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(54) Title: ALTERNARIA PEPTIDES

(57) Abstract: Pharmaceutical formulations,which may be used for preventing or treating allergy to moulds of the Alternaria and/or Cladosporiumgenus, comprising a pharmaceutically acceptable carrier or diluent and a polypeptide or a pharmaceutically acceptable salt thereof selected from at least three of: (a)a polypeptide comprising the amino acid sequence of WSWKIGPAIATGNT(Alt28; SEQ ID NO: 101) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; (b)a polypeptide comprising the amino acid sequence of KYRRVVRAGVKVAQTAR(Alt34A; SEQ ID NO: 107) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; (c) a polypeptide comprising the amino acid sequence of KYAGVFVSTGTLGGG (SEQ ID NO: 112) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; (d)a polypeptide comprising the amino acid sequence of AEVYQKLKALAKKTYGQ(Alt13A; SEQ ID NO: 83) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; (e)a polypeptide comprising the amino acid sequence of SLGFNIKATNGGTLD(Alt01A; SEQ ID NO: 60)or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; (f) a polypeptide comprising the amino acid sequence of SAKRMKVAFKLDIEK(Alt06; SEQ ID NO: 72) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; (g)a polypeptide comprising the amino acid sequence of DITYVATATLPNYCR(SEQ ID NO: 111) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; and (h)a polypeptide comprising the amino acid sequence of GWGVMVSHRSGET(Alt14;SEQ ID NO: 84) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; wherein a T cell epitope-containing variant sequence of a said amino acid sequence is said amino acid sequence having up to seven amino acid modifications, each of which is independently a deletion, substitution or insertion, and each polypeptide is up to 30 amino acids in length.

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ALTERNARIA PEPTIDES

Field of the Invention

The present invention relates to polypeptides and pharmaceutical formulations which may be used for preventing or treating allergy to moulds of the *Alternaria* and/or *Cladosporium* genus.

Background to the Invention

Mould allergens are recognised as a major cause of allergic diseases in humans and animals, including asthma, allergic rhinitis, allergic conjunctivitis and allergic dermatitis. In colder climates, moulds can be found in the outdoor air starting in the late winter, and peaking in the late summer to early fall months (July to October). In warmer climates, mould spores may be found throughout the year, with the highest levels found in the late summer to early fall months. While indoor moulds can occur year round and are dependent on moisture levels in the home, indoor mould levels are higher when outdoor mold levels are higher. Therefore, a common source of indoor mould is from the outside environment, although can also be from indoor mould contamination.

There are thousands of types of mould; however, only a few of these are commonly associated with allergy. The following are the most likely causes of allergic disease based on the types of mould spores collected in the air: *Alternaria*, *Cladosporium*, *Aspergillus, Penicillium, Helminthosporum, Epicoccum, Fusarium, Aureobasidium*, *Phoma*, *Rhizopus, Mucor*, Smuts and Yeasts. Moulds in the genus *Alternaria*, in particular *Alternaria Alternata*, and the genus *Cladosporium* are considered to be among the most important allergenic fungi.

Cladosporium is the most common airborne outdoor mould. *Alternaria* is one of the main allergens affecting children. In temperate climates, airborne *Alternaria* spores are detectable from for most of the year (typically May to November in the northern hemisphere), with peaks in late summer and autumn. Dispersion of *Alternaria* spores occurs during dry periods. These feature higher wind velocity and lower relative humidity, which result in peak dispersion during sunny afternoon periods

Although considered to be an outdoor mould, *Alternaria* will grow anywhere that provides sufficient moisture and a suitable growth substrate. Accordingly, *Alternaria* is commonly found indoors, in particular in damp areas such as basements, kitchens or bathrooms. *Alternaria* is commonly found in refrigerator drip trays, air conditioners, waste containers, mattresses, foam rubber pillows, or even in condensation on windows. It is one of the most common mould spores found in house dust in both North America and Europe. It is effectively impossible to avoid *Alternaria* allergens.

Summary of the Invention

The invention provides a pharmaceutical formulation comprising a pharmaceutically acceptable carrier or diluent and a polypeptide or a pharmaceutically acceptable salt thereof selected from at least three of:

(a) a polypeptide comprising the amino acid sequence of WSWKIGPAIATGNT (Alt28; SEQ ID NO: 101) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(b) a polypeptide comprising the amino acid sequence of KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(c) a polypeptide comprising the amino acid sequence of KYAGVFVSTGTLGGG (SEQ ID NO: 112) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof ;

(d) a polypeptide comprising the amino acid sequence of AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(e) a polypeptide comprising the amino acid sequence of SLGFNIKATNGGTLD (Alt01A; SEQ ID NO: 60) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(f) a polypeptide comprising the amino acid sequence of SAKRMKVAFKLDIEK (Alt06; SEQ ID NO: 72) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(g) a polypeptide comprising the amino acid sequence of DITYVATATLPNYCR (SEQ ID NO: 111) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; and

(h) a polypeptide comprising the amino acid sequence of GWGVMVSHRSGET (Alt14; SEQ ID NO: 84) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

wherein a T cell epitope-containing variant sequence of a said amino acid sequence is said amino acid sequence having up to seven amino acid modifications, each of which is independently a deletion, substitution or insertion, and each polypeptide is up to 30 amino acids in length.

The invention further provides a pharmaceutical formulation of the invention for use in a method of treating or preventing allergy to *Cladosporium* and/or *Alternaria*.

The invention also provides a method of treating an individual for allergy to *Alternaria* and/or *Cladosporium* or of preventing in an individual allergy to *Alternaria* and/or *Cladosporium*, which method comprises administering to said individual a therapeutically or prophylactically effective amount of a pharmaceutical formulation of the invention.

The invention further provides use of the at least three polypeptides or salts described above for the manufacture of a medicament for the prevention or treatment of allergy to *Alternaria* and/or *Cladosporium*.

The invention additionally provides an *in vitro* method of determining whether T cells recognise a polypeptide of a pharmaceutical formulation of the invention, which method comprises contacting said T cells with said pharmaceutical formulation and detecting whether said T cells are stimulated by a said polypeptide.

The invention also provides a method of preparing a pharmaceutical formulation of the invention, comprising combining at least three polypeptides or salts described above with a pharmaceutically acceptable carrier or diluent.

The invention further provides a polypeptide, or a pharmaceutically acceptable salt thereof, which is up to 30 amino acids in length and comprises:

(I) the amino acid sequence:

(a) WSWKIGPAIATGNT (Alt28; SEQ ID NO: 101),

(b) KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107), or

(c) KYAGVFVSTGTLGGG (SEQ ID NO: 112); or

(II) a T cell epitope-containing variant sequence which is a said amino acid sequence (I) having up to seven amino acid modifications, each of which is independently a deletion, substitution or insertion.

The invention also provides a polypeptide or salt of the invention for use in a method of treating or preventing allergy to *Alternaria* and/or *Cladosporium*, and use of a polypeptide or salt of the invention for the manufacture of a medicament for the prevention or treatment of allergy to *Alternaria* and/or *Cladosporium*. The invention additionally provides method of treating an individual for allergy to *Alternaria* and/or *Cladosporium* or of preventing in an individual allergy to *Alternaria* and/or *Cladosporium*, which method comprises administering to said individual a therapeutically or prophylactically effective amount of a polypeptide or salt of the invention.

Description of the sequences

SEQ ID NOS: 1 to 118 provide amino acid sequences as set out in Examples 1 to 10. In more detail:

SEQ ID NOS: 1 to 6, 59 to 65 and 111 correspond to amino acid sequences derived from protein Alt a1.

SEQ ID NOS: 7 to 11, 66 to 78 and 113 correspond to amino acid sequences derived from protein Alt a2.

SEQ ID NOS: 12 to 22 and 79 to 87 correspond to amino acid sequences derived from protein Alt a6.

SEQ ID NOS: 23 to 29, 88, 89, 112 and 114 correspond to amino acid sequences derived from protein Alt a7.

SEQ ID NOS: 30 to 35 and 90 to 98 correspond to amino acid sequences derived from protein Alt a8.

SEQ ID NOS: 36 to 48 and 99 to 101 correspond to amino acid sequences derived from protein Alt a10.

SEQ ID NOS: 49 to 58, 102 to 107 and 115 correspond to amino acid sequences derived from protein Alt a13.

SEQ ID NOS: 108 to 110 correspond to amino acid sequences derived from homologues of the above Alternaria proteins.

SEQ ID NOS: 116 to 118 correspond to amino acid sequences of control polypeptides used in Example 9.

NCBI accession numbers for the proteins referred to above are provided in Examples 1 to 10.

Detailed Description of the Invention

The present invention is concerned with preventing or treating allergy to *Cladosporium* and/or *Alternaria* and provides combinations of polypeptides, and pharmaceutically acceptable salts thereof, suitable for this use. The combinations of polypeptides or salts may be provided in pharmaceutical formulations.

Amino acid sequences and variant amino acid sequences

A polypeptide of the invention may preferably comprise, consist or consist essentially of an amino acid sequence as shown in any one of:

(a) WSWKIGPAIATGNT (Alt28; SEQ ID NO: 101),
(b) KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107),
(c) KYAGVFVSTGTLGGG (Alt18; SEQ ID NO: 112),
(d) AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83),
(e) SLGFNIKATNGGTLD (Alt01A; SEQ ID NO: 60),
(f) SAKRMKVAFKLDIEK (Alt06; SEQ ID NO: 72),
(g) DITYVATATLPNYCR (SEQ ID NO: 111), or
(h) GWGVMVSHRSGET (Alt14; SEQ ID NO: 84);

Other polypeptides of the invention comprise, consist or consist essentially of an amino acid sequence as shown in:

(i) IEKLRSNITVQYDI (Alt33; SEQ ID NO: 105),
(j) SAFRSIEPELTVY (Alt10; SEQ ID NO: 77),
(k) GYTGKIKIAMDVASSE (Alt15; SEQ ID NO: 86),

Alternatively, a polypeptide included in a pharmaceutical formulation of the invention may comprise, consist or consist essentially of a T cell epitope-containing variant sequence which is an amino acid sequence as shown in any one of (a) to (k) having up to seven amino acid modifications, each of which is independently a deletion, substitution or insertion.

It is preferred that the modifications in a variant sequence do not alter the functional properties of a T cell epitope present in the corresponding original amino acid sequence. The functional properties of T cell epitopes are discussed further below.

In preferred variant sequences, sufficient contiguous amino acids of the corresponding original amino acid sequence are retained to contain a T cell epitope. Typically, such a variant sequence retains at least 8, preferably at least 9, contiguous amino acids of the original amino acid sequence. The variant sequence may retain from 8 to 12 amino acids or from 9 to 12 amino acids of the original amino acid sequence.

A variant sequence may have fewer than seven amino acid modifications. For example, said variant sequence may have up to six or up to five amino acid modifications, preferably up to four said amino modifications, more preferably up to three amino acid modifications, and most preferably only one or two amino acid modifications. All said modifications are independently a deletion, substitution or insertion.

In a particularly preferred embodiment, the variant sequence has one or two amino acid modifications, the or each of which independently is a deletion or substitution.

Deletions

Where a T cell epitope-containing variant sequence has an amino acid modifications that is a deletion, the deleted amino acid is preferably removed from the N- or C-terminus of the corresponding original amino acid sequence. That is, the variant sequence is a truncation of the original amino acid sequence formed by removing one or more contiguous amino acids from the N- and/or C-terminus of the original sequence. Such a variant sequence may optionally have no other deletions or no other modifications.

A deleted amino acid may less preferably be removed from an internal position in the corresponding original amino acid sequence. By removal from an internal position it is meant that a deleted amino acid is not itself at the N- or C-terminus of the original amino acid sequence and nor is it removed as part of a sequence of contiguous amino acids including the N- or C-terminus of the original amino acid sequence. That is, to be considered to be deletion from an internal position, said deletion must occur independently of deletion from the N- or C-terminus of the original amino acid sequence.

For example, given an original sequence ABCDEFGH, an example variant sequence having an internal deletion of two amino acids could be ADEFGH, that is B and C are removed from internal positions and the original terminal residues A and H are retained. By contrast, a deletion of two contiguous amino acids from the N-terminus of the same original sequence would result in the variant sequence CDEFGH, in which A and B are removed and C is now at the N-terminus. The deletion of B in this case is not a removal from an internal position, because it is removed as one of the two contiguous amino acids including the N-terminus of the original sequence.

Where more than one deletion occurs in a variant sequence, the deleted amino acids may be removed from any combination of the N-terminus and/or the C-terminus and/or an internal position. Preferred variant sequences have no more than one deletion from an internal position. In particularly preferred variant sequences there is no deletion from an internal position, and the deleted amino acids are removed from any combination of the N- and/or C-terminus of the original sequence. That is, the deleted amino acids may all be removed from the N-terminus of the original sequence, or they may all be removed from the C-terminus of the original sequence, or some amino acids may be removed from each end of the original sequence.

Thus, in one embodiment, a variant sequence is an amino acid sequence of any one of (a) to (k) having one, two, three, four, five, six or seven amino acids removed from the N-terminus of said sequence of (a) to (k).

In another embodiment, a variant sequence is an amino acid sequence of any one of (a) to (k) having one, two, three, four, five, six or seven amino acids removed from the C-terminus of said sequence of (a) to (k).

In another embodiment, a variant amino acid sequence is an amino acid sequence of any one of (a) to (k) having a number of amino acids removed from both the N- and C-terminus of said sequence, provided that said sequence has no more than six modifications in total. A preferred embodiment of such a variant sequence is an amino acid sequence of any one of (a) to (k) having one, two or three amino acids removed from the N- and/or C-terminus of said sequence, and optionally no other modifications.

Specific examples of variant amino acid sequences which have at least one deletion include:

- the variant sequence QKLKALAKKTYGQ (SEQ ID NO: 18), which is the amino acid sequence of AEVYQKLKALAKKTYGQ (SEQ ID NO: 83) having four amino acids removed from the N-terminus;
- the variant sequence DITYVATATLPNY (SEQ ID NO: 5) which is the amino acid sequence of DITYVATATLPNYCR (SEQ ID NO: 111) having two amino acids removed from the C terminus;
- the variant sequence RVVRAGVKVAQTA (SEQ ID NO: 58). which is the amino acid sequence of KYRRVVRAGVKVAQTAR (SEQ ID NO: 107) having three amino acids removed from the N-terminus and one amino acid removed from the C terminus; and
- the variant sequence YEKYRRVVRAGVKV (SEQ ID NO: 106) which is the amino acid sequence of KYRRVVRAGVKVAQTAR (SEQ ID NO: 107) having five amino acid residues removed from the C-terminus, and an N-terminal extension of two amino acids corresponding to the two contiguous amino acids immediately N-terminal to KYRRVVRAGVKVAQTAR in the native sequence of Alt a 13.

Substitutions

Where a T cell epitope-containing variant sequence has an amino acid modification that is a substitution, the substitution may occur at any position in the original amino acid sequence. It is preferred that said substitution does not introduce a proline or a cysteine. It is also preferred that said substitution is a conservative substitution.

By conservative substitution, it is meant that an amino acid may be substituted with any alternative amino acid having similar properties. The following is a non-exhaustive list of examples:

The amino acids with basic side chains, such as lysine, arginine or histidine, may each be independently substituted for each other.

The amino acids with acidic side chains, such as aspartate and glutamate, may each be independently substituted for each other, or for their amide derivatives, asparagine and glutamine. A glutamate or glutamine may also preferably be replaced with pyroglutamate. A variant sequence having pyroglutamate substituted for glutamate or glutamine is particularly preferred where said pyroglutamate will correspond to the N-terminus of a polypeptide of the invention which comprises, consists or consists essentially of the variant sequence. Polypeptides with pyroglutamate at the N-terminus typically have improved stability during manufacture.

The amino acids with aliphatic side chains, such as glycine, alanine, valine, leucine and isoleucine, may each be independently substituted for each other. Particularly preferred substitutions in this category are limited to the amino acids with smaller aliphatic side chains, that is glycine, alanine, valine, which may preferably each be independently substituted for each other.

Other preferred substitutions include the substitution of methionine with norleucine (Nle).

Additionally, in more general terms, a neutral amino acid may be substituted with another neutral amino acid, a charged amino acid may be substituted with another charged amino acid, a hydrophilic amino acid may be substituted with another hydrophilic amino acid, a hydrophobic may be substituted with another hydrophobic amino acid, a polar amino acid may be substituted with another polar amino acid, and an aromatic amino acid may be substituted with another aromatic amino acid. Some properties of the 20 main amino acids which can be used to select suitable substituents are as follows:

Ala	aliphatic, hydrophobic, neutral	Met	hydrophobic, neutral
Cys	polar, hydrophobic, neutral	Asn	polar, hydrophilic, neutral
Asp	polar, hydrophilic, charged (-)	Pro	hydrophobic, neutral
Glu	polar, hydrophilic, charged (-)	Gln	polar, hydrophilic, neutral
Phe	aromatic, hydrophobic, neutral	Arg	polar, hydrophilic, charged (+)
Gly	aliphatic, neutral	Ser	polar, hydrophilic, neutral
His	aromatic, polar, hydrophilic, charged (+)	Thr	polar, hydrophilic, neutral
Ile	aliphatic, hydrophobic, neutral	Val	aliphatic, hydrophobic, neutral
Lys	polar, hydrophilic, charged(+)	Trp	aromatic, hydrophobic, neutral
Leu	aliphatic, hydrophobic, neutral	Tyr	aromatic, polar, hydrophobic

Specific examples of variant amino acid sequences which have at least one substitution are:

- The variant sequence SAKR-Nle-KVAFKLDIEK (SEQ ID NO: 73) is the amino acid sequence of SAKRMKVAFKLDIEK (SEQ ID NO: 72) having one substitution. The amino acid M at position 5 of SEQ ID NO: 72 is substituted with norleucine; and
- The variant sequence DITYVATATLPNYSR (SEQ ID NO: 62) is the amino acid sequence of DITYVATATLPNYCR (SEQ ID NO: 111) having one substitution. The amino acid C at position 14 of SEQ ID NO: 111 is substituted with Serine. Other preferred variant sequences of SEQ ID NO: 111 include sequences with alternative, preferably similar, substitutions at position 14. For example, instead of substituting with S, the C amino acid at position 14 could be replaced with T, G, A or V.

In some variant sequences there may be substitutions and deletions. Specific examples are:

- the variant sequence AEVYQKLKSLTK (SEQ ID NO: 108) is the amino acid sequence of AEVYQKLKALAKKTYGQ (SEQ ID NO: 83) having five deletions at the C-terminus and two substitutions made at positions 9 (Ser for Ala) and 11 (Thr for Ala). Other preferred variant sequences of SEQ ID NO: 83 include sequences with alternative, preferably similar, substitutions at positions 9 and 11. For example, instead of substituting with S and T, both the A amino acids at positions 9 and 11 could be independently replaced with G or V; and
- the variant sequence of SAKR-Nle-KVAFK (SEQ ID NO: 113) is the amino acid sequence of SAKRMKVAFKLDIEK (Alt06; SEQ ID NO: 72) having five deletions at the C-terminus and one substitution made at position 5 (Nle for Met).

Insertions

Where a variant sequence has an amino acid modification that is an insertion, the added amino acid may be inserted at any position in the original amino acid sequence. It is preferred that the insertion does not introduce a proline or a cysteine.

Preferably, an amino acid may be inserted at the N-terminus and/or C-terminus of the original sequence. That is, the variant sequence is an extension of the original amino acid sequence formed by adding amino acids to the N- and/or C-terminus of the original sequence. Such a variant sequence may optionally have no other insertions or no other modifications.

Less preferably, an amino acid may be inserted at an internal position. By insertion at an internal position it is meant that an amino acid is inserted at any position which is C-terminal to the amino acid at the N-terminus of the original sequence, or that an amino acid is inserted at any position which is N-terminal to the amino acid at the C-terminus of the original sequence.

Where more than one insertion occurs in a variant sequence, the added amino acids may be inserted at any combination of the N-terminus and/or the C-terminus and/or an internal position. Preferred variant sequences have no more than one insertion at an internal position. In particularly preferred variant sequences there is no insertion at an internal position, and the added amino acids are inserted at any combination of the N- and/or C-terminus of the original sequence. That is, the added amino acids may all be inserted at the N-terminus of the original sequence, or they may all be inserted at the C-terminus of the original sequence, or some amino acids may be inserted at each end of the original sequence. That is, the added amino acids may be considered to extend the original sequence at the N- and/or C-terminus.

Thus, in one embodiment, a variant sequence is an amino acid sequence of any one of (a) to (k) having one, two, three, four, five, six or seven amino acids inserted at the N-terminus of said sequence of (a) to (k).

In another embodiment, a variant sequence is an amino acid sequence of any one of (a) to (k) having one, two, three, four, five, six or seven amino acids inserted at the C-terminus of said sequence of (a) to (k).

In another embodiment, a variant sequence is an amino acid sequence of any one of (a) to (k) having a number of amino acids inserted at both the N- and C-terminus of said sequence of (a) to (k), provided that said sequence has no more than seven modifications in total. A preferred embodiment of such a variant sequence is an amino acid sequence of any one of (a) to (k) having one, two or three amino acids inserted at the N- and/or C-terminus of said sequence of (a) to (k), and optionally no other modifications.

A variant sequence having a charged amino acid inserted at the N- and/or C-terminus is particularly preferred where said charged amino acid will correspond to the N- and/or C- terminus of the polypeptide of the invention which comprises, consists or consists essentially of the variant sequence. Charged residues at the N- and/or C-terminus of a polypeptide can improve the solubility of a polypeptide. Preferred charged amino acids include lysine, arginine and histidine. Lysine is particularly preferred. Thus, a particularly preferred variant sequence is an amino acid sequence of any one of (a) to (k) having one or more charged amino acids, preferably one or more lysine residues, inserted at the N- and/or C-terminus of said sequence of (a) to (k).

Specific examples of variant amino acid sequences which have at least one insertion include:

- the variant sequence KSAFRSIEPELTVYK (SEQ ID NO: 78), which is the amino acid sequence of SAFRSIEPELTVY (SEQ ID NO: 77) having a lysine inserted at the N-terminus and at the C terminus; and
- the variant sequence KKYAGVFVSTGTLGGGK (SEQ ID NO: 89), which is the amino acid sequence of KYAGVFVSTGTLGGG (SEQ ID NO: 112) having a lysine inserted at the N-terminus and at the C terminus.

Polypeptides

A polypeptide included in a pharmaceutical formulation of the invention is up to 30 amino acids in length and comprises, consists or consists essentially of an amino acid sequence or variant sequence as defined above.

Said polypeptide may preferably be up to 25 amino acids in length, more preferably up to 20 amino acids in length or up to 17 amino acids in length, and most preferably up to 15 amino acids in length. Put another way, the polypeptide may have a maximum length of 30, 25, 20, 17 or 15 amino acids.

A polypeptide included in a pharmaceutical formulation of the invention is preferably at least 8 amino acids in length, more preferably at least 9 amino acids in length, most preferably at least 12 amino acids in length. Put another way, the polypeptide may have a minimum length of 8, 9, or 12 amino acids.

A polypeptide included in a pharmaceutical formulation of the invention may be of a length defined by any combination of a said minimum and a said maximum length. For example, the polypeptide may be 8 to 30, 8 to 25, 8 to 20, 8 to 17 or 8 to 15 amino acids in length. The polypeptide may be 9 to 30, 9 to 25, 9 to 20, 9 to 17 or 9 to 15 amino acids in length. The polypeptide may be 12 to 30, 12 to 25, 12 to 20, 12 to 17 or 12 to 15 amino acids in length. A preferred polypeptide is of 9 to 30 amino acids in length, more preferably 9 to 20 amino acids in length. A particularly preferred polypeptide is of 12 to 17 amino acids in length.

A polypeptide included in a pharmaceutical formulation of the invention may comprise an amino acid sequence or variant sequence as defined above. Therefore, said polypeptide may include additional amino acids which are not defined by said amino acid sequence or variant sequence. The additional amino acids may be described as flanking said amino acid sequence or variant sequence. That is, the additional amino acids are included at the N-terminus and/or C-terminus of said amino acid sequence or variant sequence.

Put another way, a polypeptide included in a pharmaceutical formulation of the invention may have a sequence consisting of said amino acid sequence or variant sequence having an N-terminal and/or C-terminal extension of a number of amino acids. The maximum number of amino acids in the N-terminal and/or C-terminal extension is determined by the maximum length of the polypeptide, as defined above.

The amino acids in an N-terminal extension of a said amino acid sequence or variant sequence preferably correspond to the amino acids immediately N-terminal to the said amino acid sequence in the native sequence of the protein from which it derives.

The amino acids in a C-terminal extension of a said amino acid sequence or variant sequence preferably correspond to the amino acids immediately C-terminal to the said amino acid sequence in the native sequence of the protein from which it derives.

The N-terminal and/or C-terminal extension may be the one, two, three, four, five, six, seven, eight, nine or ten amino acids corresponding respectively to the one, two, three, four, five, six, seven, eight, nine or ten contiguous amino acids immediately

N- terminal or C-terminal to said amino acid sequence in the sequence of the protein from which it derives.

That is, the N-terminal and/or C-terminal extension is of from one to ten amino acids corresponding respectively to the one to ten contiguous amino acids immediately N-terminal or C-terminal to the said amino acid sequence in the native sequence of the protein from which it derives.

Preferably, the N-terminal and/or C-terminal extension is of from one to six amino acids corresponding respectively to the one to six contiguous amino acids immediately N-terminal or C-terminal to the said amino.

More preferably, the N-terminal and/or C-terminal extension is of from one to four amino acids corresponding respectively to the one to four contiguous amino acids immediately N-terminal or C-terminal to the said amino.

Most preferably, the N-terminal and/or C-terminal extension is of from one to two amino acids corresponding respectively to the one to two contiguous amino acids immediately N-terminal or C-terminal to the said amino acid sequence.

Specific examples of polypeptides which include an N-terminal and/or C-terminal extension to an amino acid sequence or variant sequence include the following:

AEVYQKLKALAKKTYGQ (SEQ ID NO: 83) may have an N-terminal and/or a C-terminal extension of one, two, three, four, five or six amino acids corresponding respectively to the one, two, three, four, five or six contiguous amino acids immediately N- or C-terminal to AEVYQKLKALAKKTYGQ in the native sequence of Alt a 6, that is the amino acids E, A, M, R, Q and G at the N-terminus and S, A,G, N, V and G at the C-terminus. For example, where a one amino acid extension is present both at the N- and C-terminus, the polypeptide of the invention has the amino acid sequence of GAEVYQKLKALAKKTYGQS (SEQ ID NO:12; N- and C-terminal extensions are underlined).

SLGFNIKATNGGTLD (SEQ ID NO: 60) may have an N-terminal and/or a C-terminal extension of one, two, three, four, five or six amino acids corresponding to the one, two, three, four, five or six contiguous amino acids immediately N-and/or C-terminal to SLGFNIKATNGGTLD in the native sequence of Alt a 1. For example, where six contiguous amino acids are present in the N-terminal extension and two contiguous amino acids are present in the C-terminal extension, the polypeptide of the invention has the amino acid sequence of EGTYYNSLGFNIKATNGGTLDFT (SEQ ID NO: 2; N- and C-terminal extensions are underlined).

IEKLRSNITVQYDI (SEQ ID NO: 105) may have a N-terminal extension of one, two or three amino acids corresponding to the one, two, or three contiguous amino acids immediately N-terminal to IEKLRSNITVQYDI in the native sequence of Alt a 13, that is the amino acids P, K and T. It may also have a C-terminal extension of one, two or three amino acids corresponding to the one, two or three contiguous amino acids immediately C-terminal to IEKLRSNITVQYDI in the native sequence of Alt a 13. That is the amino acids L, E and R. For example, where all three contiguous amino acids are present in the N-terminal extension and all three contiguous amino acids are present in the C-terminal extension the polypeptide of the invention has the amino acid sequence of PKTIEKLRSNITVQYDILER (SEQ ID NO: 115; N and C-terminal extensions are underlined).

GWGVMVSHRSGET (Alt18; SEQ ID NO: 84) may have a N-terminal extension of one, two, three, four, five or six amino acids corresponding to the one, two, three, four, five or six amino acids immediately N-terminal to GWGVMVSHRSGET in the native sequence of Alt a 7, that is the amino acids K, D, A, F, G and A. It may also have a C-terminal extension of one, two or three amino acids corresponding to the one, two, or three contiguous amino acids immediately C-terminal to GWGVMVSHRSGET in the native sequence of Alt a 7. That is the amino acids E, D and V. For example, where all six amino acids are present in the N-terminal extension and all three contiguous amino acids are present in the C-terminal extension the polypeptide of the invention has the amino acid sequence of KDAFGAGWGVMVSHRSGETEDV (SEQ 15, N- and C-terminal extensions underlined).

The amino acids in the N-terminal and/or C-terminal extension may not correspond exactly to amino acids in the native sequence of the protein from which an amino acid sequence or variant sequence derives. The N-terminal and/or C-terminal extension may include a sequence derived from said native sequence which has been modified, for example to improve stability, solubility or manufacturability of the polypeptide. For example, a methionine in the native sequence may be substituted with nor-leucine, and/or one or more charged residues may be added at the N-terminus of a N-terminal extension and/or the C-terminus of a C-terminal extension. Preferably positively charged residues such as arginine and lysine are added. Amino acids selected from histidine, glutamate and aspartate may be added.

Alternatively, the amino acids of an N-terminal and/or C-terminal extension may not correspond to amino acids in native sequence of the protein from which an amino acid sequence or variant sequence derives. They may instead be any suitable amino acids, preferably selected to improve stability, solubility or manufacturability of the polypeptide. For example, one or more charged residues may be added at the N and/or C terminus of any of the amino acid sequences or variant sequences of the invention. Preferably positively charged residues such as arginine and lysine are added. Amino acids selected from histidine, glutamate and aspartate may be added.

T cell epitopes

A polypeptide included in a pharmaceutical formulation of the invention is up to 30 amino acids in length and comprises, consists or consists essentially of an amino acid sequence or variant sequence as defined above. Each said amino acid sequence and said variant sequence contains a T cell epitope. The T cell epitope is preferably an MHC Class II-binding T cell epitope. It is preferred that the modifications in a variant sequence do not alter the functional properties of a T cell epitope present in the corresponding original amino acid sequence.

In preferred variant sequences, sufficient contiguous amino acids of the corresponding original amino acid sequence are retained to contain a T cell epitope. Typically, such a variant sequence retains at least 8, preferably at least 9, contiguous amino acids of the original amino acid sequence.

The presence of a T cell epitope may preferably be confirmed by analysis performed *in silico*, for example using bioinformatic software as described in Examples 1 to 5. Alternatively, the presence of a T cell epitope may be confirmed by direct evaluation of its functional properties. Particular functional properties of T cell epitopes include the ability of a polypeptide comprising the epitope to bind to an MHC molecule, preferably an MHC Class II molecule, and/or the ability of a polypeptide comprising the epitope to activate a T cell, preferably when bound to an MHC Class II molecule.

The ability of a polypeptide to bind to an MHC molecule may be evaluated using any suitable method, such as a competition assay. A preferred *in vitro* assay is described in Example 6.

The ability of a polypeptide to activate a T cell may also be evaluated using any suitable method. Preferred methods include the measurement of one or more parameters associated with T cell activation, such as proliferation or cytokine release. Preferred assays for these parameters are described in Example 7. Relevant cytokines include IFN-gamma, IL-13 and IL-10. In the context of the present invention, a polypeptide is typically considered to have activated a T cell if it induces release of one, two, or all of IFN-gamma, IL-13 and IL-10. The polypeptide preferably induces a release of greater than 50 pg/ml of the given cytokine(s).

As mentioned above, it is preferred that the modifications in a variant sequence do not alter the functional properties of a T cell epitope present in the corresponding original amino acid sequence. Thus, a polypeptide comprising, consisting or consisting essentially of a variant amino acid sequence should have substantially the same MHC class II binding properties and substantially the same T cell activation properties as a polypeptide comprising, consisting or consisting essentially of the corresponding original amino acid sequence.

Typically, a polypeptide has substantially the same MHC Class II binding characteristics as another polypeptide if both polypeptides are capable of binding specifically to one or more MHC Class II molecules belonging to the same MHC Class II allele supertype family. Examples of MHC Class II allele supertype families include HLA-DR1, HLA-DR3, HLA-DR4, HLA-DR7, HLA-DR8, HLA-DR11, HLA-DR13, HLA-DR15 and HLA-DR51. Most preferably, both polypeptides will bind specifically to the same MHC Class II molecule, that is to an MHC Class II molecule encoded by the same allele.

Typically, a polypeptide has substantially the same T cell activation properties as another polypeptide if both polypeptides specifically activate a T cell expressing the same T cell receptor. Preferably, there should be no significant difference in the level of activation induced by each polypeptide. The level of activation may be assessed by monitoring proliferation and/or cytokine release, as described above.

Suitable polypeptides comprising, consisting or consisting essentially a variant sequence may be derived empirically or selected according to known criteria. Within a single polypeptide there are certain residues which contribute to binding within the MHC antigen binding groove and other residues which interact with hypervariable regions of the T cell receptor (Allen et al (1987) Nature 327: 713-5). Advantageously, peptides may be designed to favour T-cell proliferation and induction of desensitisation. Metzler and Wraith have demonstrated improved tolerogenic capacity of polypeptides in which substitutions increasing polypeptide-MHC affinity have been made (Metzler & Wraith(1993) Int Immunol: 1159-65). That an altered polypeptide ligand can cause long-term and profound energy in cloned T cells was demonstrated by Sloan-Lancaster et al (1993) Nature 363: 156-9.

Sequence identity

T cell epitope-containing variant sequences of polypeptides included in pharmaceutical formulations of the invention may alternatively be described in terms of their sequence identity to a corresponding original amino acid sequence. For example, a variant sequence may have at least 65% identity to an amino acid sequence of any one of (a) to (k). More preferably, a variant sequence may have at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid identity to an amino acid sequence of any one of (a) to (k).

Sequence identity is typically evaluated over a number of contiguous amino acids in the original amino acid sequence. For example, sequence identity may be measured over at least 9, 10, 11, 12, 13, 14, or 15 contiguous amino acids in the original amino acid sequence, depending on the size of the peptides of comparison. It is preferred that sequence identity be measured over at least 9 contiguous amino acids in the original amino acid sequence. It is particularly preferred that sequence identity is measured over the entire length of the corresponding original amino acid sequence.

In connection with amino acid sequences, "sequence identity" refers to sequences which have the stated value when assessed using ClustalW (Thompson et al., 1994, supra) with the following parameters:

Pairwise alignment parameters -Method: accurate, Matrix: PAM, Gap open penalty: 10.00, Gap extension penalty: 0.10; Multiple alignment parameters -Matrix:

PAM, Gap open penalty: 10.00, % identity for delay: 30, Penalize end gaps: on, Gap separation distance: 0, Negative matrix: no, Gap extension penalty: 0.20, Residue-specific gap penalties: on, Hydrophilic gap penalties: on, Hydrophilic residues: G, P, S, N, D, Q, E, K, and R. Sequence identity at a particular residue is intended to include identical residues which have simply been derivatized.

Salts

The invention encompasses any pharmaceutically acceptable salt of a polypeptide of the invention. Pharmaceutically acceptable salts of a polypeptide of the invention include, for example, mineral acid salts such as chlorides, hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A hydrochloride salt or an acetate salt is preferred.

Synthesis

A polypeptide of the invention can be prepared by any suitable technique. Solid-phase peptide synthesis (SPPS) is a preferred technique. This involves formation of the peptide on small solid beads.

Using SPPS, the peptide remains covalently attached to a bead during synthesis. The peptide is synthesised using repeated cycles of coupling-washing-deprotection-washing. In particular, the free N-terminal amine of a solid-phase attached peptide is coupled to a single N-protected amino acid unit. This unit is then deprotected, revealing a new N-terminal amine to which a further protected amino acid is attached. These steps are repeated until the peptide is complete. The peptide is then cleaved from the beads using a suitable reagent.

Suitable protecting groups, reagents, solvents and reaction conditions for SPPS are well known to those skilled in the art and as such conditions can be determined by one skilled in the art by routine optimization procedures.

Pharmaceutically acceptable salts of polypeptides can be prepared by any suitable technique. Typically, salification involves reaction of the polypeptide or a salt thereof with a suitable reagent, typically acid, to obtain the pharmaceutically acceptable salt selected.

For example, a hydrochloride salt of a polypeptide can be prepared by initially cleaving the polypeptide from the solid phase using trifluoroacetic acid. The polypeptide will thus initially be a trifluoroacetate salt. The trifluoroacetate salt can then be converted into a hydrochloride salt by any known technique, such as ion exchange on a suitable column using hydrochloric acid as an eluent.

The polypeptide or polypeptide salt products can be purified, where required, by any suitable technique. High pressure liquid chromatography (HPLC) can be used, for example.

The term "polypeptide" includes not only molecules in which amino acid residues are joined by peptide (-CO-NH-) linkages but also molecules in which the peptide bond is reversed. Such retro-inverso peptidomimetics may be made using methods known in the art, for example such as those described in Meziere et al (1997) J. Immunol.159, 3230-3237. This approach involves making pseudopolypeptides containing changes involving the backbone, and not the orientation of side chains. Meziere et al (1997) show that, at least for MHC class II and T helper cell responses, these pseudopolypeptides are useful. Retro-inverse polypeptides, which contain NH-CO bonds instead of CO-NH peptide bonds, are much more resistant to proteolysis.

Similarly, the peptide bond may be dispensed with altogether provided that an appropriate linker moiety which retains the spacing between the carbon atoms of the amino acid residues is used; it is particularly preferred if the linker moiety has substantially the same charge distribution and substantially the same planarity as a peptide bond. It will also be appreciated that the peptide may conveniently be blocked at its N-or C-terminus so as to help reduce susceptibility to exoproteolytic digestion. For example, the N-terminal amino group of the polypeptides may be protected by reacting with a carboxylic acid and the C-terminal carboxyl group of the peptide may be protected by reacting with an amine. Other examples of modifications include glycosylation and phosphorylation. Another potential modification is that hydrogens on the side chain amines of R or K may be replaced with methylene groups ($-NH_2 \rightarrow -NH(Me)$ or $-N(Me)_2$).

Analogues of polypeptides according to the invention may also include peptide variants that increase or decrease the polypeptide’s half-life in vivo. Examples of analogues capable of increasing the half-life of polypeptides used according to the invention include peptoid analogues of the peptides, D-amino acid derivatives of the peptides, and peptide-peptoid hybrids. A further embodiment of the variant polypeptides used according to the invention comprises D-amino acid forms of the polypeptide. The preparation of polypeptides using D-amino acids rather than L-amino acids greatly decreases any unwanted breakdown of such an agent by normal metabolic processes, decreasing the amounts of agent which needs to be administered, along with the frequency of its administration.

The polypeptides provided by the present invention may be derived from splice variants of the parent proteins encoded by mRNA generated by alternative splicing of the primary transcripts encoding the parent protein chains. The polypeptides may also be derived from amino acid mutants, glycosylation variants and other covalent derivatives of the parent allergen proteins. Exemplary derivatives include molecules wherein the polypeptides of the invention are covalently modified by substitution, chemical, enzymatic, or other appropriate means with a moiety other than a naturally occurring amino acid. Further included are naturally occurring variant amino acid sequences of the parent proteins. Such a variant amino acid sequence may be encoded by an allelic variant or represent an alternative splicing variant.

Modifications as described above may be prepared during synthesis of the peptide or by post-production modification, or when the polypeptide is in recombinant form using the known techniques of site-directed mutagenesis, random mutagenesis, or enzymatic cleavage and/or ligation of nucleic acids.

The polypeptides described herein may also be modified to improve physicochemical characteristics. Thus, for example, original amino acid sequences may be altered to improve their solubility, and accordingly a polypeptide of the invention having a variant sequence will preferably be more soluble than a polypeptide having the corresponding original amino acid sequence under equivalent conditions. Methods for evaluating the solubility of polypeptides are well known in the art.

Improved solubility is advantageous for the tolerisation of subjects to allergens from which the polypeptides of the invention derive, since administration of poorly soluble agents to subjects causes undesirable, non-tolerising inflammatory responses. The solubility of the polypeptides may be improved by altering the residues which flank the region containing a T cell epitope. For example, N and C terminal to the residues of the polypeptide which flank a T cell epitope, at least one amino acid may be added selected from arginine, lysine, histidine, glutamate and aspartate. In other examples:

i) any hydrophobic residues in the up to three amino acids at the N or C terminus of the native sequence of the polypeptide, which are not comprised in a T cell epitope, are deleted; and/or

ii) any two consecutive amino acids comprising the sequence Asp-Gly in the up to four amino acids at the N or C terminus of the native sequence of the polypeptide, which are not comprised in a T cell epitope, are deleted; and/or

iii) one or more positively charged residues are added at the N and/or C terminus of the native sequence of the polypeptide.

Optionally, any polypeptides containing cysteine residues may be engineered to prevent dimer formation such that any cysteine residues are replaced with serine or 2-aminobutyric acid.

Polypeptide combinations

The invention provides combinations of polypeptides including at least three polypeptides or salts thereof. Each polypeptide is up to 30 amino acids in length and is preferably independently selected from the polypeptides of (a) to (h) as set out above. The combination of polypeptides may also be independently selected from the polypeptides of (a) to (k) as set out above. Such a combination of peptides is preferably provided in a pharmaceutical formulation as described below.

Three, four, five, six, seven, eight or more polypeptides selected from the polypeptides of (a) to (k), or said salts thereof, may be provided together in combination. It is preferred that only one polypeptide, or salt thereof, is selected from each of (a) to (k).

More preferably, three, four, five, six, seven, or eight polypeptides selected from the polypeptides of (a) to (h) or said salts thereof, are provided together in combination. It is preferred that only one polypeptide, or salt thereof is selected from each of (a) to (h).

It is particularly preferred that the above combinations of at least three polypeptides comprise a polypeptide of (a) or a said salt thereof. That is a polypeptide, or a salt thereof, comprising, consisting essentially or consisting of the amino acid sequence of (Alt28; SEQ ID NO: 101), or a corresponding variant sequence.

The above combinations of at least three polypeptides may also preferably comprise at least one polypeptide of (b), (c) or (d), or a said salt thereof. That is a polypeptide, or a salt thereof, comprising, consisting essentially or consisting of the amino acid sequence of any one of KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107), KYAGVFVSTGTLGGG (SEQ ID NO: 112), or AEVYQKLKALAKKTYGQ (Alt13A;SEQ ID NO: 83), or a corresponding variant sequence of any thereof.

A preferred variant sequence of SEQ ID NO: 107 is YEKYRRVVRAGVKV (Alt34, SEQ ID NO: 106). Alt34 may be used in place of SEQ ID: 107 in any polypeptide combination and pharmaceutical formulation described herein. A preferred variant sequence of SEQ ID NO: 112 is KKYAGVFVSTGTLGGGK (Alt18; SEQ ID NO: 89). Alt18 may be used in place of SEQ ID: 112 in any polypeptide combination and pharmaceutical formulation described herein.

It is particularly preferred that the above combinations of at least three polypeptides comprise a polypeptide or salt of (a), (b) and (c). It is also particularly preferred that the above combinations of at least three polypeptides comprise a polypeptide of (d) or a said salt thereof. That is a polypeptide, or a salt thereof, comprising, consisting essentially or consisting of the amino acid sequence of AEVYQKLKALAKKTYGQ (Alt13A;SEQ ID NO: 83) or a corresponding variant sequence. Another preferred combination of at least three polypeptides comprises a polypeptide or salt of (a), (b) and (d).

The above combinations of at least three polypeptides may also preferably comprise at least one polypeptide of (e) or (f), or a said salt thereof. That is a polypeptide, or a salt thereof, comprising, consisting essentially or consisting of the amino acid sequence of SLGFNIKATNGGTLD (Alt01A; SEQ ID NO: 60), or SAKRMKVAFKLDIEK (Alt06; SEQ ID NO: 72, or a corresponding variant sequence of either thereof. A preferred variant sequence of Alt06 is SAKR-Nle-KVAFKLDIEK (Alt06A, SEQ ID NO: 73). Alt06A may be used in place of Alt06 in any polypeptide combination and pharmaceutical formulation described herein.

The above combinations of at least three polypeptides may also preferably comprise at least one polypeptide of (e) or (f), or a said salt thereof. That is a polypeptide, or a salt thereof, comprising, consisting essentially or consisting of the amino acid sequence of DITYVATATLPNYCR (SEQ ID NO: 111), or GWGVMVSHRSGET (Alt14;SEQ ID NO: 84), or a corresponding variant sequence of any thereof. Preferred variant sequences of SEQ ID NO: 111 are KDITYVATATLPNY

(Alt02; SEQ ID NO: 61) and DITYVATATLPNYSR (Alt02A; SEQ ID NO: 62). Alt02 or Alt02A may be used in place of SEQ ID: 111 in any polypeptide combination and pharmaceutical formulation described herein. A preferred variant sequence of Alt14 is GWGV-Nle-VSHRSGET (Alt14A, SEQ ID NO: 85). Alt14A may be used in place of Alt14 in any polypeptide combination and pharmaceutical formulation described herein.

The invention also provides a combination of at least three polypeptides comprising a polypeptide of (d), or a said salt thereof, and at least two further polypeptides selected from the polypeptides of (a) to (c) and (e) to (h) or said salts thereof. For example, a combination of the polypeptides of (b), (c) and (d) or salts thereof may be provided. The invention further provides a combination of at least three polypeptides comprising a polypeptide of (b), or a said salt thereof, and at least two further polypeptides selected from the polypeptides of (a), (c) and (d) to (h) or said salts thereof. The invention additionally provides a combination of at least three polypeptides comprising a polypeptide of (c), or a said salt thereof, and at least two further polypeptides selected from the polypeptides of (a), (b) and (d) to (h) or said salts thereof.

The above combinations of at least three polypeptides may further comprise at least one additional polypeptide selected from:

(l) a polypeptide comprising the amino acid sequence of KKVSMAIAKAAAAEK (Alt11: SEQ ID NO: 79) or a T cell epitope-containing variant sequence derived from said amino acid sequence;

(m) polypeptide comprising the amino acid sequence of SYNVAKAGCIHLAK (Alt22; SEQ ID NO: 92) or a T cell epitope-containing variant sequence derived from said amino acid sequence;

(n) polypeptide comprising the amino acid sequence of KLWHSMIPMGRDAK (Alt24; SEQ ID NO: 95) or a T cell epitope-containing variant sequence derived from said amino acid sequence;

(o) polypeptide comprising the amino acid sequence of KRSLLVFAVRSSMELRK (Alt27; SEQ ID NO: 99) or a T cell epitope-containing variant sequence derived from said amino acid sequence; and

(p) polypeptide comprising the amino acid sequence of NWLTLHTAALGPTAK (Alt31; SEQ ID NO:103) or a T cell epitope-containing variant sequence derived from said amino acid sequence;

wherein a T cell epitope-containing variant sequence of a said amino acid sequence is as defined above and each polypeptide is up to 30 amino acids in length.

A preferred variant sequence of Alt11 is Alt11A (SEQ ID NO:81). A preferred variant sequence of Alt22 is Alt22A (SEQ ID NO: 93). A preferred variant sequence of Alt24 is Alt24A (SEQ ID NO: 96). A preferred variant sequence of Alt27 is Alt27A (SEQ ID NO: 100).

The above combinations of at least three polypeptides may also further comprise a polypeptide, or a salt thereof, comprising, consisting essentially or consisting of the amino acid sequence of any one of IEKLRSNITVQYDI (Alt33; SEQ ID NO: 105), GYTGKIKIAMDVASSE (Alt15; SEQ ID NO: 86), or SAFRSIEPELTVY (Alt10; SEQ ID NO: 77), or a corresponding variant thereof, A preferred variant sequence of Alt15 (SEQ ID NO: 86) is GYTGKIKIA-Nle-DVASSE (Alt15A, SEQ ID NO: 87).

All of the above selections are subject to the combination preferably comprising twelve polypeptides in total or less, more typically, ten polypeptides or less, preferably less than nine, more preferably less than eight polypeptides, such as seven or six polypeptides or less. The combination may comprise four, five, six or seven polypeptides. The combination of the invention most preferably comprises six or seven polypeptides.

A preferred core polypeptide combination is (1):

- a polypeptide having the amino acid sequence WSWKIGPAIATGNT (Alt28; SEQ ID NO: 101), or a corresponding variant sequence, or a said salt thereof;
- a polypeptide having the amino acid sequence KYAGVFVSTGTLGGG (SEQ ID NO: 112) or a corresponding variant sequence (particularly preferably Alt18), or a said salt thereof;
- a polypeptide having the amino acid sequence KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107) or a corresponding variant sequence, or a said salt thereof; and

- a polypeptide having the amino acid sequence AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83) or a corresponding variant sequence, or a said salt thereof.

Preferably, one or both of the following additional polypeptides may be added to the core polypeptide combination of (1) to create a combination of five or six polypeptides:

- a polypeptide having the amino acid sequence SLGFNIKATNGGTLD (Alt01A; SEQ ID NO: 60) or a corresponding variant sequence, or a said salt thereof; and
- a polypeptide having the amino acid sequence SAKRMKVAFKLDIEK (Alt06; SEQ ID NO: 72) or a corresponding variant sequence (such as Alt06A), or a said salt thereof.

Optionally, one or two of the following further additional polypeptides may be added to the combination of (1) or to the above combination of five or six polypeptides to create a combination of six, seven or eight polypeptides:

- a polypeptide having the amino acid sequence DITYVATATLPNYCR (SEQ ID NO: 111) or a corresponding variant sequence (such as Alt02 or Alt02A), or a said salt thereof; and
- a polypeptide having the amino acid sequence GWGVMVSHRSGET (Alt14; SEQ ID NO: 84) or a corresponding variant sequence (such as Alt14A), or a said salt thereof.

Another preferred core polypeptide combination is (2):

- a polypeptide having the amino acid sequence WSWKIGPAIATGNT (Alt28; SEQ ID NO: 101), or a corresponding variant sequence, or a said salt thereof;
- a polypeptide having the amino acid sequence KYAGVFVSTGTLGGG (SEQ ID NO: 112) (particularly preferably Alt18) or a corresponding variant sequence, or a said salt thereof;
- a polypeptide having the amino acid sequence KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107) or a corresponding variant sequence, or a said salt thereof;

- a polypeptide having the amino acid sequence AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83) or a corresponding variant sequence, or a said salt thereof; and
- a polypeptide having the amino acid sequence SLGFNIKATNGGTLD (Alt01A; SEQ ID NO: 60) or a corresponding variant sequence, or a said salt thereof.

Optionally, one or two of the following further additional polypeptides may be added to the core combination of (2) to create a combination of six or seven polypeptides:

- a polypeptide having the amino acid sequence SAKRMKVAFKLDIEK (Alt06; SEQ ID NO: 72) or a corresponding variant sequence (such as Alt06A), or a said salt thereof;
- a polypeptide having the amino acid sequence DITYVATATLPNYCR (SEQ ID NO: 111) or a corresponding variant sequence (such as Alt02 or Alt02A), or a said salt thereof; and
- a polypeptide having the amino acid sequence GWGVMVSHRSGET (Alt14; SEQ ID NO: 84) or a corresponding variant sequence (such as Alt14A), or a said salt thereof.

An especially preferred polypeptide combination comprises Alt28 (SEQ ID NO: 101), or a said salt thereof; Alt18, or a said salt thereof; Alt34A (SEQ ID NO: 107) or a corresponding variant sequence (such as Alt34), or a said salt thereof; Alt13A (SEQ ID NO: 83), or a said salt thereof; and Alt01A (SEQ ID NO: 60), or a said salt thereof. One, two or three peptides, each selected from one of the following groups of peptides, may also preferably be added to the especially preferred polypeptide combination: (I) Alt06 or Alt06A or a said salt of either thereof, (II) Alt02 or Alt02A, or a said salt of either thereof, and (III) Alt14 or Alt14A, or a said salt of either thereof. The especially preferred polypeptide combination may comprise a polypeptide from group (I) and a polypeptide from group (II), a polypeptide from group (I) and a polypeptide from group (III), or a polypeptide from group (I) and a polypeptide from group (II).

The above polypeptide combinations may be suitable for use in preventing or treating allergy to *Alternaria* and/or *Cladosporium*. The invention provides polypeptide combinations which are suitable for tolerisation against both *Alternaria* and

Cladosporium allergens by virtue of representing epitope regions which are homologous between these moulds. In this aspect, the following polypeptides, or salts thereof, may preferably be used.

SEQ ID NOs 83 to 87 represent sequences derived from Alt a 6 which contain epitope regions which are homologous with Cla h 6. SEQ ID NO: 108 is a sequence derived from Cla h 6 which contains an epitope region which is homologous with Alt a 6. SEQ ID NO: 108 may be used in place of, or in addition to any Alt a 6 peptide in a combination described herein.

SEQ ID NOs 90, 91, and 94 to 98 represent sequences derived from Alt a 8 which contain epitope regions which are homologous with Cla h 8. SEQ ID NOs: 109 and 110 are sequences derived from Cla h 8 which contains epitope regions which are homologous with Alt a 8. One or more of SEQ ID NOs: 109 and 110 may be used in place of, or in addition to any Alt a 8 peptide in a combination described herein.

SEQ ID NO 101 represents a sequence derived from Alt a 10 which contains an epitope region which is homologous with Cla h 10. SEQ ID NO: 101 may be used in place of, or in addition to any Alt a 10 peptide in a combination described herein.

In a broader aspect, the invention provides combinations of polypeptides including at least three polypeptides each of which is up to 30 amino acids in length and comprise the amino acid sequence of any of SEQ ID NOs 1 to 110 or a corresponding variant sequence. Such combinations typically include i) at least one polypeptide comprising the amino acid sequence of any of SEQ ID NOS: 1 to 6 and 59 to 65 (which are derived from Alt a1), or a corresponding variant sequence; ii) at least one polypeptide comprising the amino acid sequence of SEQ ID NOS: 7 to 11 and 66 to 78 (which are derived from Alt a2), or a corresponding variant sequence; and iii) at least one polypeptide comprising the amino acid sequence of SEQ ID NOS: 12 to 22 and 79 to 87 (which are derived from Alt a6), or a corresponding variant sequence, preferably where in said polypeptide comprises AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83) or a corresponding variant sequence.

Combining polypeptides, or salts thereof, derived from different Alt allergens may allow for broad coverage of mould allergy observed in the general population by providing tolerising epitopes from more than one mould allergen. The above combinations comprising polypeptides, or salts thereof, from Alt a1, Alt a2, and Alt a6 may further comprise:

(iv) at least one polypeptide comprising the amino acid sequence of any of SEQ ID NOS: 23 to 29 and 88 to 89 (which are derived from Alt a7) or a corresponding variant sequence, or a said salt thereof; and/or

(v) at least one polypeptide comprising the amino acid sequence of any of SEQ ID NOS: 30 to 35 and 90 to 98 (which are derived from Alt a8) or a corresponding variant sequence, or a said salt thereof; and/or

(vi) at least one polypeptide comprising the amino acid sequence of any of SEQ ID NOS: 36 to 48 and 99 to 101 (which derived from Alt a 10) or a corresponding variant sequence, or a said salt thereof; and/or

(vii) at least one polypeptide comprising the amino acid sequence of any of SEQ ID NOS: 49 to 58 and 102 to 107 (which are derived from Alt a 13) or a corresponding variant sequence, or a said salt thereof.

Non-limiting examples of such combinations include:

(1) a polypeptide or salt comprising AEVYQKLKALAKKTYGQ (Alt13A;SEQ ID NO: 83) or a corresponding variant sequence, at least two polypeptides or salts selected from group (ii), and at least two polypeptides or salts selected from group (iii);

(2) a polypeptide or salt comprising AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83) or a corresponding variant sequence, at least one, preferably two polypeptides or salts selected from group (ii), at least two, preferably two polypeptides or salts selected from group (iii), and at least one polypeptide or salt selected from group (vi); and

(3) a polypeptide or salt comprising AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83) or a corresponding variant sequence, at least one, preferably two polypeptides or salts selected from group (ii), at least two, preferably two polypeptides or salts selected from group (iii), and at least one, preferably two polypeptides or salts selected from group (vii).

Any of the polypeptide combinations described above may optionally comprise no further polypeptides or no further peptides derived from Alternaria and/or Cladosporium allergens. Any of the polypeptide combinations described above may be incorporated in a pharmaceutical formulation of the invention as described in more detail below.

In a broader aspect, the invention provides a polypeptide, or a pharmaceutically acceptable salt thereof which is up to 30 amino acids in length and comprises, consists essentially or consists of the amino acid sequence of any one of SEQ ID NOs 1 to 110 or a corresponding variant sequence.

The polypeptide, or pharmaceutically acceptable salt thereof, preferably comprises:

(I) the amino acid sequence:

(a) WSWKIGPAIATGNT (Alt28; SEQ ID NO: 101),

(b) KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107), or

(c) KYAGVFVSTGTLGGG (SEQ ID NO: 112); or

(II) a T cell epitope-containing variant sequence which is a said amino acid sequence (I) having up to seven amino acid modifications, each of which is independently a deletion, substitution or insertion.

Other polypeptides of the invention or pharmaceutically acceptable salts thereof, comprise the amino acid sequence (d) AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83), (e) SLGFNIKATNGGTLD (Alt01A; SEQ ID NO: 60), (f) SAKRMKVAFKLDIEK (Alt06; SEQ ID NO: 72); (g) DITYVATATLPNYCR (SEQ ID NO: 111); and (h) GWGVMVSHRSGET (Alt14; SEQ ID NO: 84), or a corresponding variant sequence as described above.

Preferably, a polypeptide of the invention comprises, consists or consists essentially of the amino acid sequence of any one of SEQ ID NOs 83, 60, 61, 62, 72, 73, 106, 107, 101, 84, 85, or 89.

The invention also provides a pharmaceutical formulation comprising a polypeptide of the invention, and a pharmaceutically acceptable carrier or diluent. The invention further provides a polypeptide of the invention for use in a method of treating or preventing allergy to *Alternaria* and/or *Cladosporium*. The invention additionally provides use of a polypeptide of the invention for the manufacture of a medicament for the prevention or treatment of allergy to *Alternaria* and/or *Cladosporium*.

Medical uses and methods

A preferred aspect of the invention is the prevention or treatment of allergy. In this aspect, the invention provides a pharmaceutical formulation of the invention (which comprises at least three polypeptides or salts) for use in a method of treating or preventing allergy to *Alternaria* and/or *Cladosporium*. The pharmaceutical formulation of the invention may prevent or treat the allergy by tolerisation. The tolerisation may be to one or more protein allergens of the *Alternaria* and/or *Cladosporium* genus.

The invention further provides a use of the at least three polypeptides or salts described above for the manufacture of a medicament for the prevention or treatment of allergy to *Alternaria* and/or *Cladosporium*.

The invention further provides a method of treating an individual for allergy to *Alternaria* and/or *Cladosporium* or of preventing in an individual allergy to *Alternaria* and/or *Cladosporium*, which method comprises administering to said individual a therapeutically or prophylactically effective amount of a polypeptide or salt of the invention or of a pharmaceutical formulation of the invention. The method may thus reduce or ameliorate the symptoms of allergy in the individual suffering from the allergy. The method may improve the condition of the individual suffering from the allergy. The method may prevent or delay the appearance of symptoms of allergy in the individual. Symptoms of allergy to mould are discussed below.

In each of the methods and uses mentioned in this section, a polypeptide or salt may be replaced with a combination of polypeptides or salts as was defined in the previous section. As such, the invention encompasses a scenario in which a combination of polypeptides or salts is used in a method of treating or preventing allergy to *Cladosporium* and/or *Alternaria*. In said scenario, the polypeptides in a combination need not be administered together, and/or need not be not part of the same pharmaceutical formulation. The multiple peptides of this method may each be administered simultaneously, sequentially or concurrently.

The pharmaceutical formulation of the invention may treat or prevent the allergy by desensitising or tolerising to *Cladosporium* and/or *Alternaria* allergens. A polypeptide comprised in the pharmaceutical formulation may be used to tolerise or desensitise an individual to the allergen from which it is derived. Desensitising an individual to the allergens means inhibition or dampening of allergic tissue reactions induced by the allergens in appropriately sensitised individuals. The term “tolerisation” refers to an ability to suppress, or abolish a response to an antigen, such as an allergic response to a protein allergen. Tolerisation is also an ability to diminish or abolish an unwanted immune response, or to desensitise a subject to a protein allergen. Tolerisation may be determined by *in vitro* analysis of T cell responses or by observation of a reduction in the symptoms in an individual.

In more detail, T cells can be selectively activated, and then rendered unresponsive. Moreover the energising or elimination of these T-cells leads to desensitisation of the patient for a particular allergen. The desensitisation manifests itself as a reduction in response to an allergen or allergen-derived peptide, or preferably an elimination of such a response, on second and further administrations of the allergen or allergen-derived peptide. This second administration may be made after a suitable period of time has elapsed to allow desensitisation to occur; this is preferably any period between one day and several weeks. An interval of around four weeks is preferred.

The individual to whom the pharmaceutical formulation is administered may be asymptomatic. A prophylactically effective amount of the pharmaceutical formulation is administered to such an individual. A prophylactically effective amount is an amount which prevents the onset of one or more symptoms of allergy.

Alternatively, the individual to whom the pharmaceutical formulation is administered may be in need thereof. That is, the individual may exhibit one or more symptoms of allergy. A therapeutically effective amount of the r pharmaceutical formulation is administered to such an individual. A therapeutically effective amount is an amount which is effective to ameliorate one or more symptoms of allergy.

The individual to whom the pharmaceutical formulation is administered is preferably human. The individual may be known to be sensitised to mould allergens, at risk of being sensitised or suspected of being sensitised. The individual can be tested for sensitisation using techniques well known in the art and as described herein. Alternatively, the individual may have a family history of allergy to mould.

It may not be necessary to test an individual for sensitisation to mould because the individual may display symptoms of allergy when exposed to mould. By exposure is meant proximity to, for example, a mould or a substance or product derived from a mould. By proximity is meant 10 metres or less, 5 metres or less, 2 metres or less, 1 metre or less, or 0 metres from the items described above. Symptoms of allergy can include an itching nose, sneezing, ocular tearing, an itchy throat, itchy palate, itchy eyes, runny nose, breathing difficulties, bronchospasm, asthma, red itchy skin or rash.

The individual may be of any age. However, preferably, the individual may be in the age group of 1 to 90, 5 to 60, 10 to 40, or more preferably 18 to 35.

Preferably, the individual is from a population that has MHC allele frequencies within the range of frequencies that are representative of the Caucasian population. Reference population allele frequencies for 11 common DRB1 allele families are shown in Table 1 (Data from HLA Facts Book, Parham and Barber).

Table 1

DRB1	1	3	4	7	8	11	12	13	14	15	16
%	6.4	14.7	15.7	8.8	3.4	8.3	3.9	14.7	2.9	17.6	2.5
Reference population %	9.4	11.1	12.8	13.2	3.7	13.4	2.3	10.2	3.2	10.7	3.6

Reference frequencies were obtained by analysis of multiple studies reporting frequencies and the figures shown are mean values. Preferably therefore, the individual to be treated is from a population that has equivalent MHC allele frequencies as the reference population for the alleles referred to Table 1 (such as for at least 1, 2, 3, 4, 5 or all of the alleles), for example within the ranges of those figures plus or minus 1, 2, 3, 5, 10, 15 or 20%.

Preferably the individual is from a population where the allele frequencies of the following DRB1 alleles is:

4 – at least 9%
7 – at least 10%
11 – at least 8%.

The individual may have had allergy to mould for at least 2 weeks, 1 month, 6 months, 1 year, 5 years or more than 5 years. The individual may suffer from a rash, nasal congestion, nasal discharge and/or coughing caused by the allergy. The individual may or may not have been administered with other compositions/compounds which treat mould allergy. The individual may live in a geographical region which has a temperate, semi-tropical, tropical, or arctic climate. The individual typically suffers from allergy to mould in a particular season but the allergy may be perennial. Seasonal allergy to mould may commonly occur in autumn in the Northern hemisphere.

The allergic individual is typically allergic to moulds of the *Alternaria* genus, particularly *Alternaria alternata*. The allergic individual may be allergic to moulds of the *Cladosporium* genus, particularly *Cladosporium herbarium* and/or *Cladosporium cladosporoides*. The allergic individual may be allergic both to moulds of the *Alternata* and *Cladosporium*.

The polypeptides or salts described herein and the pharmaceutical formulations of the invention may be screened in panels of mould allergic individuals to confirm their suitability for use. The panel of mould allergic individuals may comprise individuals known or not known to be allergic to moulds of the *Alternaria* and *Cladosporium* genus. In particular where multiple polypeptides are provided in combination in a pharmaceutical formulation, they may be screened for their ability to cause T cell proliferation in at least 20 % of samples of T cells, wherein each sample is obtained from different mould allergic individuals in the population. Preferably, the pharmaceutical formulation will induce T cell proliferation in at least 30 % of samples of T cells obtained from of a panel of mould allergic individuals. More preferably, the pharmaceutical formulation will induce T cell proliferation in 35% or more, 40 % or more, 50 % or more, 60 % or more, 70% or more, 80 % or more, or 90 % or more of samples in the panel. The number of individuals in a panel of mould allergic individuals may be any number greater than one, for example at least 2, 3, 5, 10, 15, 20, 30, 50, 80, or at least 100 individuals.

It is also preferred that the polypeptides or salts described herein and the pharmaceutical formulations of the invention cause T cell proliferation, but do not lead to the release of histamine from leucocyte samples from a sensitised individual. The histamine release profile of a polypeptide, salt or pharmaceutical formulation may thus be confirmed. Suitable leucocyte samples include enriched basophils or mast cell preparations. There may be some histamine release, but preferably the amounts released are not significant. Significant histamine release may be considered to be the release of 20% or more of the total available leukocyte histamine when a sample of leukocytes from an individual is stimulated with a pharmaceutical formulation in vitro. A polypeptide or salt described herein or a pharmaceutical formulation of the invention preferably causes the release of less than 5%, less than 4%, less than 3%, less than 2% or less than 1% of the total available leukocyte histamine when a sample of leukocytes from an individual is stimulated with a composition in vitro. A normal individual typically has an approximate leukocyte histamine content of 150ng/10^7 cells.

Pharmaceutical formulations

Each polypeptide or salt described herein may be provided to an individual in an isolated, substantially isolated, purified or substantially purified form. For example, where polypeptides or salts of a combination described herein are not administered together, a polypeptide or salt described herein may be provided to an individual substantially free from other polypeptides or salts thereof. Whilst it may be possible for the polypeptides or salts to be presented in raw form, it is preferable to present them as a pharmaceutical formulation.

A pharmaceutical formulation of the invention preferably comprises at least three polypeptides or salts as described above and a pharmaceutically acceptable carrier or diluent. The pharmaceutical formulation may comprise any combination of polypeptides or salts described above.

The carrier(s) or diluent(s) present in the pharmaceutical formulation must be 'acceptable' in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof. Typically, carriers for injection, and the final formulation, are sterile and pyrogen free. Preferably, the carrier or diluent is water. The carrier or diluent may comprise thioglycerol, methionine or thioanisole.

A composition containing at least three polypeptides or salts as described above can be combined with one or more pharmaceutically acceptable excipients or vehicles to produce a pharmaceutical formulation. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances and the like, may be present in the excipient or vehicle. These excipients, vehicles and auxiliary substances are generally pharmaceutical agents that do not induce an immune response in the individual receiving the composition, and which may be administered without undue toxicity. Pharmaceutically acceptable excipients include, but are not limited to, liquids such as water, saline, polyethyleneglycol, hyaluronic acid, glycerol, thioglycerol and ethanol. Pharmaceutically acceptable salts can also be included therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients, vehicles and auxiliary substances is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

The polypeptides or salts are typically present at 0.1% to 50% by weight in the pharmaceutical formulation, more preferably at 0.1% to 5% by weight. The polypeptides or salts may be present at less than 0.1% by weight in the pharmaceutical formulation.

The pharmaceutically acceptable carrier or diluent is typically present at 50% to 99.9 % by weight in the pharmaceutical formulation, more preferably at 95% to 99.9 % by weight. The pharmaceutically acceptable carrier or diluents may be present at more than 99. 9% by weight in the pharmaceutical formulation.

Pharmaceutical formulations include, but are not limited to pharmaceutically acceptable solutions, lyophilisates, suspensions, emulsions in oily or aqueous vehicles, pastes, and implantable sustained-release or biodegradable formulations. Such pharmaceutical formulations may further comprise one or more additional ingredients including, but not limited to, suspending, stabilizing, or dispersing agents. A lyophilisate may comprise one or more of trehalose, thioglycerol, methionine and thioanisole. In one embodiment of a pharmaceutical formulation for parenteral administration, the active ingredient is provided in dry form (e.g., a lyophilisate, powder or granules) for reconstitution with a suitable vehicle (e. g., sterile pyrogen-free water) prior to parenteral administration of the reconstituted pharmaceutical formulation.

The invention further provides a method of preparing a pharmaceutical formulation of the invention, comprising combining at least three polypeptides or salts as described above with a pharmaceutically acceptable carrier or diluent. Preferably, said method prepares a pharmaceutical formulation for parenteral administration, and comprises providing said polypeptides, or salts in dry form and reconstituting said polypeptides, or salts with a said pharmaceutically acceptable carrier or diluent.

The pharmaceutical formulations may be prepared, packaged, or sold in the form of a sterile injectable aqueous or oily suspension or solution. This suspension or solution may be formulated according to the known art, and may comprise, in addition to the active ingredient, additional ingredients such as the dispersing agents, wetting agents, or suspending agents described herein. Such sterile injectable formulations may be prepared using a non-toxic parenterally-acceptable diluent or solvent, such as water or 1,3-butane diol, for example. Other acceptable diluents and solvents include, but are not limited to, Ringer's solution, isotonic sodium chloride solution, and fixed oils such as synthetic mono-or di-glycerides.

Other parenterally-administrable pharmaceutical formulations which are useful include those which comprise the active ingredient in microcrystalline form, in a liposomal preparation, or as a component of a biodegradable polymer systems. pharmaceutical formulations for sustained release or implantation may comprise pharmaceutically acceptable polymeric or hydrophobic materials such as an emulsion, an ion exchange resin, a sparingly soluble polymer, or a sparingly soluble salt.

Alternatively, the polypeptides described herein may be encapsulated, adsorbed to, or associated with, particulate carriers. Suitable particulate carriers include those derived from polymethyl methacrylate polymers, as well as PLG microparticles derived from poly(lactides) and poly(lactide-co-glycolides). See, e.g., Jeffery et al. (1993) Pharm. Res. 10:362-368. Other particulate systems and polymers can also be used, for example, polymers such as polylysine, polyarginine, polyornithine, spermine, spermidine, as well as conjugates of these molecules.

The formulation of any of the polypeptides mentioned herein will depend upon factors such as the nature of the polypeptide and the method of delivery. The pharmaceutical formulation may be administered in a variety of dosage forms. It may be administered orally (e.g. as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules), topically, parenterally, subcutaneously, by inhalation, intravenously, intramuscularly, intralymphatically (such as to lymph nodes in the groin), intrasternally, transdermally, intradermally, epidermally, sublingually, intranasally, buccally or by infusion techniques. The administration may be intratonsillar. The administration may be as suppositories. The administration may be made by iontophoresis. Preferably, the administration is intradermal, epidermal or transdermal. The administration may be made by a patch, such as a microtine patch.

A physician will be able to determine the required route and means of administration for each particular individual.

The pharmaceutical formulations of the invention are preferably provided sealed in a container. Where the pharmaceutical formulation is a pharmaceutically acceptable solution, the solution may be provided in an ampoule, sealed vial, syringe, cartridge, flexible bag or glass bottle. Where the pharmaceutical formulation is a lyophilisate, it is preferably provided in a sealed vial.

The pharmaceutical formulations of the invention will comprise a suitable concentration of each polypeptide to be effective without causing adverse reaction. Where the pharmaceutical formulation is for example a lyophilisate, the relevant concentration will be that of each polypeptide following reconstitution. Typically, the concentration of each polypeptide in the pharmaceutical formulation when in solution will be in the range of 0.03 to 200 nmol/ml. The concentration of each polypeptide may be more preferably in the range of 0.3 to 200 nmol/ml, 3 to 180 nmol/ml, 10 to 150 nmol/ml, 50 to 200nmol/ml or 30 to 120 nmol/ml. The pharmaceutical formulation should have a purity of greater than 95% or 98% or a purity of at least 99%.

An adjuvant or further therapeutic agent may be used in combination with the polypeptides described herein. An adjuvant is preferably administered in an amount which is sufficient to augment the effect of the polypeptide(s) or vice versa. The adjuvant or further therapeutic agent may be an agent that potentiates the effects of a polypeptide described herein. For example, the further therapeutic agent may be an immunomodulatory molecule which enhances the response to the polypeptide of the invention. Non-limiting examples of adjuvants include vitamin D, rapamycin and glucocorticoid steroids such as dexamethasone, fluticasone, budesonide, mometasone, beclomethasone, hydrocortisone, cortisone acetate, prednisone, prednisolone, methylprednisolone, betamethasone and triamcinolone. A preferred glucocorticoid is dexamethasone.

In an embodiment where the polypeptides described herein are used for therapy in combination with one or more other therapeutic agents or adjuvants, the other therapeutic agents or adjuvants may be administered separately, simultaneously or sequentially. They may be administered in the same or different pharmaceutical formulations. A pharmaceutical formulation may therefore be prepared which comprises a polypeptide described herein and also one or more other therapeutic agents or adjuvants. A pharmaceutical formulation of the invention may alternatively be used simultaneously, sequentially or separately with one or more other therapeutic compositions as part of a combined treatment. Accordingly, in a method of preventing or treating allergy according to the invention as described below, the subject may also be treated with a further therapeutic agent.

Routes of administration

Where a polypeptide or salt described herein is to be administered to an individual in a pharmaceutical formulation, it is preferred to administer the formulation to a site in the body of the individual where the polypeptide or salt will have the ability to contact suitable antigen presenting cells, and where it, or they, will have the opportunity to contact T cells of the individual.

Once formulated the pharmaceutical formulations of the invention can be delivered to a subject in vivo using a variety of known routes and techniques. For example, a pharmaceutical formulation can be provided as an injectable solution, suspension or emulsion and administered via parenteral, subcutaneous, epidermal, intradermal, intramuscular, intralymphatic, intraarterial, intraperitoneal, or intravenous injection using a conventional needle and syringe, a microneedle and syringe or using a liquid jet injection system. The administration may be made using a patch, such as a microtine patch. Pharmaceutical formulations can also be administered topically to skin or mucosal tissue, such as nasally, intratonsillarly, intratracheally, intestinal, rectally or vaginally, or provided as a finely divided spray suitable for respiratory or pulmonary administration. Other modes of administration include oral administration, suppositories, sublingual administration, and active or passive transdermal delivery techniques.

Dosages

Administration of the polypeptides or salts described herein or of the pharmaceutical formulations of the invention may be by any suitable method as described above. Suitable amounts of the polypeptides or salts to be administered may be determined empirically, but typically are in the range given below. A single administration of each polypeptide or salt may be sufficient to have a beneficial effect for the patient, but it will be appreciated that it may be beneficial if the polypeptide or salt is administered more than once, in which case typical administration regimes may be, for example, once or twice a week for 2-4 weeks every 6 months, or once a day for a week every four to six months. As will be appreciated, each polypeptide or salt in a combination of polypeptides or salts may be administered to a patient singly or in combination.

Dosages for administration will depend upon a number of factors including the nature of the pharmaceutical formulation, the route of administration and the schedule and timing of the administration regime. Suitable doses of a polypeptide or salt described herein may be in the order of up to 10 μg, up to 15μg, up to 20μg, up to 25μg, up to 30μg, up to 50μg, up to 100μg, up to 500 μg or more per administration. Suitable doses may be less than 15μg, but at least 1ng, or at least 2ng, or at least 5ng, or at least 50ng, or least 100ng, or at least 500ng, or at least 1μg, or at least 10μg. For some polypeptides described herein, the dose used may be higher, for example, up to 1 mg, up to 2 mg, up to 3 mg, up to 4 mg, up to 5 mg or higher. Such doses may be provided in a liquid formulation, at a concentration suitable to allow an appropriate volume for administration by the selected route. It will be understood that the above doses refer to total dose in the case of a combination of peptides or salts. For example, “up to 35μg” refers to a total peptide or salt concentration of up to 35μg in a composition comprising a combination or more than one peptide or salt.

Nucleic acids and vectors

The polypeptides described herein may be administered directly, or may be administered indirectly by expression from an encoding sequence. For example, a polynucleotide may be provided that encodes a polypeptide described herein. A polypeptide described herein may thus be produced from or delivered in the form of a polynucleotide which encodes, and is capable of expressing, it. Any reference herein to the use, delivery or administration of a peptide described herein is intended to include the indirect use, delivery or administration of such a peptide via expression from a polynucleotide that encodes it.

The terms “nucleic acid molecule” and “polynucleotide” are used interchangeably herein and refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Non-limiting examples of polynucleotides include a gene, a gene fragment, messenger RNA (mRNA), cDNA, recombinant polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may be provided in isolated or purified form.

Polynucleotides can be synthesised according to methods well known in the art, as described by way of example in Sambrook et al (1989, Molecular Cloning - a laboratory manual; Cold Spring Harbor Press).

The above polynucleotides may be used in vitro, ex vivo or in vivo in the production of a polypeptide described herein. Such polynucleotides may be administered or used in the prevention or treatment of allergy to *Alternaria* and/or *Cladosporium*.

Methods for gene delivery are known in the art. See, e.g., U.S. Patent Nos. 5,399,346, 5,580,859 and 5,589,466. The nucleic acid molecule can be introduced directly into the recipient subject, such as by standard intramuscular or intradermal injection; transdermal particle delivery; inhalation; topically, or by oral, intranasal or mucosal modes of administration. The molecule alternatively can be introduced *ex vivo* into cells that have been removed from a subject. For example, a polynucleotide, expression cassette or vector may be introduced into APCs of an individual ex vivo. Cells containing the nucleic acid molecule of interest are re-introduced into the subject such that an immune response can be mounted against the peptide encoded by the nucleic acid molecule. The nucleic acid molecules used in such immunization are generally referred to herein as “nucleic acid vaccines.”

Antigen presenting cells (APCs)

The invention encompasses the use in vitro of a method of producing a population of APCs that present the polypeptides described herein, such as a combination of at least three polypeptides described herein, on their surface. Said population of APCs may be subsequently used in therapy. Said method of production may be carried out *ex vivo* on a sample of cells that have been obtained from a patient. The APCs produced in this way therefore form a pharmaceutical agent that can be used in the treatment or prevention of allergy to *Cladosporium* and/or *Alternaria*. The cells should be accepted by the immune system of the individual because they derive from that individual. Delivery of cells that have been produced in this way to the individual from whom they were originally obtained, thus forms a therapeutic embodiment of the invention.

Where an APC is to be administered, it is preferred to administer the APC to a site in the body where it will have the ability to contact, and activate, suitable T cells of the individual.

In vitro method

The invention further provides an *in vitro* method of determining whether T cells recognize one or more polypeptides or salts of a pharmaceutical formulation of the invention, which method comprises contacting said T cells with said pharmaceutical formulation and detecting whether said T cells are stimulated by said polypeptides.

The above method may be carried out to determine whether an individual has, or is at risk of having, an allergy to *Cladosporium* and/or *Alternaria*.

The invention is illustrated by the following Examples:

Example 1

MHC Class II binding search

The aim of this study is to identify a distinct panel of polypeptides with strong affinities for the seven most common human MHC Class II HLA-DRB1* allotypes (covering in total around 63% of the allotypes found in the average Caucasian population). In order to identify said polypeptides in the major Alternaria allergens Alt a 1, Alt a 2, Alt a 6. Alt a 7, Alt a 8 and Alt a 10 from *Alternaria Alternata*, an *in silico* approach known as "peptide threading" was performed using the commercially available EpiMatrix algorithm (EpiVax Inc.) This is a bioinformatic analysis of analysing a polypeptide having a given sequence for the potential to be accommodated within the binding groove of MHC class II HLA-DR molecules.

EpiMatrix is a matrix-based algorithm that ranks 10 amino acid long segments, overlapping by 9 amino acids, from any polypeptide sequence by estimated probability of binding to each of the selected MHC molecules. (De Groot et al., AIDS Research and Human Retroviruses 13:539-41 (1997)). The procedure for developing matrix motifs was published by Schafer et al, 16 Vaccine 1998 (1998). In this Example, binding potential for HLA DR1, DR2, DR3, DR4, DR7, DR8, DR11, DR13 and DR15 is assessed. Putative MHC ligands are selected by scoring each 10-mer frame in a protein sequence. This score is derived by comparing the sequence of the 10-mer to the matrix of 10 amino acid sequences known to bind to each MHC allele. Retrospective studies have demonstrated that EpiMatrix accurately predicts published MHC ligands (Jesdale et al., in Vaccines '97 (Cold Spring Harbor Press, Cold Spring Harbor, N.Y., 1997)). Successful prediction of polypeptides which bind to multiple MHC molecules has also been confirmed.

Estimated probability of binding to a selected MHC molecule is calculated by EpiMatrix as follows. The polypeptides having a given sequence are scored by estimating the relative promotion or inhibition of binding for each amino acid, compared to known MHC binders for a given MHC allele. This information is summed across the polypeptide and a summary score (EMX score) is assigned to the entire polypeptide. After comparing the EMX score to the scores of known MHC ligands, EpiMatrix arrives at an "estimated binding probability" (abbreviated as EBP, but not strictly a probability). The EBP describes the proportion of polypeptides with EpiMatrix scores as high or higher that will bind to a given MHC molecule. EBPs range from 100% (highly likely to bind) to less than 1% (very unlikely to bind).

EpiMatrix analyses were performed on the entire sequence of known isoforms of Alt a 1 (NCBI accession nos: P79085.1; Q6Q128; PQ8NJ79). These analyses identified core polypeptides (and their flanking sequences) derived from the above sequences which are predicted to have good MHC class-II binding. These sequences are shown below in Table 2.

In Table 2: “Residues in sequence” gives the location of the sequence within the sequence of the polypeptide that was analysed. The core sequence (middle amino acids in bold) defines the actual binding sequence that was identified during the analysis. The stabilizing flanks (N-terminal and C-terminal, not bold) were included for use with the core sequence and are typically required to aid manufacture of a polypeptide. “Number of hits” refers to the number of high predicted binding affinities for all MHC types tested within the sequence. The “EpiMatrix Cluster Score” is derived from the number of hits normalized for the length of the cluster. Cluster Score is thus the excess or shortfall in predicted aggregate MHC binding properties relative to a random polypeptide standard. A score above 10 is considered to indicate broad MHC binding properties.

Table 2 – Alt a 1

INPUT SEQUENCE	RESIDUES IN SEQUENCE (Incl. FLANKS)	SEQUENCE	Hydro-phobicity	EpiMatrix HITS (Excl FLANKS)	EpiMatrix CLUSTER SCORE (Excl FLANKS)	Peptide ID NO	SEQ ID NO
AAM90320	1 - 21	MQ**FTTIASLFAAAGLAAA**APL	1.43	11	14.96	P1	1
AAM90320	51 - 73	EGT**YYNSLGFNIKATNGGTL**DFT	-0.42	11	17.74	P2	2
AAM90320	113 - 135	SDD**ITYVATATLPNYCRAGG**NGP	-0.35	14	20.83	P3	3
AAM90320	144 - 157	ADA**YITLVTLPKS**S	0.47	7	12.34	P4	4
Q6Q128	1 - 21	MQ**FTTIASLFAAAGLAAA**APL	1.43	11	14.96	P5	-
Q6Q128	51 - 73	EGT**YYNSLGFNIKATNGGTL**DFT	-0.42	11	17.74	P6	-
Q6Q128	113 - 135	SDD**ITYVATATLPNYCRAGG**NGP	-0.35	14	20.83	P7	-
Q6Q128	144 - 157	ADA**YITLVTLPKS**S	0.47	7	12.34	P8	-
Q8NJ79	1 - 21	MQ**FTTIASLFAAAGLAAA**APL	1.43	11	14.96	P9	-
Q8NJ79	51 - 73	EGT**YYNSLGFNIKATNGGTL**DFT	-0.42	11	17.74	P10	-

Based on a further analysis of Epimatrix data, the following additional sequences from Alt a 1 were also identified as having suitable MHC-binding properties: DITYVATATLPNY (SEQ ID NO: 5), DAYITLVTLPKSS (SEQ ID NO: 6), DITYVATATLPNYCR (SEQ ID NO: 111).

Example 2

EpiMatrix analyses as above were performed on the entire sequence of the known isoform of Alt a 2 (NCBI accession no: AAD00097). This analysis identified core sequences (with their flanking sequences) derived from said Alt a 2 isoform which are predicted to have good MHC class-II binding properties. These sequences are shown below in Table 3. Headings and notes for Table 3 are as with Table 2 above.

Table 3 – Alt a 2

INPUT SEQUENCE	RESIDUES IN SEQUENCE (Incl. FLANKS)	SEQUENCE	Hydro-phobicity	EpiMatrix HITS (Excl FLANKS)	EpiMatrix CLUSTER SCORE (Excl FLANKS)	Peptide ID NO:	SEQ ID NO:
AAD00097	38 - 60	WAQ**LLMLSAKRMKVAFKLDI**EKD	0.00	17	28.06	P11	7
AAD00097	75 - 98	RNG**FKRCLQFTLYRPRDLLSL**LNE	-0.55	14	20.04	P12	8
AAD00097	129 - 147	EDL**WKEYQKIFPSIQV**ITS	-0.37	10	16.7	P13	9

Based on a further analysis of Epimatrix data, the following additional sequences from Alt a 2 were also identified as having suitable MHC-binding properties: QLLMLSAKRMKVA (SEQ ID NO: 10), TLYRPRDLLSLLN (SEQ ID NO: 11);

Example 3

EpiMatrix analyses as above were performed on the entire sequence of the known isoform of Alt a 6 (NCBI accession no: Q9HDT3). This analysis identified core sequences (with flanking sequences) derived from said Alt a 6 isoform which are predicted to have good MHC class-II binding. These sequences are shown below in Table 4. Headings and notes for Table 4 are as with Table 2 above.

Table 4 – Alt a 6

INPUT SEQUENCE	RESIDUES IN SEQUENCE (Incl. FLANKS)	SEQUENCE	Hydro-phobicity	EpiMatrix HITS (Excl FLANKS)	EpiMatrix CLUSTER SCORE (Excl FLANKS)	Peptide ID NO.	SEQ ID NO.
Q9HDT3	186 - 204	GAE**VYQKLKALAKKTY**GQS	-0.73	14	25.24	P14	12
Q9HDT3	234 - 254	EAG**YTGKIKIAMDVASSE**FYK	-0.22	8	11.35	P15	13
Q9HDT3	335 - 357	AIE**LKSCNALLLKVNQIGTI**TEA	0.56	11	13.18	P16	14
Q9HDT3	362 - 383	KDA**FGAGWGVMVSHRSGET**EDV	-0.43	9	13.36	P17	15
Q9HDT3	385 - 400	IAD**IVVGLRSGQI**KTG	0.59	6	10.53	P18	16

Based on a further analysis of Epimatrix data, the following additional sequences from Alt a 6 were also identified as having suitable MHC-binding properties: VSMAIAKAAAAEK (SEQ ID NO: 17), QKLKALAKKTYGQ (SEQ ID NO: 18), EFIKKAIELKSCN (SEQ ID NO: 19), IELKSCNALLLK (SEQ ID NO: 20), GYTGKIKIAMDVASSEF (SEQ ID NO: 21), GYTGKIKIAMDVASSEFY (SEQ ID NO: 22). Based on homology with Alt a 6 and further design and screening, the following sequence derived from Cla h 6 was also identified as having suitable MHC-binding properties: SEQ ID NO: 108 (Cla16; AEVYQKLKSLTK).

Example 4

EpiMatrix analyses as above were performed on the entire sequence of the known isoform of Alt a 7 (NCBI accession no: P42058). This analysis identified core sequences (with flanking sequences) derived from the said Alt a 7 isoform which are predicted to have good MHC class-II binding. These sequences are shown below in Table 5. Headings and notes for Table 5 are as with Table 2 above.

Table 5 – Alt a 7

INPUT SEQUENCE	RESIDUES IN SEQUENCE (Incl. FLANKS)	SEQUENCE	Hydro-phobicity	EpiMatrix HITS (Excl FLANKS)	EpiMatrix CLUSTER SCORE (Excl FLANKS)	Peptide ID NO.	SEQ ID NO.

P42058	6 - 27	AIV**YYSMYGHIKKMADAEL**KGI	0.15	9	12.42	P19	23
P42058	32 - 48	GDA**KLFQVAETLPQ**EVL	0.12	8	16.31	P20	24
P42058	104 - 125	GAF**WGKYAGVFVSTGTLGG**GQE	0.15	12	19.42	P21	25
P42058	139 - 162	GFI**YVPLGYKTAFSMLANLDE**VHG	0.45	12	17.33	P22	26
P42058	180 - 199	PSE**LELNIAQAQGKAFY**EAV	-0.14	8	11.28	P23	27

Based on a further analysis of Epimatrix data, the following additional sequences from Alt a 7 were also identified as having suitable MHC-binding properties: DAKLFQVAETLPQEVLDK (SEQ ID NO: 28), GVFVSTGTLGGGQ (SEQ ID NO: 114), SELELNIAQAQGKAFYE (SEQ ID NO: 29), KYAGVFVSTGTLGGG (SEQ ID NO: 112).

Example 5

EpiMatrix analyses as above were performed on the entire sequence of the known isoform of Alt a 8 (NCBI accession no: P0C0Y4). This analysis identified core sequences (with flanking sequences) derived from the said Alt a 8 isoform which are predicted to have good MHC class-II binding. These sequences are shown below in Table 6. Headings and notes for Table 6 are as with Table 2 above.

Table 6 – Alt a 8

INPUT SEQUENCE	RESIDUES IN SEQUENCE (Incl FLANKS)	SEQUENCE	Hydro-phobic ity	EpiMatrix HITS (Excl FLANKS)	EpiMatrix CLUSTER SCORE (Excl FLANKS)	Peptide ID NO:	SEQ ID NO:
P0C0Y4	41 - 63	CAE**YGADLAITYNSRAEGAE**KNA	-0.55	10	15.58	P24	30
P0C0Y4	141 - 167	AVG**LHFRERKTGSLVITSSMSGHI**ANF	0.15	13	18.69	P25	31
P0C0Y4	189 - 203	ANE**WRDFARVNS**ISP	-0.80	5	10.04	P26	32
P0C0Y4	219 - 239	QKL**WHSMIPMGRDAKATE**LKG	-0.72	8	11.04	P27	33
P0C0Y4	234 - 254	ATE**LKGAYVYFASDASSY**CTG	0.05	10	13.22	P28	34

Based on a further analysis of Epimatrix data, the following additional sequence from Alt a 8 was also identified as having suitable MHC-binding properties: FVPQDIQKL (SEQ ID NO: 35). Based on homology with Alt a 8 and further design and screening, the following sequences derived from Cla h 8 were also identified as having suitable MHC-binding properties: SEQ ID NO: 109 (Alt25, VAITYASRAQGAEK) and SEQ ID NO:110 (Alt26, GHHFKERGTGSLVIT).

Example 6

EpiMatrix analyses as above were performed on the entire sequence of the known isoform of Alt a 10 (NCBI accession no: P42041). This analysis identified core sequences (with flanking sequences) derived from the said Alt a 10 isoform which are predicted to have good MHC class-II binding. These sequences are shown below in Table 7. Headings and notes for Table 7 are as with Table 2 above.

Table 7 – Alt a 10

INPUT SEQUENCE	RESIDUES IN SEQUENCE (Incl. FLANKS)	SEQUENCE	Hydro-phobicity	Epi Matrix HITS (Excl FLANKS)	Epi Matrix CLUSTER SCORE (Excl FLANKS)	Peptide ID NO:	SEQ ID NO:
P42041	144 - 170	PDS**FNYIRKSLLVFAVRSSMELPI**LMW	0.44	20	29.57	P29	36
P42041	169 - 189	MWS**WKIGPAIATGNTVVL**KTA	0.48	8	10.62	P30	37
P42041	209 - 231	PPG**VINVITGFGKIAGAAMS**AHM	0.82	9	10.82	P31	38
P42041	281 - 300	AIH**WVNFGIYFNHGQAC**CAG	0.45	8	10.6	P32	39
P42041	310 - 330	YDK**FIQRFKERAAQNAVG**DPF	-0.89	10	15.94	P33	40
P42041	408 - 430	ADV**IKIGNNTTYGLSAAVHT**SNL	0.15	10	14.49	P34	41
P42041	431 - 447	TTA**IEVANALRAGT**VWV	0.78	8	12.5	P35	42
P42041	476 - 495	LDN**YIQTKTVSIRLGDVLFG**	0.25	9	12.8	P36	43
P42041.2	170 - 190	MWS**WKIGPAIATGNTVVL**KTA	0.48	8	10.62	P37	-
P42041.2	210 - 232	PPG**VINVITGFGKIAGAAMS**AHM	0.82	9	10.82	P38	-
P42041.2	282 - 301	AIH**WVNFGIYFNHGQAC**CAG	0.45	8	10.6	P39	-
P42041.2	311 - 331	YDK**FIQRFKERAAQNAVG**DPF	-0.89	10	15.94	P40	-

P42041.2	410 - 432	ADV**IKIGNNTTYGLAAAVHT**SNL	0.27	11	16.79	P41	44
P42041.2	433 - 449	TTA**IEVANALRAGT**VWV	0.78	8	12.5	P42	-

Based on a further analysis of Epimatrix data, the following additional sequences from Alt a 10 were also identified as having suitable MHC-binding properties: SLLVFAVRSSMEL (SEQ ID NO: 45), SLLVFAVRSSMELPIL (SEQ ID NO: 46), WSWKIGPAIATGN (SEQ ID NO: 47), DNYIQTKTVSIRL (SEQ ID NO: 48).

Example 7

EpiMatrix analyses as above were performed on the entire sequence of the known isoform of Alt a 13 (NCBI accession no: Q6R4B4). This analysis identified core sequences (with flanking sequences) derived from the said Alt a 13 isoform which are predicted to have good MHC class-II binding. These sequences are shown below in Table 8. Headings and notes for Table 8 are as with Table 2 above.

Table 8

INPUT SEQUENCE	RESIDUES IN SEQUENCE (Incl. FLANKS)	SEQUENCE	Hydro-phobicity	Epi Matrix HITS (Excl FLANKS)	Epi Matrix CLUSTER SCORE (Excl FLANKS)	Peptide ID NO:	SEQ ID NO:
Q6R4B4	4 - 27	KPS**ELAVQKLVLFAVKGTATS**THN	0.05	14	19.42	P43	49
Q6R4B4	41 - 56	PHE**IYVVDRVSAP**WFT	0.01	6	11.83	P44	50
Q6R4B4	108 - 126	SSD**INNWLTLHTAALG**PTA	0.05	10	17.67	P45	51
Q6R4B4	126 - 143	AKY**WLYFYKLHPEKL**PKT	-0.83	10	18.28	P46	52
Q6R4B4	141 - 158	PKT**IEKLRSNITVQY**DIL	-0.34	9	15.34	P47	53
Q6R4B4	150 - 171	NIT**VQYDILERRLNEPGQQ**YLA	-0.72	8	10.9	P48	54

Based on a further analysis of Epimatrix data, the following additional sequences from Alt a 13 were also identified as having suitable MHC-binding properties: NWLTLHTAALGP (SEQ ID NO: 55), EKLRSNITVQYDI (SEQ ID NO:

56), EKYRRVVRAGVKV (SEQ ID NO: 57). RVVRAGVKVAQTA (SEQ ID NO: 58).

Example 8

The sequences set out in Table 9 were selected by the inventors as having desirable characteristics, based on the analyses performed in Examples 1 to 7 and a consideration of solubility and other physicochemical characteristics. For example, the sequences of SEQ ID NOS: 62 and SEQ ID NO: 89 are preferred variant sequences derived from SEQ ID NOS 111 and 112 respectively. These variant sequences were selected for improved solubility and/or manufacturability relative to the original amino acid sequences. Polypeptides consisting of the sequences of Table 9 were produced and were particularly preferred for screening in subsequent assays.

Table 9

Peptide	Sequence	Residues in parent	SEQ ID NO.
Alt01	TYYNSLGFNIKATNGGTL	53-70 (Alt a 1)	59
Alt01A	SLGFNIKATNGGTLD	57-71	60
Alt02	KDITYVATATLPNY	K115-127 (Alt a 1)	61
Alt02A	DITYVATATLPNYSR	115-129	62
Alt02B	KTYVATATLPNY	K117-127	63
Alt03	KDAYITLVTLPKSS	K145-157 (Alt a 1)	64
Alt03A	KKDAYITLVTLPKSS	KK145-157	65
Alt04	IFRSLSKEDPDY	12-23 (Alt a 2)	66
Alt04A	IFRSLSKEEPDY	12-23	67
Alt05	KQLLMLSAKRMKVAFK	K40-54 (Alt a 2)	68
Alt05A	KQLL-Nle-LSAKR-Nle-KVAFK		69
Alt05B	KQLL-Nle-LSAKRMKVAFK		70
Alt05C	KQLLMLSAKR-Nle-KVAFK		71
Alt06	SAKRMKVAFKLDIEK	45-59 (Alt a 2)	72
Alt06A	SAKR-Nle-KVAFKLDIEK		73
Alt07	LQFTLYRPRDLLS	82-94 (Alt a 2)	74
Alt08	TLYRPRDLLSLLNE	85-98 (Alt a 2)	75

Alt09	KEYQKIFPSIQVI	133-145 (Alt a 2)	76
Alt10	SAFRSIEPELTVY	147-159 (Alt a 2)	77
Alt10A	KSAFRSIEPELTVYK	K147-159K	78
Alt11	KKVSMAIAKAAAAEK	KK113-126 (Alt a 6)	79
Alt11A	KKVS-Nle-AIAKAAAAEK		80
Alt12	AEVYQKLKALAKK	187-199 (Alt a 6)	81
Alt13	PyrKLKALAKKTYGQ	191-203 (Alt a 6)	82
Alt13A	AEVYQKLKALAKKTYGQ*	187-203 (Alt a 6)	83
Alt14	GWGVMVSHRSGET*	368-380 (Alt a 6)	84
Alt14A	GWGV-Nle-VSHRSGET*	368-380 (Alt a 6)	85
Alt15	GYTGKIKIAMDVASSE*	236-251 (Alt a 6)	86
Alt15A	GYTGKIKIA-Nle-DVASSE*	236-251 (Alt a 6)	87
Alt17	KLFQVAETLPQEVLDK	35-50 (Alt a 7)	88
Alt18	KKYAGVFVSTGTLGGGK	109-125 (Alt a 7)	89
Alt20	LAITYNSRAEGAEK*	48-61 (Alt a 8)	90
Alt21	GLHFRERKTGSLVIT*	143-157 (Alt a 8)	91
Alt22	SYNVAKAGCIHLAK	173-186 (Alt a 8)	92
Alt22A	SYNVAKAGSIHLAK		93
Alt23	NEWRDFARVNSISP*	190-203 (Alt a 8)	94
Alt24	KLWHSMIPMGRDAK*	220-233 (Alt a 8)	95
Alt24A	KLWHS-Nle-IP-Nle-GRDAK*		96
Alt24B	KLWHS-Nle-IPMGRDAK*		97
Alt24C	KLWHSMIP-Nle-GRDAK*		98
Alt27	KRSLLVFAVRSSMELRK	KR153-166RK(Alt a 10)	99
Alt27A	KRSLLVFAVRSS-Nle-ELRK		100
Alt28	WSWKIGPAIATGNT*	170-183 (Alt a 10)	101
Alt30	HEIYVVDRVSAP	42-53 (Alt a 13)	102
Alt31	NWLTLHTAALGPTAK	112-127 (Alt a 13)	103
Alt32	KYWLYFYKLHPEK	127-139 (Alt a 13)	104
Alt33	IEKLRSNITVQYDI	144-157 (Alt a 13)	105
Alt34	YEKYRRVVRAGVKV	193-206 (Alt a 13)	106
Alt34A	KYRRVVRAGVKVAQTAR	195-211	107

Nle: Norleucine; Pyr: pyroglutamate. Asterisk (*) denotes potentially cross-reactive epitopes between a given *Alternaria* allergen and its *Cladosporium* homologue. Other instances of such epitopes are provided in Examples 1-7.

Example 9

In vitro binding analysis

Polypeptides having the sequences identified in Examples 1 to 8 are pre-screened for solubility in an aqueous, acidic milieu and the polypeptides are tested in an in vitro MHC Class II binding assay.

Methods

The assay employed is a competitive MHC class II binding assay, wherein each polypeptide is analysed for its ability to displace a known control binder from each of the human MHC class II allotypes investigated. The allotypes and control polypeptides used in this study are typically those shown below:

Allotype	Control Polypeptide	Sequence
DRB1*0301	Myco. tuberculosis/leprae hsp 65 2-16	AKTIAYDEEARRGLE (SEQ ID NO:116)
DRB1*1101	Influenza haemagglutinin 307-319	PKYVKQNTLKLAT (SEQ ID NO:117)
DRB1*1501	Human myelin basic protein 85-99	ENPVVHFFKNIVTPR (SEQ ID NO:118)

Each polypeptide is analysed in the competition assay and screened for relative binding compared to the control polypeptides. Due to the nature of the competitive assay the data for each polypeptide is determined as a ratio of its own IC50 to that of the control polypeptide. Thus, a polypeptide that has an IC50 value that is parity to the control polypeptide has an identical binding affinity, while polypeptides with a ratio less than one have a higher affinity and those with a ratio greater than one have a lower affinity.

Solubility in aqueous solution is an essential criterion for a polypeptide to be an effective therapeutic agent. Therefore, as a consequence of the solubility screen very hydrophobic polypeptides with a high frequency of large hydrophobic amino acid residues in multiple binding registers will be eliminated. This is a characteristic of promiscuous HLA-DRB1* binders. Polypeptides which bind to one or more of the MHC Class II allotypes are identified. It would be expected that such polypeptides would have the ability to bind similar allotypes that have not been tested through the homology of MHC structures.

Example 10

The following methods were used to evaluate T cell activation characteristics of polypeptides having the sequences identified in Examples 1 to 8.

Cell proliferation assay

The cell proliferation assay is performed on PBMC's ($140x10^6$ cells required for all parameters to be tested). Proliferation is measured by the incorporation of the radiolabelled compound 3H-thymidine. In more detail, 100μl of the appropriate antigen or polypeptide concentration is distributed into the appropriate wells of 96 well plates. The plates are then placed into a humidified 5% CO2 incubator set at 37°C for a maximum of 4 hours. PBMC's isolated as described above are prepared to a concentration of $2x10^6$ cells/ml in complete medium at room temperature. 100μl of cell solution is then distributed into each of the wells of the 96 well plates containing antigen/polypeptide. The plates are then incubated for 6 to 8 days. The cultures are pulsed with tritiated thymidine solution by adding 10μl of tritiated thymidine stock solution (1.85MBq/ml in serum-free RPMI medium) to each well. The plates are then returned to the incubator for between 8 and 16 hours. Cultures are then harvested using a Canberra Packard FilterMate 196 cell harvester. Dried filter mats are counted using an appropriate beta scintillation counter.

Counts from wells containing polypeptide are compared statistically to wells containing media alone (12 wells per group). The non-parametric Mann-Whitney test is used. The same statistical test is used for all subjects. A statistically significant difference between media only wells and polypeptide-stimulated wells is considered a positive stimulation of PBMC's by the polypeptide.

Cytokine release assay

Polypeptides for use in this assay were manufactured at small scale (approximately 10mg batch size, non-GMP). The purity of each polypeptide was at least 95% by HPLC. 96 well culture plates containing polypeptides and controls (the negative control was culture medium and the positive controls were staphylococcal enterotoxin B (SEB) 25ng/ml and whole *Alternaria* allergen extract 100 μg/ml) were prepared in advance and stored at -20°C prior to the day of assay. Polypeptides were added to wells in a volume of 100 µl containing polypeptides at a concentration of 200 µg/ml, such that subsequent addition of 100 µl of cells would create a final assay concentration of 100 µg/ml.

Peripheral blood mononuclear cells (PBMCs) were isolated from heparinised blood by Ficoll density gradient centrifugation. A 100 µl aliquot of a 5x106 cell/ml PBMC suspension was then added to each well and the plates placed in a humidified 5% CO2 incubator at 37°C for 5 days. Following stimulation, culture supernatants (100 µl) were harvested for testing by multiplex bead assay.

Multiplex cytokine bead assays (IL-10, IL-13, Interferon gamma (IFN-g)) were performed on thawed culture supernatants according to the manufacturer's instructions. Single measurements were performed for each culture supernatant sample. After completion of the multiplex assay, individual cytokine levels were determined by interpolation from the standard curve generated in the assay. A positive result was taken as a cytokine release of greater than 50 pg/ml in one or more of the IL-13, IL-10 and IFN-g assays. The number of responders out of 50 mould allergic subjects tested was calculated for each polypeptide for the three cytokines.

Results for the polypeptides having the sequences of Table 9 are summarized in Table 10.

<u>Table 10</u>

Peptide	% responders	Peptide	% responders
Alt01	20	Alt13A	86
Alt01A	26	Alt14	44
Alt02	36	Alt14A	56
Alt02A	30	Alt15	56
Alt02B	22	Alt15A	42
Alt03	22	Alt17	30
Alt03A	16	Alt18	50
Alt04	6	Alt20	38
Alt04A	4	Alt21	38
Alt05	2	Alt22	46
Alt05A	10	Alt22A	44
Alt05B	12	Alt23	40
Alt05C	16	Alt24	34
Alt06	16	Alt24A	40
Alt06A	10	Alt24B	30
Alt07	10	Alt24C	36
Alt08	10	Alt27	40
Alt09	6	Alt27A	42

Alt10	42	Alt28	52
Alt10A	34	Alt30	36
Alt11	36	Alt31	58
Alt11A	44	Alt32	36
Alt12	38	Alt33	44
Alt13	40	Alt34	38
		Alt34A	38

As shown, the top performing peptide was Alt13A. A polypeptide combination including a polypeptide having the sequence of Alt13A is preferred for treatment or prevention of *Alternaria* allergy. Other top performing polypeptides which induce responses individually in a high proportion of subjects include Alt10, Alt11A, Alt13, Alt14, Alt14A, Alt15, Alt15A, Alt18, Alt22, Alt22A, Alt24A, Alt27, Alt27A, Alt28, Alt31 and Alt33. One or more of these polypeptides may also be preferably included in any peptide combination of the invention.

An analysis of population coverage was carried out to determine what polypeptides could advantageously capture additional responses from the population when included in combination with other peptides. The number of subjects in the population displaying IL-13 or IFN-g responses to at least one, two or three polypeptides included in a given combination was analysed. Results are shown below in Table 11.

Table 11

Peptides	Subjects showing responses to at least 1 peptide	Subjects showing responses to at least 2 peptides	Subjects showing responses to at least 3 peptides
All polypeptides from Table 9	46	40	36
Alt01A, Alt02A, Alt06, Alt13A	43	18	6
Alt01A, Alt02A, Alt06, Alt13A, Alt33	43	32	12
Alt01A, Alt02A, Alt06, Alt13A, Alt33, Alt34A	44	32	24
Alt01A, Alt02A, Alt06,	44	30	23

Alt13A, Alt15, Alt18			
Alt01A, Alt02A, Alt06, Alt10, Alt13A, Alt33, Alt34A	45	34	27
Alt01A, Alt02A, Alt06, Alt13A, Alt28, Alt33, Alt34A	44	36	26
Alt01A, Alt02A, Alt06, Alt 10, Alt13A, Alt 15, Alt 18	45	33	25
Alt01A, Alt02A, Alt06, Alt13A, Alt 15, Alt 18, Alt28	44	35	23

The effect of adding different polypeptides can be seen by comparing the number of additional subjects responding to the different combinations.

Two polypeptides derived from Alt a1 (Alt01A and Alt02A) and one peptide from Alt a2 (Alt06) were able to provide for an increase in the number of subjects showing a response to at least one polypeptide, in particular those not showing a response to top-performing polypeptide Alt13A (86% response, i.e 34/50 individuals). A combination including any of Alt01A, Alt02A or Alt06 is thus preferred to increase population coverage, in particular in combination with polypeptide Alt13A.

Two polypeptides derived from Alt a 13 (Alt33 and Alt34A) were also particularly effective in increasing population coverage. When included in a combination above, they increased the number of subjects responding to at least two polypeptides from 18 to 32 and the number of subjects responding to at least three polypeptides from 6 to 24. Thus Alt33 and Alt34A are also preferred to increase population coverage, in particular in combination with polypeptide Alt13A and/or one or more polypeptides from Alt01A, Alt02A or Alt06.

Alternatively polypeptides Alt 15 and Alt 18 could be substituted for polypeptides Alt 33 and Alt 34. When included in a combination above they achieved 30 subjects responding to at least 2 peptides and 23 subjects responding to at least 3 polypeptides. Thus Alt15 and Alt18 are also preferred to increase population coverage, in particular in combination with polypeptide Alt13A and/or one or more polypeptides from Alt01A, Alt02A or Alt06.

Polypeptides Alt10 (from Alt a2) and Alt28 (from Alt10) gave further increases in population coverage when added to a mixture containing Alt01A, Alt02A, Alt06, Alt 13A, Alt 33 and Alt34A, providing respectively for 34 or 36 subjects responding to at least 2 peptides and 27 or 26 subjects responding to at least 3 polypeptides. Thus, Alt10 and Alt28 are also preferred in a vaccine to increase population coverage, in particular in combination with polypeptide Alt13A and/or one or more polypeptides from Alt01A, Alt02A, Alt06, Alt33 or Alt34A.

Polypeptides Alt10 or Alt28 may also be used as an alternative to polypeptides Alt 33 or Alt 34A. As shown above, a combination including Alt10 and Alt28 in place of polypeptides Alt33 and Alt34A provided respectively for 33 or 35 subjects responding to at least 2 polypeptides and 25 or 23 subjects responding to at least 3 polypeptides. Thus, Alt10 and Alt28 may be preferably provided in combination with polypeptide Alt13A and/or one or more polypeptides from Alt01A, Alt02A, Alt06, Alt15 or Alt18.

Example 11

The polypeptides identified in Example 10 as providing a basis for combinations of polypeptides capable of covering responses in a polymorphic population were analysed for their pharmaceutical development characteristics. An analysis of population coverage was then carried out for additional combinations of polypeptides identified as having preferable pharmaceutical development characteristics. The number of subjects in the population displaying IL-13 or IFN-g responses to at least one, two or three polypeptides included in a given combination was analysed. Results are shown below in Table 12.

Table 12

Peptides	Subjects showing responses to at least 1 peptide	Subjects showing responses to at least 2 peptides	Subjects showing responses to at least 3 peptides

All polypeptides from Table 9	46	40	36
Alt01A, Alt28, Alt34A	32	20	3
Alt18, Alt28, Alt34A	28	22	17
Alt01A, Alt13A,Alt28,Alt34A	42	27	19
Alt13A, Alt18, Alt28, Alt34A	39	26	21
Alt13A, Alt18, Alt28, Alt34	39	26	19
Alt01A,Alt13A,Alt18,Alt28,Alt34A	42	28	22
Alt01A,Alt13A,Alt18,Alt28,Alt34	42	28	22
Alt13A, Alt18, Alt28, Alt34A, Alt01A, Alt06	43	29	22
Alt13A, Alt18, Alt28, Alt34, Alt01A, Alt06	43	29	22
Alt13A, Alt18, Alt28, Alt34A, Alt01A, Alt06, Alt02	43	34	24
Alt13A, Alt18, Alt28, Alt34, Alt01A, Alt06, Alt02	43	34	24
Alt13A, Alt18, Alt28, Alt34A, Alt01A, Alt06, Alt14	43	29	24
Alt13A, Alt18, Alt28, Alt34, Alt01A, Alt06, Alt14	43	29	24

The effect of adding different polypeptides can be seen by comparing the number of additional subjects responding to the different combinations.

Two three peptide combinations: (a) Alt01A, Alt28 and Alt34A and (b) Alt18, Alt28 and Alt34A, both lacking top performing peptide Alt13A, were compared to assess differences in population coverage in the absence of Alt13A. The three peptide combination of (b) provided enhanced coverage in terms of the number of subjects who respond to all three peptides.

Addition of top performing peptide Alt13A in combinations of four peptides, such as the combination of Alt18, Alt28, Alt34A and Alt13A significantly improved coverage in terms of subjects responding to at least one peptide, as expected from the results in Example 10.

Addition of polypeptides such as Alt01A, Alt06, Alt02 and Alt14 further improved population coverage in terms of subjects responding to at least one, two and three peptides in the various combinations.

Thus, Alt01A, Alt06, Alt02 and Alt14 may preferably be provided in combination with the polypeptides Alt18, Alt28, Alt34A and Alt13A as a basis for effective coverage of responses in a polymorphic mould allergic population.

Example 12 – Preparation of peptides, salts and pharmaceutical formulations

Peptides are prepared as follows. Synthesis is performed in a solid phase peptide synthesis (SPPS) reactor and started by suspending the substituted resin in N,N-dimethylformamide (DMF). After washing of the resin with DMF, each coupling procedure is performed by addition of the N-α-protected amino acid derivative or the N-α-protected dipeptide to the preceding amino acid in the presence of N-[(1H-Benzotriazol-1-yl)(dimethylamino)methylene]-N-methylmethanaminium tetrafluoroborate N-oxide (TBTU) and N,N-diisopropylethylamine (DIPEA) in DMF or diisopropylcarbodiimide (DIC) and 1-hydroxybenzotriazole (HOBt) in a mixture of methylene chloride (DCM) and DMF. For each single step, the solvents and/or reagents are added and the reaction mixture is stirred and subsequently filtered to remove solvents and/or reagents from the resin.

After each successful coupling or capping procedure, an Fmoc-deprotection procedure is performed. It consists of washing of the resin with DMF, cleaving the Fmoc-group with 20% (V/V) piperidine in either DMF or 1-Methyl-2-pyrrolidone (NMP), and subsequent washings with DMF and isopropanol (IPA). For each single step, the solvents and/or reagents are added, and the reaction mixture is stirred and then filtered to remove the solvents and/or reagents from the resin.

Fmoc-deprotection and coupling procedures are repeated until the resin carries the complete peptide sequence of the required peptide. The SPPS is completed by a final Fmoc-deprotection and drying of the peptide resin under reduced pressure.

Acetate or hydrochloride salts of the specified peptides are prepared by the following methods. The peptide resin is treated with cold trifluoroacetic acid (TFA) at room temperature for 1.5 to 3 hours in the presence of 1,2-ethanedithiol (EDT), triisopropylsilane (TIS), and water. After filtering off and washing the resin with TFA, the product is precipitated in cold diisopropyl ether (IPE). It is then filtered off, washed with IPE, and dried under reduced pressure. The product is then reconstituted and purified by high-performance liquid chromatography (HPLC).

For preparation of acetate salts, the trifluoroacetate salt is reconstituted in 5% (V/V) aqueous acetic acid and loaded onto an ion exchange resin. The elution is performed with 5% (V/V) aqueous acetic acid. The acetate is filtered through a 0.2 µm membrane filter and lyophilized to yield the final product as a white to off-white powder.

For preparation of hydrochloride salts, the trifluoroacetate salt is reconstituted in 0.01 M HCl in purified water and filtered where necessary. The solution is loaded onto a preparative HPLC column for ion exchange into the hydrochloride salt. The ion exchange is performed by washing the column with a 0.1 M ammonium chloride solution followed by 0.01 M HCl. Subsequently, the hydrochloride is filtered through a 0.2 µm membrane filter and lyophilized to yield the final product as a white to off-white powders.

An exemplary pharmaceutical formulation of the present invention contains the components set out in Table 13. The peptide salt is a acetate or hydrochloride salt.

Table 13

Raw material	**Function**	**Nominal concentration**
Alt28 salt	Active ingredient	40 to 220µM
Alt34A salt	Active ingredient	40 to 220µM
Alt18 salt	Active ingredient	40 to 220µM
Alt13A salt	Active ingredient	40 to 220µM
Alt01A salt (optional)	Active ingredient	40 to 220µM
Alt06 salt (optional)	Active ingredient	40 to 220µM
Alt02 salt (optional)	Active ingredient	40 to 220µM
Alt14 salt (optional)	Active ingredient	40 to 220µM
L-Methionine	Antioxidant	5mM
Phosphoric acid or Hydrochloric acid	pH adjustment	As required

Trehalose dihydrate	Tonicity agent	260 mM

The formulation is prepared in solution prior to being subjected to freeze-drying to produce a lyophilisate.

CLAIMS

1. A pharmaceutical formulation comprising a pharmaceutically acceptable carrier or diluent and a polypeptide or a pharmaceutically acceptable salt thereof selected from at least three of:

(a) a polypeptide comprising the amino acid sequence of WSWKIGPAIATGNT (Alt28; SEQ ID NO: 101) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(b) a polypeptide comprising the amino acid sequence of KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(c) a polypeptide comprising the amino acid sequence of KYAGVFVSTGTLGGG (SEQ ID NO: 112) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof ;

(d) a polypeptide comprising the amino acid sequence of AEVYQKLKALAKKTYGQ (Alt13A; SEQ ID NO: 83) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(e) a polypeptide comprising the amino acid sequence of SLGFNIKATNGGTLD (Alt01A; SEQ ID NO: 60) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(f) a polypeptide comprising the amino acid sequence of SAKRMKVAFKLDIEK (Alt06; SEQ ID NO: 72) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

(g) a polypeptide comprising the amino acid sequence of DITYVATATLPNYCR (SEQ ID NO: 111) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof; and

(h) a polypeptide comprising the amino acid sequence of GWGVMVSHRSGET (Alt14; SEQ ID NO: 84) or a T cell epitope-containing variant sequence derived from said amino acid sequence, or a said salt thereof;

wherein a T cell epitope-containing variant sequence of a said amino acid sequence is said amino acid sequence having up to seven amino acid modifications, each of which is independently a deletion, substitution or insertion, and each polypeptide is up to 30 amino acids in length.

2. A pharmaceutical formulation according to claim 1, wherein a polypeptide of (a) to (h) consists respectively of the amino acid sequence or variant sequence recited in (a) to (h).

3. A pharmaceutical formulation according to claim 1 or 2, wherein the variant sequence of a said amino acid sequence is said amino acid sequence having one or two amino acid modifications, the or each of which independently is a deletion or substitution.

4. A pharmaceutical formulation according to any one of the preceding claims, wherein the or each substitution is a conservative substitution.

5. A pharmaceutical formulation according to any one of the preceding claims, wherein the variant sequence of a said amino acid sequence is said amino acid sequence having up to two amino acids deleted from the N-terminus and/or up to two amino acids deleted from the C-terminus.

6. A pharmaceutical formulation according to any one of the preceding claims, wherein each polypeptide is up to 20 amino acids in length.

7. A pharmaceutical formulation according to any one of the preceding claims, wherein at least one polypeptide has an amino acid sequence or variant sequence as defined in the preceding claims having a N-terminal and/or C-terminal extension of from one to six amino acids corresponding respectively to the one to six amino acids immediately N-terminal or C-terminal to the said amino acid sequence in the native sequence of the protein from which said amino acid sequence is derived.

8. A pharmaceutical formulation according to any one of the preceding claims, which comprises a polypeptide or salt of (a).

9. A pharmaceutical formulation according to any one of the preceding claims, which comprises at least one polypeptide or salt of (b), (c), or (d).

10. A pharmaceutical formulation according to any one of the preceding claims, which comprises a polypeptide or salt of (a), (b) and (c).

11. A pharmaceutical formulation according to claim 9 or 10, which comprises a polypeptide having the amino acid sequence YEKYRRVVRAGVKV (Alt34, SEQ ID NO: 106).

12. A pharmaceutical formulation according to any one of claims 9 to 11, which comprises a polypeptide having the amino acid sequence KKYAGVFVSTGTLGGGK (Alt18, SEQ ID NO: 89).

13. A pharmaceutical formulation according to any one of the preceding claims, which comprises a polypeptide or salt of (a), (b) and (d).

14. A pharmaceutical formulation according to any one of the preceding claims, which comprises a polypeptide or salt of (a), (b), (c) and (d).

15. A pharmaceutical formulation according to any one of the preceding claims, which comprises at least one polypeptide or salt of (e) or (f).

16. A pharmaceutical formulation according to claim 15, which comprises a polypeptide having the amino acid sequence SAKR-Nle-KVAFKLDIEK (Alt06A, SEQ ID NO: 73) , or a salt thereof.

17. A pharmaceutical formulation according to any one of the preceding claims, which comprises at least one polypeptide or salt of (g) or (h).

18. A pharmaceutical formulation according to claim 17, which comprises a polypeptide having the amino acid sequence KDITYVATATLPNY (Alt02; SEQ ID NO: 61), or DITYVATATLPNYSR (Alt02A; SEQ ID NO: 62), or a salt of either thereof.

19. A pharmaceutical formulation according to claim 17 or 18, which comprises a polypeptide having the amino acid sequence GWGV-Nle-VSHRSGET (Alt14A, SEQ ID NO: 85), or a salt thereof.

20. A pharmaceutical formulation according to any one of the preceding claims, which comprises a polypeptide or salt of (a), (b), (c), (d), and (e).

21. A pharmaceutical formulation according to claim 20, which comprises at least one polypeptide or salt of (f), (g) or (h).

22. A pharmaceutical formulation according to any one of the preceding claims, which is sealed in a container.

23. A pharmaceutical formulation according to any one of the preceding claims, which is a pharmaceutically acceptable solution or a lyophilisate.

24. A pharmaceutical formulation according to claim 23, wherein the solution is formulated for intradermal administration, subcutaneous administration, oral administration, nasal administration, topical administration, sublingual administration, buccal administration or epidermal administration.

25. A pharmaceutical formulation according to claim 23 or 24, wherein the solution is provided in an ampoule, sealed vial, syringe, cartridge, flexible bag or glass bottle.

26. A pharmaceutical formulation according to claim 23, wherein the lyophilisate is provided in a sealed vial.

27 A pharmaceutical formulation according to any one of the preceding claims for use in a method of treating or preventing allergy to *Alternaria* and/or *Cladosporium*.

28. An *in vitro* method of determining whether T cells recognize a polypeptide of a pharmaceutical formulation according to any one of claims 1 to 21, which method comprises contacting said T cells with said pharmaceutical formulation and detecting whether said T cells are stimulated by a said polypeptide.

29. A method according to claim 28 which is carried out to determine whether an individual has, or is at risk of having, an allergy to *Alternaria* and/or *Cladosporium*.

30. A method of treating an individual for allergy to *Alternaria* and/or *Cladosporium* or of preventing in an individual allergy to *Alternaria* and/or *Cladosporium*, which method comprises administering to said individual a therapeutically or prophylactically effective amount of a pharmaceutical formulation as defined in any one of claims 1 to 21.

31. Use of at least three polypeptides or salts as defined in claims 1 to 21 for the manufacture of a medicament for the prevention or treatment of allergy to *Alternaria* and/or *Cladosporium*.

32. A method of preparing a pharmaceutical formulation of the invention, comprising combining at least three polypeptides or salts as defined in any one of claims 1 to 21 with a pharmaceutically acceptable carrier or diluent.

33. A polypeptide, or a pharmaceutically acceptable salt thereof, which is up to 30 amino acids in length and comprises:

(I) the amino acid sequence:

(a) WSWKIGPAIATGNT (Alt28; SEQ ID NO: 101),

(b) KYRRVVRAGVKVAQTAR (Alt34A; SEQ ID NO: 107), or

(c) KYAGVFVSTGTLGGG (SEQ ID NO: 112); or

(II) a T cell epitope-containing variant sequence which is a said amino acid sequence (I) having up to seven amino acid modifications, each of which is independently a deletion, substitution or insertion.

34. A polypeptide or salt according to claim 33, wherein the polypeptide has an amino acid sequence selected from KKYAGVFVSTGTLGGGK (Alt18, SEQ ID NO: 89), and YEKYRRVVRAGVKV (Alt34, SEQ ID NO: 106).

35. A polypeptide or salt according to claim 33 or 34, for use in a method of treating or preventing allergy to *Alternaria* and/or *Cladosporium*.

36. Use of a polypeptide or salt according to claim 33 or 34 for the manufacture of a medicament for the prevention or treatment of allergy to *Alternaria* and/or *Cladosporium*.

37. A method of treating an individual for allergy to *Alternaria* and/or *Cladosporium* or of preventing in an individual allergy to *Alternaria* and/or *Cladosporium*, which method comprises administering to said individual a therapeutically or prophylactically effective amount of a polypeptide or salt according to claim 33 or 34.

INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2013/051439

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K14/37 A61K39/35 A61P37/08
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2009/022154 A2 (CIRCASSIA LTD [GB]; HAFNER RODERICK PETER [GB]; LARCHE MARK [CA]) 19 February 2009 (2009-02-19) page 2, line 10 - line 11 page 9, line 23 - line 24 page 78 - page 83; example 6 -----	1-37
X	WO 2012/038540 A2 (ALERGENETICA SL [ES]; DUNN-COLEMAN NIGEL STUART [ES]; DIAZ-TORRES MARI) 29 March 2012 (2012-03-29) abstract page 74, line 27 - line 31 page 77, line 17 - line 18 page 77, line 20 - line 22 sequences 172, 459 page 88 - page 91; example 7 page 90, line 17 - line 18 ----- -/--	1-37

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search 11 July 2013	Date of mailing of the international search report 23/07/2013
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C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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A	KARAMLOO FARIBA ET AL: "Prevention of allergy by a recombinant multi-allergen vaccine with reduced IgE binding and preserved T cell epitopes", EUROPEAN JOURNAL OF IMMUNOLOGY, WILEY - V C H VERLAG GMBH & CO. KGAA, DE, vol. 35, no. 11, 1 November 2005 (2005-11-01), pages 3268-3276, XP002464627, ISSN: 0014-2980, DOI: 10.1002/EJI.200425522 abstract -----	1-37
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C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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A	TERESA E TWAROCH ET AL: "Carrier-Bound Alt A 1 Peptides without Allergenic Activity for Vaccination Against Alternaria Alternata Allergy", CLINICAL & EXPERIMENTAL ALLERGY, vol. 42, no. 6, 1 March 2012 (2012-03-01), pages no-no, XP055070980, ISSN: 0954-7894, DOI: 10.1111/j.1365-2222.2012.03996.x abstract page 970, right-hand column, paragraph 5 - page 971, left-hand column, paragraph 1 figures 3, 4c, 5b -----	1-37

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/GB2013/051439

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摘 要

本发明公开一种药物制剂，其可用于预防或治疗对链格孢属和/或枝孢属的霉菌的过敏症，该药物制剂包括药学上可接受的载剂或稀释剂和选自以下多肽中的至少三种的多肽或其药学上可接受的盐：(a)包括氨基酸序列WSWKIGPAIATGNT(A1t28; SEQ ID NO: 101)或者来源于该氨基酸序列的含T细胞表位的变异序列的多肽，或者它的盐；(b)包括氨基酸序列KYRRVVRAGVKVAQTAR(A1t34A; SEQ ID NO: 107)或者来源于该氨基酸序列的含T细胞表位的变异序列的多肽，或者它的盐；(c)包括氨基酸序列KYAGVFVSTGTLGGG (SEQ ID NO: 112)或者来源于该氨基酸序列的含T细胞表位的变异序列的多肽，或者它的盐；(d)包括氨基酸序列AEVYQKLKALAKKTYGQ(A1t13A; SEQ ID NO: 83)或者来源于该氨基酸序列的含T细胞表位的变异序列的多肽，或者它的盐；(e)包括氨基酸序列SLGFNIKATNGGTLD(A1t01A; SEQ ID NO: 60)或者来源于该氨基酸序列的含T细胞表位的变异序列的多肽，或者它的盐；(f)包括氨基酸序列SAKRMKVAFKLDIEK(A1t06; SEQ ID NO: 72)或者来源于该氨基酸序列的含T细胞表位的变异序列的多肽，或者它的盐；(g)包括氨基酸序列DITYVATATLPNYCR(SEQ ID NO: 111)或者来源于该氨基酸序列的含T细胞表位的变异序列的多肽，或者它的盐；(h)包括氨基酸序列GWGVMVSHRSGET(A1t14;SEQ ID NO: 84)或者来源于该氨基酸序列的含T细胞表位的变异序列的多肽，或者它的盐；其中所述氨基酸序列的含T细胞表位的变异序列为其中具有多达7个氨基酸修饰的所述氨基酸序列，其中每一种修饰独立地为缺失、替换或者插入，并且每一个多肽的长度都多达30个氨基

摘 要

酸。