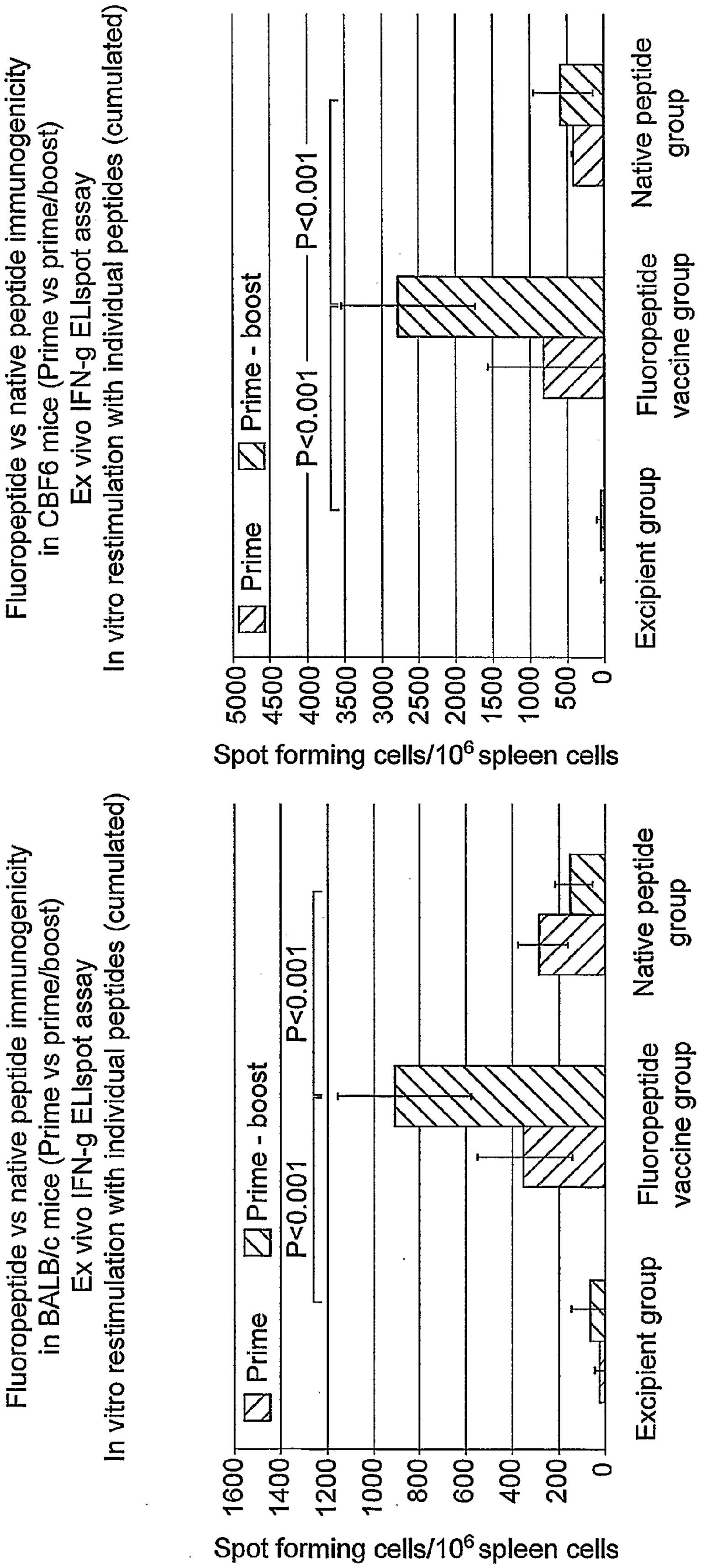
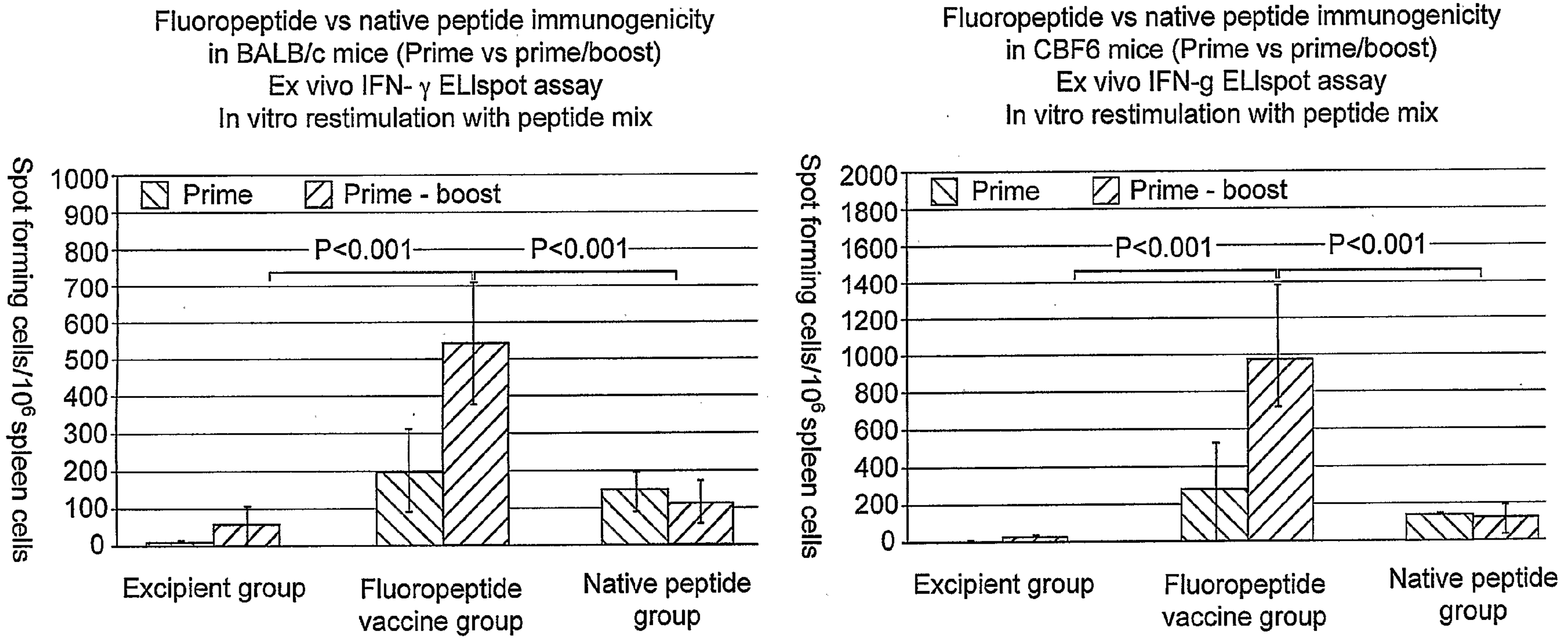

Fluoropeptide vs native peptide immunogenicity
in BALB/c mice (Prime vs prime/boost)
Ex vivo IFN-g ELIspot assay
In vitro restimulation with individual peptides (cumulated)
Prime
Prime - boost
P<0.001
P<0.001
Spot forming cells/10⁶ spleen cells
1600
1400
1200
1000
800
600
400
200
0
Excipient group
Fluoropeptide vaccine group
Native peptide group
Fluoropeptide vs native peptide immunogenicity
in CBF6 mice (Prime vs prime/boost)
Ex vivo IFN-g ELIspot assay
In vitro restimulation with individual peptides (cumulated)
Prime
Prime - boost
P<0.001
P<0.001
Spot forming cells/10⁶ spleen cells
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
Excipient group
Fluoropeptide vaccine group
Native peptide group

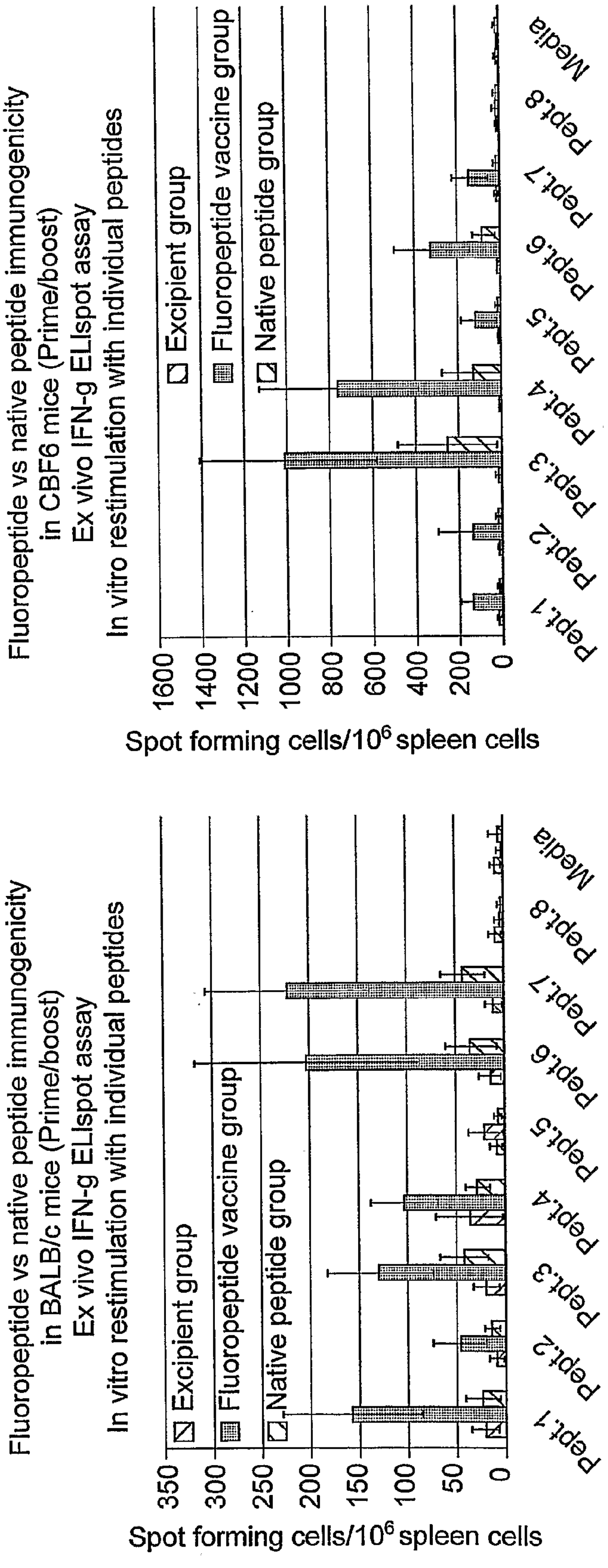
FIG. 1



Fluoropeptide vs native peptide immunogenicity
in BALB/c mice (Prime vs prime/boost)
Ex vivo IFN- γ ELIspot assay
In vitro restimulation with peptide mix

Fluoropeptide vs native peptide immunogenicity
in CBF6 mice (Prime vs prime/boost)
Ex vivo IFN-g ELIspot assay
In vitro restimulation with peptide mix

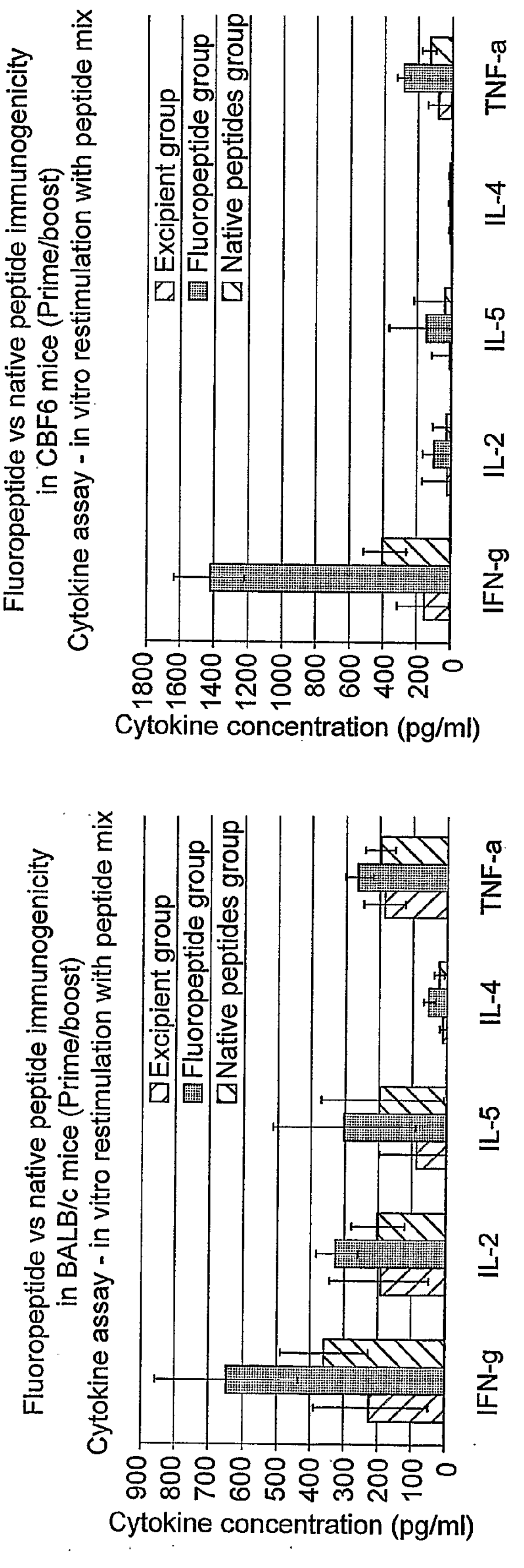
FIG. 2



Fluoropeptide vs native peptide immunogenicity in BALB/c mice (Prime/boost) Ex vivo IFN-g ELIspot assay In vitro restimulation with individual peptides

Fluoropeptide vs native peptide immunogenicity in CBF6 mice (Prime/boost) Ex vivo IFN-g ELIspot assay In vitro restimulation with individual peptides

FIG. 3



Fluoropeptide vs native peptide immunogenicity in CBF6 mice (Prime/boost) Cytokine assay - in vitro restimulation with peptide mix

Fluoropeptide vs native peptide immunogenicity in BALB/c mice (Prime/boost) Cytokine assay - in vitro restimulation with peptide mix

FIG. 4

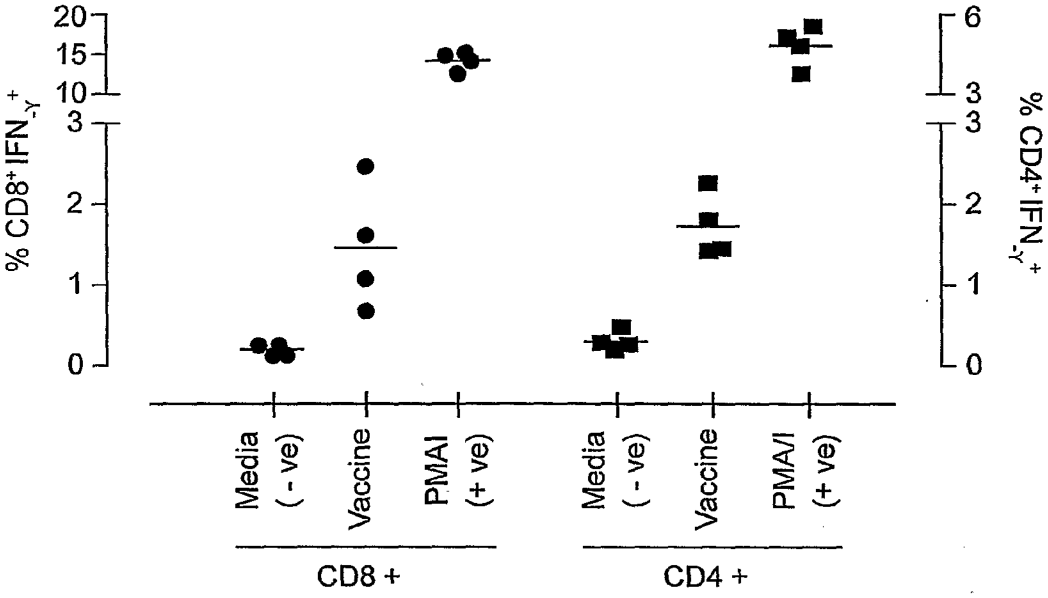

20
15
10
3
2
1
0
% CD8⁺ IFN-γ⁺
6
3
3
2
1
0
% CD4⁺ IFN-γ⁺
Media (- ve)
Vaccine
PMAI (+ ve)
Media (- ve)
Vaccine
PMA/I (+ ve)
CD8 +
CD4 +

FIG. 5

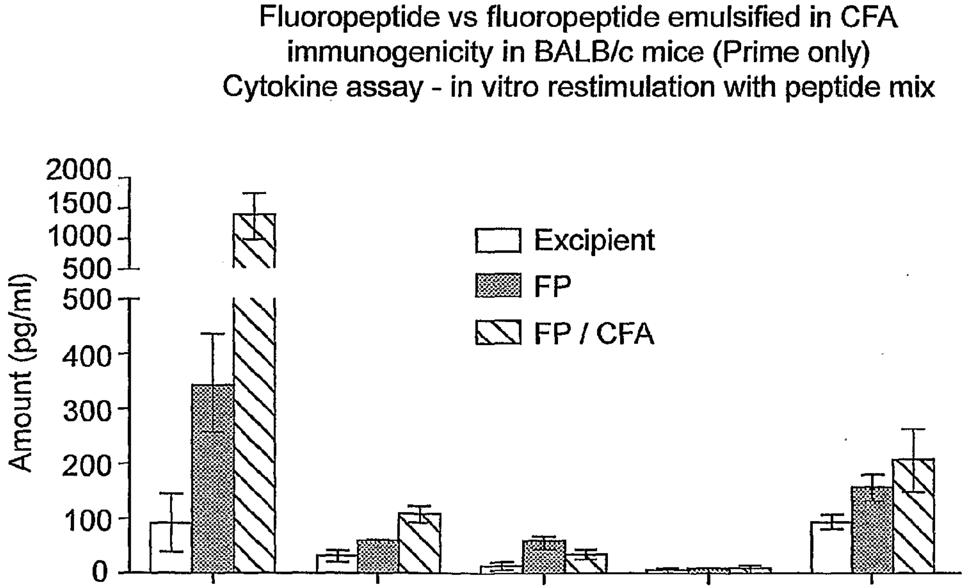
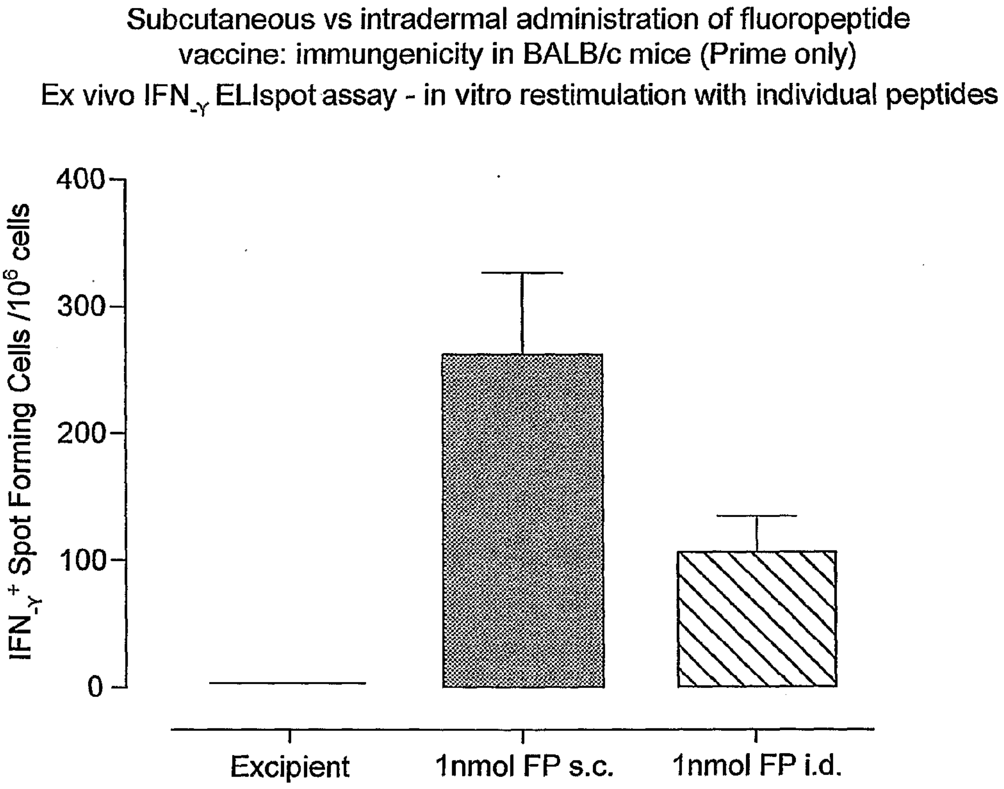

Fluoropeptide vs fluoropeptide emulsified in CFA
immunogenicity in BALB/c mice (Prime only)
Cytokine assay - in vitro restimulation with peptide mix
2000
1500
1000
500
500
400
300
200
100
0
Amount (pg/ml)
Excipient
FP
FP / CFA
IFN-γ
IL-2
IL-5
IL-4
TNF-α
Cytokine

FIG. 6



Subcutaneous vs intradermal administration of fluoropeptide vaccine: immungenicity in BALB/c mice (Prime only)

Ex vivo IFN$_{-\gamma}$ ELIspot assay - in vitro restimulation with individual peptides

FIG. 7