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Tumour-associated peptides that bond to MHC molecules

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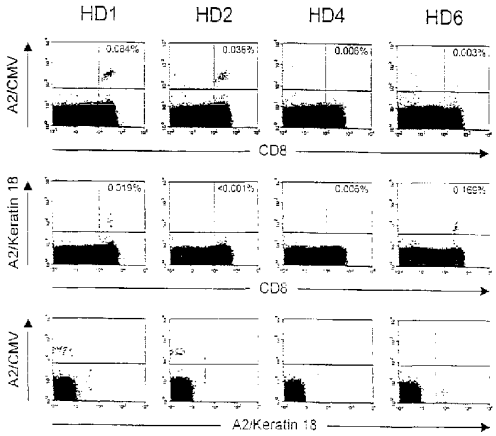

(57) Abstract: The invention relates to a tumour-associated peptide containing an amino acid sequence, which is selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 79 of the enclosed sequence protocol. Said peptide has the capacity to bond to a molecule of the human major histocompatibility complex (MHC) class I. The invention also relates to the use of the peptides for producing a medicament and for treating tumorous diseases. The invention further relates to a pharmaceutical composition, which comprises at least one of the peptides.

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Zur Erklärung der Zweibuchstaben-Codes und der anderen Abkürzungen wird auf die Erklärungen ("Guidance Notes on Codes and Abbreviations") am Anfang jeder regulären Ausgabe der PCT-Gazette verwiesen.

(57) Zusammenfassung: Die Erfindung betrifft ein Tumor-assoziiertes Peptid mit einer Aminosäuresequenz, die ausgewählt ist aus der Gruppe bestehend aus SEQ ID-Nr. 1 bis SEQ ID-Nr. 79 aus dem beiliegenden Sequenzprotokoll, wobei das Peptid die Fähigkeit aufweist, an ein Molekül des menschlichen Haupt-Histokompatibilitäts-Komplexes (MHC) Klasse-I zu binden. Die Erfindung betrifft darüber hinaus die Verwendung der Peptide zur Herstellung eines Arzneimittels und zur Behandlung von Tumorerkrankungen. Ferner wird eine pharmazeutische Zusammensetzung beschrieben, die mindestens eines der Peptide aufweist.

Tumor-associated peptides binding to MHC-molecules

The present invention relates to tumor-associated peptides having the ability to bind to a molecule of human major histocompatibility (MHC), class I.

Such peptides are used - for example - in immunotherapy of tumor-associated diseases.

When tumor cells are eliminated by the immune system the identification of tumor-associated antigens (TAA) by components of the immune system plays a pivotable role. This mechanism is based on the fact that there exist qualitative or quantitative differences between tumor cells and normal cells. To induce an anti-tumor-response, the tumor cells have to express antigens which induce an immune response being sufficient for the elimination of the tumor.

In particular, CD8-expressing cytotoxic T-lymphocytes (in the following CTL) are involved in rejection of tumors. To induce such an immune reaction by cytotoxic T-cells foreign proteins/peptides have to be presented to T-cells. Antigens are recognized as peptide fragments by T-cells only if they are presented by MHC-molecules on cell surfaces. These MHC ("major histocompatibility complex") molecules are peptide receptors which normally bind peptides intracellularly and transport them to the cell surface. This complex of peptide and MHC-molecule is recognized by T-cells. Human MHC-molecules are also designated as human leukocyte antigens (HLA).

There are two classes of MHC-molecules: MHC class-I-molecules, which are present on most cells having a nucleus, present peptides generated by degradation of endogenous proteins. MHC class-II-molecules are present on professional antigen-presenting cells (APC) only and present peptides of exogenous proteins, which are taken up and processed during endocytosis. Peptide/MHC-class-I complexes are recognized by CD8-positive cytotoxic T-lymphocytes, peptide/MHC class-II-complexes are recognized by CD4 helper T-cells.

In order to induce a cellular immune response a peptide has to bind to a MHC-molecule. This action depends on the allele of the MHC-molecule and on the amino acid sequence of the peptide. MHC-class-I-binding peptides, being - as a general rule - of 8 to 10 residues in length, comprise two conserved residues ("anchor") in their sequence, that engage complementary pockets located in the MHC-molecule.

In order for the immune system to induce an effective CTL-response directed against tumor-associated peptides, these peptides have not only to be able to bind to specific MHC-class-I-molecules expressed by tumor cells but have also to be able to be recognized by T-cells having specific T-cell receptors (TCR).

When developing a tumor vaccine a main aim is to identify and to characterize tumor-associated antigens which are recognized by $CD8^+$ CTL.

The antigens - or their epitopes, respectively - which are recognized by tumor-specific cytotoxic T-lymphocytes can be molecules of all classes of proteins, such an enzymes, receptors, transcription factors, etc. Another important class of tumor-associated antigens are tissue-specific structures such as the cancer-testis antigens, which are expressed in various kinds of tumors and healthy testis tissue.

In order for the T-lymphocytes to identify proteins as tumor-specific antigens and in order to use them in therapy, certain requirements have to be met: The antigen has to be expressed mainly by tumor cells and not by normal cells or at least to a minor extent as in tumors. Further, it is desirable if the specific antigen is present not only in one kind of tumor but also in other kinds in high concentrations. Further, the presence of epitopes in the amino acid sequence of the antigen is essentially since those peptides derived from tumor-associated antigens are supposed to induce a T-cell-response, either *in vitro* or *in vivo*.

Thus, TAA represent a starting point for developing a tumor vaccine. Methods for identification and characterization of TAA are based on the utilization of patient-derived CTL or on the generation of differential transcription profiles between tumors and normal tissue.

Identification of genes which are overexpressed in tumorous tissues or which are selectively expressed in such tissues does not provide precise information about utilization of antigens transcribed from these genes for immune therapy. This is based on the fact that only several epitopes of these antigens are suitable for such an utilization since a T-cell response is induced - via MHC presentation - by epitopes of the antigens only and not by the antigen as a whole. Thus it is important to select those peptides of overexpressed or selectively expressed proteins, that are presented by MHC-molecules, thereby generating points of attack for specific tumor recognition by cytotoxic T-lymphocytes.

In view of the above it is an object of the present invention to provide at least one new amino acid sequence of such a peptide which can bind to a molecule of the human major histocompatibility complex (MHC)-class-I.

This object is achieved, according to the invention, by providing a tumor-associated peptide containing an amino acid sequence which is selected from the group consisting of SEQ ID-No. 1 to SEQ ID-No. 79 of the enclosed sequence protocol, the peptide having the ability to bind to a molecule of the human major histocompatibility complex (MHC)-class-I.

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Accordingly in a first aspect of the invention there is provided an isolated and/or purified tumor-associated peptide, wherein the tumor-associated peptide is a HLA-A*02 ligand which contains an amino acid sequence having the ability to bind to a molecule of the human major histocompatibility complex (MHC) Class - 1, wherein the peptide sequence comprises at position 2 and the C-terminal amino acid position a non-polar amino acid.

In a second aspect of the invention there is provided the first aspect of the invention namely an isolated and/or purified tumor associated peptide, wherein:

a) the non-polar amino acid at position 2 is selected from the group consisting of Leucine, Valine, Isoleucine, Alanine and Methionine, and

b) the non-polar amino acid at the C-terminal position is selected from the group consisting of Leucine, Valine, Isoleucine and Alanine.

In a third aspect of the invention there is provided an isolated and/or purified tumor-associated peptide comprising the amino acid sequence YVDPVITSI (SEQ ID No. 1), the peptide having the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-1.

It is understood that peptides identified from the tumor may be synthesized or be expressed in cells in order to obtain larger amounts and in order to utilize them for purposes described below.

The inventors were able to identify the above-mentioned peptides as specific ligands of MHC-class-1-molecules from tumorous tissue. In this connection, with the term "tumor-associated", peptides are denoted herein, which have been isolated and identified from tumorous material. These peptides - being presented on genuine (primary) tumors - are subject to antigen processing in a tumor cell.

The specific ligands can be used in cancer therapy, for example to induce an immune response directed against tumor cells, which express the corresponding antigens from which the peptides derive.

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On the one hand, such an immune response in terms of an induction of CTL can be achieved *in vivo*. For that purpose a peptide is administered - for example in form of a pharmaceutical composition - to the patient, who suffers from a tumor disease associated with the TAA.

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On the other hand, a CTL-response against a tumor expressing the antigen from which the peptides derive can be induced *ex vivo*. For this purpose the CTL-precursor cells are incubated together with antigen-presenting cells and the peptides. The

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CTL stimulated thereby are then cultivated, and these activated CTL are administered to the patient.

A further possibility is to load APC *ex vivo* with the peptides and to administer those loaded APC to a patient, who, in tumor tissue, expresses the antigen from which the peptide is derived. The APC can in turn present the peptide to the CTL *in vivo* and activate them.

The peptides according to the invention can further be utilized as diagnostic reagents.

In that way, the peptides can be used to find out if, in a CTL population, there exist CTL specifically directed against the peptide or if the CTL were induced by a therapy.

Further, the increase of precursor T-cells, which show reactivity against the defined peptide, can be tested with the peptide.

In addition, the peptide can be used as a marker to assess the disease course of a tumor expressing the antigen from which the peptide derives.

In the enclosed Table 1 the identified peptides are listed. They are disposed according to the respective HLA-types they are binding to. Further, in the table the proteins are disposed, from which the peptide is deriving, and the respective position of the peptide in the corresponding protein. In doing so, the English denotation of the proteins was kept to avoid misleading translations. Further, the Acc-numbers are quoted,

which are listed in the gene bank of the "National Center for Biotechnology Information" of the National Institute of Health (see http://www.ncbi.nlm.nih.gov).

The inventors were able to isolate the peptides (or ligands) from renal cell carcinomas of two patients, RCC01 and RCC13. In doing so, 68 ligands from tumorous tissue of patient RCC01 were isolated and 13 ligands from tumorous tissue of patient RCC13. Two of the ligands identified in both patients were identical. Those were the peptides having the sequence ID No. 1 and 3 (YVDPVITSI of met-protooncogene (C-Met) and ALLNIKVKL of keratin 18).

79 ligands could be identified from the tumors of the patients, 30 of which were bound to the HLA-subtypes HLA-A*02, 13 were bound to HLA-A*68, 34 to HLA-B*18 or HLA-B*44 and 2 to HLA*24.

HLA-A*02-ligands were all exhibiting the allele-specific peptide motif: (Leucine/Valine, Isoleucine, Alanine or Methionine on position 2; Leucine/Valine, Isoleucine or Alanine at the C-terminus.

Some of the ligands derived from abundantly expressed so-called housekeeping genes, which are expressed equally in most tissues, but many were distinguished by tumor-association.

The peptide having the sequence ID No. 1 YVDPVITSI, for example, is concerning a ligand, which, in particular, is associated with tumors and which derives from the met-protooncogene (c-Met) (position 654-662). Peptides having the sequence ID Nos. 2, 22 and 23 derive from adipophilin (also denoted as

"adipose differentiation related" protein) and comprise positions 129-137, 62-71 and 349-358 in this protein, whereby the last two are among HLA-A*68 presented peptides. The ligand having the sequence ID No. 3 is a ligand, which is derived from keratin 18 and is located at position 365-373.

The major part of the ligands was comprising the amino acid glutamic acid (E) on position 2, which is an anchor-amino acid of the HLA-B*44-subtype. In that way, peptides could be identified, which derive from proteins, that have proven to be immunogenic in earlier experiments, for example peptide having sequence ID No. 5, which derives from protein Annexin II (position in Annexin II: 55-63). This protein proved to be immunogenic in respect of MHC class-II-molecules in melanoma patients (see Heinzel et al., The self peptide annexin II (208-223) presented by dendritic cells sentisizes autologous CD4+ T-lymphocytes to recognize melanoma cells, 2001, Cancer Immunol. Immunother. 49: 671-678).

Further, some peptides could be identified, which derive from proteins, that are, in particular, overexpressed in tumorous tissue. Thus, fragments of Vimentin (EEIAFLKKL, position 229-237) and Caldesmon (DEAAFLERL, position 92-100) could be identified. Young et al., Expression profiling of renal epithelial neoplasms: a method for tumor classification and discovery of diagnostic molecular markers, 2001, Am. J. Pathol., 158: 1639-1651) disclosed that these proteins were overexpressed in renal cell carcinoma tissues.

The inventors were further able - among other things - to identify ligands, which derived from ets-1 (NEFSLKGVDF, position

86-95), Alpha-Catenin (NEQDLGIQY, position 169-177) and Galectin 2 (SEVKFTVTF, position 80-88).

The inventors further isolated fragment YYMIGEQKF (sequence ID No. 79) which derives from the enzyme Nicotinamid-N-Methyl-transferase (position 203-211). Takahashi et al., Gene expression profiling of clear cell renal cell carcinoma: gene identification and prognostic classification, 2001, Proc. Natl. Acad. Sci. USA, 98: 9754-9749, disclosed that this enzyme was overexpressed in renal cells carcinoma.

Surprisingly, the inventors were able to detect cytotoxic T-lymphocytes specific for one of the identified peptides in donor blood. Thus, it is possible to induce a CTL-response specific against the tumors.

The inventors were able to demonstrate, in their own experiments, that by using two exemplarily selected peptides cytotoxic T-lymphocytes (CTL) could be generated *in vivo*, which were specific for peptides having sequence ID No. 1 (c-Met-protoocogene-fragment or c-Met-peptide) or specific for the peptide having the sequence ID No. 2 (adipophilin fragment or adipophiline peptide). These CTL were able to specifically kill tumor cells, which expressed the respective proteins and which derived from different tumor cell lines of different patients. The inventors could further demonstrate that with the mentioned CTL dendritic cells, for example, could be lysed, which were previously pulsed (loaded) with the respective peptides. The inventors demonstrated with these experiments that human T-cells can be activated *in vitro* by using the peptides according to the invention as epitopes. The inventors could not only

demonstrate that CTL, which were obtained from peripheral blood mononuclear cells (PBMNC) of a patient and which were specific for a certain peptide, were able to kill cells of the same kind of tumor of another patient. The inventors further demonstrated that even cells of other kinds of tumors could be lysed with these CTL.

In a preferred embodiment, peptides may be used for stimulation of an immune response, too, which comprise sequence ID No. 1 to 79 and in the sequence of which at least one amino acid may be replaced by another amino acid with similar chemical features.

With respect to the respective MHC-subtypes, these are, for example, anchor amino acids, which may be replaced by amino acids with similar chemical features. For example, in peptides, which are associated with MHC-subtype HLA-A*02, Leucine on position 2 may be replaced with Isoleucine, Valine or with Methionine and vice versa, and Leucine at the C-terminus with Valine, Isoleucine and Alanine, which all comprise non-polar side chains.

Further, it is possible to use peptides having sequence ID Nos. 1 to 79, which comprise at least one additional amino acid at the N- or C-terminus, or in the sequence of which at least one amino acid may be deleted.

Further, peptides having sequence ID Nos. 1 79 can be used, which comprise at least one amino acid being chemically modified.

The varying amino acid(s) is (are) chosen in that way that the variation does not effect the immunogenity of the peptide, that is the peptide still displays a similar binding affinity to the MHC-molecule and the ability to stimulate T-cells.

According to the invention, the peptide can be used for treatment of tumor diseases and/or adenomatous diseases.

Tumor diseases to be treated comprise, for example, renal, breast, pancreas, gastric, testis and/or skin cancer. Listing of tumor diseases is supposed to be merely illustrative and shall not limit the scope of usage.

The inventors were able to demonstrate, in their own experiments, that the peptides according to the invention are suitable for such use. Thus, it was demonstrated that with specifically generated CTL, which were specific for certain peptides, tumor cells could be effectively and selectively killed.

To use tumor-associated antigens in a tumor vaccine there are, as a general rule, several possible forms of application. Tighe et al., 1998, Gene vaccination: plasmid DNA is more than just a blueprint, Immunol. Today 19(2): 89-97, demonstrated that the antigen could be administered either as recombinant protein with suitable adjuvants or carrier systems or - in plasmid vectors - as cDNA encoding the antigen. In the latter cases, to induce an immune response, the antigen has to be processed and presented by antigen-presenting cells (APC) in the patient's body.

Melief et al., 1996, Peptide-based cancer vaccines, Curr. Opin. Immunol. 8: 651-657, demonstrated a further possibility, i.e. to use synthetic peptides as vaccine.

In a preferred embodiment the peptide can be used in addition of adjuvants, or on its own.

As an adjuvant, the granulocate-macrophage-colony-stimulating-factor (GM-CSF) can be used for example.

Further examples for such adjuvants are aluminumhydroxide, emulsions of mineral oils, such as Freund's adjuvants, saponines or silicon compounds.

Use of adjuvants is of advantage, since the immune response induced by the peptide can be boosted and/or the peptide can be stabilized.

In another preferred embodiment the peptide is administered when bound to an antigen-presenting cell.

This step is advantageously since the peptides can be presented to the immune system, in particular to cytotoxic T-lymphocytes (CTL). In that way, CTL can identify and specifically kill the tumor cells. For example, dendritic cells, monocytes or B-lymphocytes are suitable as antigen-presenting cells for that purpose.

In doing so, the cells are, for example, loaded with the peptides *ex vivo*. On the other hand, the cells may be transfected

with DNA or the corresponding RNA encoding the peptides in order for the peptides being expressed on the cells.

The inventors were able to demonstrate, in their own experiments, that dendritic cells (DC) could be loaded with specific peptides and that these loaded dendritic cells activated peptide-specific CTL. That means, that the immune system can be stimulated to produce CTL directed against the tumors which express the respective peptides.

The antigen-presenting cells carrying the peptide may be used either in a direct manner or may be activated with heat shock protein gp96 prior use. This heat shock protein induces expression of MHC-class-I-molecules and of costimulating molecules such as B7, and, in addition, stimulates production of cytokins. In that way the induction of immune responses is enhanced all in all.

In another preferred embodiment the peptides are used to label leukocytes, in particular T-lymphocytes.

This use is of advantage, if the peptides are used, in a CTL-population, to detect CTL specifically directed against the peptides.

The peptide can further be used as a marker to assess a therapy course of a tumor disease.

The peptide can also be used for monitoring therapy in other immunizations or therapies. In that way the peptide may not

only be used in a therapeutical way but also in a diagnostic way.

In a further embodiment the peptides are used for generating an antibody.

Polyclonal antibodies can be obtained, in a general manner, by immunization of animals by means of injection of the peptides and subsequent purification of the immunoglobuline.

Monoclonal antibodies can be generated according to standardized protocols, for example as described in Methods Enzymol. (1986), 121, Hybridoma technology and monoclonal antibodies.

In a further aspect the invention relates to a pharmaceutical composition comprising one or more peptides.

This composition may for example be applied parenterally, for example subcutaneously, intradermally or intramuscularly or may be administered orally. In doing so the peptides are dissolved or suspended in a pharmaceutically acceptable carrier, preferably an aqueous carrier. The composition can further comprise additives, for example buffers, binders, diluents etc.

The peptides can also be administered together with immunostimulating substances, for example cytokins. An extensive description of additives which can be used in a composition of this nature is given, for example, in A. Kibbe, Handbook of Pharmaceutical Excipients, 3. ed., 2000, American Pharmaceutical Association and pharmaceutical press.

The composition may be used for prevention, prophylaxis and/or therapy of tumor diseases and/or adenomatous diseases.

The pharmaceutical composition comprising at least one of the peptides having sequence ID Nos. 1 to 79 is administered to a patient who suffers from a tumor disease, the respective peptide or antigen is associated with. Thereby, a tumor-specific immune response can be induced on basis of tumor-specific CTL.

The amount of the peptide or of the peptides being present in the pharmaceutical composition is a therapeutically effective amount. In this connection the peptides contained in the composition can bind to at least two different HLA-types.

The present invention relates, in a further aspect, to nucleic acid molecules encoding the peptides with sequence ID Nos. 1 to 79.

The nucleic acid molecules can represent DNA- or RNA-molecules and can be used for immune therapy of cancer as well. Thereby the peptide expressed by the nucleic acid molecule induces an immune response against tumor cells, which express the peptide.

According to the invention the nucleic acid molecules can be provided in a vector.

The invention further relates to a cell genetically modified by means of the nucleic acid molecule so that the cell is producing a peptide having sequence ID Nos. 1 to 79.

For this purpose, the cells are transfected with DNA or corresponding RNA encoding the peptides, thereby expressing the peptides on the cells. For this purpose, for example dendritic cells, monocytes or B-lymphocytes are suitable as antigen-presenting cells.

It will be understood that the features which are mentioned above and the features still to be explained below can be used not only in the combinations which are in each case specified but also in other combinations or on their own without departing from the scope of the present invention.

Embodiments of the invention are displayed and explained in the figures below.

Fig. 1 shows the detection of $CD8^+$-T-lymphocytes specific for keratin 18;

Fig. 2a-d show the induction of CTL-responses *in vitro*, specific for the c-Met-peptide (SEQ ID No. 1), Fig. 2a+b, or the adipophilin-peptide (SEQ ID No. 2), Fig. 2c+d;

Fig. 3a-f show antigen-specific lysis of tumor cell lines expressing c-Met or adipophilin, mediated by c-Met-peptide (SEQ ID No. 1), Fig. 3a-d, or adipophilin-peptide (SEQ ID No. 2), Fig. 3e-f, induced CTL;

Fig. 4a-c show lysis-inhibition assays with ^{51}Cr-labeled tumor cells and unlabeled pulsed T2-cells mediated by c-Met-peptide (SEQ ID No. 1), Fig. 4a+b, or adipophilin-peptide (SEQ ID No. 2), Fig. 4c) induced CTL;

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Fig. 5a+b show lysis of autologous dendritic cell transfected with tumor RNA mediated by c-Met-peptide (SEQ ID NO. 1), Fig. 51, or adipophilin-peptide (SEQ ID NO. 2), Fig. 5b, inducted CTL;

Fig. 6 shows that adipophilin-specific autologous CTL induced *in vitro* recognize autologous tumor cells of a patent with chronic lymphatic leukaemia but not autologous dendritic or B-cells.

Fig. 7 shows the detection of Tumor Associated Peptides on the surface of tumor cells obtained from randomly obtained HLA-A*02 positive renal cell carcinoma (RCC) patients.

Fig. 8 shows T-cell responses in patients suffering from advanced renal cell carcinoma dosed with eight courses of IMA901 vaccine.

Fig. 9 shows T-cell responses for the TUMAPs contained in the IMA901 vaccine.

EXAMPLE 1

1.1 Patient samples

Samples of patients having histologically confirmed renal cell carcinoma were obtained from the department of urology, University of Tübingen. Both patients had not received preoperative therapy. Patient No. 1 (in the following designated RCC01) had the following HLA-typing: HLA-A*02 A*68 B*18 B*44; patient No. 2 (in the following designated RCC13) HLA-A*02 A*24 B*07 B*40.

1.2 Isolation of MHC-class-I-bound peptides

Shock-frozen tumor samples were processed as described in Schirle, M. *et al.*, Identification of tumor-associated MHC-class I ligands by a novel T cell-independent approach, 2000, European Journal of Immunology, 30: 2216-2225. Peptides were isolated according to standard protocols using monoclonal antibody W6/32 being specific for HLA class I or monoclonal antibody BB7.2 being specific for HLA-A2. Production and utilization of these antibodies is described by Barnstable, C.J. *et*

al., Production of monoclonal antibodies to group A erythrocytes, HLA and other human cell surface antigens - New tools for genetic analysis, 1978, Cell, 14:9-20 and Parham, P. & Brodsky, F.M., Partial purification and some properties of BB7.2. A cytotoxic monoclonal antibody with specificity for HLA-A2 and a variant of HLA-A28, 1981, Hum. Immunol., 3: 277-299.

1.3 Mass spectrometry

Peptides from tumor tissue of patient RCC01 were separated by reversed phase HPLC (SMART-system, µRPC C2/C18 SC 2.1/19, Amersham Pharmacia Biotech) and fractions were analyzed by nanoESI MS. In doing so it was proceeded as described in Schirle, M. et al., Identification of tumor-associated MHC class I ligands by a novel T cell-independent approach, 2000, European Journal of Immunology, 30: 2216-2225.

Peptides from tumor tissue of patient RCC13 were identified by online capillary LC-MS as mentioned above with minor modifications: Sample volumes of about 100 µl were loaded, desalted and preconcentrated on a 300 µm * 5 mm C18 µ-precolumn (LC packings). A syringe pump (PHD 2000, Harvard Apparatus, Inc.) equipped with a gastight 100 µl-syringe (1710 RNR, Hamilton), delivered solvent and sample at 2 µl/min. For peptide separation, the preconcentration column was switched in line with a 75 µm * 250 mm C-18-column (LC packings). Subsequently a binary gradient of 25 % - 60 % B within 70 min was performed, applying a 12 µl/min flow rate reduced to approximately 300 nl/min with a precolumn using a TEE-piece (ZT1C, Valco) and a 300 µm * 150 mm C-18-column.

A blank run was always included to ensure that the system was free of residual peptides. On-line fragmentation was performed as described and fragment spectra were analyzed manually. Database searches (NCBInr, EST) were made using MASCOT (http://www.matrixscience.com).

1.4 Identification of 77 MHC-class-I-ligands of tumorous tissue of patient RCC01

In the enclosed Table 1 the ligands are listed which were bound to HLA-A*02, HLA-A*68, HLA-B*18 or HLA-B*44. Peptides that bound to HLA-A*02 reflected the allele-specific peptide motif: On position 2 Leucine, Valine, Isoleucine, Alanine or Methionine and at the C-terminus Leucine, Valine, Isoleucine or Alanine. Most ligands were derived from so-called housekeeping proteins but ligands from proteins with reported tumor-associated associations could be detected also.

HLA-A*68 ligands were identified by their anchor amino acid Threonine, Isoleucine, Valine, Alanine or Leucine on position 2 and Arginine or Lysine at the C-terminus. This indicated to subtype HLA-A*6801. Two other ligands from adipophilin were found among HLA-A*68 presented peptide, MTSALPEIQK and MAGDIYSVFR, and further ETIPLTAEKL deriving from tumor-associated cycline D1. Peptide TIVNILTNR derives from Annexin II, this protein proved as immunogenic in connection with MHC-class-II in melanoma patients (see Heinzel et al., The self peptide annexin II (208 - 223) presented by dendritic cells sentisizes autologous CD4+ T-lymphocytes to recognize melanoma cells, 2001, Cancer Immunol. Immunother. 49: 671-678). Further ligands were carrying glutamic acid on position 2 which is an

anchor amino acid of the HLA-B*44-subtype. Since the peptide motif of HLA-B*18 is unknown the distinction between ligands of these two HLA-B-molecules was not possible.

1.5 MHC-class-I-ligands of tumorous tissue of patient RCC13

With this tumorous tissue, too, the same ligands could be identified, which have been identified in patient RCC01 and which derived from met-protooncogene (c-Met) and keratin 18: peptides having sequence ID Nos. 1 and 3. In addition, further ligands could be obtained from this tumorous tissue: A ligand could be identified which derives from nicotinamide-N-methyltransferase (NNMT); this gene is overexpressed in more than 95 % of all renal carcinoma. Further, some other ligands overlap with the peptide repertoire of RCC01.

1.6 Detection of keratin 18-specific T-cells in normal $CD8^+$-T-cell repertoire

Peripheral blood mononuclear cells from healthy patients were stained with HLA-A*0201-tetramers which were folded with adipophilin-, keratin 18- or met-protooncogene (c-Met)-peptides: For generation of the tetramers, recombinant HLA-A*0201-molecules were folded *in vitro* with the peptides SVASTITGV (SEQ ID No. 2, adipophilin), ALLNIKVKL (SEQ ID No. 3, keratin 18) or YVDPVITSI (SEQ ID No. 1, met-protooncogene, c-Met), purified by means of gel filtration, biotinylated and mixed with streptavidin to link the monomers.

Unexpectedly, a significant population of $CD8^+$-T-lymphocytes specific for keratin 18 was found in four out of 22 healthy

individuals. In Fig. 1 the results of double staining are shown in dotplots, whereby in the middle row the results of staining with keratin 18 is shown. Between 0.02 and 0.2 % of the $CD8^+$-positive T-cells were specific for keratin 18. As can be seen from the lower row of the dotplots, binding of the keratin 18-tetramer was specific.

Example 2

To analyze presentation of the peptides with SEQ ID No. 1 (YVDPVITSI) (peptide fragment of c-Met-protooncogene) and SEQ ID No. 2 (peptide fragment of adipophilin) by tumor cells and their recognition by CTL, CTL were induced *in vitro*, which were specific for the c-Met-peptide (peptide with SEQ ID No. 1) and CTL which were specific for the adipophilin-peptide (SEQ ID No. 2). In doing so, dendritic cells (DC) derived from healthy HLA-A*02-positive donors were used.

2.1 Generation of DC

Peripheral blood mononuclear cells (PBMNC) were isolated by Ficoll/Paque-(Biochrom, Berlin, Germany)-density gradients centrifugation of heparinized blood obtained from buffy coat preparations of healthy volunteers from the blood bank of the University of Tübingen. Cells were seeded (1×10^7 cells / 3 ml per well) into 6-well plates (Falcon, Heidelberg, Germany) in RP10 media (RPMI 1640, supplied with 10 % heat-inactivated fetal calf serum and with antibiotics). After 2 hours of incubation at 37°C and 5 % CO_2, non-adherent cells were removed and the adherent blood monocytes were cultured in RP10 medium supplemented with the following cytokins: human recombinant GM-CSF

(granulocyte makrophage colony stimulating factor; Leukomax, Novartis; 100 ng/ml), Interleukin IL-4 (R&D Systems, Wiesbaden, Germany, 1000 IU/ml) and TNF-α (tumor necrosis factor α) (R&D Systems, Wiesbaden, Germany, 10 ng/ml).

2.2 Synthesis of peptides

Exemplary, two HLA-A*02-binding peptides (c-Met SEQ ID No. 1, YVDPVITSI) or adipophilin (SEQ ID No. 2, SVASTITGV) which were identified as described above) were synthesized using standard F-moc chemistry on a peptide synthesizer (432A, Applied Biosystems, Weiterstadt, Germany) and analyzed by reversed phase HPLC and mass spectrometry. In that way, sufficient amounts of the identified peptides can be generated.

2.3 Induction of antigen-specific CTL-response using HLA-A*02 restricted synthetic peptides

For CTL induction, the DC obtained in step 2.1 (5×10^5) were pulsed with the peptides obtained in step 2.2 with SEQ ID No. 1 or SEQ ID No. 2, each with 50 µg/ml for 2 hours, washed and incubated with $2,5 \times 10^6$ autologous PBMNC in RP10 medium.

After 7 days of culture, cells were restimulated with autologous PBMNC pulsed with peptides. In doing so, 1 ng/ml human recombinant Interleukin IL-2 (R&D Systems) was added on days 1, 3 and 5. The cytolytic activity of thereby induced CTL was analyzed on day 5 after the last restimulation in a standard ^{51}Cr-release-assay (see below, under 2.4: CTL-assay).

2.4 CTL-Assay

In the CTL-assays, tumor cells, peptide-pulsed cells of different cell lines and autologous DC were used as target cells. Peptide-pulsed cells were pulsed with 50 µg/ml peptide (SEQ ID No. 1 or SEQ ID No. 2) for 2 hours. All target cells were labeled with [^{51}Cr] sodium chromate in RP10 (RPMI 1640, supplemented with 10 % heat inactivated calf serum and antibiotics) for 1 hour at 37°C. Subsequently, 10^4 cells/well were transferred to a 96-well round bottomed plate. Varying numbers of CTL were added to give a final volume of 200 µl and incubated for 4 hours at 37°C. At the end of the assays, supernatants (50 µl/well) were harvested and counted in a beta-plate counter. The percent-specific lysis was calculated as: 100 x (experimental release - spontaneous release / maximal release - spontaneous release). The spontaneous and maximal release were determined in the presence of either medium or 2 % Triton X-100, respectively.

2.5 Results of the CTL-induction

a) CTL-cytotoxic activity against peptide-pulsed DC

In Fig. 2, the results of the ^{51}Cr-release-assay (see under 2.4) with respect to the cytotoxic activity of induced CTL (see under 2.3) against T2- or DC-cells is shown. The T2-cell line is HLA-A*02-positive and TAP (transporter associated with antigen processing) deficient; (TAP-peptide-transporter transport peptide fragments of a proteinous antigen from the cytosol to the endoplasmatic reticulum, where they associate with MHC-molecules).

In Figs. 2a and 2b, the cytotoxic activity of CTL induced with peptide with SEQ ID No. 1 against T2-cells and DC is shown, both cell types had previously been pulsed with the (c-Met-)peptide with SEQ ID No. 1 (black filled boxes) or an irrelevant peptide (Survivin (= "Sv"; ELTLGEFLKL; SEQ ID No. 80) or HIV (ILKEPVHGV; Pol. HIV-1 reverse transcriptase peptide, position 476-484; SEQ ID No. 81). In Figs. 2c and 2d the cytotoxic activity of CTL induced with peptide with SEQ ID No. 2 against T2- and DC-cells is shown, which had previously been pulsed with the (adipophilin)-peptide with the SEQ ID No. 2.

The specific lysis, which is demonstrated in the release of ^{51}Cr, is, in Figs. 2a - 2d, - as well as in the CTL-lysis-diagrams of Figs. 3 – 5 - shown vs. different ratios of effector cells (CTL) to target cells (^{51}Cr-labeled cells to be lysed).

As can be seen from Figs. 2a - 2d, an antigen-specific killing of cells could be demonstrated with a CTL-cell line, which has been generated after 2-weekly restimulation: Only cells were lysed by an increasing amount of CTL, which presented either the c-Met-peptide with the SEQ ID No. 1 (Figs. 2a and 2b) or the adipophilin-peptide with the SEQ ID No. 2 (Figs. 2c and 2d) (see in the Figs. 2a - 2d curves with black filled boxes, respectively); while control cells pulsed with irrelevant peptides were not lysed (curves with empty boxes). Thereby the specifity of the cytolytic activity could be demonstrated.

b) CTL-cytotoxic activity against tumor cell lines

Next, it was tested, in a standard tumor ^{51}Cr-release-assays again, whether CTL specific for the c-Met-peptide with SEQ ID

No. 1 or for adipophilin-peptide with SEQ ID No. 2 recognized and lysed tumor cells, which endogeously express the c-Met-protooncogene or adipophilin.

In doing so, the following cell lines, ^{51}Cr-labeled, HLA-A*02-positive, were used: HCT 116 (colon cancer; obtained from Prof. G. Pawelec, Tübingen, Germany), A 498, MZ 1257 and MZ 1774 (renal cell carcinoma; obtained fro Prof. A. Knuth, Frankfurt, Germany), MCF-7 (breast cancer; obtained from ATCC, American Type Culture Collection), Mel 1479 (Malignant melanoma; obtained from Prof. G. Pawelec, Tübingen, Germany) and U 266 (multiple myeloma; obtained from Prof. G. Pawelec, Tübingen, Germany). These cell lines express c-Met-protooncogene and adipophilin as target structures ("targets").

In the experiments CEBV (Epstein-Barr-virus)-immortalized B-cell line Croft, HLA-A*01-positive; obtained from O.J. Finn, Pittsburgh, USA) and cell line SK-OV-3 (ovarian cancer; HLA-A*03-positive; obtained from O.J. Finn, Pittsburgh, USA) were used as negative controls. K 562-cells (for example obtainable at the German Collection of Mikro Organisms and Cell Cultures DSMZ; ACC 10) were used to determine the activity of natural killer cells (NK) since the cell line is highly sensitive for these killer cells.

All cell lines were cultivated in RP10 medium (RPMI 1640, supplemented with 10 % heat-inactivated fetal calf serum and antibiotics).

With the above-mentioned tumor cell lines and the CTL induced ^{51}Cr-release assays (see under 2.4.) were carried out as mentioned above.

Figs. 3a - 3f show the results of these CTL-assays, whereby in Figs. 3a - 3d CTL were used which were induced using c-Met-peptide with SEQ ID No. 1, and in Figs. 3e - 3f CTL were used, which were induced using adipophilin peptide with SEQ ID No. 2.

As can be seen from Figs. 3a - 3f, the CTL specific for c-Met-peptide with SEQ ID No. 1 (Fig. 3a - 3d) or specific for adipophilin peptide with SEQ ID No. 2 (Fig. 3e and 3f) were able to efficiently lyse tumor cells expressing both HLA-A*02 and c-Met or adipophilin (that is in Fig. 3a cell line HCT 116, in Fig. 3b cell line A 498, in Fig. 3c cell lines MZ 1257 and MEL 1479 and in Fig. 3d cell lines MCF-7 and U 266; in Fig. 3e cell lines A 494, U 266 and MCF-7, in Fig. 3f cell lines MZ 1774, Mel 1479 and MZ 1257). Specific lysis was measured - as mentioned under 2.4. - via ^{51}Cr release. There was no lysis of the control cell line SK-OV-3 (HLA-A-*02-negative), neither through CTL, which were induced by the peptide with SEQ ID No. 1 nor through CTL, which were induced by the peptide with SEQ ID No. 2. Thus, it could be demonstrated that both peptides have to be presented on tumor cells in connection with HLA-A*02-molecules to efficiently lyse the target cells. Further, the antigen-specifity and the MHC-restriction of the CTL is proved in that way.

CTL-cells induced *in vitro* with the peptide having SEQ ID No. 1 did not recognize the K562 cell line (see Figs. 3a, 3b and 3d),

indicating that the cytotoxic activity was not mediated by natural killer (NK)-cells.

c) Inhibition-Assays

To further verify the antigen-specifity and the MHC-restriction of the *in-vitro*-induced CTL, inhibition assays with non-^{51}Cr-labeled ("cold") inhibitor cell lines were performed.

In doing so, the ability of peptide-pulsed cell lines was analyzed to inhibit the lysis of tumor cells (competition assay). For this purpose, an excess of inhibitor (that is an excess of unlabeled pulsed cells) was used. The ratio of inhibitor (peptide-pulsed cells) to target (tumor cells) was 20:1. When inhibitor cell lines were lysed, no ^{51}Cr was released, since the inhibitor cell lines were unlabeled.

Cell line T2 (HLA-A*02; TAP-deficient; see under 2.5.a)) was used as inhibitor. Previous to the assay, this cell line T2 was pulsed with the relevant peptides (SEQ ID Nos. 1 or 2) or an irrelevant control peptide (Survivin (= Sv), SEQ ID No. 80), respectively.

Results of these tests are shown in Figs. 4a - 4c, whereby in Figs. 4a and 4b CTL were used which were c-Met-peptide-induced (SEQ ID No. 1) and in Fig. 4c CTL were used, which were adipophilin-peptide-induced (SEQ ID No. 2).

In Figs. 4a and 4b lysis of the ^{51}Cr-labeled cell lines U 266 and A 498 was tested without inhibitor cell line (see the curve with black filled boxes); lysis with inhibitor cell line T2,

pulsed with an irrelevant peptide (Survivin; SEQ ID No. 80; negative control, curves with the filled triangles); and lyses with the inhibitor cell line T2 pulsed with the c-Met-peptide with SEQ ID No. 1 (curves with the empty rhombus).

Without inhibitor cells, lysis of tumor cells by CTL could be demonstrated (see in Figs. 4a - 4d curves with black filled boxes, respectively). Further, as can be seen from Fig. 4a and 4b, when using an excess of inhibitor target tumor cells were not lysed (and no ^{51}Cr was released), if the inhibitor target was pulsed with c-Met-peptide with SEQ ID No. 1 (see curves with the empty rhombus symbols, respectively). The activity of the CTL was directed against the excess unlabeled T-cells, so that these cells and not the tumor cells were lysed. The T2-cells pulsed with an irrelevant peptide (Survivin respectively; SEQ ID No. 80) were not able to inhibit the lysis of tumor cells by CTL, so that released ^{51}Cr could be measured (see in Figs. 4a and 4b curves with black filled triangles).

A similar event could be shown when using CTL induced with adipophilin peptide with SEQ ID No. 2 (see Fig. 4c):

MHC-restriction and antigen-specifity of the cytotoxic activity of the adipophiline-induced CTL could be demonstrated by using a HLA-A*02-specific monoclonal antibody and in an inhibition assay with unlabeled ("cold") inhibitor: The results of this experiment are shown in Fig. 4c. A 498-tumor cells were blocked when adding HLA-A*02-specific antibody (monoclonal antibody BB7.2, IgG2b, obtained from S. Stefanovic, Tübingen) so that they were not lysed by the added CTL and no ^{51}Cr was released (see Fig. 4c curve with filled triangle-symbols). As a control

a non-specific antibody was used, which did not block the HLA-A*02-molecule (ChromPure Maus IgG, Dianova, Germany; see in Fig. 4c curve with filled boxes). With these inhibition assays, the cells were incubated with 10 µg/ml antibody previous to seeding on the 96-well-plates for 30 min.

Further it could be demonstrated that the T2-competition cell line pulsed with the irrelevant peptide Survivin (SEQ ID No. 80) (T2/SV), was not able to inhibit CTL-induced lysis of tumor cell line A 498 (see in Fig. 4c curve with black filled circles), but T2-inhibitor cell line pulsed with adipophilin peptide with SEQ ID No. 2 (T2/AD) was able to inhibit the lysis of the tumor cell line, so that - refrain to the latter case - no ^{51}Cr release could be measured (see in Fig. 4c curve with x-symbols).

d) Specific lysis of transfected DC

In a next experiment, the cytotoxic activity of CTL in an autologous setting was analyzed. In doing so, autologous DC, generated from the same PBMNC that were utilized for CTL induction (see under 2.2.), were used as target cells. Prior to the CTL-assay, the DC were electroporated with RNA, which was previously isolated either from tumor cell lines or which represented control-RNA (*in vitro* transcribed EGFP-RNA, enhanced Green fluorescent protein-RNA); plasmide: pSP64 Poly(A) EGFPII, obtained from Van Tendeloo, Antwerp, Belgium). Total RNA of tumor cells was isolated with the QIAGEN Rneasy Mini Kit (QIAGEN, Hilden, Germany) according to the manufacturer's protocol. Quantity and purity of RNA were determined by spectrophotometry and stored in aliquots at -80°C.

Prior to electroporation on day 6, immature DC were washed twice with serum-free X-VIVO 20 medium (BioWhittaker, Walkersville, USA) and resuspended to a final concentration of 2 x 10^7 cells/ml. Subsequently, 200 µl of the cell suspension were mixed with 10 µg of total RNA and electroporated in a 4 mm-cuvette using an Easyject Plus™ (Peglab, Erlangen, Germany) (parameters: 300 V, 150 µF, 1540 Ω, pulse time 231 ms). After electroporation the cells were immediately transferred into RP10 medium and returned to the incubator. More than 80 % of the cells proved to be viable after electroporation.

The results of these experiments are shown in Figs. 5a and 5b. In Fig. 5a CTL were used, which were induced with c-Met-peptide with SEQ ID No. 1, in Fig. 5b CTL were used which were induced with adipophilin peptide with SEQ ID No. 2.

After performing the CTL-assay with the CTL induced by c-Met-peptide (SEQ ID No. 1) (see under 2.4.) a specific lysis of DC could be demonstrated which were electroporated with RNA of c-Met-expressing tumor cell lines (A 498 and MCF-7) (see in Fig. 5a, curves with black filled symbols). DC electroporated with RNA of the non-C-met-expressing tumor cell line Croft were not lysed (see curve with the empty rhombus).

CTL induced with adipophilin-peptide with SEQ ID No. 2 lysed DC which were electroporated with RNA of the adipophilin-expressing cell line A 498 (see in Fig. 5b curve with black filled triangles). Further, DC were lysed which were pulsed with the adipophilin-peptide SEQ ID No. 2 (see in Fig. 5b curve with black filled rhombus). On the other hand, DC electropo-

rated with control (EGFP) RNA were not lysed (see in Fig. 5b curve with the empty triangles).

Thus it could be demonstrated that - after transfection of the DC with RNA of c-Met- or adipophilin-positive tumor cells - the identified peptides, that is c-Met-peptide with SEQ ID No. 1 and adipophilin-peptide with SEQ ID No. 2, were processed and presented.

e) Induction of adipophilin-specific CTL in a patient with chronic lymphatic leukemia

In a further experiment, CTL were generated from PBMNC of HLA-A*0201-positive patient with chronic lymphatic leukemia (CLL), which were specific for adipophilin-peptide with SEQ ID No. 2. The patient was in remission after treatment with fludarabine. Further, autologous CLL-cells and DC of this patient were used as ^{51}Cr-labeled targets in an assay, in which ^{51}Cr-release is mediated by the peptide-induced CTL.

As shown in Fig. 6, the peptide-induced CTL efficiently lysed autologous DC from this patient that were pulsed with the adipophilin peptide with SEQ ID No. 2 ("DC + AD") as well as the autologous CLL-cells ("CLL cells"). DC which were pulsed with the irrelevant peptide Survivin with SEQ ID No. 80 were - on the other hand - not lysed ("DC + SV"). Also, non-malignant B-cells and cell line K 562 were not lysed by CTL.

The specifity of the CTL-response was further confirmed in a target inhibition assay, using the cell line T2 (see above) as inhibitor cells, which were pulsed with the adipophilin peptide

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with SEQ ID NO. 2 or with the irrelevant peptide Survivin with SEQ ID NO. 80, respectively. The CTL induced with adipophilin-peptide with SEQ ID NO. 2 lysed the excess inhibitor cell lines which were pulsed with the relevant peptide with SEQ ID NO. 2 so that ^{51}Cr-labeled tumor cells were not lysed in this case (see in Fig. 6 the curve with empty boxes).

In conclusion, the inventors could show that the identified peptides represent promising substances in the scope of an immune therapy for many (tumor) diseases.

As will be demonstrated below, Immatics developed a vaccine (designated as IMA901) containing 9 HLA-A02 and 1 HLA-DR TUMAPs that were identified and validated using Immatics' novel technology. Each of the TUMAPS in this vaccine has been shown to demonstrate immunogenic activity (discussed below). Thus, Immatics method of discovery and validation of immunogenic TUMAPs has been shown to predict *in vivo* immunogenicity.

EXAMPLE 3

A Vaccine Preparation

A vaccine containing 10 Tumor associated peptides (TUMAPs) was prepared (IMA901). These TUMAPs have been identified as being naturally presented in primary renal cell carcinoma (RCC) tissues. The vaccine includes nine HLA-class I-binding peptide epitopes with the capacity to activate cytotoxic T cells (CD8+ T cells) and one HLA class II-binding peptide with the capacity to activate T helper cells (CD4+ T cells). The IMA901 vaccine includes the peptide from c-met proto-oncogene (having the amino acid sequence YVDPVITSI (SEQ ID NO. 1)). This peptide is designated as IMA-MET-001 in the attached data. The vaccine also contains one additional peptide from hepatitis B virus (HBV) core antigen (HBV-001, an HLA-A0201 binding immunogenic peptide antigen) to serve as a marker peptide.

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B Identification of SEQ ID NO. 1 on the surface of renal carcinoma tissues (RCC)

Pre-clinical studies confirmed, using mass spectrometry-based detection of peptides presented by and eluted from HLA-A*02 molecules that all naturally processed tumor associated peptides (TUMAPs) included in the vaccine, in particular the peptide IMA-MET-001 from c-met proto-oncogene, are in fact presented on the surface of tumor cells obtained from randomly selected HLA-A*02 positive renal cell carcinoma (RCC) patients. The peptide from c-met (SEQ ID NO. 1) having the sequence of YVDPVITSI was detected in 7/7 cases. See Fig. 7.

C *In vitro* validation platform using ELISpot and HLA-Tetramer Assays

Two generally accepted but different assays for monitoring clinical immune responses were used to detect the *in vivo* immune response: ELISpot Assay and HLA-Tetramer Assay.

The ELISpot assay measures the release of IFN-γ by T cells after specific recognition of a peptide. Triplicate measurements of IFN-γ spots in the assay were performed to provide a reliable statistical calculation. The ELISpot assay verifies the presence of the c-met peptide (IMA-MET-001) (or any desired peptide) in patient blood. This assay can be used to demonstrate effector T cell functions in response to stimulation of T cells from patient blood with the antigen (peptide) of interest.

The HLA-tetramer assay measures the frequency of a T-cell population specifically recognising a MHC/peptide complex. A single cell measurement by cytometric analysis (FACS) was performed to provide a reliable statistical calculation. This assay uses HLA-A*02 tetramers that are complexed with the peptide of interest, *e.g.* the peptide from c-met. This complex will specifically bind only to those T cells isolated from the peripheral blood of patients vaccinated with the vaccine (comprising the peptide from c-met) that bear the respective T cell receptor ("TCR") on their surface. The T cells are then detected by cytometric analysis (FACS) with the use of a fluorophore.

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Both of these *in vitro* assays were performed for all single peptides present in the IMA901 vaccine, including the c-met peptide (SEQ ID NO. 1).

The ELISpot assay is a method that allows detecting living activated CD8+ T cells from sample material, *e.g.* patient peripheral blood mononuclear cells (PBMC), in an antigen-(HLA/peptide-complex-) specific manner by measuring the secretion of interferon-gamma (IFN-g) in response to a specific stimulus, *i.e.* the matching HLA/peptide-complex for a particular T cell receptor (TCR). In brief, this sensitive and easy-to-perform assay was employed in a clinical phase 1 study in patients for assessing the frequency of CD8+ T cells reacting against tumor-associated HLA ligands. The enzyme-linked immunosorbent (ELISpot) technique quantifies T cells that produce certain cytokines, *e.g.* IFN-gamma, on a single cell level of sensitivity, thus offering the most sensitive assay for detecting antigen-specific T cells currently available.

Purified T cells obtained from patient-derived PBMC at different points in time before or during treatment with the IMA901 vaccine, according to the clinical study protocol had been kept in cell culture and re-stimulated with the antigen of choice (*e.g.* CCN-001, a peptide originating from the cell cycle control and tumor antigen Cyclin D1) for 12 days before they were incubated for 20-24 hours in the ELISpot microtiter plates coated with the anti-IFN-gamma-antibody. Those T cells with the appropriate T cell receptor (TCR) recognising the CCN-001 peptide bound to the HLA-A*02 receptor secrete IFN-gamma in response to the stimulus.

The secreted IFN-gamma is bound by the antibody coated on the well. After a washing step, IFN-gamma release is visualised by an enzyme-labelled detection antibody and its corresponding chromogenic substrate, which becomes insoluble and attached to the surface of the well at the site of reaction. Each coloured spot on the wells represents an area where at least one cell secreted IFN-gamma. Spots can be quantified manually or automatically by using a CCD camera and the according image analysis software. The significance of the differences

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between, *e.g.* T cells purified from pooled blood samples taken before and during the first day of vaccination with SEQ ID NO. 1 and T cells present in PBMC after several rounds of vaccination is determined by generally accepted statistical methods for conducting analyses of this kind. Results from analysis showed that the CCN-001 peptide included in SEQ ID NO. 1 induced the proliferation (increase in the number of spots over the course of treatment) of T cells specifically recognising the CCN-001 peptide when displayed by the HLA-A*02 receptor. At the same time, T cells recognising an irrelevant peptide representing a *bona fide* epitope from a viral antigen from the H1 virus, which was used as a negative control, were not increased in number. (Results not shown).

A second assay, the HLA-tetramer assay, was also performed. The peptide (c-met peptide) triggered the expansion of killer T cells. In this assay, the presence or absence of antigen-specific T cells recognising a particular HLA/peptide-complex of interest, *i.e.* peptides such as the MET-001 peptide derived from the tumor antigen c-met proto-oncogene, is visualised by using aggregates (referred to as HLA tetramers) consisting of four covalently linked synthetic HLA/peptide complexes, which specifically bind to only those T cells that carry the appropriate T cell receptor (TCR). Staining and counting of antigen-specific T cells in this way is a generally accepted method for the quantification of T cells.

In contrast to an ELISpot assay, no additional information regarding the functionality of T cells (*e.g.* production of certain activation markers such as IFN-gamma) is acquired. For providing information about particular cell populations of interest, multiparametric analysis of different surface markers, *e.g.* the CD8 co-receptor and a TCR binding the HLA-A*02/MET-001 peptide-complex, T cells are incubated first with an anti-CD8-antibody, a secondary fluorescence-labelled antibody, and HLA-tetramers that are also directly or indirectly linked to a chromophore.

After washing the cells, the cells are passed through a detector with a laser at a wavelength suitable for exciting light emission from the fluorescent dyes attached

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to the agents used for detection. Events measured by the detectors can be visualized by *e.g.* dot plots showing the number of double and single-positive cells *i.e.* cells having both the CD8 co-receptor as well as a matching TCR on its surface, or only cells being positive for only one of the parameters under investigation. In dot plots of this kind, double-positive populations always show up in the upper right corner. In case of the MET-001 peptide, the presence of a discrete double-positive population demonstrates the existence of a MET-001-responsive T cell population after beginning of vaccination of patients with the product IMA901 vaccine containing the MET-001 peptide as an active pharmaceutical ingredient. (Results not shown).

D *In vivo* immunogenicity, determination for SEQ ID NO. 1 and for the other TUMAPs in the IMA901 vaccine

1. A phase I study to assess safety, immunogenicity, and anti-tumor activity of tumor vaccination with eight courses of intradermally (i.d.) applied IMA901 plus GM-GSF as adjuvant was performed in patients suffering from advanced renal cell carcinoma (RCC).

The study involved 30 patients with histologically confirmed RCC of states III and IV and who were also HLA type HLA-A*02 positive. Eight vaccinations were given within 10 weeks. Each vaccination comprised the i.d. injection of GM-CSF (75 µg) followed by the i.d. injection of 4.5 mg IMA901 (413 µg per peptide per vaccination).

The results showed that 74% of evaluable patients (27 out of 30) showed a vaccine-induced T cell response to at least one HLA class I TUMAP and 30% of evaluable patients were multi-peptide responders (*i.e.* > I vaccine-induced T cell response). T cell responses were detectable by day 15. See Fig. 8.

2. In a phase I trial, the induction of T cell responses *in vivo* against two or more of the HLA-A*02 binding TUMAPS included in the vaccine correlated with a clinical stabilisation of the disease. A Wilcoxon two-sample test showed a

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significant difference regarding growth/shrinkage of target lesion in patients with one or multiple TUMAP responses.

Immunogenicity was seen for 8 of the 9 HLA class I TUMAPs. IMA901 induced a T cell response against TUMAPs in the majority of advanced RCC patients (74%). For the peptide of MET-001, 15% of the patients showed a T cell response. See Fig. 9.

E. The c-met peptide (SEQ ID NO. 1) triggers an immune response in caner patients who received the peptide as a therapeutic vaccine

Not only does the peptide IMA-Met-001 from c-met lead to a strong and specific stimulation of T cells *in vitro*, it also triggers an immune response in cancer patents who received the peptide as a therapeutic vaccine. Four out of 27 patients with advanced renal cell carcinoma mounted an immune response against the IMA-MET-001 peptide. In addition, eight out of the nine HLA-A*02 binding TUMAPS included in the vaccine triggered an immune response *in vivo*. See Fig. 9.

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Table 1

	Sequence	Position/Gene	Acc. No.	SEQ ID-No.
Patient RCC01				
HLA-A*02				
1.	YVDPVITSI	654-662 met proto-oncogen	J02958	SEQ ID-Nr. 1
2.	SVASTITGV	129-137 adipose differentiation-related protein	X97324	SEQ ID-Nr. 2
3.	ALLNIKVKL	365-373 keratin 18	M26326	SEQ ID-Nr. 3
4.	ALFDGDPHL	1-9 KIAA0367	AB002365	SEQ ID-Nr. 4
5.	RLLDYVVNI	679-687 hypothetical protein **FLJ20004**	AB040951	SEQ ID-Nr. 5
6.	ALANGIEEV	101-109 apolipoprotein L, 3	AY014906	SEQ ID-Nr. 6
7.	QLIDKVWQL	593-601 SEC14 (S. cerevisiae)-like 1	D67029	SEQ ID-Nr. 7
8.	ALSDLEITL	389-397 mitogen inducible 2	Z24725	SEQ ID-Nr. 8
9.	ILDTGTIQL	174-182 kidney- and liver-specific gene	AB013094	SEQ ID-Nr. 9
10.	SLLGGDVVSV	27-36 delta sleep inducing peptide, immunoreactor	AF153603	SEQ ID-Nr. 10
11.	FLDGNELTL	167-175 chloride intracellular channel 1	U93205	SEQ ID-Nr. 11
12.	NLLPKLHIV	179-187 chloride intracellular channel 1	U93205	SEQ ID-Nr. 12
13.	ALASHLIEA	507-515 EH-domain containing 2	AF181263	SEQ ID-Nr. 13
14.	SLYGGTITI	296-304 hypothetical protein FLJ11189	AK000697	SEQ ID-Nr. 14

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16.	FLDGNEMTL	178-186 chloride intracellular channel 4	AF097330	SEQ ID-Nr. 16
17.	AIVDKVPSV	147-155 coat-protein gamma-cop	AF100756	SEQ ID-Nr. 17
18.	DVASVIVTKL	241-250 signal recognition particle 54kD	U51920	SEQ ID-Nr. 18
19.	LASVSTVL	130-137 hemoglobin, alpha 2	AF230076	SEQ ID-Nr. 19
20.	VMAPRTLVL	3-11 HLA-A		SEQ ID-Nr. 20
21.	LLFDRPMHV	267-275 hnRNP M	L03532	SEQ ID-Nr. 21
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22.	MTSALPIIQK	62-71 adipose differentiation-related protein	X97324	SEQ ID-Nr. 22
23.	MAGDIYSVFR	349-358 adipose differentiation-related protein	X97324	SEQ ID-Nr. 23
24.	ETIPLTAEKL	115-124 cyclin D1/PRAD1	X59798	SEQ ID-Nr. 24
25.	DVMVGPFKLR	934-943 A kinase (PRKA) anchor protein 2	AJ303079	SEQ ID-Nr. 25
26.	TIIDILTKR	64-72 annexin A1	X05908	SEQ ID-Nr. 26
27.	TIVNILTNR	55-63 annexin A2	BC001388	SEQ ID-Nr. 27
28.	TIIDIITHR	385-393 annexin A6	J03578	SEQ ID-Nr. 28
29.	SIFDGRVVAK	107-116 putative membrane protein	AB020980	SEQ ID-Nr. 29
30.	STIEYVIQR	115-123 Sec23 (S. cerevisiae) homolog B	BC005032	SEQ ID-Nr. 30
31.	ELIKPPTILR	132-141 adaptor-related protein complex 3	AF092092	SEQ ID-Nr. 31

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33.	ETIGEILKK	95-103 hnRNP K	BC000355	SEQ ID-Nr. 33
34.	SLADIMAKR	86-94 ribosomal protein L24	BC000690	SEQ ID-Nr. 34

HLA-B*44 oder HLA-B*18

35.	EEIAFLKKL	229-237 vimentin	M14144	SEQ ID-Nr. 35
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38.	DEVKFLTV	191-198 annexin A4	M82809	SEQ ID-Nr. 38
39.	NENSLFKSL	935-943 clathrin, heavy polypeptide (Hc)	D21260	SEQ ID-Nr. 39
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42.	DEVKLPAKL	158-166 polymerase I and transcript release factor	AF312393	SEQ ID-Nr. 42
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44.	NEFSLKGVDF	86-95 ets-1	J04101	SEQ ID-Nr. 44
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46.	EERIVELF	306-313 signal transducer and activator of transcription 3	BC000627	SEQ ID-Nr. 46
47.	EEIREAFRVF	84-93 calmodulin 3	J04046	SEQ ID-Nr. 47
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51.	IETIINTF	12-19 calgranulin B	M26311	SEQ ID-Nr. 51
52.	KENPLQFKF	61-69/72-80 villin 2 (ezrin)/(radixin)	J05021/ L02320	SEQ ID-Nr. 52
53.	DEVRTLTY	41-48 hnRNP methyltransferase, S. cerevisiae-like 2	Y10807	SEQ ID-Nr. 53
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55.	EEVLIPDQKY	385-394 F-box and leucine-rich repeat protein 3A	AF126028	SEQ ID-Nr. 55
56.	DEGRLVLEF	163-171 sterol O-acyltransferase 1	L21934	SEQ ID-Nr. 56
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58.	VEVLLNYAY	83-91 NS1-binding protein	AF205218	SEQ ID-Nr. 58
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62.	EEFGQAFSF	77-85 MHC, class II, DP alpha 1	X03100	SEQ ID-Nr. 62
63.	VEAIFSKY	33-40 hnRNP C (C1/C2)	M29063	SEQ ID-Nr. 63
64.	DERTFHIFY	277-285 myosin, heavy polypeptide 10, non-muscle	M69181	SEQ ID-Nr. 64

65.	TEKVLAAVY	206-214 aldolase B, fructose-bisphosphate	K01177	SEQ ID-Nr. 65
66.	VESPLSVSF	159-167 hypothetical protein FLJ22318	AK025971	SEQ ID-Nr. 66
67.	SEAGSHTLQW	MHC-I		SEQ ID-Nr. 67
68.	DEGKVIRF	56-63 EST reading frame-1	BF431469	SEQ ID-Nr. 68

Patient RCC13

HLA-A*02

69.	ALAAVVTEV	frameshift, DDX3 reading frame +2	AF061337	SEQ ID-Nr. 69
70.	TLIEDILGV	209-217 transient receptor protein 4 associated protein	AL132825	SEQ ID-Nr. 70
71.	ALFGALFLA	2-10 phospholipid transfer protein	L26232	SEQ ID-Nr. 71
72.	VLATLVLLL	72-80 EST	AA483794	SEQ ID-Nr. 72
73.	TLDDLIAAV	325-333 hypothetical protein FLJ10042	AK000904	SEQ ID-Nr. 73
74.	YLDNGVVFV	316-324 damage-specific DNA binding protein 1 (127kD)	U18299	SEQ ID-Nr. 74
75.	SVFAGVVGV	581-589 guanylate cyclase 1, soluble, alpha 3	U58855	SEQ ID-Nr. 75
76.	SLINVGLISV	48-57 acidic protein rich in leucines	BC000476	SEQ ID-Nr. 76
77.	ALADGVQKV	176-184 apolipoprotein L, 1)	AF323540	SEQ ID-Nr. 77

HLA-A*24

78.	TYGEIFEKF	107-115 NADH dehydrogenase (ubiquinone) 1, (B14.5b)	AF070652	SEQ ID-Nr. 78
79.	YYMIGEQKF	203-211 nicotinamide-n-methyltrans-ferase	U08021	SEQ ID-Nr. 79

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An isolated and/or purified tumor-associated peptide comprising the amino acid sequence YVDPVITSI (SEQ ID No. 1), the peptide having the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-1.

2. The peptide according to claim 1, wherein said peptide comprises one additional amino acid at the N- or/and C-terminus.

3. The peptide according to claim 1 or 2, wherein at least one amino acid is deleted.

4. The peptide according to any one of claims 1 to 3, wherein at least one amino acid is chemically modified.

5. The use of the peptide according to any one of claims 1 to 4, for the manufacture of a medicament for the treatment of tumor diseases and/or adenomatous diseases.

6. The use of the peptide according to any one of claims 1 to 4, for the production of a pharmaceutical composition for the treatment of tumor diseases and/or adenomatous diseases.

7. The use according to claim 5 or 6, wherein the disease is renal, breast, pancreatic, stomach, bladder and/or testicular cancer.

8. The use according to claim 6 or 7, wherein the peptide is used together with an adjuvant.

9. The use according to claim 6 or 7, wherein the peptide being used is bound to an antigen presenting cell.

10. The use of the peptide according to any one of claims 1 to 4, for in vitro labeling of leukocytes, in particular of T-lymphocytes.

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11. The use according to claim 10 for evaluation of the course of a therapy for a tumor disease.

12. The use of the peptide according to any one of claims 1 to 4 for the production of an antibody.

13. A pharmaceutical composition containing the peptide according to any one of claims 1 to 4.

14. A nucleic acid molecule encoding the peptide according to any one of claims 1 to 4.

15. A vector, comprising the nucleic acid molecule according to claim 14.

16. An isolated and/or purified cell that has been genetically altered using the nucleic acid molecule according to claim 14 or using the vector according to claim 15, to produce a peptide according to any one of claims 1 to 4.

IMMATICS BIOTECHNOLOGIES GMBH

WATERMARK PATENT & TRADE MARK ATTORNEYS

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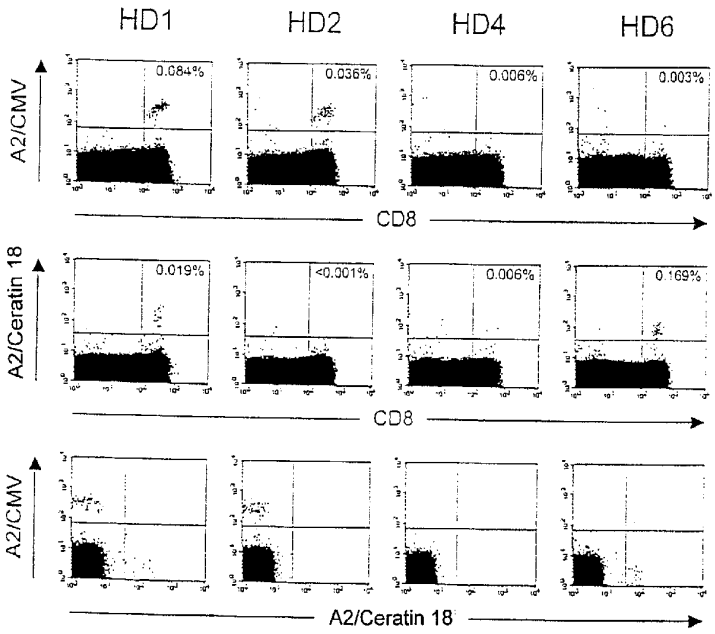

Fig. 1

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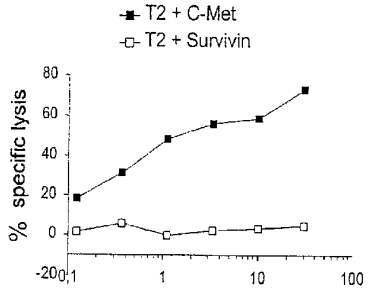
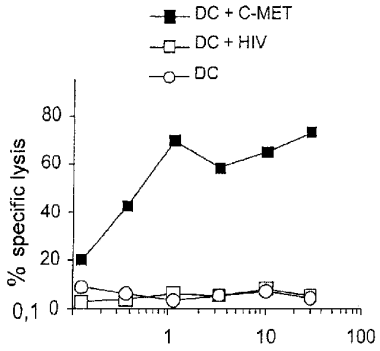


Fig. 2a



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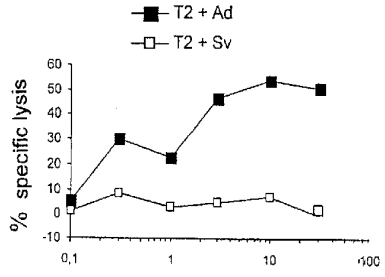

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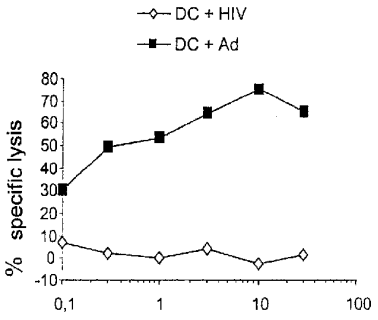

Fig. 2d

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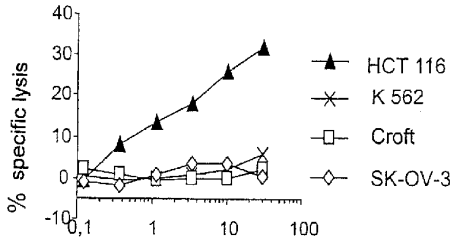

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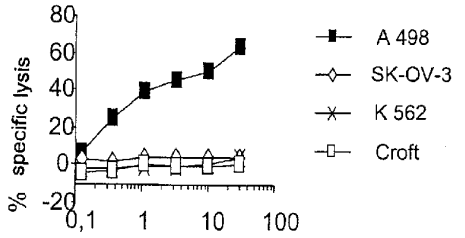

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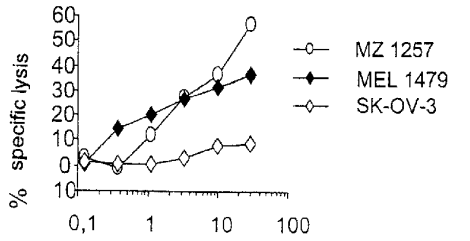

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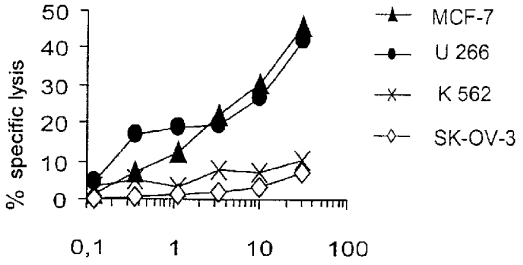

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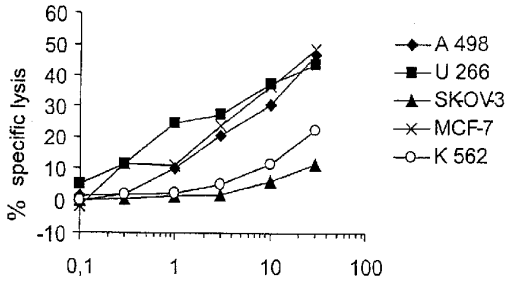

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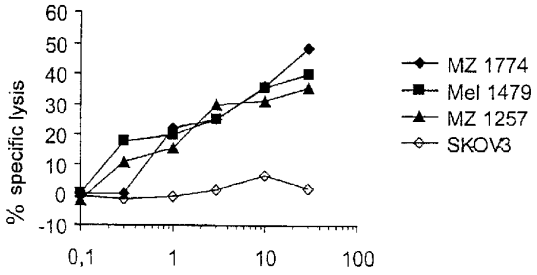

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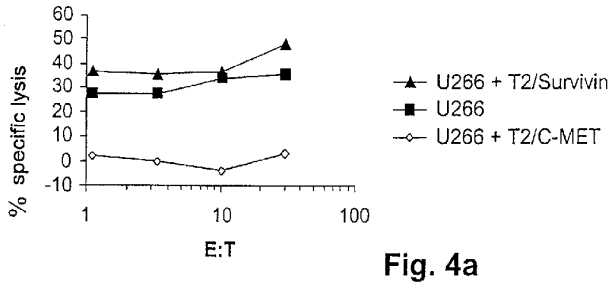

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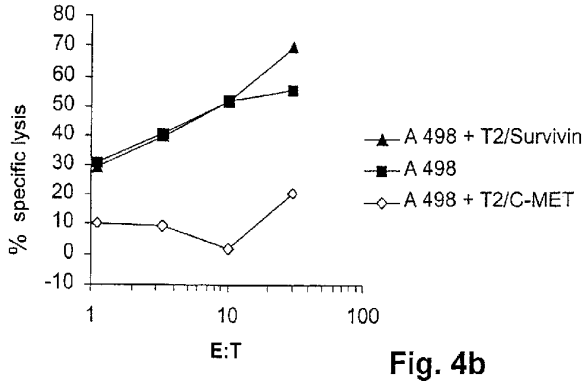

Fig. 4b

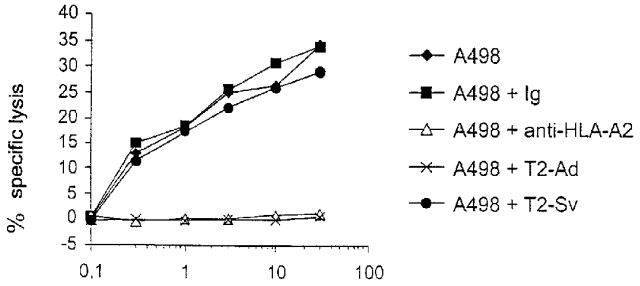

Fig. 4c

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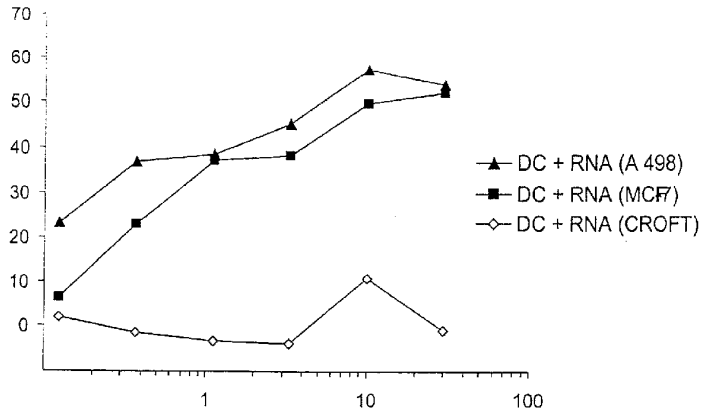

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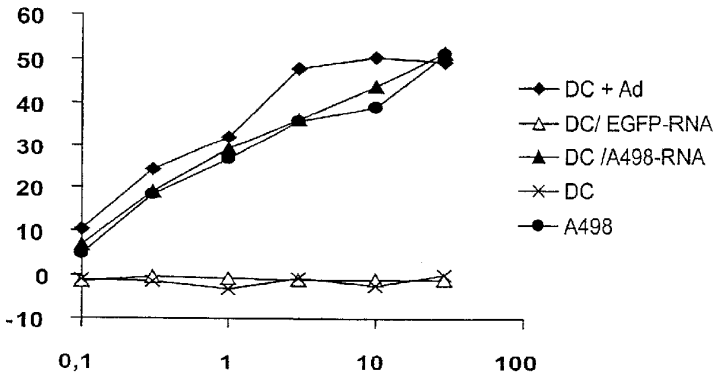

Fig. 5b

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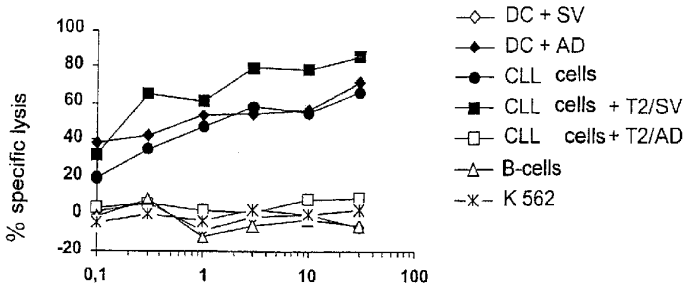


Fig. 6

Fig. 7

Detection of IMA901 TUMAPs on ccRCC samples

			TUMAP detected (+) or not detected (-) in mass spectrometric analysis								
No.	**ccRCC[1] sample**	**Tumor mass (g)**	**IMA-ADF-001**	**IMA-ADF-002**	**IMA-APO-001**	**IMA-CCN-001**	**IMA-GUC-001**	**IMA-K67-001**	**IMA-MET-001**	**IMA-MUC-001**	**IMA-RGS-001**
1	RCC208	33.9	+	+	+	-	+	+	+	-	-
2	RCC212	29.1	+	+	+	-	+	+	+	-	-
3	RCC294	9.8	+	+	+	-	+	+	+	-	-
4	RCC284	9.1	+	+	+	-	+	+	+	-	-
5	RCC202	7.0	+	+	+	-	+	+	+	-	-
6	RCC172	6.4	+	+	+	-	+	+	+	-	-
7	RCC197	6.1	+	+	+	-	+	+	+	-	-
	Total detected[2]		**7**	**7**	**7**	**0**	**7**	**7**	**7**	**0**	**0**

[1] ccRCC clear cell renal cell carcinoma

[2] TUMAP detected in x of 7 ccRCC

Fig. 8

Summary of vaccine-induced T cell responses (ITT/PP; N=27)

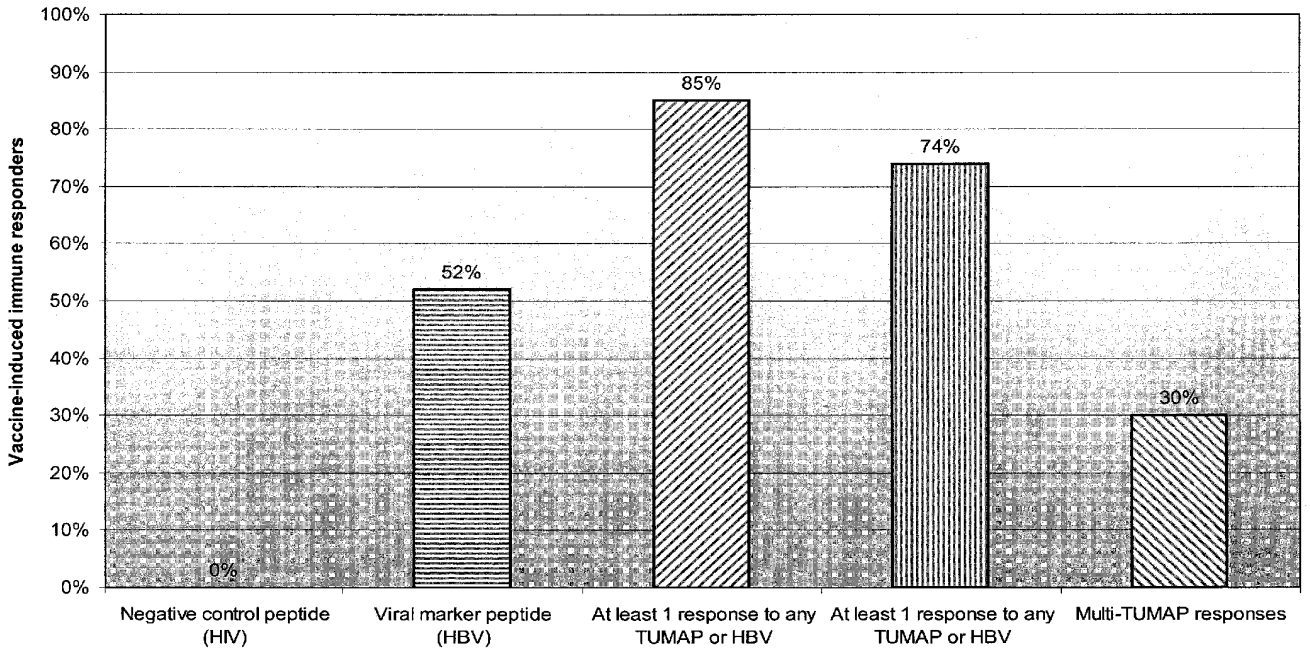
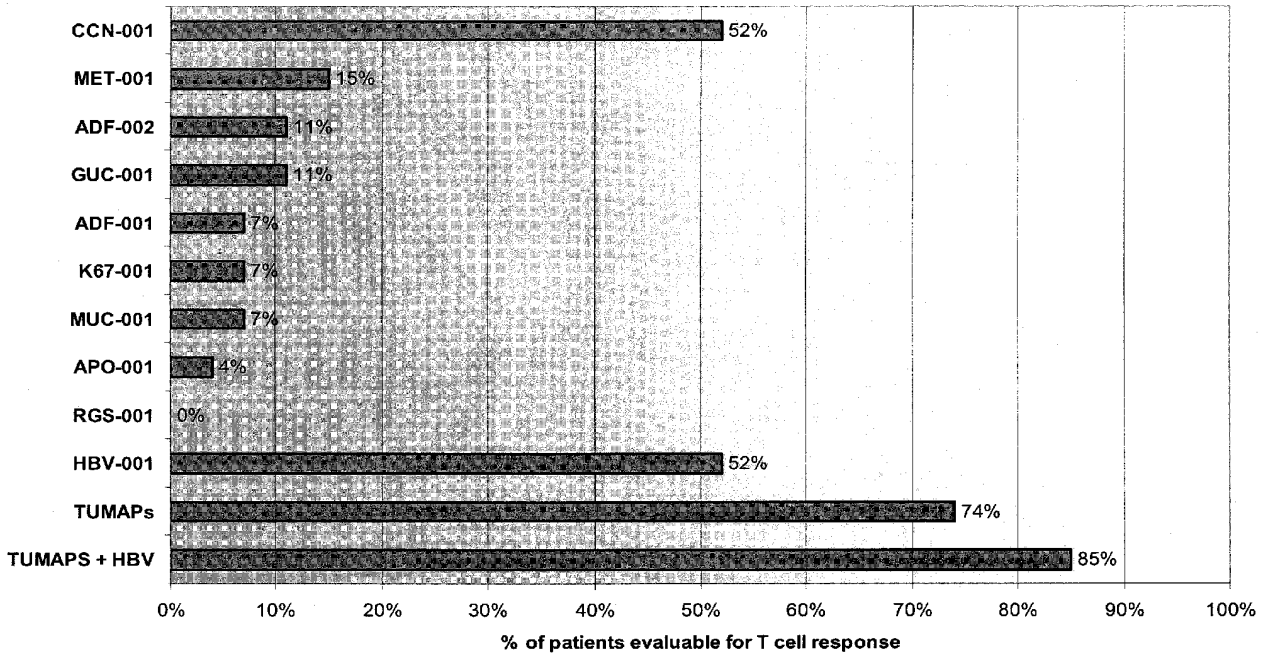


Fig. 9

Vaccine-induced single-peptide responses (ITT/PP; N=27



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Asp Glu Arg Thr Phe His Ile Phe Tyr
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Val Leu Ala Thr Leu Val Leu Leu Leu
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Thr Leu Asp Asp Leu Ile Ala Ala Val
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Tyr Leu Asp Asn Gly Val Val Phe Val
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Ser Val Phe Ala Gly Val Val Gly Val
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Tyr Tyr Met Ile Gly Glu Gln Lys Phe
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