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(54) **Title**: TREATING INFLAMMATORY SKIN DISEASES

(57) **Abstract**: A method for treating inflammatory skin disease comprises applying peripheral blood from a patient to an apheresis column loaded with a solid support comprising one or more binding reagents capable of specifically binding to a chemokine receptor, optionally the chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 immobilized directly or indirectly on the support thus removing one or more chemokine receptor, optionally CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells from the peripheral blood of the patient or subject. Various companion diagnostic methods and useful binding reagents are also described.

TREATING INFLAMMATORY SKIN DISEASES

FIELD OF THE INVENTION

The various embodiments of the present invention relates to products for and methods of treating inflammatory conditions, such as inflammatory skin diseases, in particular psoriasis and atopic dermatitis. Companion diagnostics are also described.

BACKGROUND OF THE INVENTION

Inflammatory skin disease defines a broad category of disorders characterised by mild to severe irritation and inflammation of the skin. These disorders can affect people of all ages, and include conditions such as acne, eczema or dermatitis, Rosacea and psoriasis. In most cases, there is no cure and patients with such conditions receive treatments to manage their symptoms.

Psoriasis and atopic dermatitis represent two of the commonest chronic inflammatory disorders of the skin, although, in both cases, the precise etiology of these diseases remains unknown. Psoriasis is characterised clinically by keratinocyte hyperproliferation and increased migration of inflammatory cells into the skin leading to epithelial hyperplasia and an excessive inflammatory response at the site of psoriatic plaques or lesions. Atopic dermatitis typically develops as an allergic reaction following exposure to irritants and/or environmental allergens and is associated with a dysregulated immune response occurring at the affected site.

In all inflammatory disorders of the skin, including psoriasis and atopic dermatitis, crosstalk between epidermal keratinocytes and cells of the immune system appears to play a central role in the pathogenesis of disease. For example, dendritic cells and effector T cells have been identified as key players in the development of psoriasis, and cytokines produced by these cells are known to stimulate keratinocyte proliferation and increase migration of inflammatory cells in the skin. In atopic dermatitis, cytokines released by immune cells trigger the inflammatory activation of keratinocytes.

Apheresis is a treatment used for depletion of blood components, such as antibodies, low-density lipoproteins (LDL) and blood cells. Leukapheresis is the apheresis treatment used for removal of white blood cells, leukocytes. The patient is connected to an extracorporeal blood circulating system; the blood is drawn from a vein in one arm, passed through a column device and returned into the other arm of the patient. WO2010/029317 describes apheresis columns useful for treating inflammatory conditions including a chemokine immobilised on a solid support.

SUMMARY OF THE INVENTION

Chemokines are a class of cytokine molecules involved in cell recruitment and activation in inflammation. Chemokines cause chemotaxis and activation of various subpopulations of cells in the immune system. The activity of chemokines is mediated primarily through tight

binding to their receptors on the surface of leukocytes. In certain embodiments the present invention is based on the realisation that the interaction between chemokines and cells expressing their receptors may be exploited for the treatment of inflammatory skin diseases. In particular, various inflammatory skin diseases, such as psoriasis and atopic dermatitis include an inflammatory component. The inventors have determined that targeting increased recruitment of specific chemokine receptor-expressing cells to the site of inflammation presents a new therapeutic approach to treat such conditions. Moreover, in such conditions, chemokine receptor expression on each cell may be increased again providing a therapeutic approach to treat such conditions. It is shown herein that subjects suffering from inflammatory skin disorders such as psoriasis exhibit increased frequency of chemokine receptor expressing cells in the peripheral blood, in particular CCR4 expressing cells such as CCR4 expressing T lymphocytes, compared to healthy controls. It is also shown herein that the CCR4 expressing cells can be removed using a suitable binding reagent, in particular MDC (in biotinylated form) immobilized on a suitable matrix. Similarly, it is shown herein that CXCR1 and CXCR2-expressing cells, in particular neutrophils, can be depleted in psoriasis patients using a suitable binding reagent, in particular IL-8, in biotinylated form, immobilized on a suitable matrix.

Thus, in certain embodiments the invention serves to reduce the recruitment of inflammatory leukocytes, which express characteristic chemokine receptors, and possibly express characteristic chemokine receptors at increased levels, to sites of inflammation linked to inflammatory skin diseases such as psoriasis and atopic dermatitis. This is achieved using specific binding reagents to capture specific chemokine receptor-expressing inflammatory leukocytes from the patient. Accordingly, in certain embodiments the invention provides in a first aspect a method for treating inflammatory skin disease comprising applying peripheral blood from a patient to an apheresis column loaded with a solid support comprising one or more binding reagents capable of specifically binding to one or more chemokine receptors, in particular to a chemokine receptor selected from CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23, immobilized directly or indirectly on the support thus removing one or more chemokine receptor, in particular one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23, expressing cells from the peripheral blood of the patient. The peripheral blood from which the chemokine receptor expressing cells have been removed may then be returned to the patient in order to complete the treatment. The invention may thus rely on a continuous extracorporeal circuit in some embodiments. Alternatively, the invention may comprise steps of obtaining peripheral blood from the patient, applying the peripheral blood to the column and subsequently returning the peripheral blood from which the chemokine receptor expressing cells have been removed to the patient.

As shown herein, suitable binding reagents can be immobilized onto a solid support, either directly or indirectly, to generate an apheresis column suitable for capturing relevant chemokine receptor-expressing cells. Where increased levels of chemokine receptor expression are observed, such cells may be preferably removed from the peripheral blood

using the columns of the various embodiments of the invention. Thus, the methods of the various embodiments of the invention may preferably target one or more of CCR4hi, CXCR1hi, CXCR2hi, CCR2hi, CCR6hi, CCR3hi, CCR5hi, CCR1hi and CCR9hi cells as defined herein for removal from the peripheral blood. "High" expression may be determined according to standard flow cytometry techniques. The level may be measured relative to levels of expression of the chemokine receptor in cells taken from a healthy subject. The attached Figure 15 provides an example of a gating strategy.

Herein, reference to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23 is intended to encompass selection of any one or more, up to all, of the chemokine receptors listed. In addition, the combination of CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23 is explicitly contemplated as a separate grouping, to include any one or more of CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23.

In other embodiments the invention further provides a binding reagent capable of specifically binding to one or more chemokine receptors, in particular to a chemokine receptor/the chemokine receptor selected from CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23, for use in the treatment of inflammatory skin disease, wherein the one or more binding reagents is immobilized, directly or indirectly, on a solid support contained within an apheresis column, to which is applied peripheral blood from a patient thus removing one or more chemokine receptor/ CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23, expressing cells from the peripheral blood of the patient. In certain embodiments the invention also provides for use of one or more binding reagents capable of specifically binding to a chemokine receptor/the chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23, for use in the manufacture of an apheresis column for treatment of inflammatory skin disease, wherein the one or more binding reagents is immobilized on a solid support contained within the apheresis column, to which is applied peripheral blood from a patient thus removing one or more of chemokine receptor/ CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23, expressing cells from the peripheral blood of the patient.

All embodiments described in respect of the methods of treatment of the various embodiments of the invention apply to these aspects *mutatis mutandis* and are not repeated for reasons of conciseness. Thus, the following discussion made with reference to the methods of treatment is also applicable to the medical use aspects of the various embodiments of the invention.

In certain embodiments the invention aims to treat a range of inflammatory skin diseases. By treatment is meant a reduction in the specific chemokine receptor expressing cells in the peripheral blood of the patient but the term patient may include both human and non-human animal subjects in some embodiments. The reduction may comprise a reduction in cells that express chemokine receptors, in particular one or more of CCR4, CXCR1, CXCR2, CCR2,

CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23, at increased levels in diseased patients. The patient is typically a human patient. In the context of the various embodiments of the present invention, this typically involves a reduction in one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, such as one or more of "$CCR4^{hi}$, $CXCR1^{hi}$, $CXCR2^{hi}$, $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$ and $CCR9^{hi}$"expressing cells, in the peripheral blood of the patient. The CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells comprise, consist essentially of or consist of monocytes, lymphocytes, neutrophils, macrophages, eosinophils, basophils and dendritic cells, in particular plasma dendritic cells, in certain embodiments. In specific embodiments, the cells removed in order to treat inflammatory skin disorders including psoriasis comprise T cells, in particular CCR4 expressing T cells. In other embodiments, the cells removed in order to treat inflammatory skin disorders including psoriasis comprise neutrophils, in particular CXCR1 and CXCR2 expressing neutrophils.

Monocytes are produced by the bone marrow from haematopoietic stem cell precursors called monoblasts. Monocytes may differentiate into macrophages or dendritic cells. Monocytes and their macrophage and dendritic cell progeny serve a number of functions in the immune system including phagocytosis, antigen presentation and cytokine production. Monocytes may be characterized with reference to expression of the cell surface marker CD14, optionally together with CD16. Classical monocytes may be characterized by high level expression of the CD14 cell surface receptor (CD14++ CD16- monocyte). Non-classical monocytes may be characterized by low level expression of CD14 and with additional co-expression of the CD16 receptor (CD14+CD16++ monocyte). Intermediate monocytes may be characterized by high level expression of CD14 and low level expression of CD16 (CD14++CD16+ monocytes). Macrophages are derived from monocytes and are responsible for protecting tissues from foreign substances. They are cells that possess a large smooth nucleus, a large area of cytoplasm and internal vesicles for processing foreign material. The term "macrophage" may refer to a monocyte-derived cell expressing one or more of the following cell surface markers CD14, CD11b, Lysozyme M, MAC-1/MAC-3 and CD68. The term macrophage includes both activated and un-activated macrophages. Activated macrophages may be characterized by expression of one or more of CD69, ENG, FCER2 and IL2RA, HLA-DR, CD86. Un-activated macrophages have not yet received activating signals through for example TLR receptors and therefore they express less activation markers on the cell surface which correlates with lesser maturation. M1 macrophages may be characterized by expression of one or more of $CD16^{+}CD32^{+}CD64^{+}$ and secrete mainly IL-23 and IL-1, TNF, IL-6 and high levels of IL-12 and in addition effector molecules such as iNOS and ROI. M1 macrophages have cytotoxic features as opposed to M2 macrophages. M2 macrophages may be characterized by expression of one or more of $SRA/B^{+}CD163^{+}MR^{+}CD14^{+}$ and express TGFβ, IL-10 and IL-1Ra. Tumour associated macrophages (TAMs) share many characteristics with the M2 macrophages and are considered as M2 polarised macrophages. The M1/M2 paradigm can also be found in monocyte subsets where $CD14^{+}CD16^{-}CXC3R1^{low}$ monocytes are considered the "inflammatory" subset and the $CD14^{low}CD16^{+}CXC3R1^{high}$ are "resident" monocytes.

The three major types of lymphocyte are T cells, B cells and natural killer (NK) cells. The term "T-lymphocyte" includes $CD4^+$ T cells such as T helper cells (Th1 cells and Th2 cells), and $CD8^+$ T cells such as cytotoxic T cells. Th1 cells may be characterized by expression of CCR5 and/or by production of IFN-γ. Th2 cells may be characterized by expression of CCR3 and/or by production of IL-4.

The claimed methods may, in particular, target eosinophils. Eosinophilia is an important component of allergic conditions and may be defined as the presence of more than 500 eosinophils/microlitre of blood. Thus, reducing numbers of circulating eosinophils represents an important therapeutic approach. Eosinophils, or eosinophil granulocytes, are white blood cells and represent an important immune system component. Along with mast cells, they also control mechanisms associated with allergy and asthma. They are granulocytes that develop during haematopoiesis in the bone marrow before migrating into blood.

The name "eosinophil" derives from the eosinophilic "acid-loving" properties of the cell. Normally transparent, it is this affinity that causes them to appear brick-red after staining with eosin, a red dye, using the Romanowsky method. The staining is concentrated in small granules within the cellular cytoplasm, which contain many chemical mediators, such as histamines and proteins such as eosinophil peroxidase, ribonuclease (RNase), deoxyribonucleases, lipase, plasminogen, and major basic protein. These mediators are released by a process called degranulation following activation of the eosinophil, and are toxic to both parasite and host tissues.

Eosinophils develop and mature in bone marrow. They differentiate from myeloid precursor cells in response to the cytokines interleukin 3 (IL-3), interleukin 5 (IL-5), and granulocyte macrophage colony-stimulating factor (GM-CSF). Eosinophils produce and store many secondary granule proteins prior to their exit from the bone marrow. After maturation, eosinophils circulate in blood and migrate to inflammatory sites in tissues in response to chemokines such as CCL11 (eotaxin-1), CCL24 (eotaxin-2), CCL5 (RANTES) and MCP1/4. Eosinophils may be activated by Type 2 cytokines released from a specific subset of helper T cells (Th2); IL-5, GM-CSF, and IL-3 are important for eosinophil activation as well as maturation. CD44 and CD69 have been shown to represent different types of cell-surface activation markers for human eosinophils. CD69 is absent from "fresh" eosinophils but expressed following activation (using cytokines). CD44 on the other hand is constitutively expressed but expression is significantly up-regulated in response to activation (Matsumoto et al., Am. J. Respir. Cell Mol. Biol., Volume 18, Number 6, June, 1998 860-866). Cell specific markers for eosinophils include CD9 and CDw125

Basophils may also be known as basophil granulocyte. In contrast to eosinophils, these leukocytes are basophilic, i.e., they are susceptible to staining by basic dyes. Basophils contain large cytoplasmic granules which obscure the cell nucleus under the microscope.

However, when unstained, the nucleus is visible and it usually has 2 lobes. Basophils store histamine, which is secreted by the cells upon stimulation.

Basophils have protein receptors on their cell surface that bind IgE, an immunoglobulin involved in macroparasite defense and allergy. It is the bound IgE antibody that confers a selective response of these cells to environmental substances, for example, pollen proteins or helminth antigens. Recent studies in mice suggest that basophils may also regulate the behavior of T cells and mediate the magnitude of the secondary immune response. Basophils may display an immunophenotype based upon expression (or lack thereof, indicated as "+" or "-" respectively of one or more of the following markers: FcεRI+, CD123, CD49b(DX-5)+, CD69+, Thy-1.2+, 2B4+, CD11bdull, CD117(c-kit)–, CD24–, CD19–, CD80–, CD14–, CD23–, Ly49c–, CD122–, CD11c–, Gr-1–, NK1.1–, B220–, CD3–, γδTCR–, αβTCR–, α4 and β4-integrin negative.

When activated, basophils degranulate to release histamine, proteoglycans (e.g. heparin and chondroitin), and proteolytic enzymes (e.g. elastase and lysophospholipase). They also secrete lipid mediators like leukotrienes, and several cytokines. Histamine and proteoglycans are pre-stored in the cell's granules while the other secreted substances are newly generated. Each of these substances contributes to inflammation. Recent evidence suggests that basophils are an important source of the cytokine, interleukin-4, perhaps more important than T cells. Interleukin-4 is considered one of the critical cytokines in the development of allergies and the production of IgE antibody by the immune system. There are other substances that can activate basophils to secrete which suggests that these cells have other roles in inflammation.

Dendritic cells (DCs) are the most important class of "antigen presenting cells" and as such, play a central role in the activation of the immune response. Immature DCs reside in tissues thoughout the body are may become activated in response to a variety of stimuli indicating the presence of antigen. Once activated, DCs can release a plethora of cytokines that activate cells of the innate immune system including eosinophils, macrophages and NK cells. Activated DCs also take up and process antigen and, as a result, actively transport antigen to secondary lymphoid organs. At these sites, antigen is presented on the surface of mature DCs, in the context of MHC class I and class II complexes, to immature T and B cells leading to both cellular and humoral immune responses.

DCs represent a heterogeneous class of cells of which there are two main subypes: myeloid DCs (mDCs) and plasmacytoid DCs (pDCs). These subtypes can be further divided into different subsets which may be classified according to the differential expression of a variety of cell surface markers. Importantly, the different subsets of DCs appear to drive different immune effector responses; for example, CD14+ mDCs appear to specialize in the generation of humoral immunity whereas BDCA3+ mDCs elicit CD8+ T cell responses. Furthermore, pDCs can be distinguished by the surface expression of CD2, and are typically

involved in the generation of anti-viral immune responses as a result of rapid type I interferon production.

The methods of the invention may involve specific binding interactions with any one or more of these further cell-surface (and cell-specific) markers in addition to the removal based upon binding to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23. Suitable binding reagents can be prepared to specifically bind to these cell-surface markers. The discussion of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 specific binding reagents thus applies *mutatis mutandis*.

CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressed on these aforementioned cells are bound by chemokines such as monocyte chemoattractant protein-1 (MCP-1), MCP-2, MCP-3, MCP-4, MCP-5, MIP-3alpha, CCL25, Chemerin, RANTES, MDC and/or IL-8. MCP-1 is a major chemoattractant for monocytes and memory T cells by means of their binding to its specific cell-surface receptor, CC-chemokine receptor-2 (CCR2). CCR2 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) receptor 2. The HGNC ID for this gene is 1603. The gene is located at chromosome position 3p21. The previous symbol and name for the gene is CMKBR2. Synonyms for this gene include CC-CKR-2, CD192, CKR2, FLJ78302 and MCP-1-R. The NCBI Reference Sequence is NM_001123041.2.

CCR1 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) receptor 1. The HGNC ID for this gene is 1602. The gene is located at chromosome position 3p21. The previous symbol and name CMKBR1, SCYAR1. Synonyms for this gene include CD191, CKR-1, MIP1aR. The Entrez Gene reference sequence for CCR1 is 1230 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCR3 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) receptor 3. The HGNC ID for this gene is 1604. The gene is located at chromosome position 3p21.3. The previous symbol and name for the gene is CMKBR3. Synonyms for this gene include CC-CKR-3, CD193 and CKR3. The Genbank reference sequence for CCR3 is AF247361.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCR5 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) receptor 5. The HGNC ID for this gene is 1605. The gene is located at chromosome position 3p21. The previous symbol and name for the gene is CMKBR5. Synonyms for this gene include CC-CKR-5, CD195 CKR-5, IDDM22 and CKR5. The Entrez Gene reference sequence for CCR5 is 1234 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCR6 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) receptor 6. The HGNC ID for this gene is 1607. The gene is located at chromosome position 6q27. The previous symbol and name for the gene is STRL22. Synonyms for this gene include BN-1, CD196, CKR-L3, CMKBR6, DCR2, DRY-6, GPR-CY4, GPR29. The Genbank reference sequence for CCR6 is U68030.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCR9 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) receptor 9. The HGNC ID for this gene is 1610. The gene is located at chromosome position 3p22. The previous symbol and name for the gene is GPR28. Synonyms for this gene include CDw199, GPR-9-6. The Genbank reference sequence for CCR9 is AJ132337.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CMKLR1 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine receptor-like 1, also known as ChemR23. The HGNC ID for this gene is 2121. The gene is located at chromosome position 12q24.1. The Genbank reference sequence for CMKLR1 is U79526.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCR4 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) receptor 4. The HGNC ID for this gene is 1605. The gene is located at chromosome position 3p24-p21.3. Synonyms for this gene include CC-CKR-4, CD194, ChemR13, CKR4, CMKBR4, k5-5. The Genbank reference sequence for CCR4 is X85740.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CXCR1 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-X-C motif) receptor 1. The HGNC ID for this gene is 6026. The gene is located at chromosome position 2q35. The previous symbol and name for the gene is CMKAR1, IL8RA, "interleukin 8 receptor, alpha". Synonyms for this gene include CD181, CDw128a, CKR-1. The Genbank reference sequence for CXCR1 is U11870.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CXCR2 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-X-C motif) receptor 2. The HGNC ID for this gene is 6027. The gene is located at chromosome position 2q35. The previous symbol and name for the gene is IL8RB, "interleukin 8 receptor, beta". Synonyms for this gene include CD182, CMKAR2. The Genbank reference sequence for CXCR2 is U11869.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

Treatment according to the various embodiments of the invention may result in alleviation or amelioration of symptoms, prevention of progression, regression of the condition, or complete recovery. Measurable parameters of successful treatment may be based upon, *inter alia*, the

measures normally used to assess the severity of psoriasis in dermatological practice. These include the proportion of the body surface area (BSA) affected and the Psoriasis Area and Severity Index (PASI). It is generally accepted that patients with a greater than 5% affected BSA have moderate to severe psoriasis and in most recent clinical trials a PASI above 10 or 12 has been used as an inclusion criteria to define moderate to severe psoriasis. An affected BSA greater than 10% and a PASI score of 12 or higher have been proposed as criteria for severe psoriasis for use in clinical trials. While some authors define moderate psoriasis as a PASI between 7 and 12 and severe psoriasis as a PASI higher than 12, others prefer to use the "rule of tens" criteria, which define severe psoriasis as a PASI higher than 10, an affected BSA of more than 10%, or a Dermatology Life Quality Index (DLQI) score greater than 10.

In specific embodiments, a single treatment is sufficient to cause a depletion of around 10%, 20%, 30%, 40%, 50%, 60% or 70%, or higher up to 80%, 90%, 95% or more, or any range of values between and including these amounts, of one or more of the specific chemokine receptor, in particular CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23, expressing cells from the peripheral blood of the patient. In specific embodiments, at least around 50% depletion is achieved in a single treatment. Thus, successful treatment may be defined with reference to depletion of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells. Treatment may lead to depletion of between approximately 100 and 500 million CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23, expressing cells, such as monocytes, dendritic cells and T lymphocytes, in certain embodiments and more particularly to about 100, 150, 200, 250, 300, 350, 400, 450, or 500 million CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23 expressing cells. In specific embodiments, the cells removed in order to treat inflammatory skin disorders including psoriasis comprise T cells, in particular CCR4 expressing T cells. In other embodiments, the cells removed in order to treat inflammatory skin disorders including psoriasis comprise neutrophils, in particular CXCR1 and CXCR2 expressing neutrophils.

By binding to the column through the binding reagent-chemokine receptor interaction, chemokine receptor expressing cells are immobilized. These immobilized cells express further unoccupied chemokine receptors, which may be of the same or different type to those used for capture. These additional chemokine receptors may permit circulating chemokines which contribute to the inflammatory condition to be captured from the peripheral blood. Thus, a reduction in circulating (specific) chemokine levels may provide a measure of successful treatment.

The duration of treatment may be readily determined by one skilled in the art and will depend upon factors such as the flow rate of the peripheral blood. Duration of treatment may be tied into monitoring of the treatment itself, with the treatment considered complete once a measurable parameter of treatment has reached a defined threshold. Any suitable parameter may be employed as discussed herein. Thus, for example, treatment may be considered complete when a reduction in one or more of CCR4, CXCR1, CXCR2, CCR2,

CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, such as a 50% reduction in one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, has been achieved. The apheresis system may be operated at a flow rate of around 10-80 mL/min, or more specifically between around 20-70 mL/min, or between around 30-60 mL/min. In specific embodiments, the treatment is performed for a period of around 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110,120 etc., or any range of values between and including these amounts, minutes. The treatment is typically not aimed to remove all of the cells expressing the chemokine receptor in the peripheral blood, as a basal level of those cells is required in healthy subjects. However, it has been found that only low blood volumes need to be applied to the columns of the various embodiments of the invention in order to achieve effective levels of depletion of the chemokine receptor-expressing cells. Thus, in certain embodiments, around 10-80% or more specifically around 20, 30, 40 or 50%, or any range of values between and including these amounts, of the patient's blood is applied to the column in a single treatment. The volume of blood circulated through the apheresis column or system may be in the region of around 1000-3000ml, such as around 1000, 1200, 1400, 1600, 1800 or 2000ml or any range of values between and including these amounts. The treatment may be considered complete once this volume of blood has been circulated. The patient may be administered anticoagulants prior to each treatment session. A suitable solution, such as a sterile saline solution, optionally including an anticoagulant such as Heparin, may be used for priming the apheresis (extracorporeal) system. An additional volume of anticoagulant may be added to the circuit at the start of each treatment session, for example as a bolus injection.

In certain embodiments the invention relies upon a binding reagent which is capable of specifically binding to a chemokine receptor. This specific binding reaction permits cells expressing the chemokine receptor to be removed from the peripheral blood of the patient when the blood is passed over the solid support upon or within which the binding reagent is immobilized. Specific chemokine receptors of interest include CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23. The binding reagent can be any binding reagent capable of specifically binding to the receptor in question. By "specific binding" is meant that the binding reagent displays sufficient specificity of binding and appropriate binding affinity/kinetics to permit removal of cells expressing one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 from the peripheral blood. Whilst it is not precluded that the binding reagent is capable of binding to other molecules, such as other chemokine receptors, the binding reagent will preferentially bind to cells expressing one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 and in particular to cells expressing increased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 (as defined further herein). The binding reagent capable of specifically binding to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 may be either an agonist or an antagonist of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23, respectively. As the disease condition relies upon up-regulation of expression of or signaling via CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5,

CCR1, CCR9 or ChemR23, in certain embodiments the binding reagent capable of specifically binding to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 is an antagonist of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23, respectively. Chemokines are typically, although not necessarily exclusively (particularly in the case of truncated or modified forms) agonists of their cognate receptor and serve to activate the cells expressing the relevant receptor, as would be appreciated by one skilled in the art. Antibodies against the relevant chemokine receptor are generally considered to be antagonists, as would be appreciated by one skilled in the art. Specific examples of binding reagents include proteins or polypeptides, such as antibodies and receptor ligands, in particular chemokines. The binding reagent may be a nucleic acid molecule in certain embodiments. In some embodiments, the nucleic acid is an aptamer. Nucleic acid aptamers are polynucleotides of approximately 15-40 nucleotides long. Nucleic acid aptamers can be made using the SELEX process (systemic evolution of ligands by exponential enrichment) or any other process known to those of skill in the art.

In other embodiments, the binding reagent may be a peptide, and in certain instances, a peptide aptamer. Peptide aptamers are artificial recognition molecules that consist of a variable peptide sequence inserted into a constant scaffold protein (Baines IC, Colas P. Peptide aptamers as guides for small molecule drug discovery. Drug Discov Today. 2006;11:334–341, incorporated herein by reference). A number of methodologies, such as phage display, ribosome display and yeast two-hybrid screening systems are available for screening a library of potential peptide-based binding agents. Similarly protein scaffolds based on domains such as fibronectins, ankyrin repeats, protein A, SH3 domains, lipocalins and ubiquitin can be used as the binding agent. Again a number of technologies such as phage display andribosome display are available for screening a library of protein – based binding agents. Similarly, libraries of candidate chemical compounds can be screened for specific binding to the relevant chemokine receptor using suitable screening techniques known in the art, which may be high throughput screens in certain embodiments. The candidate binding agent may be immobilized on a solid support and the ability of the agent to specifically retain cells expressing the chemokine receptor of interest or labelled chemokine receptors determined. A range of cell types may be applied to the solid supports to confirm specificity of binding, or alternatively a mixed sample (such as peripheral blood) may be applied to the solid support. Retention of the cell type of interest (expressing the appropriate chemokine receptor) can be confirmed to identify suitable binding agents. A range of small-molecule antagonists of CCR-2 are discussed by Xia M and Sui Z in Expert Opin Ther Pat. 2009 Mar;19(3):295-303 - Recent developments in CCR2 antagonists, and incorporated herein by reference.

In the context of the various embodiments of the present invention the term “chemokine” also comprises biotinylated or otherwise labelled chemokines. The term “chemokine” also comprises modified and truncated versions of the chemokine and chemokine fragments with the proviso that the modified or truncated form retains its ability to bind to its cognate receptor (and thus remains functional in the context of the various embodiments of the invention). The

chemokine does not necessarily need to retain biological activity as it is specific binding affinity for CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 that is required. In certain embodiments, the chemokine lacks biological activity, for example in terms of activation of the (CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23) receptor. Modifications may be made to improve protein synthesis, for example uniformity of product and yield. As known to those skilled in the art, exemplary modifications may comprise amino acid additions, substitutions, deletions or other modifications to one or more amino acids in the chemokine. Modifications may comprise substitution of the wild type amino acid with non-natural amino acids such as norleucine (NLeu) and derivatized amino acids such as pyroglutamic acid (pyroGlu). Such modifications may be made to minimize side-product formation during storage and use of the columns of the various embodiments of the invention. Modifications may be made to improve labelling, for example inclusion of a polyethylene glycol (PEG) spacer to facilitate biotinylation. The biotinylation and/or conjugation with fluorochromes or other labelling groups of the chemokine is performed in a manner which does not substantially affect the receptor binding capacity. Site specific biotinylation or other labelling is preferred as non-selective labelling of chemokines may compromise receptor binding activity. Bioinylation or other labelling is generally preferred at or towards the C-terminus of the protein as the inventors have found that modifications in this area are generally well tolerated (in terms of a minimal effect on receptor binding capability). Biotinylation may be carried out site-specifically at any suitable amino acid. Examples of suitable amino acids include lysine, diaminopropionic acid and ornithine. Generally, reference may be made to Natarajan S et al, Int. J. Pept. Protein Res., 1992, 40, 567-74; Baumeister B, Int. J. Peptide Res. And Therapeutics, 2005, 11, 139-141; Bioconjugate techniques 2nd edition, Greg T. Hermanson, incorporated by reference herein in its entirety.

Truncations may involve deletion of either N or C terminal amino acids as appropriate, or both. Typically, the truncated version will retain the residues required for the chemokine to fold correctly, for example to retain a chemokine fold structure, consistent with the requirement that a truncated version must retain the ability to bind to the relevant receptor (expressed by (on the surface of) a leukocyte). Chemokine molecules typically include disulphide bonds between the 1st and 3rd and 2nd and 4th cysteine residues respectively, as would be understood by one skilled in the art. Where sequences are presented herein, it is assumed that these disulphide bonds will form in the folded protein (unless otherwise stated). Truncated versions may comprise anywhere between 1 and 100 less amino acids, such as 1, 2, 3, 4, 5 etc amino acids, than the wild type amino acid sequence in certain embodiments. Of course, truncated versions may comprise further modification as detailed herein. The modified or truncated version may have 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more overall amino acid sequence identity with the full length wild type chemokine (where a deletion is counted as a difference in amino acid sequence) in certain embodiments. Over the common sequence between the molecules (i.e the amino acids that have not been deleted), there may be 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% amino acid sequence identity in certain embodiments. Sequence identity

may be determined using known algorithms, such as BLAST or GAP analysis (GCG Program) (applying default settings), which are freely available. Chemokines may lack the N-terminal signal peptide which is cleaved off during synthesis *in vivo*.

Specific chemokines useful in the various embodiments of the present invention include MCP-1, MCP-2, MCP-3, MCP-4, MCP-5, MIP-3alpha, CCL25, Chemerin and/or CCL5 (RANTES). MDC and/or IL-8 may also be useful in the present invention. Both MCP-1 and MCP-5 bind solely to the chemokine receptor CCR2 and so these chemokines may be preferred in some embodiments. Each chemokine is able to bind to a chemokine receptor implicated in inflammatory skin disease. More specifically, each of MCP-1, MCP-2, MCP-3, MCP-4, MCP-5, MIP-3alpha, CCL25, Chemerin, RANTES, MDC and/or IL-8 are useful for removing one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells from the blood of a patient. In specific embodiments, the chemokine is selected from MCP-1, MCP-2, MCP-3, MCP-4 and MCP-5 and the chemokine receptor is CCR2. In other embodiments, the chemokine is MIP-3alpha and the chemokine receptor is CCR6. In still further embodiments, the chemokine is RANTES and the chemokine receptor is selected from CCR3, CCR1, CCR5 or CCR9. In still further embodiments, the chemokine is MDC and the chemokine receptor is CCR4. In yet further embodiments, the chemokine is IL-8 and the chemokine receptor is selected from CXCR1 and CXCR2. The chemokines described in greater detail herein (with reference to the relevant figures and amino acid sequences, as set forth in the SEQ ID NOs) may each be applied according to the various embodiments of the present invention.

The modified and truncated chemokines described in greater detail herein (with reference to the relevant amino acid sequences, as set forth in the SEQ ID NOs and accompanying experimental examples) may each be applied according to the present invention. Such modified forms may instruct the skilled person regarding additional modified forms of the same and other chemokines which may be suitable for use in the invention.

Chemokines show variable sequence homology varying from less than 20% to over 90% but all share very similar tertiary structures consisting of a disordered N-terminus, followed by a long loop (the N-loop) that ends in a 3_{10} helix, a 3-stranded β-sheet and a C-terminal helix. The overlall topology is stabilsed by disulphide bonds. This common tertiary structure is a common feature of the chemokine protein family (Fernandez EJ annd Lolis E., Annu. Rev. Pharmacol. Toxicol., 202, 42, 469-99; Allen SJ et al, Annu. Rev. Immunol., 2007, 25, 787-820, incorporated herein by reference).

Truncations within this N-terminal region can maintain binding to the receptor but can lead to a change or loss of function (for examples Zhang YJ et al, J. Biol. Chem., 1994, 269, 15918, ; Gong J-H and Clark-Lewis I., *J. Exp. Med.*, 1995, 181, 631-640; Fernandez EJ annd Lolis E., Annu. Rev. Pharmacol. Toxicol., 202, 42, 469-99; Allen SJ et al, Annu. Rev. Immunol., 2007, 25, 787-820, each of which is incorporated herein by reference).

Truncations at the C-terminus of the chemokine can also be made and maintain receptor binding activity (Treating Inflammatory Disorders, Ola Winqvist and Graham Cotton, WO2010/029317, incorporated herein by reference in its entirety).

In other embodiments, fragments and variants of chemokines are used in the devices and methods as disclosed herein. More particularly, such fragments and variants retain the ability to specifically bind to their cognate chemokine receptor. Chemokines are known by those skilled in the art to share specific receptor binding domains, including a similar monomeric fold, characterized, for example, by a disordered amino-terminal domain, followed by a conserved core region, consisting of the so called "N-loop," three anti-parallel β-strands, and a carboxyl-terminal α-helix. While not being bound by theory, it is believed that the chemokine-chemokine receptor interaction is a two-step mechanism, in which the core of the chemokine interacts first with a binding site formed by the extracellular domains of the receptor, while another interaction is formed between the chemokine N terminus and a second binding site on the receptor in order to trigger receptor activation. Thus, a "fragment," such as a functional fragment of a chemokine is intended to mean a portion of the amino acid sequence of the protein that retains binding for its cognate receptor. The fragment may include, for example, the monomeric fold region, or portions thereof such as the amino-terminal domain, the conserved core region and/or the "N-loop," the anti-parallel β-strands, and/or the carboxyl-terminal α-helix or combinations and portions thereof.

Further, it is recognized that a polypeptide can be considerably mutated without materially altering one or more of the polypeptide's functions, for example, without altering specific binding and/or the folding of the protein. The genetic code is well known to be degenerate, and thus different codons encode the same amino acids. Even where an amino acid substitution is introduced, the mutation can be conservative and have no material impact on the essential functions of a protein (see for example, Stryer, Biochemistry 4th Ed., W. Freeman & Co., New York, NY, 1995). This includes, for example, the ability of the protein to bind and interact with other proteins, such as a truncated chemokine binding to its cognate receptor.

In some examples, part of a polypeptide chain can be deleted without impairing or eliminating all of its functions. For example, the deletion of between about 1 and about 20 amino acids on the C- and/or N-terminus, such as deletions of about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids at the C- and/or N-terminus, can result in a chemokine that retains function, such as specific binding of its cognate receptor. Such truncations can retain the full function of an entire protein, and/or can allow for retained functions such as protein-protein interactions as in the case of ligand-receptor interactions. Chemokines having deletions of a small number of amino acids, for example, less than about 20% (such as less than about 18%, less than about 15%, less than about 10%, less than about 8%, less than about 5%, less than about 2%, or less than about 1%) of the total number of amino acids in the wild type chemokine can also be used in the methods and devices disclosed herein. Moreover, insertions or additions can be made in the polypeptide

chain for example, adding epitope tags, without impairing or eliminating its functions (Ausubel et al., Current Protocols in Molecular Biology, Greene Publ. Assoc. and Wiley-Intersciences, 1998). Other modifications that can be made without materially impairing one or more functions of a polypeptide include, for example, in vivo or in vitro chemical and biochemical modifications or the incorporation of unusual amino acids. In some examples, a functional fragment of a chemokine may consist of about 10 or more, about 25 or more, about 50 or more, about 75 or more, about 100 or more, about 125 or more, about 150, about 175 or more, or about more or 200 or more amino acid residues of a chemokine amino acid sequence.

In some examples, the chemokine or a functional fragment thereof has an amino acid that has at least about 60% or 65% sequence identity, about 70% or 75% sequence identity, about 80% or 85% sequence identity, about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity over its full length as compared to a reference sequence, such as those detailed herein, for example using the NCBI Blast 2.0 gapped BLAST set to default parameters. Alignment may also be performed manually by inspection. One or more conservative amino acid modifications can also be made in the chemokine amino acid sequence, whether an addition, deletion or modification, that does not substantially alter the 3-dimensional structure of the polypeptide or its ability to bind to the cognate receptor. For example, a conservative amino acid substitution does not affect the ability of the chemokine to specifically bind its cognate receptor. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following six groups each contain amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

Peptides, such as chemokines and fragments thereof, can be modified by a variety of chemical techniques to produce derivatives having essentially the same activity or function—such as binding to a cognate receptor—as the unmodified peptides, and optionally having other desirable properties. For example, carboxylic acid groups of the protein, whether carboxyl-terminal or side chain, may be provided in the form of a salt of a pharmaceutically-acceptable cation or esterified to form a C1-C16 ester, or converted to an amide of formula NR1R2 wherein R1 and R2 are each independently H or C1-C16 alkyl, or combined to form a heterocyclic ring, such as a 5- or 6- membered ring. Amino groups of the peptide, whether amino-terminal or side chain, may be in the form of a pharmaceutically-acceptable acid addition salt, such as the HCl, HBr, acetic, benzoic, toluene sulfonic, maleic, tartaric and other organic salts, or may be modified to C1-C16 alkyl or dialkyl amino or further converted to an amide.

Hydroxyl groups of the peptide side chains can be converted to C1-C16 alkoxy or to a C1-C16 ester using well-recognized techniques. Phenyl and phenolic rings of the peptide side chains can be substituted with one or more halogen atoms, such as F, Cl, Br or I, or with C1-

C16 alkyl, C1-C16 alkoxy, carboxylic acids and esters thereof, or amides of such carboxylic acids. Methylene groups of the peptide side chains can be extended to homologous C2-C4 alkylenes. Thiols can be protected with any one of a number of well-recognized protecting groups, such as acetamide groups. Those skilled in the art will also recognize methods for introducing cyclic structures into the peptides of this disclosure to select and provide conformational constraints to the structure that result in enhanced stability. For example, a C- or N-terminal cysteine can be added to the peptide, so that when oxidized the peptide will contain a disulfide bond, generating a cyclic peptide. Other peptide cyclizing methods include the formation of thioethers and carboxyl- and amino-terminal amides and esters.

Peptidomimetic and organomimetic embodiments are also within the scope of the present disclosure, whereby the three-dimensional arrangement of the chemical constituents of such peptido- and organomimetics mimic the three-dimensional arrangement of the peptide backbone and component amino acid side chains, resulting in such peptido- and organomimetics of the proteins of this disclosure. For computer modeling applications, a pharmacophore is an idealized, three-dimensional definition of the structural requirements for biological activity. Peptido- and organomimetics can be designed to fit each pharmacophore with current computer modeling software (using computer assisted drug design or CADD). See Walters, “Computer-Assisted Modeling of Drugs”, in Klegerman & Groves, eds., 1993, Pharmaceutical Biotechnology, Interpharm Press: Buffalo Grove, IL, pp. 165 174 and Principles of Pharmacology Munson (ed.) 1995, Ch. 102, for descriptions of techniques used in CADD. Also included within the scope of the disclosure are mimetics prepared using such techniques.

Amino acids in a peptide, polypeptide, or protein generally are chemically bound together via amide linkages (CONH). Additionally, amino acids may be bound together by other chemical bonds. For example, linkages for amino acids or amino acid analogs can include CH2NH-, -CH2S-, -CH2-CH2 -, -CH=CH-- (cis and trans), -COCH2 --, -CH(OH)CH2-, and -CHH2SO- (These and others can be found in Spatola, in Chemistry and Biochemistry of Amino Acids, Peptides, and Proteins, B. Weinstein, eds., Marcel Dekker, New York, p. 267 (1983); Spatola, A. F., Vega Data (March 1983), Vol. 1, Issue 3, Peptide Backbone Modifications (general review); Morley, Trends Pharm Sci pp. 463-468, 1980; Hudson, et al., Int J Pept Prot Res 14:177-185, 1979; Spatola et al. Life Sci 38:1243-1249, 1986; Harm J. Chem. Soc Perkin Trans. 1307-314, 1982; Almquist et al. J. Med. Chem. 23:1392-1398, 1980; Jennings-White et al. Tetrahedron Lett 23:2533, 1982; Holladay et al. Tetrahedron. Lett 24:4401-4404, 1983; and Hruby Life Sci 31:189-199, 1982.

CCL2 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) ligand 2, also known as MCP-1. The HGNC ID for this gene is 10618. The gene is located at chromosome position 17q11.2-q21.1. The previous symbol and name for the gene is SCYA2 “small inducible cytokine A2 (monocyte chemotatic protein 1, homologus to mouse Sig-je)”. Synonyms for this gene include GDCF-2, HC11, MCP1, MGC9434, SMC-CF, “monocyte chemoattractant protein-1", "monocyte chemotactic and

activating factor", "monocyte chemotactic protein 1, homologous to mouse Sig-je", "monocyte secretory protein JE", "small inducible cytokine subfamily A (Cys-Cys), member 2". The Genbank reference sequence for CCL2 is BC009716.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCL8 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) ligand 8, also known as MCP-2. The HGNC ID for this gene is 10635. The gene is located at chromosome position 17q11.2. The previous symbol and name for the gene is SCYA8, "small inducible cytokine subfamily A (Cys-Cys), member 8 (monocyte chemotactic protein 2)". Another synonym for this gene is HC14. The Genbank reference sequence for CCL8 is X99886.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCL7 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) ligand 7, also known as MCP-3. The HGNC ID for this gene is 10634. The gene is located at chromosome position 17q11.2-q12. The previous symbol and name for the gene is SCYA6, SCYA7, "small inducible cytokine A7 (monocyte chemotactic protein 3)". Synonyms for this gene include FIC, MARC, MCP-3, MCP3, NC28, "monocyte chemoattractant protein 3", "monocyte chemotactic protein 3". The Genbank reference sequence for CCL7 is AF043338 as available on 13 June 2011, which is incorporated herein by reference in its entirety

CCL13 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) ligand 13, also known as MCP-4. The HGNC ID for this gene is 10634. The gene is located at chromosome position 17q11.2-q12. The previous symbol and name for the gene is SCYA6, SCYA7, "small inducible cytokine A7 (monocyte chemotactic protein 3)". Synonyms for this gene include FIC, MARC, MCP-3, MCP3, NC28, "monocyte chemoattractant protein 3", "monocyte chemotactic protein 3". The Genbank reference sequence for CCL13 is AJ001634 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

MCP-5 is a mouse chemokine in the CC chemokine family. It is also known as Chemokine (C-C motif) ligand 12 (CCL12) and, due to its similarity with the human chemokine MCP-1, sometimes it is called MCP-1-related chemokine. The gene for MCP-5 is found in a cluster of CC chemokines on mouse chromosome 11. The NCBI reference sequence for CCL12 is NC_000077.5 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCL20 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) ligand 20, also known as MIP-3alpha. The HGNC ID for this gene is 10619. The gene is located at chromosome position 2q33-q37. The previous symbol and name for the gene is SCYA20, "small inducible cytokine subfamily A (Cys-Cys), member 20". Synonyms for this gene include CKb4, exodus-1, LARC, MIP-3a, ST38. The Genbank

reference sequence for CCL20 is D86955.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCL5 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) ligand 5, also known as RANTES. The HGNC ID for this gene is 10632. The gene is located at chromosome position 17q11.2-q12. The previous symbol and name for the gene is D17S136E, SCYA5, "small inducible cytokine A5 (RANTES)". Synonyms for this gene include "beta-chemokine RANTES", MGC17164, RANTES, "regulated upon activation, normally T-expressed, and presumably secreted", "SIS-delta", SISd, "small inducible cytokine subfamily A (Cys-Cys), member 5", "T-cell specific protein p288", "T-cell specific RANTES protein", TCP228. The Genbank reference sequence for CCL5 is AF043341.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCL25 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) ligand 25. The HGNC ID for this gene is 10624. The gene is located at chromosome position 19p13.2. The previous symbol and name for the gene is SCYA25, "small inducible cytokine subfamily A (Cys-Cys), member 25". Synonyms for this gene include “Ck beta-15", Ckb15, TECK, "TECKvar", "thymus expressed chemokine". The Genbank reference sequence for CCL25 is U86358.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

RARRES2 is the gene symbol approved by the HUGO Gene Nomenclature Committee for retinoic acid receptor responder (tazarotene induced) 2, also known as Chemerin. The HGNC ID for this gene is 9868. The gene is located at chromosome position 7q36.1. Synonyms for this gene include "chemerin", HP10433, TIG2. The Genbank reference sequence for CXCR7 is U77594.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

CCL22 is the gene symbol approved by the HUGO Gene Nomenclature Committee for chemokine (C-C motif) ligand 22. The HGNC ID for this gene is 10621. The gene is located at chromosome position 16q13. The previous symbol and name for the gene is SCYA22, "small inducible cytokine subfamily A (Cys-Cys), member 22". Synonyms for this gene include A-152E5.1, ABCD-1, DC/B-CK, MDC, MGC34554, STCP-1. The Genbank reference sequence for CCL22 is U83171.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

IL8 is the gene symbol approved by the HUGO Gene Nomenclature Committee for interleukin 8, also known as CXCL8. The HGNC ID for this gene is 6025. The gene is located at chromosome position 4q13-q21. Synonyms for this gene include 3-10C, AMCF-I, b-ENAP, "chemokine (C-X-C motif) ligand 8", CXCL8, GCP-1, IL-8, K60, LECT, LUCT, LYNAP, MDNCF, MONAP, NAF, NAP-1, SCYB8, TSG-1. The Genbank reference sequence

for CXCL8 is Y00787.1 as available on 13 June 2011, which is incorporated herein by reference in its entirety.

An example of a chemokine of the various embodiments of the invention containing both modifications and a truncation and specifically adapted for use in the invention is described in detail herein. The truncated CCL25 corresponds to residues 1 to 74 of the full length mature protein (and thus lacks amino acids 75 to 127 and the N-terminal signal peptide of 23 amino acids) and thus retains the chemokine fold. In addition, a methionine to Norleucine substitution is incorporated, to prevent oxidation of the residue during chain assembly. The N terminal glutamine residue is substituted with pyroglutamine to permit uniformity of product during synthesis. Biotinylation is achieved via a PEG spacer at the ε-functionality of the lysine residue found at position 72. The amino acid sequence of the linear molecule (i.e. without the PEG spacer and biotin molecule at amino acid 72 shown) comprises, consists essentially of or consists of the amino acid sequence presented as SEQ ID NO: 9. The final protein may thus comprise, consist essentially of or consist of the amino acid sequence of SEQ ID NO: 11 (see Example 6 below).

Examples of suitable modified chemokines of the various embodiments of the invention containing modifications and/or truncations and specifically adapted for use in the invention are described in detail herein. MCP-1 has been produced with residue 75, which may be a lysine, as the site of biotinylation on the chemokine (numbering based upon the mature protein having the amino acid sequence of SEQ ID NO: 2). Biotinylation permits immobilization of MCP-1 on a solid support (via a biotin-avidin interaction). The basic amino acid sequence of MCP-1, including a 23 amino acid leader sequence is set forth as SEQ ID NO: 1. The amino acid sequence of the mature protein is set forth as SEQ ID NO: 2. The inventors have determined that chemokines may display improved binding properties where the chemokine is biotinylated via a spacer group. The spacer may prevent the biotin group from impacting on the binding affinity of the chemokine. Any suitable spacer group may be employed. Further modifications may provide the molecule with advantageous properties. The invention also relates to derivatives of truncated MCP-1 chemokines. The amino acid sequence of the truncated version is set forth as SED ID NO:3.

Accordingly, in certain embodiments the invention also provides a modified MCP-1 chemokine comprising, consisting essentially of or consisting of the amino acid sequence set forth as SEQ ID NO: 1, SEQ ID NO: 2 or SEQ ID NO: 3 in which one or more of the following modifications have been made:

a) the glutamine residue 1 of SEQ ID NO: 2 has been replaced with pyroglutamine

b) the C terminus is produced as an amide derivative (this may be achieved by synthesis on an amide linker)

c) the (C terminal region) residue at position 98 of SEQ ID NO: 1 or position 75 of SEQ ID NO:2 or position 67 of SEQ ID NO: 3, which may be a lysine or ornithine residue, is biotinylated, optionally via a spacer group, in order to permit immobilization of the chemokine on a solid support; and/or

d) the methionine residue at position 87 of SEQ ID NO: 1 or position 64 of SEQ ID NO: 2 or position 56 of SEQ ID NO: 3 has been replaced with norleucine.

The (C terminal region) amino acid, which may be a lysine residue or a functional equivalent, at position 98 of SEQ ID NO: 1 or position 75 of SEQ ID NO:2 or position 67 of SEQ ID NO: 3 may be biotinylated via a suitable spacer group, such as a polyethylene glycol (PEG) spacer group, in order to permit immobilization of the chemokine on a solid support. In specific embodiments, the PEG spacer is 3,6-dioxo aminooctanoic acid. The sequence and biotinylation of the modified MCP-1 chemokines of the invention are shown in figures 7 to 9 respectively. The modified MCP-1 chemokines may be agonists or antagonists of CCR2 activity. They can be tested for activity in a suitable assay, such as cell-based assays. In particular, agonist and antagonist properties may be determined in functional cell-based assay on human CCR2 receptor.

MCP-5 only binds CCR2 and should be selective in its removal of CCR2 expressing cells. The full length amino acid sequence, including the signal peptide, is set forth as SEQ ID NO: 4. The amino acid sequence of N-terminal processed MCP-5 chemokine is 82 amino acids long and is set forth as SEQ ID NO: 5. An amino acid sequence alignment suggests that MCP-5 has a C-terminal extension when compared to the amino acid sequence of MCP-1. The results of this alignment are shown in figure 10. C-terminal truncated versions of MCP-5 can thus be synthesised. This truncated version will comprise, consist essentially of or consist of MCP-5 residues 1-76, set forth as SEQ ID NO: 6.

Accordingly, the various embodiments of the invention also provide a modified MCP-5 chemokine comprising the amino acid sequence set forth as SEQ ID NO: 4, SEQ ID NO: 5 or SEQ ID NO: 6 in which the isoleucine residue at position 97 of SEQ ID NO: 4 or at position 75 of SEQ ID NO: 5 or SEQ ID NO: 6 has been replaced with lysine. In certain embodiments, the modified MCP-5 chemokine comprises, consists essentially of or consists of the amino acid sequence of SEQ ID NO: 7. The modified MCP-5 chemokine may be biotinylated at the lysine (or a functional equivalent) residue at position 97 of SEQ ID NO: 4 or at position 75 of SEQ ID NO: 5 or SEQ ID NO: 6. Biotinylation may be via a suitable spacer group. Specific examples of the spacer group include a PEG spacer, optionally 3,6-dioxo aminooctanoic acid. In some embodiments, the C terminus is produced as an amide derivative. This may be achieved by synthesis on an amide linker. In certain embodiments, the modified MCP-5 chemokine comprises, consists essentially of or consists of the sequence and biotinylation shown in figure 11. The modified MCP-5 chemokine may be an agonist or an antagonist of CCR2 activity. They can be tested for activity in a suitable assay, such as cell-based assays. In particular, agonist and antagonist properties may be determined in a functional cell-based assay on human CCR2 receptor.

An example of a chemokine of the various embodiments of the invention containing modifications and specifically adapted for use in the invention is described in detail herein (see Example 3 below). The modified CCL8 (MCP-2) corresponds to residues 1 to 76 of the

full length mature protein (and lacks the N-terminal signal peptide of 23 amino acids, which is cleaved off) and thus retains the chemokine fold. The Gln at the N-terminus of the protein is subject to pyroGlu formation under physiological conditions. Thus Gln1 of the sequence may thus be substituted with pyroglutamine to prevent mixed species of N-terminal Gln and pyroGlu being generated (SEQ ID NO: 18). This improves the yield of synthesis and ensures a homogeneous chemokine preparation through column manufacture and use. FmocLys(ivDde)-OH is incorporated as residue 75 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 19). The naturally occurring lysine at position 75 is modified through biotinylation. A PEG spacer may be incorporated between the ε-amino functionality and the biotin (SEQ ID NO: 20).

Thus, in certain embodiments the invention also relates to a modified chemokine comprising, consisting essentially of or consisting of the amino acid sequence of SEQ ID NO: 18:
XPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTKRGKEVCADPKE
RWVRDSMKHLDQIFQNLXP
X1 = pyroGlu (but may remain as Gln in some embodiments)
X75 = an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, e.g. K(PEG-Biotin).

Or SEQ ID NO: 20
XPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTKRGKEVCADPKE
RWVRDSMKHLDQIFQNLXP
X1 = pyroGlu (but may remain as Gln in some embodiments)
X75 = K(PEG-Biotin).

A further example of a chemokine of the various embodiments of the invention containing modifications and specifically adapted for use in the invention is described in detail herein (see Example 4 below). The modified CCL5 (RANTES) corresponds to residues 1 to 68 of the full length mature protein (and lacks the N-terminal signal peptide of 23 amino acids, which is cleaved off) and thus retains the chemokine fold. The single methionine (Met67) within the sequence is mutated to lysine, to mitigate against oxidation of this residue during the chain assembly (SEQ ID NO: 15). This Met to Lys substitution provides a lysine at position 67 which can be modified through biotinylation. FmocLys(ivDde)-OH is incorporated as residue 67 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 16). The biotinylated version comprises, consists essentially of or consists of the amino acid sequence of SEQ ID NO: 17.

Thus, in other embodiments the invention also relates to a modified chemokine comprising, consisting essentially of or consisting of the amino acid sequence of SEQ ID NO: 17:

SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVC
ANPEKKWVREYINSLEXS

X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG (e.g. K(Biotin))

A further example of a chemokine of the various embodiments of the invention containing modifications and specifically adapted for use in the invention is described in detail herein (see Example below). The modified CCL2 (MCP-1) corresponds to residues 1 to 76 of the full length mature protein (and lacks the N-terminal signal peptide of 23 amino acids, which is cleaved off) and thus retains the chemokine fold (SEQ ID NO: 12). The Gln at the N-terminus of the protein (Gln1) is substituted with pyroglutamine to prevent mixed species of N-terminal Gln and pyroGlu being generated. This improves the yield of synthesis and ensures a homogeneous chemokine preparation through column manufacture and use. FmocLys(ivDde)-OH is incorporated as residue 75 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 13). A suitable spacer, such as a PEG spacer, may be incorporated between the ε-amino functionality and the biotin. The biotinylated version comprises, consists essentially of or consists of the amino acid sequence of SEQ ID NO: 14.

Thus, in other embodiments the invention also relates to a modified chemokine comprising, consisting essentially of or consisting of the amino acid sequence of:
SEQ ID NO: 12:
XPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEIC
ADPKQKWVQDSMDHLDKQTQTPKT
X = pyroGlu
And/or SEQ ID NO: 14:
XPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEIC
ADPKQKWVQDSMDHLDKQTQTPXT
X1 = pyroGlu
X75 is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, optionally K(PEG-Biotin)

A further example of a chemokine of the various embodiments of the invention containing modifications and specifically adapted for use in the invention is described in detail herein (see Example 11 below). The modified CCL20 (MIP-3α) corresponds to residues 1 to 70 of the full length mature protein (and lacks the N-terminal signal peptide of 26 amino acids, which is cleaved off) and thus retains the chemokine fold (SEQ ID NO: 27). FmocLys(ivDde)-OH is incorporated as residue 68 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 28). The naturally occurring lysine at position 68 is modified through biotinylation. A PEG spacer may be incorporated between the ε-amino functionality and the biotin. The final protein may thus comprise, consist essentially of or consist of the amino acid sequence of SEQ ID NO: 29.

Thus, in other embodiments the invention also relates to a modified chemokine comprising, consisting essentially of or consisting of the amino acid sequence of SEQ ID NO: 29:

ASNFDCCLGYTDRILHPKFIVGFTRQLANEGCDINAIIFHTKKKLSVCANPK
QTWVKYIVRLLSKKVXNM
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, in particular K(PEG-Biotin)

A further example of a chemokine of the various embodiments of the invention containing modifications and specifically adapted for use in the invention is described in detail herein (see Example 7 below). The modified CCL22 (MDC) corresponds to residues 1 to 69 of the full length mature protein (and lacks the N-terminal signal peptide of 24 amino acids, which is cleaved off) and thus retains the chemokine fold (SEQ ID NO: 30). FmocLys(ivDde)-OH is incorporated as residue 66 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 31). The naturally occurring lysine at position 66 is modified through biotinylation. A PEG spacer may be incorporated between the ε-amino functionality and the biotin. The final protein may thus comprise, consist essentially of or consist of the amino acid sequence of SEQ ID NO: 32.

Thus, other embodiments the invention also relates to a modified chemokine comprising, consisting essentially of or consisting of the amino acid sequence of SEQ ID NO: 32:

GPYGANMEDSVCCRDYVRYRLPLRVVKHFYWTSDSCPRPGVVLLTFR
DKEICADPRVPWVKMILNXLSQ
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, especially K(PEG-Biotin)

A further example of a chemokine of the various embodiments of the invention containing modifications and specifically adapted for use in the invention is described in detail herein (see Example 3 below). The modified CXCL8 (IL-8) corresponds to residues 1 to 77 of the full length mature protein (and lacks the N-terminal signal peptide of 22 amino acids, which is cleaved off) and thus retains the chemokine fold. An amino acid residue capable of biotinylation, such as lysine or ornithine, is added as residue 78 (SEQ ID NO: 21). FmocLys(ivDde)-OH may be incorporated as residue 78 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 22). The additional amino acid, in particular lysine or ornithine, at position 78 is modified through biotinylation. A suitable spacer, such as a PEG spacer, may be incorporated between the ε-amino functionality and the biotin (SEQ ID NO: 23).

Thus, in other embodiments the invention also relates to a modified chemokine comprising, consisting essentially of or consisting of the amino acid sequence of SEQ ID NO: 21 or 23:

SEQ ID NO: 21 AVLPRSAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKL SDGRELCLDPKENWVQRVVEKFLKRAENSX
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG

SEQ ID NO: 23
AVLPRSAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKL SDGRELCLDPKENWVQRVVEKFLKRAENSK(PEG-Biotin)

A further example of a chemokine of the various embodiments of the invention containing truncations and modifications and specifically adapted for use in the invention is described in detail herein (see Example 3 below). The modified CXCL8 (IL-8) corresponds to residues 6 to 77 of the full length mature protein, with the first 5 N-terminal amino acids removed, (and lacks the N-terminal signal peptide of 22 amino acids, which is cleaved off) and thus retains the chemokine fold. An amino acid residue capable of biotinylation, such as lysine or ornithine, is added as residue 78 (SEQ ID NO: 24). FmocLys(ivDde)-OH may be incorporated as residue 78 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 25). The additional amino acid, in particular lysine or ornithine, at position 78 is modified through biotinylation. A suitable spacer, such as a PEG spacer, may be incorporated between the ε-amino functionality and the biotin (SEQ ID NO: 26).

Thus, in other embodiments the invention also relates to a modified chemokine comprising, consisting essentially of or consisting of the amino acid sequence of SEQ ID NO: 24 or 26:

SEQ ID NO: 24
SAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGREL CLDPKENWVQRVVEKFLKRAENSX
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG

SEQ ID NO: 26
SAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGREL CLDPKENWVQRVVEKFLKRAENSX
X is K(PEG-Biotin)

Chemokines useful in the various embodiments of the invention may be synthesised through any suitable means known in the art. Preferably, the chemokines are chemically synthesised as this facilitates modification and labelling etc. However, recombinant DNA based approaches may also be employed in combination with appropriate labelling and modification technologies as required. Thus, in certain embodiments the invention also provides a nucleic

acid molecule encoding the chemokines of the various embodiments of the invention. In certain embodiments the invention also relates to a vector containing such a nucleic acid molecule and a host cell containing the vector. The vector may additionally comprise a suitable promoter operably linked to the nucleic acid molecule, to facilitate transcription of the corresponding mRNA molecule. The host cell may be capable of expressing the protein by transcription and translation of the nucleic acid molecule encoding a chemokine of the various embodiments of the invention.

The chemokines useful in the various embodiments of the invention can be biotinylated by methods known in the art such as described in WO 00/50088 A2, which is incorporated herein by reference in its entirety. As indicated above, site-specific labelling of the chemokines of the various embodiments of the invention is preferable, although any labelling technique which does not significantly affect the receptor-binding capacity of the chemokine may be employed. Various site-specifically biotinylated chemokines and native chemokines are available commercially, for instance from Almac, Craigavon, UK. In specific embodiments the one or more chemokines are biotinylated via a spacer group. The spacer may be employed to prevent the biotin group from impacting on the activity of the chemokine, in particular binding of the chemokine to its cognate receptor. Any suitable spacer that facilitates retention of receptor binding properties of the chemokine may be employed in the various embodiments of the invention. Thus, in the specific embodiments described above, spacers other than PEG spacers may be employed as appropriate. In specific embodiments, the spacer is a polyethylene glycol (PEG) spacer. PEG has been shown to be an effective spacer permitting attachment of biotin to the chemokine (which can then be immobilized on the solid support through interaction with streptavidin) without compromising receptor binding capability.

In the context of the present various embodiments of the invention the term “antibody” includes all immunoglobulins or immunoglobulin-like molecules with specific binding affinity for the relevant chemokine receptor (including by way of example and without limitation, IgA, IgD, IgE, IgG and IgM, combinations thereof, and similar molecules produced during an immune response in any vertebrate, for example, in mammals such as humans, goats, rabbits and mice). Specific immunoglobulins useful in the various embodiments of the invention include IgG isotypes. The antibodies useful in the various embodiments of the invention may be monoclonal or polyclonal in origin, but are typically monoclonal antibodies. Antibodies may be human antibodies, non-human antibodies, or humanized versions of non-human antibodies, or chimeric antibodies. Various techniques for antibody humanization are well established and any suitable technique may be employed. The term “antibody” also refers to a polypeptide ligand comprising at least a light chain or heavy chain immunoglobulin variable region which specifically recognizes and binds an epitope of an antigen, and it extends to all antibody derivatives and fragments that retain the ability to specifically bind to the relevant chemokine receptor. These derivative and fragments may include Fab fragments, $F(ab')_2$ fragments, Fv fragments, single chain antibodies, single domain antibodies, Fc fragments etc. The term antibody encompasses antibodies comprised of both

heavy and light chains, but also heavy chain (only) antibodies. In specific embodiments, the antibodies may be engineered so as to be specific for more than one chemokine receptor, for example bi-specific to permit binding to two different chemokine receptors. Suitable commercially available antibodies which bind to the chemokine receptors of interest are listed in table 1 below. They may or may not be labelled. General reference may be made to "Antibodies a laboratory manual: By E Harlow and D Lane. pp 726. Cold Spring Harbor Laboratory. 1988", which reference is incorporated herein in its entirety.

Antibody	Fluorophore	Supplier
CCR5	PE	Biolegend
CXCR1	APC	Biolegend
CCR6	PerCP Cy5.5	BD Biosciences
CCR4	PerCP Cy5.5	BD Biosciences
CCR9	APC	R&D Systems
CCR3	PE	Biolegend
CXCR2	APC	R&D Systems
CCR1	Alexa Fluor 647	Biolegend
CCR2	PerCP Cy5.5	Biolegend
ChemR23	APC	R&D Systems

Table 1. Commercially available fluorophore labelled antibodies against specific chemokine receptors

Anti-CCR2 antibodies are described for example in WO 2010/021697, incorporated herein by reference. Further examples of potentially useful antibodies include MLN-1202, an anti-CCR2 monoclonal antibody currently undergoing clinical trials (Millennium Pharmaceuticals).

The chemokine receptor expressing cells may thus be targeted using alternative binding agents, such as antibodies or other chemical compounds, as defined herein, rather than the natural chemokine binding partner. This approach is a new approach to treating inflammatory conditions.

Thus, in certain embodiments the invention also provides an apheresis column loaded with a solid support comprising a binding reagent capable of specifically binding to a chemokine receptor immobilized directly or indirectly on the support to permit removal of a cell expressing the chemokine receptor from the peripheral blood of a patient, wherein the binding reagent is not a chemokine. The binding reagent capable of specifically binding to the chemokine receptor may be an agonist or an antagonist of the chemokine receptor. In specific embodiments, the binding reagent capable of specifically binding to the chemokine receptor is selected from an antibody and a chemical compound.

In other embodiments the invention thus also provides a method for treating an inflammatory condition comprising applying peripheral blood from a patient/subject to an apheresis column as defined above (an apheresis column loaded with a solid support comprising a binding

reagent capable of specifically binding to a chemokine receptor immobilized directly or indirectly on the support to permit removal of a cell expressing the chemokine receptor from the peripheral blood of a patient, wherein the binding reagent is not a chemokine) thus removing chemokine receptor expressing cells from the peripheral blood of the patient/subject. The method may comprise returning the blood depleted of the chemokine receptor expressing cells to the patient/subject.

Similarly, in other embodiments the invention provides a binding reagent capable of specifically binding to a chemokine receptor for use in the treatment of an inflammatory condition, wherein the binding reagent is immobilized on a solid support contained within an apheresis column as defined above (an apheresis column loaded with a solid support comprising a binding reagent capable of specifically binding to a chemokine receptor immobilized directly or indirectly on the support to permit removal of a cell expressing the chemokine receptor from the peripheral blood of a patient/subject, wherein the binding reagent is not a chemokine), to which is applied peripheral blood from a patient thus removing chemokine receptor expressing cells from the peripheral blood of the patient.

These aspects of the various embodiments of the invention may be integrated into the more focussed therapeutic aspects of the various embodiments of the invention (i.e. treating inflammatory skin diseases and various aspects thereof) and thus, the remainder of the disclosure, including all specific embodiments applies *mutatis mutandis*.

Solid support materials for immobilizing the binding reagents of the various embodiments of the invention are known in the art. “Solid support” refers to, for example, materials having a rigid or semi-rigid surface or surfaces, and may take the form of beads, resins, gels, microspheres, or other geometric configurations. A useful support material is one that does not activate blood cells so as to make them coagulate or adhere to the support as peripheral whole blood is applied to the device. In certain embodiments, a support treated with an agent to provide it with anti-coagulation properties, in particular a heparinized support is employed. Alternatively, the blood of the patient may be treated with an anti-coagulant such as heparin prior to application to the support. Useful support materials comprise high molecular weight carbohydrates, in particular carbohydrates having a molecular weight of 100 kDa or more, such as agarose, in particulate form, optionally cross-linked, and cellulose. Other preferred support materials are polymers, such as carboxylated polystyrene, and glass. The support of the various embodiments of the invention may be provided in the form of particles or fibres. The support particles may have regular form, such as spheres or beads, or irregular form. They may be porous or non-porous. A preferred average particle size of the support is from 50 µm to 2 mm. In certain embodiments Sepharose™, a cross linked, beaded-form of agarose, is used as column matrix. It is chosen for its optimal distribution capacity and can provide a large available area for affinity binding. Solid supports may be provided in the form of magnetic beads, with the specific binding reagent immobilized on the magnetic beads. Following capture of the (CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3,

CCR5, CCR1, CCR9 or ChemR23) chemokine receptor expressing cells from the blood, the beads can be removed from the blood with the aid of an appropriate magnetic separator.

Methods for immobilizing binding reagents on a solid support are known in the art. A binding reagent, such as a chemokine, antibody, peptide, nucleic acid or chemical compound, can be immobilized on the support in a direct or indirect manner. Immobilization can be by means of a suitable linker in some embodiments. A preferred method of indirect immobilization of a binding reagent, such as a chemokine, relies upon the interaction between biotin and avidin molecules. "Avidin" or "avidin molecule" refers to any type of protein that specifically binds biotin to the substantial exclusion of other (small) molecules that might be present in a biological sample. Examples of avidin include avidins that are naturally present in egg white, oilseed protein (e.g., soybean meal), and grain (e.g., corn/maize), and streptavidin, which is a protein of bacterial origin. Thus, biotinylation of the binding reagent and use of an avidin molecule such as streptavidin immobilized on the solid support allows reliable attachment of the binding reagent to the solid support according to methods known in the art. Specifically, such a method may comprise providing the binding reagent in biotinylated form, providing a solid support having streptavidin immobilized on its surface, contacting the support with an aqueous solution of the biotinylated binding reagent, and rinsing the support with an aqueous solvent. In addition, binding pair interactions, such as antibody - antigen interactions, may also be utilised for indirect immobilisation of binding reagent onto a support. In such embodiments the support may be derivatised with one member of a binding pair, such as an antibody or fragment or derivative thereof, as defined herein, which has known affinity for a particular peptide sequence or small molecule hapten. Incorporating the other member of the binding pair, such as an antigen, peptide sequence or the hapten onto or into the binding reagent facilitates immobilisation onto a solid support coated with the corresponding antibody or fragment or derivative thereof. Thus, the binding reagent may be modified to include the peptide sequence or hapten into the linear molecule or may be added as a side chain or label. Any suitable antibody-antigen pair may be employed. The antibody fragment or derivative may be any fragment or derivative that retains specific binding affinity for the appropriate antigen. Examples include Fab, $F(ab')_2$ fragments, scFV, VH domains, single domain antibodies (such as nanobodies), heavy chain antibodies and humanized version of non-human antibodies etc. Other high affinity interactions can be utilised for immobilisation of binding reagents, as long as the binding reagent can be synthesised or derivatised with one of the interacting partners and the solid support synthesised or derivatised with the other interacting partner without loss of binding activity (i.e. binding of the binding reagent to the appropriate chemokine receptor). Immobilization may occur via essentially the same interaction in reverse in some embodiments. Thus, the binding reagent which may be a chemokine for example, may be attached to an antibody as defined herein, and the solid support derivatised with the antigen. The chemokine may be produced as a fusion protein with the antibody.

Alternatively binding reagents, such as chemokines and antibodies, can be immobilised directly onto a solid support using bioconjugation techniques established in the field. For

example direct immobilisation of proteins onto cyanogen bromide activated solid supports via amino functionalities within the primary sequence of the protein. Alternatively, sulphydryl functionalities within proteins can be used to directly immobilise the protein to alkyl halide derivatised supports or supports containing free thiol functionalities. In further embodiments, proteins containing α-thioester functionalities can be directly immobilised on supports containing 1,2 amino thiol moieties (eg N-terminal cysteine) using the native chemical ligation reaction. Alternatively proteins modified with ketones and aldehydes can be immobilised on solid supports derivatised with hydrazinyl, hydrazide and aminoxy functionalities using hydrazone / oxime bond forming ligation reactions (and vice versa). Alternatively 'Click' chemistry can be used to immobilise proteins onto solid supports, whereby the protein and the support are derivatised with the appropriate mutually reactive chemical functionalities (azides and alkynes). In other embodiments Staudinger ligation chemistry can be used to immobilise appropriately derivatised proteins onto the appropriately derivatised solid supports.

The solid support is contained within or carried by the apheresis column. Thus, by "loaded" is meant that the column carries or contains the solid support in a manner such that (peripheral) blood can flow through the column in contact with the solid support. Thus, the solid support provides a matrix within the column through which blood flows, in continuous fashion in certain embodiments. This permits cells expressing the specific chemokine receptor to be removed from the blood passing through the column, such that blood exiting the column is depleted of the specific chemokine receptor-expressing cells. In specific embodiments, the apheresis column is loaded with a support comprising streptavidin immobilized on the support and one or more biotinylated binding reagents, such as chemokines, bound to the streptavidin on the support. The solid support may be comprised of a high-molecular weight carbohydrate, optionally cross-linked, such as agarose.

As discussed above, the binding reagent is coupled to the solid support. The relative amounts of binding reagent may be controlled to ensure that coupling between the solid support and the binding reagent will be immediate, minimising the risk of binding reagent decoupling from the solid support. Thus, it may be ensured that there is a relative excess of immobilization sites for the binding reagent on the solid support. Alternatively, or additionally, following immobilization of the binding reagent on the solid support, the solid support may be washed to remove any unbound binding reagent.

The apheresis column utilised in the various embodiments of the present invention acts as a leukapheresis treatment for conditions associated with inflammatory skin diseases. The column acts to specifically remove one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 -expressing monocytes, dendritic cells or T lymphocytes by exploiting the interaction between CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressed on the cell surface and a specific binding reagent immobilized on a solid support contained within or carried by the column. The overall column typically comprises, consists of, or consists essentially of three combined

components; 1) a housing which contains or carries 2) the solid support and 3) one or more binding reagents (immobilized thereon) which specifically bind one or more chemokine receptors. The housing may be manufactured from any suitable material for clinical use. In certain embodiments the housing is composed of a plastic material. The housing includes an in flow site for entry of blood and an out flow site for blood (depleted of target cells) to exit the column. The housing may be designed to maintain a continuous blood flow through the solid support matrix. The housing (as shown for example in Figure 3) may include a top portion which comprises a distribution plate (2) at the inflow site (1) to spread the blood evenly over the entire matrix area. The distribution plate may act as a first safety barrier preventing larger particles flowing through the column and into the patient. However, the distribution plate is not essential and may be removed in some embodiments to decrease the overall resistance in the system. The column may contain one or more safety filter units (3 and 4) placed at the inflow (1) and/or outflow (5) sites of the plastic housing. Such filter units may act to prevent particles larger than blood cells passing in and/or out of the column. The safety filter units may contain a plurality of filters, such as two, three or four filters designed to be a robust barrier and stop all particles larger than blood cells passing through the column. Inclusion of safety filters (3 and 4) at both ends of the column serves to minimize the risk of leakage of particles into the patient, including in the event that the device is incorrectly connected resulting in blood flow in the opposite direction to that intended. The safety filters may comprise of any suitable pore size to prevent particles larger than blood cells from passing through the column, as would be readily understood by one skilled in the art. Suitable filters are commercially available. In specific embodiments, the pore size of the filter(s) is between approximately 60µm and 100µm, more specifically approximately 80 µm. The solid support and binding reagent components are discussed in further detail herein.

The volume of the housing may be varied depending upon the blood volumes intended to pass through the column. Typically, the volume of the housing is between approximately 40ml and 200ml, more specifically 50ml to 150ml or 60ml to 120ml.

The column is generally applied in the form of an apheresis circuit. In this context, the overall system includes the apheresis column, tubing and an appropriate pump to pump the blood around the circuit. The system is illustrated in figure 4. The patient (1) is connected to the extracorporeal circuit via sterile needles to veins in the right and the left arms. A saline bag (3) is also connected and the saline solution is pumped with a suitable pump (2). Blood is drawn from one arm of the patient through the sterile tubing system by the blood pump (4) and passed through the column (6) and back to the patient. The tubing system may be connected to the column via any suitable coupling, such as standard dialysis luer-lock couplings. The couplings on the column may be colour-coded for correct assembly. For example, red tubing for inflow to the red column top and blue tubing for outflow back to the patient. An air detector (8) may be present in the circuit. Inlet pressure (5) and/or Pven sensors (7) may additionally be employed to monitor the pressure in the circuit.

An apheresis pump, such as the 4008 ADS pump manufactured by Fresenius Medical Care or the Adamonitor pump, may monitor the patient's inflow and outflow. The pump may also monitor the pressure in the extracorporeal circulation. The pump may be able to discriminate air by a bubble catcher and air detector. A clot catcher filter may be positioned inside the bubble catcher. The pump may also incorporate an optical detector to distinguish between light, e.g. saline solution or air present in the tubing system and dark e.g. blood present in the tubing system.

A schematic diagram of a suitable pump, showing the air detector and optical filter is shown in figure 5. If the pump system detects air bubbles and optical fluctuations or if extracorporeal pressure values are out of the set range, then the pump may stop immediately. Alternatively or additionally a visual/ audible alarm may be emitted.

The treatment methods of the various embodiments of the invention may thus rely upon an extracorporeal circuit. The methods may be considered as *ex vivo* or *in vitro* methods and be defined solely with reference to steps performed outside of the patient. In some embodiments, however, the method further comprises, prior to application of the blood to the column, collecting peripheral blood from the patient. In a further embodiment, the method further comprises, following the application of the blood to the column, infusing the blood depleted of (CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23 ,) chemokine receptor expressing cells to the patient. This is then a complete leukapheresis treatment method. Thus, a leukaphereis method, for treating inflammatory skin disease, comprises collecting peripheral blood from the patient; applying the peripheral blood to an apheresis column loaded with a solid support comprising one or more binding reagents capable of specifically binding to one or more chemokine receptors, in particular the chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23 immobilized directly or indirectly on the support thus removing one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells from the peripheral blood of the patient; and infusing the depleted blood (of chemokine receptor expressing cells) to the patient.

The peripheral blood may be continuously collected from the patient. Similarly, the depleted blood may be continuously infused to the patient, through use of an appropriate circuit as described herein. Thus, the support may be disposed in a column through which the blood is made to flow. This may be achieved using a suitable pump for example, as also described herein. Blood flow through the column enables the binding reagent(s) immobilized on the solid support to capture the cells expressing the chemokine receptor, thus depleting them from the blood and preventing their contribution to the inflammatory skin disease.

The methods of the various embodiments of the invention and binding reagents for use in the methods of the various embodiments of the invention may require that the patient has been selected for treatment on the basis of detecting an increase in the level of chemokine receptor, in particular, one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5,

CCR1, CCR9 and ChemR23 expressing cells in a sample obtained from the patient. Such companion diagnostic methods are described in greater detail herein and are based, for example, on the observation that CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and/or ChemR23, expression may be elevated in patients with an inflammatory skin disease. More specifically, it is shown herein that levels of CCR4 expressing leukocytes, in particular T cells, are increased in psoriasis patients (compared with healthy controls).

Thus, (in this context) in certain embodiments the invention also provides a method of diagnosing, monitoring progression of, or monitoring treatment of inflammatory skin disease comprising determining:
a) the levels of one or more of the chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells
b) levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23; and/or
c) levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23
in a sample obtained from a subject, wherein high levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, high levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 or high levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 or increased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells compared to control, increased levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 compared to a control or increased levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 compared to a control indicate the presence or progression of inflammatory skin disease. Levels of chemokine receptor expression, as opposed to cell numbers, may also be investigated as increased levels of chemokine receptor expression per cell may also be diagnostically relevant. The cells may be lymphocytes such as CCR4 expressing lymphocytes, in particular CCR4 expressing T cells. The cells may be neutrophils such as CXCR1 and/or CXCR2 expressing neutrophils.

“Diagnosing” is defined herein to include screening for a disease/condition or pre-indication of a disease/condition, identifying a disease/condition or pre-indication of a disease/condition and checking for recurrence of disease/condition following treatment. The methods of the various embodiments of the invention may also have prognostic value, and this is included within the definition of the term “diagnosis”. The prognostic value of the methods of the various embodiments of the invention may be used as a marker of potential susceptibility to inflammatory skin disease by identifying levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expression linked to conditions associated with an inflammatory skin disease. Thus patients at risk may be identified before the disease has a chance to manifest itself in terms of symptoms identifiable in the patient.

In certain embodiments, diagnosis may be made in conjunction with other objective indicators of inflammatory skin disease. Thus, in specific embodiments, diagnosis is made in conjunction with one or more of the following indicators: the proportion of the body surface area (BSA) affected and the Psoriasis Area and Severity Index (PASI).

"Monitoring progression of" includes performing the methods to monitor the stage and/or the state and progression of the inflammatory skin disease. Monitoring progression may involve performing the diagnostic methods multiple times on the same patient to determine whether the levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells are increasing, decreasing or remaining stable over a certain time period. This may be in the context of a treatment regime.

"Monitoring the success of a particular treatment" is defined to include determining the levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells before and after a treatment. The treatment is generally one aimed at treating inflammatory skin disease and may be a treatment according to one of the methods of the various embodiments of the invention as defined herein. Successful treatment may be determined with reference to a decrease in one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells as a result of, or following, the treatment. Thus, in such methods a level of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells is determined prior to treatment. This level is recorded and a further assessment made at a predetermined time following the treatment. The comparison of levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells permits the success of the treatment to be monitored. In specific embodiments, a single treatment is sufficient to cause a depletion of around 10%, 20%, 30%, 40%, 50%, 60% or 70%, or higher, up to 80%, 90%, 95% or more, or any range of values between and including these amounts, of one or more specific chemokine receptors, in particular one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23, expressing cells from the peripheral blood of the patient. In specific embodiments, at least around 50% depletion is achieved in a single treatment. Thus, successful treatment may be defined with reference to depletion of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells. Treatment may lead to depletion of between approximately 100 and 500 million of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, such as monocytes, in certain embodiments. Additional factors may be included to determine successful treatment. For example, a lack of increase in CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells following treatment may indicate successful treatment in terms of preventing further progression of the condition, optionally combined with an improvement in other markers or staging of the inflammatory skin disease.

In specific embodiments, the inflammatory skin disease is selected from psoriasis and atopic dermatitis.

The sample in which one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cell levels, levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 and/or levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 (defined as $CCR4^{hi}$, $CXCR1^{hi}$, $CXCR2^{hi}$, $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$) are determined may comprise any suitable tissue sample or body fluid sample. Generally, the test sample is obtained from a human subject. Typically, the sample is a blood sample, in particular a peripheral blood sample. The sample may comprise a skin sample, such as a pinch biopsy, in certain embodiments. The methods may involve determining levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing monocytes, dendritic cells, macrophages or lymphocytes in certain embodiments.

Levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, levels of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 (defined as $CCR4^{hi}$, $CXCR1^{hi}$, $CXCR2^{hi}$, $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$) may be determined according to any suitable method. For example, flow cytometry may be employed in order to determine the number of cells expressing CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 in the sample, to determine levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression and/or to identify levels of $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$ cells. Flow cytometric techniques are described herein and examples of commercially available antibodies suitably labelled for use in flow cytometry are set out in Table 1 for example. Alternatively, the method may involve steps of collecting and fixing the cells in the sample, followed by incubation with a suitable binding reagent that binds specifically to the CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 chemokine receptor expressing cells in the sample. Any suitable binding reagent, as defined herein, may be employed. For example, a CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 specific antibody may be employed. A wash step may be adopted following an incubation period to remove any unbound reagent. Suitable wash steps and incubation conditions would be well known to one skilled in the art. The binding reagent may be directly labeled in order to permit antibody binding to be directly determined. Alternatively a secondary binding reagent, such as an antibody, may be employed which binds to the first binding reagent and carries a label. Again, suitable incubation conditions and wash steps would be apparent to one skilled in the art. The primary and secondary binding reagents may form two halves of a binding pair. The binding interaction should not prevent the primary binding reagent binding to the CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 receptor expressing cells,

unless a competition assay is being employed. The two halves of a binding pair may comprise an antigen-antibody, antibody-antibody, receptor-ligand, biotin-streptavidin pair etc. in certain embodiments. Other techniques used to quantify chemokine (CCR2) receptor expressing cell levels, to quantify levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression and/or to quantify levels of CCR4hi, CXCR1hi, CXCR2hi, CCR2hi, CCR6hi, CCR3hi, CCR5hi, CCR1hi, CCR9hi or ChemR23hi cells include PCR-based techniques such as QT-PCR and protein based methods such as western blot. Quantitation may be achieved with reference to fixed cell lines carrying known numbers of various receptor expressing cells and/or known levels of receptor expression per cell. Such fixed cell lines are available commercially (for example ChemiScreen^{TM} cell lines from Millipore). Methods analogous to the treatment methods of the various embodiments of the invention may also be employed, with binding of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells to the solid support being determined following peripheral blood being passed through the column.

The levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, levels of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 (defined as CCR2^{hi}, CCR6^{hi}, CCR3^{hi}, CCR5^{hi}, CCR1^{hi}, CCR9^{hi} or ChemR23^{hi}) may be determined relative to a suitable control. When diagnosing an inflammatory skin disease, a threshold level of cells, level of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or level of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 (defined as CCR2^{hi}, CCR6^{hi}, CCR3^{hi}, CCR5^{hi}, CCR1^{hi}, CCR9^{hi} or ChemR23^{hi}) may be set at or over which a positive diagnosis is made. This threshold may be determined based upon measuring levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, levels of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 (defined as CCR4^{hi}, CXCR1^{hi}, CXCR2^{hi}, CCR2^{hi}, CCR6^{hi}, CCR3^{hi}, CCR5^{hi}, CCR1^{hi}, CCR9^{hi} or ChemR23^{hi}) in samples obtained from diseased patients and comparing these levels with levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, levels of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 (defined as CCR4^{hi}, CXCR1^{hi}, CXCR2^{hi}, CCR2^{hi}, CCR6^{hi}, CCR3^{hi}, CCR5^{hi}, CCR1^{hi}, CCR9^{hi} or ChemR23^{hi}) in samples obtained from healthy subjects.

In certain embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is diagnosed on the basis of levels of chemokine receptor expressing cells, such as CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells. A positive diagnosis may be made in subjects based upon the presence of greater than about

10%, greater than about 20%, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 55%, greater than about 60%, greater than about 65%, greater than about 70%, greater than about 75%, greater than about 80%, greater than about 85%, greater than about 90%, greater than about 95%, or more chemokine receptor expressing cells in the sample, as a percentage of total cells in the sample. In other embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is diagnosed on the basis of the presence of a about a 1.2 fold or greater increase, such as about a 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 10, 20, 50 or 100 or greater fold increase in chemokine receptor expressing cells, relative to healthy controls.

In specific embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is diagnosed on the basis of levels of CCR4 expressing cells, in particular lymphocytes such as T lympohcytes. A positive diagnosis may be made in subjects based upon the presence of greater than about 10%, greater than about 12% or greater than about 15% CCR4 expressing T cells in the sample, as a percentage of total cells in the sample. Inflammatory skin disease such as psoriasis or atopic dermatitis may also be diagnosed on the basis of the presence of a about a 1.2 fold or greater increase, such as about a 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 10, 20, 50 or 100 or greater fold increase in the specific chemokine receptor expressing cells, relative to healthy controls.

In certain embodiments, progression of inflammatory skin disease such as psoriasis or atopic dermatitis, which may be in the context of a treatment regime, is monitored on the basis of levels of chemokine receptor expressing cells at different time points. Progression of inflammatory skin disease such as psoriasis or atopic dermatitis may be indicated in subjects based upon an increase of greater than about 10%, such as an increase of greater than about 15%, greater than about 20%, greater than about 25%, greater than about 30%, greater than about 35%, greater than about 40%, greater than about 45%, greater than about 50%, greater than about 55%, greater than about 60%, greater than about 65%, greater than about 70%, greater than about 75% or more chemokine receptor expressing cells in the sample, as a percentage of total cells in the sample, compared to a sample taken from the same subject at an earlier time point. In other embodiments, progression of inflammatory skin disease such as psoriasis or atopic dermatitis is confirmed on the basis of the presence of a about a 1.2 fold or greater increase, such as about a 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 10, 20, 50 or 100 or greater fold increase in chemokine receptor expressing cells, relative to a sample taken from the same subject at an earlier time point.

In specific embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is monitored on the basis of levels of CCR4 expressing cells, in particular lymphocytes such as T lympohcytes. Progression of the disease, which may be in the context of a treatment regime, may be indicated in subjects based upon the presence of an increase of greater than about 3%, such as greater than about 4%, greater than about 5%, greater than about 6%, greater than about 7%, greater than about 8%, greater than about 10%, greater than about 15%, greater than about 20%, greater than about 25%, greater than about 30%, greater than

about 35%, greater than about 40%, greater than about 45% or more chemokine receptor expressing cells in the sample, as a percentage of total cells in the sample, compared to a sample taken from the same subject at an earlier time point. In other embodiments, progression of inflammatory skin disease such as psoriasis or atopic dermatitis is confirmed on the basis of the presence of a about a 1.2 fold or greater increase, such as about a 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 10, 20, 50 or 100 or greater fold increase in CCR4 expressing cells, in particular lymphocytes such as T lympohcytes, relative to a sample taken from the same subject at an earlier time point.

Regression or successful treatment may be monitored based upon similar decreases over various time points. For example, regression or successful treatment may be indicated in subjects based upon a decrease of about 3%, such as a decrease of about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 11%, about 15%, about 20%, about 25%, about 30%, about 35% or more chemokine receptor expressing cells in the sample, as a percentage of total cells in the sample, compared to a sample taken from the same subject at an earlier time point. In other embodiments, regression of inflammatory skin disease such as psoriasis or atopic dermatitis is confirmed on the basis of the presence of a about a 1.2 fold or greater decrease, such as about a 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 10, 20, 50 or 100 or greater fold decrease in chemokine receptor expressing cells, relative to a sample taken from the same subject at an earlier time point.

In specific embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is monitored on the basis of levels of CCR4 expressing cells, in particular lymphocytes such as T lympohcytes. Regression or successful treatment of the disease may be made in subjects based upon a decrease of about 2%, such as such as a decrease of about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 15% or more CCR4 expressing cells, in particular lymphocytes such as T lympohcytes in the sample, as a percentage of total cells in the sample or by a decrease of about 2%, such as such as a decrease of about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 15% or more CCR4 expressing cells, in particular lymphocytes such as T lympohcytes in the sample, as a percentage of total cells in the sample, compared to a sample taken from the same subject at an earlier time point. In other embodiments, regression of inflammatory skin disease such as psoriasis or atopic dermatitis is confirmed on the basis of the presence of a about a 1.2 fold or greater decrease, such as about a 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 10, 20, 50 or 100 or greater fold decrease in CCR4 expressing cells, in particular lymphocytes such as T lympohcytes, relative to a sample taken from the same subject at an earlier time point.

Suitable software is freely available (such as the R project for statistical computing) to perform the necessary statistical analysis of the data obtained to calculate a useful threshold. The threshold may be set to maximize sensitivity and/or specificity of the test. Performance of the test in these respects may be measured by plotting a receiver operating characteristics (ROC) curve (sensitivity versus specificity). The area under the curve provides an indication

of the overall performance of the test. Thus, once thresholds have been set for diagnosing the condition, a separate control experiment does not necessarily have to be run each time a sample is tested. Rather reference can simply be made to the pre-existing thresholds to determine the diagnosis. However, in certain embodiments, the sample is tested together with a control sample taken from a healthy subject to provide a comparator based upon essentially identical experimental conditions. The test sample is generally tested in parallel with the control sample. The test sample level of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, levels of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 (defined as $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$) can then be compared with that of the control sample to make the diagnosis. A control sample from a disease patient may also be tested in certain embodiments. Reference to controls permits relative levels ("high", "low" etc.) of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells in the test sample to be readily identified and the significance thereof interpreted. Reference to controls also permits relative levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression ("high", "low" etc.) within the cell population to be determined and the significance thereof interpreted. Such determination may, for example, indicate the average levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression per cell in the test sample.

Thus, in specific embodiments, high or higher levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells or high or higher levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expression, for example average CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression per cell, or high or higher levels of one or more of $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ and $ChemR23^{hi}$ cells correlate with active inflammatory skin disease or more active inflammatory skin disease. Similarly, lower or low levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, or low or lower levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expression, for example average CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression per cell, or low or lower levels of one or more of $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ and $ChemR23^{hi}$ cells may correlate with a lack of active inflammation or inflammatory skin disease. This may be defined as "less active disease". It can readily be envisaged that control samples may be assessed and levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, levels of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 (defined as $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$) determined across the range of severities of conditions associated with inflammatory skin disease. This may assist

in correlating the levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, levels of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 (defined as $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$) in the test sample with the relative severity of the condition.

When monitoring progression of, or monitoring treatment of inflammatory skin disease, the control samples may be taken from the subject at an earlier time point. They may, however, be based upon known reference values as discussed above. Thus, relative levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, relative levels of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression including relative levels of average CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression per cell or relative levels of $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$ cells may be with reference to samples taken from the same subject at a different point in time. In certain embodiments, decreased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, decreased relative levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expression including decreased relative levels of average CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression per cell, or decreased relative levels of one or more of $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$ cells correlate with successful treatment. The treatment may be any suitable treatment, but in specific embodiments is a treatment according to the various embodiments of the invention.

When monitoring progression of inflammatory skin disease, increased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells increased relative levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expression including increased relative levels of average CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expression per cell or increased relative levels of one or more of $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ and $ChemR23^{hi}$ cells may indicate the progression of condition or disease. Thus, if levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 and/or levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 (defined as $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$) are increased in a sample taken later than a sample from the same patient this may indicate progression of the condition.

Since the levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, levels of one or more of CCR4, CXCR1,

CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expression or levels of one or more of $CCR2^{hi}$, $CCR6^{hi}$, $CCR3^{hi}$, $CCR5^{hi}$, $CCR1^{hi}$, $CCR9^{hi}$ or $ChemR23^{hi}$ cells are diagnostically relevant, determining such levels in a sample obtained from a subject may influence treatment selection for that subject. Accordingly, in a related aspect the various embodiments of the invention provides a method of selecting a suitable treatment for inflammatory skin disease comprising determining:

a) the levels of one or more of the chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells

b) levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 ; and/or

c) levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23

in a sample obtained from a subject, wherein high levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, high levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 or high levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 or ChemR23 or increased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells compared to control, increased levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 compared to a control or increased levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 compared to a control, result in selection of a treatment as defined herein for treatment of the inflammatory skin disease. In certain embodiments, the chemokine receptor expressing cells are high chemokine receptor expressing cells, in particular, high CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells. The cells may be lymphocytes such as CCR4 expressing lymphocytes, in particular CCR4 expressing T cells. The cells may be neutrophils such as CXCR1 and/or CXCR2 expressing neutrophils.

In specific embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is treated on the basis of measuring levels of chemokine receptor expressing cells. Thus, a treatment according to the various embodiments of the invention may be applied based upon the presence of greater than about 10%, greater than about 15%, greater than about 20%, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 55%, greater than about 60%, greater than about 65%, greater than about 70%, greater than about 75%, greater than about 80%, greater than about 85%, greater than about 90%, greater than about 95%, or more chemokine receptor expressing cells in the sample, as a percentage of total cells in the sample. In other embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is treated according to the various embodiments of the invention on the basis of the presence of a about a 1.5 fold or greater increase, such as about a 2, 2.5, 3, 3.5, 4, 4.5, 5, 10, 20, 50 or 100 or greater fold increase in chemokine receptor expressing cells, relative to healthy controls.

In specific embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is treated on the basis of measuring levels of CCR4 expressing cells, in particular lymphocytes such as T lympohcytes. Thus, a treatment according to the various embodiments of the invention may be applied based upon the presence of greater than about 10%, greater than about 15% or greater than about 20% CCR4 expressing T cells in the sample, as a percentage of total cells in the sample. In other embodiments, inflammatory skin disease such as psoriasis or atopic dermatitis is treated according to the various embodiments of the invention on the basis of the presence of a about a 1.5 fold or greater increase, such as about a 2, 2.5, 3, 3.5, 4, 4.5, 5, 10, 20, 50 or 100 or greater fold increase in CCR4 expressing cells, in particular lymphocytes such as T lympohcytes, relative to healthy controls.

For the avoidance of doubt, all embodiments described in respect of the methods of the various embodiments of the invention apply to these aspects *mutatis mutandis* and are not repeated for reasons of conciseness. Specifically, inflammatory skin disorders may be indicated in conjunction with one or more of the following indicators:
the proportion of the body surface area (BSA) affected and the Psoriasis Area and Severity Index (PASI).The inflammatory skin disease may be selected from psoriasis and atopic dermatitis. In specific embodiments, the sample is a peripheral blood sample.

The methods and medical uses of the various embodiments of the invention thus can be tailored to the need of individual patients or groups of patients on the basis of the various diagnostic methods of the various embodiments of the invention. By removing from the circulation one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, such as monocytes, lymphocytes, neutrophils, macrophages, eosinophils, dendritic cells and basophils upregulated in various inflammatory skin diseases, an important factor in the inflammatory process of inflammatory skin disease can be controlled. The method of the invention may be effective in treating or reversing conditions such as psoriasis and atopic dermatitis.

The various embodiments of the invention will now be described in more detail by reference to the following non-limiting embodiments and examples:

DESCRIPTION OF THE FIGURES

FIG. 1a, 1b & 1c - the binding of biotinylized MCP-1 by CD4+, CD8+ T-cells and CD14+ monocytes respectively, obtained from peripheral blood of a healthy donor.
FIG. 1d, 1e & 1f - the binding of biotinylized CCL25 by CD4+, CD8+ T-cells and CD14+ monocytes respectively, obtained from peripheral blood of a healthy donor;
FIG. 1g, 1h & 1i- the binding of biotinylized CCL25 by CD4+, CD8+ T-cells and CD14+ monocytes respectively, obtained from peripheral blood of a patient with CD;

FIG. 2a – binding of MCP-1 to monocytes (dashed line) in peripheral blood taken from IBD patients. The graph represents a summary of four tests.

FIG. 2b – binding of CCR2-antibody to monocytes (line) in peripheral blood taken from IBD patients. The graph represents a summary of four tests.

FIG. 3 - The plastic house and top showing the distribution plate (2) and safety filter units (3 and 4).

FIG. 4 - The overall leukapheresis system

FIG. 5 - The pump with air detector and optical detector (4).

FIG. 6a – Results of in vitro depletion tests performed on the bMCP-1 coupled matrix showing ability to eliminate CCR2-expressing cells from blood from three healthy donors.
FIG. 6b – Results of in vitro depletion tests performed on the biotinylated RANTES coupled matrix showing ability to eliminate chemokine receptor-expressing cells from peripheral blood of a healthy donor.
FIG. 6c – Results of in vitro depletion tests performed on the biotinylated MIP-3a coupled matrix showing ability to eliminate CCR6-expressing lymphocytes from blood from three healthy donors.
FIG. 6d -Depletion of CCR9-expressing cell populations in one blood donor. Total cell populations are unaffected after the column passage.
FIG. 6e - Depletion of CCR9-expressing cell populations in one IBD patient. Total cell populations are unaffected after the column passage.

FIG. 7 – Sequence and biotinylation, via a spacer group, of mature protein MCP-1 derivative containing Gln to pyroGlu modification

FIG. 8 - Sequence and biotinylation, via a spacer group, of mature protein MCP-1 derivative containing Gln to pyroGlu modification and Met to Norleu substitution

FIG. 9 - Sequence and biotinylation, via a spacer group, of truncated MCP-1 derivative containing Met to Norleu substitution

FIG. 10 – Alignment of MCP-1 and MCP-5 amino acid sequences

FIG. 11 - Sequence and biotinylation, via a spacer group, of (C-terminal) truncated MCP-5 derivative containing Ile to Lys modification

FIG. 12 - Sequence and biotinylation, of RANTES derivative

FIG. 13 - HPLC of purified folded Biotin-TECK(Nleu).

FIG. 14 - Electrospray ionisation with tandem mass spectrometry (ES/MS) data of purified folded Biotin-TECK(Nleu).

FIG. 15 - example of gating criteria for CCR2 expressing monocytes.

FIG. 16 - Frequency of CCR4 expressing T cells in one patient with psoriasis. The expression of chemokine receptors and specific cell markers were analysed with flow cytometry.

FIG. 17 - Expression of CCR4 compared to binding of bMDC to blood T cells from a patient with psoriasis. The expression of chemokine receptors, binding of chemokine, and specific cell markers were analysed with flow cytometry.

FIG. 18 - Depletion of CCR4 expressing T cells with Sepharose Streptavidin-matrix conjugated with bMDC. Blood cells from a healthy control were incubated with biotinylated MDC-Sepharose Streptavidin-matrix. Unbound cells were retrieved by washing the matrix. The cells (After Depletion) were then analysed with flow cytometry and compared with cells that had not been incubated with bMDC-matrix (Before Depletion).

FIG. 19 - Expression of CXCR1 and CXCR2 on neutrophils from a patient with psoriasis. The expression of chemokine receptors, binding of chemokine and specific cell markers were analysed with flow cytometry.

FIG. 20 - Binding of the chemokine bIL-8 to neutrophils in blood from a psoriasis patient. Blood from a psoriasis patient was incubated with bIL-8 and analysed with flow cytometry. The neutrophils were characterized as CD16 positive cells.

FIG. 21 - Depletion of CXCR2 expressing neutrophils with Sepharose Streptavidin-matrix conjugated with bIL-8. Blood cells from a psoriasis patient were incubated with bIL-8 Sepharose Streptavidin-matrix. Unbound cells were retrieved by washing the matrix with Phosphate Buffer Saline. The cells (After Depletion) were then analysed with flow cytometry and compared with cells that had not been incubated with bIL-8-matrix (Before Depletion).

DESCRIPTION OF PREFERRED EMBODIMENTS

Patients with psoriasis and AD have an increased number of circulating CCR2 expressing monocytes or increased proinflammtory properties of CCR2 expressing monocytes compared to healthy controls. When investigating the skin from patients with psoriasis and AD there is a selective infiltration of CCR2 expressing monocytes in affected skin areas. To support this notion keratinocytes produce high amounts of MCP-1 thus recruiting CCR2 expressing cells.

The expression of RANTES is increased in psoriatic lesions, produced by the keratinocytes. Skin infiltrating T cell infiltrates are an important cell population involved in disease development. Supporting these ideas is that CCR6 deficient mice fail to develop IL-23 induced, IL-22 dependent psoriasis-like inflammation demonstrating the importance

recruitment of CCR6 expressing T cells for the development of the disease.. Moreover animal models of contact dermatitis can be abolished using RANTES antagonists.

It is shown herein that subjects suffering from inflammatory skin disorders such as psoriasis exhibit increased frequency of chemokine receptor expressing cells in the peripheral blood, in particular CCR4 expressing cells such as CCR4 expressing T lymphocytes, compared to healthy controls. It is also shown herein that the CCR4 expressing cells can be removed using a suitable binding reagent, in particular MDC (in biotinylated form) immobilized on a suitable matrix. Similarly, it is shown herein that CXCR1 and CXCR2-expressing cells, in particular neutrophils, can be depleted in psoriasis patients using a suitable binding reagent, in particular IL-8, in biotinylated form, immobilized on a suitable matrix.

EXAMPLES 1 and 2

Materials and methods

Isolation of peripheral blood leukocytes. Heparinized peripheral blood from healthy blood donors or inflammatory bowel disease (IBD) patients was fixed with 4% paraformaldehyde for 4 minutes, hemolyzed for 15 minutes with a 0.83 % ammonium chloride solution and washed twice in FACS buffer to obtain a suspension of blood leukocytes.

Chemokines. The leukocytes were incubated for 30 min in the dark at 4 ºC with biotinylated and Alexa647 Fluor® labeled chemokine (e.g. MCP-1) (in concentrations 10 ng/µL and 50 ng/µL). The cells were then washed with FACS-buffer and analyzed by flow cytometry. All chemokines used in the Examples were provided by Almac Sciences Scotland Ltd, Edinburgh, Scotland.

Flow cytometry assay. The flow cytometry assay was performed on a two laser FACS Calibur cytometer (BD Immunocytometry systems, San José, Ca, USA). Ten thousand cells were counted and analysed in each sample. For data analyses, Cell Quest Pro software from Becton Dickinson was used.

EXAMPLE 1 - *Binding of monocytes to MCP-1*. In the experiment with biotinylated MCP-1 it was found that about 90% of the monocytes obtained from peripheral blood of healthy donors had bound to the cytokine after 30 min of incubation (Fig. 1a), whereas CD4+ and CD8+ lymphocytes had not bound (Fig. 1b and 1c).

EXAMPLE 2 - Monocytes were investigated for their expression of CCR2 (FIG. 2b) and their ability to bind MCP-1 (FIG. 2a). CCR2 expression was noted an all monocytes with the majority of monocytes expressing high levels, using an anti-CCR2 antibody (FIG. 2b). The MCP-1 binding to monocytes shown in FIG. 2a corresponds to the $CCR2^{hi}$ expressing population shown in FIG. 2b. Thus, MCP-1 binds favourably to $CCR2^{hi}$ expressing cells.

EXAMPLE 3 - *Affinity of blood cells to CCL25*. In the experiment with biotinylated CCL25 it was found that neither T-cells (CD4+ lymphocytes; CD8+ lymphocytes) nor monocytes

(CD14+ monocytes) from the peripheral blood of a healthy donor (Fig. 1d, 1e and 1f) bound to the biotinylated chemokine. In contrast, about 80% of the CD8+ lymphocytes and about 90% of the CD4+ lymphocytes and the monocytes from a patient with Crohn's disease bound to CCL25 (Fig 1g, 1h and 1i).

EXAMPLE 4 - *Tailored leukapheresis*

COLUMN DESIGN AND PROPERTIES

Introduction

Apheresis is an established treatment used for depletion of blood components, such as antibodies, low-density lipoproteins (LDL) and blood cells. Leukapheresis is the apheresis treatment used for removal of white blood cells, leukocytes. The patient is connected to an extracorporeal blood circulating system; the blood is drawn from a vein in one arm, passed through a column device and returned into the other arm of the patient. Side effects of leukapheresis treatments are varying from mild events like headache, dizziness, hypotension, palpitation and flush seen in 0.1 to 5% of treated patients.

The column

The column is intended to be used as a leukapheresis treatment for inflammatory skin disease. It will specifically remove CCR2-expressing leukocytes, in particular monocytes, through the use of a binding reagent, more specifically an MCP-1, MCP-2, MCP-3, MCP-4 and/or MCP-5 containing resin, exploiting the CCR2-chemokine interaction. The column consists of three combined components, the plastic house, the streptavidin (SA) Sepharose™ BigBeads matrix and one or more of bMCP-1 bound to the matrix. The treatment is conducted using the same techniques as a standard apheresis procedure.

The plastic house (FIG. 3)

The plastic house, designed to keep a continuous blood flow through the matrix, consists of a transparent body and red-coloured top. The top has a distribution plate (2) at the inflow site (1) to spread the blood evenly over the entire matrix area. The plate is the first safety barrier preventing larger particles flowing through the column and into the patient. Safety filter units (3 and 4) are placed at the inflow (1) and outflow (5) sites of the plastic housing. The safety filter unit contains three filters designed to be a robust barrier and stop all particles larger than blood cells passing through the column. The plastic housing design is shown in Figure 3. The design with safety filters (3 and 4) at both ends of the column device will minimize the risk of leakage of particles into the patient, including in the event that the device is placed up side down with the blood flow in the opposite direction to that anticipated.

Streptavidin Sepharose™ BigBeads

The second component in the device is the affinity matrix called streptavidin Sepharose™ BigBeads (Sepharose™ GE Healthcare, Sweden). Sepharose™ is a cross linked, beaded-form of agarose, which is a polysaccharide extracted from seaweed. Sepharose™ and agarose are commonly used as column matrices in biomedical affinity techniques. It is

chosen for its optimal distribution capacity and can provide a large available area for affinity binding.

Binding reagent

Coupled to the matrix is the third component of the device, one or more binding reagents that bind specifically to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23. One or more chemokines selected from the group consisting of: MCP-1. MCP-2, MCP-3, MCP-4,MCP-5, MIP-3alpha, RANTES, CCL25 and/or Chemerin may be employed. These peptides may be synthetic, engineered versions of the human chemokine, which are truncated and biotinylated, but retain binding activity to the CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 receptor. By biotinylating the engineered chemokine, it is able to bind to the streptavidin molecules in the Sepharose™ matrix. The biotin-streptavidin binding is known be one of the strongest biological interactions with a Kd in the order of 4×10^{-14} M. The calculated ratio of streptavidin:biotin binding sites in the column is 10:1. Therefore, the coupling between the matrix and chemokine will be immediate, minimising the risk of chemokine decoupling from the matrix.

The apheresis system

To conduct the leukapheresis the following components are needed; the column, tubing system, and a 4008 ADS pump (Fresenius Medical Care).

The circuit

The system is illustrated in Figure 4. The patient (1) is connected to the extracorporeal circuit via sterile Venflon needles to veins in the right and the left arms. A saline bag (3) is also connected and the saline solution is pumped with an ACD pump (2). Blood is drawn from one arm of the patient through the sterile tubing system by the blood pump (4) and passed through the column (6) and back to the patient. The tubing system is connected to the column via standard dialysis luer-lock couplings. The couplings on the column are colour-coded for correct assembly; red tubing for inflow to the red column top and blue tubing for outflow back to the patient. An air detector (8) is present. Inlet pressure(5) and Pven sensors (7) are employed to monitor the pressure in the circuit.

The 4008 ADS pump

An apheresis pump, from Fresenius Medical Care, monitors the patient's inflow and outflow, the pressure in the extracorporeal circulation and can discriminate air by a bubble catcher and air detector. A clot catcher filter is placed inside the bubble catcher. The pump also has an optical detector to distinguish between light, e.g. saline solution or air present in the tubing system and dark e.g. blood present in the tubing system.

A schematic diagram of the pump, showing the air detector and optical filter is shown in Figure 5. If the pump system detects air bubbles and optical fluctuations or if extracorporeal pressure values are out of the set range, then the pump stops immediately and a visual/ audible alarm are emitted.

Legend for FIG. 5:

1. Monitor
2. Holder for waste bag
3. Modules (left to right – Blood pump, ACD pump, Air detector)
4. Reserve places for further modules
5. Absorber holder
6. Drip detector
7. IV pole

Preparation of the patient

The patient will be administered anticoagulants prior to each treatment session. A sterile saline solution with 5000 IE Heparin will be used for priming the extracorporeal system, thereafter a bolus injection with 4000 IE Heparin will be added into the circuit at the start of each treatment session.

Leukapheresis time and flow rate

The apheresis system should be operated at a flow rate of 30-60 mL/min. A treatment is finalised after 1800mL of blood has been circulated.

Storage conditions

The column devices should be stored between 1 and 25°C avoiding freezing and more elevated temperatures. Stability data > 3 months indicate no difference in functionality over time or by temperature (room temperature and refrigerated). The columns will be kept in refrigerated conditions until use. Mechanical damage as those resulting from violent vibrations and trauma should be avoided. Column stored outside of these recommendations should not be used.

Transport conditions

The column devices will be transported under refrigerated condition, avoiding freezing and more elevated temperatures. Mechanical damage such as those resulting from violent vibrations and trauma should be avoided.

In-vitro depletion of target cell populations – MCP-1

To investigate the ability to eliminate CCR2-expressing cells, in vitro tests have been performed on the bMCP-1 coupled matrix. Blood was collected from blood donors and passed through the column device containing bMCP-1 coupled matrix. Blood samples were taken before and after column passage and analyzed by flow cytometry (FACS) for the depletion of CCR2-expressing cells.

The results demonstrate significant depletion of the target population CCR2-expressing monocytes post matrix perfusion. Depletion tests were performed on blood from three healthy donors. The results are shown in Figure 6a.

In conclusion, the in-vitro results demonstrate a specific reduction of up to 80% of the CCR2-expressing cells by the column. Notably, individuals with fewer CCR2 expressing cells initially achieved lower depletion. The remaining levels of monocytes were around 20-30% in

each case, irrespective of the starting point. Non-CCR2-expressing cells remained unaffected (data not shown).

In-vitro depletion of target cell populations – RANTES

To investigate the ability to eliminate CCR1, 3 and 5-expressing cells, in vitro tests have been performed on the biotinylated RANTES coupled matrix. Blood was collected from blood donors and passed through a magnetic column device containing biotinylated RANTES coupled to MACs beads. Blood samples were taken before and after column passage and analyzed by flow cytometry (FACS) for the depletion of CCR1, 3 and 5-expressing cells. The results demonstrate significant depletion of the target population chemokine receptor-expressing cells post matrix perfusion. Depletion tests were performed on blood from a healthy donor. The results are shown in Figure 6b.

The in-vitro results demonstrate a specific reduction of around 20% of the chemokine receptor-expressing cells by the column. Non-CCR1, 3 or 5-expressing cells remained unaffected (data not shown).

In-vitro depletion of target cell populations – MIP-3a

To investigate the ability to eliminate CCR6-expressing cells, in vitro tests have been performed on the biotinylated MIP-3a coupled matrix. Blood was collected from blood donors and passed through the column device containing biotinylated MIP-3a coupled matrix. Blood samples were taken before and after column passage and analyzed by flow cytometry (FACS) for the depletion of CCR6-expressing cells.

The results demonstrate significant depletion of the target population CCR6-expressing lymphocytes post matrix perfusion. Depletion tests were performed on blood from three healthy donors. The results are shown in Figure 6c.

The in-vitro results demonstrate a specific reduction of up to around 15% of the CCR6-expressing cells by the column. Non-CCR6-expressing cells remained unaffected (data not shown).

The RANTES molecule was synthesized by Almac. The amino acid sequence of the biotinylated RANTES molecule is set forth as SEQ ID NO: 8:

H2N-
SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVREYI
NSLEKS
-CO2H

This molecule has the naturally occurring methionine at position 67 replaced with lysine to facilitate biotinylation at position 67.

The side-chain of Lys 67 was directly biotinylated to given the protein primary structure shown in figure 12. The protein was folded and disulphide bonds formed between the first and third cysteine in the sequence and between the 2nd and 4th cysteines.

In-vitro depletion of target cell populations - TECK
To investigate the ability to eliminate CCR9-expressing cells, in vitro tests have been performed on the bTECK coupled matrix. Blood was collected from blood donors and IBD patients and passed through the column device containing bTECK coupled matrix. Blood samples were taken before and after column passage and analyzed by flow cytometry (FACS) for the depletion of CCR9-expressing cells.
The results demonstrate significant depletion of the target population CD14- positive CCR9-expressing cells post matrix perfusion; while total CD14-positive cells remain unchanged. Depletion tests were performed on blood from healthy donors and IBD patients confirming similar effects. The results are shown in Figures 6d and 6e respectively.

In conclusion, the in-vitro results demonstrate a specific reduction of 50-75% of the CCR9-expressing cells by the column. Non-CCR9-expressing cells remained unaffected.

EXAMPLE 5 - MCP1 DERIVATIVES
MCP-1 has been produced with residue 75 as the site of biotinylation on the chemokine (numbering based upon the mature protein having the amino acid sequence of SEQ ID NO: 2). Biotinylation permits immobilization of MCP-1 on a solid support (via a biotin-avidin interaction). The basic amino acid sequence of MCP-1, including a 23 amino acid leader sequence is set forth as SEQ ID NO: 1,
MKVSAALLCL LLIAATFIPQ GLAQPDAINA PVTCCYNFTN RKISVQRLAS YRRITSSKCP KEAVIFKTIV AKEICADPKQ KWVQDSMDHL DKQTQTPKT

The amino acid sequence of the mature protein is set forth as SEQ ID NO: 2,
QPDAINA PVTCCYNFTN RKISVQRLAS YRRITSSKCP KEAVIFKTIV AKEICADPKQ KWVQDSMDHL DKQTQTPKT

The inventors have determined that chemokines may display improved binding properties where the chemokine is biotinylated via a spacer group. The spacer may prevent the biotin group from impacting on the binding affinity of the chemokine.

Thus, MCP-1 derivatised at the ε-amino side chain functionality of Lys75 with PEG-Biotin (TFA salt) will be synthesised. The PEG spacer will be 3,6, - dioxoaminooctanoic acid. The Gln at the N-terminus of the proteins is subject to pyroGlu formation under physiological conditions. Thus the first glutamine (Gln1) of the sequence will be substituted with pyroglutamine. The molecule will be synthesised as a C-terminal amide (via synthesis on an amide linker). The molecule is shown schematically in Figure 7.

A biotinMCP-1 Met to Nleu analogue will also be synthesised. The single methionine within the sequence will be altered to Norleucine, to mitigate against oxidation of this residue during the chain assembly and improve stability of the final product. This molecule is shown schematically in Figure 8.

Once synthesised, the activity of the various biotinMCP-1 derivatives will be determined in cell-based assays. In particular, agonist and antagonist properties will be determined in aequorin functional cell-based assay on human CCR2 receptor.

EXAMPLE 6 - SYNTHESIS OF A CCR2 ANTAGONIST BIOTINMCP-1 WHICH BINDS TO THE RECEPTOR WITHOUT ACTIVATION

Antagonist Activity (J-H Gong and I. Clark-Lewis, J. Exp. Med., 1995, 181, 63) has been shown for an MCP-1 derivative truncated at the N-terminus. In particular, deletion of residues 1-8, results in binding to CCR2 with Kd 8.3 nM. This protein was unable to cause chemotaxis of CCR2 positive cells. (inhibition of chemotaxis IC50 20nM)

The amino acid sequence of the truncated version is set forth as SEQ ID NO :3:
VTCCYNFTN RKISVQRLAS YRRITSSKCP KEAVIFKTIV AKEICADPKQ KWVQDSMDHL DKQTQTPKT

A derivative of this truncated version will be synthesised comprising residues 9 to 76 of the mature protein (MCP-1 9-76) with Met64 to Nleu substitution and derivatised at the ε-amino side chain functionality of Lys75 with PEG-Biotin (TFA salt). This molecule is shown schematically in Figure 9. The PEG spacer will be 3,6, - dioxoaminooctanoic acid.

Once synthesised, the activity of the various biotinMCP-1 derivatives will be determined in cell-based assays. In particular, agonist and antagonist properties will be determined in aequorin functional cell-based assay on human CCR2 receptor.

EXAMPLE 7 - DEMONSTRATE REMOVAL OF CCR2 EXPRESSING CELLS USING AN ALTERNATIVE CHEMOKINE LIGAND TO MCP-1

CCR2 also binds chemokines MCP-2, MCP-3, MCP-4, MCP-5, and HCC-4 in addition to MCP-1. MCP-5 only binds CCR2 and should be selective in its removal of CCR2 expressing cells. MCP5 is a mouse chemokine shown to chemotact human CCR2 cells with EC50 < 3 nM.

The full length amino acid sequence, including the signal peptide, is set forth as SEQ ID NO: 4
MKISTLLCLL LIATTISPQV LAGPDAVSTP VTCCYNVVKQ KIHVRKLKSY RRITSSQCPR EAVIFRTILD KEICADPKEK WVKNSINHLD KTSQTFILEP SCLG

The amino acid sequence of N-terminal processed MCP-5 chemokine is 82 amino acids long and is set forth as SEQ ID NO: 5
GPDAVSTP VTCCYNVVKQ KIHVRKLKSY RRITSSQCPR EAVIFRTILD KEICADPKEK WVKNSINHLD KTSQTFILEP SCLG

An amino acid sequence alignment suggests that MCP-5 has a C-terminal extension when compared to the amino acid sequence of MCP-1. The results of this alignment are shown in figure 10. On this basis a C-terminal truncated version of MCP-5 will be synthesised. This truncated version will comprise MCP-5 residues 1-76, set forth as SEQ ID NO: 6:

GPDAVSTP VTCCYNVVKQ KIHVRKLKSY RRITSSQCPR EAVIFRTILD KEICADPKEK WVKNSINHLD KTSQTFIL

In the truncated version, Ile75 to be substituted with Lys, set forth as SEQ ID NO: 7:
GPDAVSTP VTCCYNVVKQ KIHVRKLKSY RRITSSQCPR EAVIFRTILD KEICADPKEK WVKNSINHLD KTSQTFKL

Following substitution, the substituted version will be biotinylated at position 75, a lysine or other suitable residue such as ornithine or diaminopropanoic acid via A PEG spacer (3,6, -dioxoaminooctanoic acid). The protein will be synthesised on an amide linker to yield a C-terminal amide derivative. This molecule is shown schematically in Figure 11.

Once synthesised, the activity of the various biotinMCP-5 derivatives will be determined in cell-based assays. In particular, agonist and antagonist properties will be determined in aequorin functional cell-based assay on human CCR2 receptor.

EXAMPLE 8 - TECK-PEG-Biotin Synthesis Summary
Target molecule:
TECK (Met to Nleu substitution) derivatised at the ε-amino side chain functionality of Lys72 with PEG-Biotin (TFA salt)

Modifications:
Truncated form of human TECK corresponding to residues 1-74 of the mature protein, which encompasses the sequence corresponding to the chemokine fold. The full length mature protein is 127 amino acids (the signal peptide is 23 amino acids in a 150 amino acid immature protein). The single methionine within the sequence was altered to Norleucine, to mitigate against oxidation of this residue during the chain assembly, which was observed during the synthesis of the natural sequence derivative. The Gln at the N-terminus of the proteins is subject to pyroGlu formation under physiological conditions. Thus Gln1 of the sequence was substituted with pyroglutamine to prevent mixed species of N-terminal Gln and pyroGlu being generated. This improves the yield of synthesis and ensures a homogeneous chemokine preparation through column manufacture and use. The naturally occurring lysine at position 72 was modified through biotinylation on the resin. A PEG spacer was incorporated between the ε-amino functionality and the biotin.

The linear amino acid sequence (SEQ ID NO: 9) is shown, prior to attachment of the PEG spacer and biotin molecules at amino acid 72 (K):

H-XGVFEDCCLAYHYPIGWAVLRRAWTYRIQEVSGSCNLPAAIFYLPKRHRKVCG NPKSREVQRAXKLLDARNXVF-OH
X = pyroGlu
X64 = Norleucine
X72 = an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, e.g. K(PEG-Biotin)

The engineered TECK sequence was assembled on a solid support, using Fmoc protocols for solid-phase peptide synthesis:
H-XGVFEDCCLAYHYPIGWAVLRRAWTYRIQEVSGSCNLPAAIFYLPKRHRKVCG NPKSREVQRAXKLLDARNXVF-RESIN
X1 = pyroGlu
X64 = Norleucine
X72 = K(ivDde)

FmocLys(ivDde)-OH was incorporated as residue 72 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 10).
Met to Nle substitution.
N-terminal Gln to pyroglutamic acid substitution.

Removal of Dde Protection:
The Dde protecting group was removed by treatment of all resin (2.5g) with a solution of 2% hydrazine in DMF (100ml) over 1 hour period to afford 2.0g resin.

Labelling steps:

1. Couple Fmoc-8-amino-3,6-dioctanoic acid

Resin (1.5g) was swollen in DMF (2ml) and then a solution of Fmoc-8-amino-3,6-dioctanoic acid (0.38g, 1mmol), DIC solution (2ml, 0.5M in DMF) and HOCt solution (2ml, 0.5M in DMF) was added. The mixture was sonicated for 2 hours and then washed with DMF.

2. Cap

The resin was capped with 0.5M acetic anhydride/DMF solution (20ml) for 5 minutes and then washed with DMF.

3. Fmoc deprotection

Fmoc deprotection was carried out by treatment with 20% piperidine in DMF solution (2 x 50ml) for 15 minutes each. The resin was washed with DMF.

4. Couple Biotin-OSu

A solution of Biotin-NHS ester (341mg, 1mmol) and DIPEA (348ul) in DMF (10ml) was added to the resin and the mixture was sonicated for 3 hours. The resin was washed thoroughly with DMF and DCM then dried in vacuo. Dry resin obtained = 1.5g.

Cleavage:

Dry peptide resin (1.5g) and the mixture was cleaved with TFA (30 ml) containing a scavenger cocktail consisting of TIS, thioanisole, water, EDT and phenol and the mixture was stirred at room temperature for 6 hours. The solution was filtered into cold ether and the resin rinsed with TFA. The peptide was centrifuged, washed with ether, centrifuged and lyophilised to give 1.0g crude peptide.

Folding Protocol:
Crude peptide (100mg) was dissolved into 6M GnHCl (233ml) and then rapidly diluted to 2M GnHCl concentration by the addition of 50mM TRIS pH8 (467ml) containing 0.5mM GSSG and 5mM GSH. The mixture was stirred at room temperature for 2.5 days and then analysed by HPLC (Jupiter C18, 250x4.6mm column, 10-60% B over 30 minutes. HPLC analysis confirmed the formation of desired product as well as mis-folded by-products.

Purification:
The folded protein was purified by reverse phase HPLC using a Jupiter C18, 250x21mm column, 9ml/min, 10-60%B over 50 minutes. 11.1mg of pure folded Nle-TECK-Biotin was afforded.
Figure 13 shows HPLC of purified folded Biotin-TECK(Nleu). The protein eluted in a single peak at 21.6 mins.
Figure 14 shows Electrospray ionisation with tandem mass spectrometry (ES/MS) data of purified folded Biotin-TECK(Nleu). The expected mass was 8959.4 Da.

Functional Assay Data:
TECK-Biotin-Nle was tested for agonist activity in an Aequorin assay against hCCR9 (Euroscreen) and an EC50 value of 63.6nM was reported. c.f. EC50 for native TECK is 67.87nM.

The desired active chemokine comprises the amino acid sequence of SEQ ID NO: 11:

H-XGVFEDCCLAYHYPIGWAVLRRAWTYRIQEVSGSCNLPAAIFYLPKRHRKVCG NPKSREVQRAXKLLDARNXVF-OH
X1 = pyroGlu
X64 = Norleucine
X72 is K(PEG-Biotin)

EXAMPLES 9 to 15
Chemokine Synthesis – GENERAL PROTOCOLS

Assembly:
Chemical synthesis of chemokines was performed using standard Fmoc solid phase peptides synthesis (SPPS) techniques on an ABI 433 peptide synthesiser. DIC (0.5 M in DMF) and OxymaPure (0.5 M in DMF) were used for activation, acetic anhydride (0.5 M in DMF) for capping, and 20 % piperidine in DMF for Fmoc deprotection. Rink Amide resin was utilised

for the generation of C-terminal amide chemokines and Wang resin for C-terminal acid chemokines. After assembly, the resin was washed with DMF and DCM and then dried *in vacuo*.

Removal of Dde Protection:
The Dde protecting group was removed by treatment of resin with a solution of 2.5% hydrazine in DMF (200ml) over a 2 hour period. The resin was then washed with DMF.

Labelling steps:
1. Couple Fmoc-8-amino-3,6-dioctanoic acid (PEG)
Resin was swollen in DMF and then a solution of Fmoc-8-amino-3,6-dioctanoic acid (0.38g, 1mmol), DIC solution (2ml, 0.5 M in DMF) and OxymaPure solution (2ml, 0.5 M in DMF) was added. The mixture was sonicated for 3 hours and then washed with DMF.
2. Capping
The resin was capped with acetic anhydride solution (0.5 M in DMF, 10ml) for 5 minutes and then washed with DMF.
3. Fmoc deprotection
Fmoc deprotection was carried out by treatment with 20% piperidine in DMF solution (2 x 50ml) for 15 minutes each. The resin was washed with DMF.
4. Couple Biotin-OSu
A solution of Biotin-OSu (341mg, 1mmol) and DIPEA (348μl) in DMF (10ml) was added to the resin and the mixture was sonicated for 3 hours. The resin was washed thoroughly with DMF and DCM then dried *in vacuo*.

Cleavage:
Dry resin was treated with TFA (10 ml) containing a scavenger cocktail consisting of TIS (500 μl), thioanisole (500 μl), water (500 μl), DMS (500 μl), EDT (250 μl), NH_4I (500 μg) and phenol (500 μg) and the mixture was stirred at room temperature for 5 hours. The solution was filtered into cold ether and the resin rinsed with TFA. The precipitated peptide was centrifuged, washed with ether, centrifuged and lyophilised.

Purification Protocol:
The crude peptide was purified by reverse phase HPLC (RP-HPLC) using a Jupiter C18, 250 x 21 mm column, 9 ml/min, eluting with an optimised gradient [Buffer A: water containing 0.1% TFA, Buffer B: acetonitrile containing 0.1% TFA].

Folding Protocol:
Pure peptide (10mg) was dissolved into 6M GnHCl (16 ml) and then rapidly diluted to 2M GnHCl concentration by the addition of 50mM TRIS pH 8.5 (84 ml) containing 0.3mM GSSG and 3mM GSH. The mixture was stirred at room temperature for 24 hours and then analysed by RP-HPLC (Jupiter C18, 250 x 4.6 mm column, 10-60% B over 30 minutes. Purification by RP-HPLC using an optimised gradient afforded the desired product.

EXAMPLE 9 – biotinMCP-1 (CCL2)

Target Molecule: MCP-1 derivatised at the ε-amino side chain functionality of Lys(75) with PEG-Biotin (TFA salt)

Modifications: Human MCP-1 corresponding to residues 1-76, is initially expressed as 99 amino acids comprising the chemokine fold, and a 23 amino acid signal peptide which is cleaved off. The Gln at the N-terminus of the protein is subject to pyroGlu formation under physiological conditions. Thus Gln1 of the sequence was substituted with pyroglutamine to prevent mixed species of N-terminal Gln and pyroGlu being generated. This improves the yield of synthesis and ensures a homogeneous chemokine preparation through column manufacture and use. The naturally occurring lysine at position 75 was modified through biotinylation on the resin. A PEG spacer was incorporated between the ε-amino functionality and the biotin.

The linear amino acid sequence (SEQ ID NO: 12) is shown, prior to attachment of the PEG spacer and biotin molecules at amino acid 75 (K):

H-XPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEIC
ADPKQKWVQDSMDHLDKQTQTPKT-NH_2
X = pyroGlu or Gln

The engineered MCP-1 sequence was assembled on a solid support (Rink Amide resin), using Fmoc protocols for solid-phase peptide synthesis as described in the general protocols section:

SEQ ID NO: 13
H-XPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEIC
ADPKQKWVQDSMDHLDKQTQTPXT-RESIN
X1 = pyroGlu or Gln
X75 = K(ivDde)

FmocLys(ivDde)-OH was incorporated as residue 75 to facilitate site-specific labelling at this position of the protein. Subsequent removal of the ivDde protecting group, followed by coupling of the PEG spacer and Biotin, was carried out as described in the general protocol section. Cleavage, purification and folding protocols were carried out as described to furnish the desired active chemokine.

SEQ ID NO: 14
H-XPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEIC
ADPKQKWVQDSMDHLDKQTQTPXT-NH_2
X1 = pyroGlu or Gln

X75 is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, optionally K(PEG-Biotin)

Electrospray ionisation with tandem mass spectrometry (ESI-TOF-MS) data of purified folded biotinMCP-1: obtained = 9032.8 Da; expected 9034.4 Da.

Functional Assay Data:
biotinMCP-1 was tested for agonist activity in an Aequorin assay against hCCR2b, (Euroscreen) and an EC50 value of 9.6nM was reported. c.f. EC50 for recombinant native MCP-1 is 3.1nM.

EXAMPLE 10 – biotinRANTES (CCL5)

Target Molecule: RANTES derivatised at the ε-amino side chain functionality of Lys(67) with Biotin (TFA salt)

Modifications: Human RANTES corresponding to residues 1-68, is initially expressed as 91 amino acids comprising the chemokine fold, and a 23 amino acid signal peptide which is cleaved off. The single methionine (Met67) within the sequence was mutated to lysine, to mitigate against oxidation of this residue during the chain assembly, which was observed during the synthesis of the natural sequence derivative. This Met to Lys substitution provided a lysine at position 67 which was modified through biotinylation on the resin.

The linear amino acid sequence (SEQ ID NO: 15) is shown, prior to attachment of the biotin molecule at amino acid 67 (K):

H-SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVC ANPEKKWVREYINSLEKS-OH

The engineered RANTES sequence was assembled on a solid support (Wang resin), using Fmoc protocols for solid-phase peptide synthesis as described in the general protocols section:

H-SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVC ANPEKKWVREYINSLEXS-RESIN
X is K(ivDde)

FmocLys(ivDde)-OH was incorporated as residue 67 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 16). Subsequent removal of the ivDde protecting group, followed by coupling of the Biotin, was carried out as described in the general protocol section. Cleavage, purification and folding protocols were carried out as described to furnish the desired active chemokine (SEQ ID NO: 17).

H-SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVC
ANPEKKWVREYINSLEXS-OH
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG (e.g. K(Biotin))

Electrospray ionisation with tandem mass spectrometry (ESI-TOF-MS) data of purified folded biotinRANTES: obtained = 8068.9 Da; expected 8070.2 Da.

Functional Assay Data:
BiotinRANTES was tested for agonist activity in an Aequorin assay against hCCR5, (Euroscreen) and an EC50 value of 0.5nM was reported.

EXAMPLE 11 – biotinMCP-2 (CCL8)

Target Molecule: MCP-2 derivatised at the ε-amino side chain functionality of Lys(75) with PEG-Biotin (TFA salt)

Modifications: Human MCP-2 corresponding to residues 1-76, is initially expressed as 99 amino acids comprising the chemokine fold, and a 23 amino acid signal peptide which is cleaved off. The Gln at the N-terminus of the protein is subject to pyroGlu formation under physiological conditions. Thus Gln1 of the sequence was substituted with pyroglutamine to prevent mixed species of N-terminal Gln and pyroGlu being generated. This improves the yield of synthesis and ensures a homogeneous chemokine preparation through column manufacture and use. The naturally occurring lysine at position 75 was modified through biotinylation on the resin. A PEG spacer was incorporated between the ε-amino functionality and the biotin.

The linear amino acid sequence (SEQ ID NO: 18) is shown, prior to attachment of the PEG spacer and biotin molecules at amino acid 75 (K):

H-XPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTKRGKEVCADPKE
RWVRDSMKHLDQIFQNLKP-NH_2
X = pyroGlu or Gln

The engineered MCP-2 sequence was assembled on a solid support (Rink Amide resin), using Fmoc protocols for solid-phase peptide synthesis as described in the general protocols section:

H-XPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTKRGKEVCADPKE
RWVRDSMKHLDQIFQNLXP-NH_2
X1 = pyroGlu or Gln
X75 = K(ivDde)

FmocLys(ivDde)-OH was incorporated as residue 75 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 19). Subsequent removal of the ivDde protecting group, followed by coupling of the PEG spacer and Biotin, was carried out as described in the general protocol section. Cleavage, purification and folding protocols were carried out as described to furnish the desired active chemokine (SEQ ID NO: 20):

H-XPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTKRGKEVCADPKE
RWVRDSMKHLDQIFQNLXP-NH_2
X1 = pyroGlu or Gln
X75 = an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, e.g. K(PEG-Biotin).

Electrospray ionisation with tandem mass spectrometry (ESI-TOF-MS) data of purified folded biotinMCP-2: obtained = 9263.6 Da; expected 9263.8 Da.

Functional Assay Data:
biotinMCP-2 was tested for activity in an Aequorin assay against hCCR2b, (Euroscreen) and was shown to be a partial agonist with an EC50 value of 50.9nM. c.f. EC50 for recombinant native MCP-2 is 23.5nM (partial agonist).

Example 12 – biotinIL-8 (CXCL8)

Target Molecule: IL-8 derivatised at the ε-amino side chain functionality of Lys(78) with PEG-Biotin (TFA salt)

Modifications: Human IL-8 corresponding to residues 1-77, is initially expressed as 99 amino acids comprising the chemokine fold, and a 22 amino acid signal peptide which is cleaved off. An additional lysine was inserted at the C-terminus at position 78, and modified through biotinylation on the resin. A PEG spacer was incorporated between the ε-amino functionality and the biotin.

The linear amino acid sequence (SEQ ID NO: 21) is shown, prior to attachment of the PEG spacer and biotin molecules:

H-AVLPRSAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKL
SDGRELCLDPKENWVQRVVEKFLKRAENSX-NH_2
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, e.g. K(PEG-Biotin)

The engineered IL-8 sequence was assembled on a solid support (Rink Amide resin), using Fmoc protocols for solid-phase peptide synthesis as described in the general protocols section:

H-AVLPRSAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKL
SDGRELCLDPKENWVQRVVEKFLKRAENSX-RESIN
X is K(ivDde)

FmocLys(ivDde)-OH was incorporated as residue 78 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 22). Subsequent removal of the ivDde protecting group, followed by coupling of the PEG spacer and Biotin, was carried out as described in the general protocol section. Cleavage, purification and folding protocols were carried out as described to furnish the desired active chemokine (SEQ ID NO: 23):

H-AVLPRSAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKL
SDGRELCLDPKENWVQRVVEKFLKRAENSX-NH_2
X is K(PEG-Biotin)

Electrospray ionisation with tandem mass spectrometry (ESI-TOF-MS) data of purified folded biotinIL-8: obtained = 9416.9 Da; expected 9417.0 Da.

Functional Assay Data:
BiotinIL-8 was tested for agonist activity in an Aequorin assay against hCXCR1, (Euroscreen) and an EC50 value of 18.9 nM was reported. c.f. EC50 for recombinant native IL-8 is 4.1 nM.

Example 13 – biotinIL-8 (6-78)

Target Molecule: IL-8 (6-78) derivatised at the ε-amino side chain functionality of Lys(78) with PEG-Biotin (TFA salt)

Modifications: Truncated form of IL-8 corresponding to residues 6-77, the first five N-terminal residues have been removed and an additional lysine was inserted at the C-terminus at position 78, and modified through biotinylation on the resin. A PEG spacer was incorporated between the ε-amino functionality and the biotin.

The linear amino acid sequence (SEQ ID NO: 24) is shown, prior to attachment of the PEG spacer and biotin molecules:

H-SAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGREL
CLDPKENWVQRVVEKFLKRAENSX-NH_2
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG

The engineered IL-8 sequence was assembled on a solid support (Rink Amide resin), using Fmoc protocols for solid-phase peptide synthesis as described in the general protocols section:

H-SAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGREL
CLDPKENWVQRVVEKFLKRAENSX-RESIN
X is K(ivDde)

FmocLys(ivDde)-OH was incorporated as residue 78 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 25). Subsequent removal of the ivDde protecting group, followed by coupling of the PEG spacer and Biotin, was carried out as described in the general protocol section. Cleavage, purification and folding protocols were carried out as described to furnish the desired active chemokine (SEQ ID NO: 26):

H-SAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGREL
CLDPKENWVQRVVEKFLKRAENSX-NH_2
X is K(PEG-Biotin)

Electrospray ionisation with tandem mass spectrometry (ESI-TOF-MS) data of purified folded biotinIL-8 (6-78): obtained = 8880.50 Da; expected 8880.4 Da.

Functional Assay Data:
BiotinIL-8 (6-78) was tested for agonist activity in an Aequorin assay against hCXCR1, (Euroscreen) and an EC50 value of 6.1nM was reported. c.f. EC50 for recombinant native IL-8 is 4.1nM.

Example 14 – biotinMIP-3α (CCL20)

Target Molecule: MIP-3α derivatised at the ε-amino side chain functionality of Lys(68) with PEG-Biotin (TFA salt)

Modifications: Human MIP-3α corresponding to residues 1-70, is initially expressed as 96 amino acids comprising the chemokine fold, and a 26 amino acid signal peptide which is cleaved off. The naturally occurring lysine at position 68 was modified through biotinylation on the resin. A PEG spacer was incorporated between the ε-amino functionality and the biotin.

The linear amino acid sequence (SEQ ID NO: 27) is shown, prior to attachment of the PEG spacer and biotin molecules at amino acid 68 (K):

H-ASNFDCCLGYTDRILHPKFIVGFTRQLANEGCDINAIIFHTKKKLSVCANPK
QTWVKYIVRLLSKKVKNM-OH

The engineered MIP-3α sequence was assembled on a solid support (Wang resin), using Fmoc protocols for solid-phase peptide synthesis as described in the general protocols section:

H-ASNFDCCLGYTDRILHPKFIVGFTRQLANEGCDINAIIFHTKKKLSVCANPK
QTWVKYIVRLLSKKVXNM-RESIN
X= K(ivDde)

FmocLys(ivDde)-OH was incorporated as residue 68 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 28). Subsequent removal of the ivDde protecting group, followed by coupling of the PEG spacer and Biotin, was carried out as described in the general protocol section. Cleavage, purification and folding protocols were carried out as described to furnish the desired active chemokine (SEQ ID NO: 29).

H-ASNFDCCLGYTDRILHPKFIVGFTRQLANEGCDINAIIFHTKKKLSVCANPK
QTWVKYIVRLLSKKVXNM-OH
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, in particular K(PEG-Biotin)

Electrospray ionisation with tandem mass spectrometry (ESI-TOF-MS) data of purified folded biotinMip-3α: obtained = 8396.4 Da; expected 8397.0 Da.

Functional Assay Data:
BiotinMIP-3α was tested for agonist activity in an Aequorin assay against hCCR6, (Euroscreen) and an EC50 value of 1.6nM was reported. c.f. EC50 for recombinant native MIP-3α is 1.0nM.

Example 15 – biotinMDC (CCL22)
Target Molecule: MDC derivatised at the ε-amino side chain functionality of Lys(66) with PEG-Biotin (TFA salt)

Modifications: Human MDC corresponding to residues 1-69, is initially expressed as 93 amino acids comprising the chemokine fold, and a 24 amino acid signal peptide which is cleaved off. The naturally occurring lysine at position 66 was modified through biotinylation on the resin. A PEG spacer was incorporated between the ε-amino functionality and the biotin.

The linear amino acid sequence (SEQ ID NO: 30) is shown, prior to attachment of the PEG spacer and biotin molecules at amino acid 66 (K):

H-GPYGANMEDSVCCRDYVRYRLPLRVVKHFYWTSDSCPRPGVVLLTFRDK
EICADPRVPWVKMILNKLSQ-NH_2

The engineered MDC sequence was assembled on a solid support (Rink Amide resin), using Fmoc protocols for solid-phase peptide synthesis as described in the general protocols section:

H-GPYGANMEDSVCCRDYVRYRLPLRVVKHFYWTSDSCPRPGVVLLTFRDK
EICADPRVPWVKMILNXLSQ-RESIN
X= K(ivDde)

FmocLys(ivDde)-OH was incorporated as residue 66 to facilitate site-specific labelling at this position of the protein (SEQ ID NO: 31). Subsequent removal of the ivDde protecting group, followed by coupling of the PEG spacer and Biotin, was carried out as described in the general protocol section. Cleavage, purification and folding protocols were carried out as described to furnish the desired active chemokine (SEQ ID NO: 32).

H-GPYGANMEDSVCCRDYVRYRLPLRVVKHFYWTSDSCPRPGVVLLTFR
DKEICADPRVPWVKMILNXLSQ-NH_2
X is an amino acid residue that can be biotinylated, such as lysine, ornithine or diaminopropionic acid and optionally is biotinylated, optionally via a spacer molecule such as PEG, especially K(PEG-Biotin)

Electrospray ionisation with tandem mass spectrometry (ESI-TOF-MS) data of purified folded biotinMDC: obtained = 8456.1 Da; expected 8456.9 Da.

Functional Assay Data:
BiotinMDC was tested for agonist activity in an Aequorin assay against hCCR4, (Euroscreen) and an EC50 value of 4.5nM was reported. c.f. EC50 for recombinant native MDC is 3.6nM.

EXAMPLE 16 – Diagnosis and Treatment of Inflammatory skin disease

Materials and methods

1. Flow cytometric analysis of peripheral blood

Peripheral blood from patients and healthy controls was collected in heparin tubes. The red blood cells were lysed using Fix Buffer (Phosphate Buffer Saline (PBS) citrate with 4% paraformaldehyde) for four minutes at 37°C and Lysing buffer (PBS with 10mM Tris and 160mM NH_4Cl, pH 7.5) for 15 min at 37°C. The cells were washed in PBS with 2% Bovine Growth Serum, incubated with 10% human serum for 15min at room temperature (RT) and stained with antibodies (Table 2) at 4°C for 30min. The cells were analysed by flow cytometry on a FACS Canto flow cytometer with the FACSDiva software (BD Biosciences).

Antibody	Fluorophore	Supplier
CCR4	PerCpCy5.5	BD
CXCR1	APC	Biolegend
CXCR2	PE	Biolegend
CD16	PECy7	BD
CD3	Horizon V450	BD
Streptavdin	APC	BD

Table 2. List of antibodies for flow cytometric analysis.

2. Chemokine Binding test

Peripheral blood from patients and healthy controls was collected in heparin tubes. The red blood cells were lysed using Fix Buffer (Phosphate Buffer Saline (PBS) citrate with 4% paraformaldehyde) for four minutes at 37°C and Lysing buffer (PBS with 10mM Tris and 160mM NH4Cl, pH 7.5) for 15 min at 37°C. The cells were washed in PBS with 2% Bovine Growth Serum, incubated with 10% human serum 15min at room temperature (RT) and stained with cell specific antibodies together with biotinylated chemokine (1µM) or the corresponding chemokine receptor antibody at 4°C for 30min (Table 1). The biotinylated chemokine was detected via the interaction between biotin and a fluorophore conjugated Streptavidin. The samples were analysed by flow cytometry on a FACS Canto flow cytometer with the FACSDiva software (BD Biosciences).

3. Cell depletion by matrix conjugated with biotinylated chemokine

Cells were prepared from peripheral blood (section 1). 1 mL Sepharose BigBeads matrix conjugated with 0.4mg/mL Streptavidin (GE Healthcare) was washed in 50 mL PBS and added to a 5 mL polystyrene tube (BD Falcon™). Biotinylated chemokine was added to the tube and incubated for 20 min at RT to enable immobilization of the chemokine on the matrix via the biotin-streptavidin interaction. Next, the cells were added to the chemokine-matrix and incubated for 20 min at RT. The cells that did not bind to the matrix were removed by washing the matrix with PBS in a sterile 40um nylon filter (BD Falcon™ Cell Strainer). The flow through cells were stained with antibodies (Table 1), analysed by flow cytometry and compared with cells from peripheral blood that had not been incubated with the chemokine-matrix.

Results and Discussion

1. Flow cytometric analysis of peripheral blood – CCR4

White blood cells from one patient with psoriasis were analysed for the expression of chemokine receptors with flow cytometry. The patient exhibited an increased frequency of CCR4 expressing T cells compared to healthy controls, based upon flow cytometry data and binding by an anti-CCR4 antibody (Figure 16).

2. Chemokine Binding test – CCR4

The chemokine receptor CCR4 is necessary for T cell migration to the skin, which leads to inflammation. The ligand for CCR4 is the chemokine MDC (CCL22) which is expressed in inflamed skin lesions.

The T cells could bind biotinylated MDC (bMDC) to a similar extent as the chemokine receptor expression (Figure 17).

3. Cell depletion by matrix conjugated with biotinylated chemokine – CCR4
The CCR4 expressing T cells could be efficiently depleted with biotinylated MDC conjugated Sepharose Streptavidin Matrix (Figure 18).

1. Flow cytometric analysis of peripheral blood – CXCR1 and CXCR2
The chemokine receptors CXCR1 and CXCR2 were expressed on neutrophils (Figure 19), based upon flow cytometry data and binding of an anti-CXCR1 and anti-CXCR2 antibody. Th17 cells produce IL-17 causing IL-8 release and attract neutrophils to sites of skin inflammation. Therefore eliminating neutrophils is predicted to be beneficial for treatment of inflammatory skin conditions such as psoriasis.

2. Chemokine Binding test – CXCR1 and CXCR2
The ligand for CXCR1 and CXCR2 is IL-8 that mediate migration of neutrophils in inflammation. In accordance with the receptor expression, biotinylated IL-8 (bIL-8) could bind to blood neutrophils from a psoriasis patient (Figure 20).

3. Cell depletion by matrix conjugated with biotinylated chemokine – CXCR1 and CXCR2
The CXCR2 expressing neutrophils could be efficiently depleted with bIL-8 conjugated Sepharose Streptavidin Matrix (Figure 21).

Conclusions
We conclude that the frequency of CCR4 expressing T cells is enhanced in psoriasis. The CCR4 expressing T cells and CXCR1 and CXCR2 expressing neutrophils could bind their respective chemokines, and could be efficiently depleted with biotinylated chemokine-Sepharose Streptavidin-matrix.

The various embodiments of the present invention are not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the various embodiments of the nvention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims. Moreover, all embodiments described herein are considered to be broadly applicable and combinable with any and all other consistent embodiments, as appropriate.

Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

CLAIMS

1. A method for treating inflammatory skin disease comprising applying peripheral blood from a patient to an apheresis column loaded with a solid support comprising one or more binding reagents capable of specifically binding to a chemokine receptor, optionally the chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 immobilized directly or indirectly on the support thus removing one or more chemokine receptor, optionally CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells from the peripheral blood of the patient or subject.

2. The method of claim 1 wherein the inflammatory skin disease is selected from psoriasis and atopic dermatitis.

3. The method of claim 1 or 2 wherein the binding reagent capable of specifically binding to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 is an agonist or an antagonist of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23, respectively.

4. The method of any preceding claim wherein the binding reagent capable of specifically binding to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 is selected from an antibody and a chemokine.

5. The method of claim 4 wherein the chemokine is selected from one or more of MCP-1, MCP-2, MCP-3, MCP-4, MCP-5, MIP-3alpha, CCL25, Chemerin, RANTES, MDC and/or IL-8.

6. The method of claim 5 wherein the chemokine is MCP-1 or MCP-5.

7. The method of claim 5 or 6 wherein the chemokine receptor is CCR2.

8. The method of claim 4 wherein the chemokine is MIP-3a.

9. The method of claim 8 wherein the chemokine receptor is CCR6.

10. The method of claim 4 wherein the chemokine is RANTES.

11. The method of claim 10 wherein the chemokine receptor is selected from CCR3, CCR1 and/or CCR5.

12. The method of any preceding claim wherein the CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells are selected from monocytes, lymphocytes, neutrophils, mast cells, macrophages, eosinophils and dendritic cells, such as plasmacytoid DC.

13. The method of claim 12 wherein the CCR2 expressing cells are monocytes, T cells, basophils, mast cells or dendritic cells or wherein the CCR4 expressing cells comprise CCR4 expressing lymphocytes, in particular CCR4 expressing T cells or wherein the CXCR1 and/or CXCR2 expressing cells comprise neutrophils.

14. The method of claim 12 wherein the CCR6 expressing cells are lymphocytes or dendritic cells.

15. The method of claim 12 wherein the CCR3 expressing cells are Th2 cells, basophils or eosinophils, the CCR5 expressing cells are monocytes or Th1 cells and/or the CCR9 expressing cells are monocytes and/or T lymphocytes

16. The method of any preceding claim wherein the patient or subject has been selected for treatment on the basis of detecting an increase in the level of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, levels of expression of one or more of CCR2, CCR6, CCR3, CCR5, CCR1 andCCR9 and/or levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 in a sample obtained from the patient or subject.

17. The method of any preceding claim wherein around 20-50% of the patient's blood is applied to the column in a single treatment.

18. A binding reagent capable of specifically binding to a chemokine receptor, optionally the chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 for use in the treatment of inflammatory skin disease, wherein the binding reagent is immobilized on a solid support contained within an apheresis column, to which is applied peripheral blood from a patient thus removing chemokine receptor, optionally CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells from the peripheral blood of the patient.

19. The binding reagent of claim 18 wherein the inflammatory skin disease is selected from psoriasis and atopic dermatitis.

20. The binding reagent of claim 18 or 19 wherein the binding reagent capable of specifically binding to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 is an antagonist of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23, respectively.

21. The binding reagent of any of claims 18 to 20 wherein the binding reagent capable of specifically binding to CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 is selected from an antibody and a chemokine.

22. The binding reagent of claim 21 wherein the chemokine is selected from one or more of MCP-1, MCP-2, MCP-3, MCP-4, MCP-5, MIP-3alpha, CCL25, Chemerin, RANTES, MDC and/or IL-8.

23. The binging reagent of claim 22 wherein the chemokine is MCP-1 or MCP-5.

24. The binding reagent of claim 22 or 23 wherein the chemokine receptor is CCR2.

25. The binding reagent of claim 21 wherein the chemokine is MIP-3a.

26. The binding reagent of claim 25 wherein the chemokine receptor is CCR6.

27. The binding reagent of claim 21 wherein the chemokine is RANTES.

28. The binding reagent of claim 27 wherein the chemokine receptor is CCR1, CCR3 and/or CCR5.

29. The binding reagent of any one of claims 18 to 28 wherein the CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells are selected from monocytes, lymphocytes, neutrophils, macrophages, eosinophils and dendritic cells such as plasmacytoid DC.

30. The binding reagent of claim 29 wherein the CCR2 expressing cells are monocytes, T cells, basophils, mast cells or dendritic cells or wherein the CCR4 expressing cells comprise CCR4 expressing lymphocytes, in particular CCR4 expressing T cells or wherein the CXCR1 and/or CXCR2 expressing cells comprise neutrophils.

31. The binding reagent of claim 29 wherein the CCR6 expressing cells are lymphocytes or dendritic cells.

32. The binding agent of claim 29 wherein the CCR3 expressing cells are Th2 cells, basophils or eosinophils, the CCR5 expressing cells are monocytes or Th1 cells and/or the CCR9 expressing cells are monocytes and/or T lymphocytes

33. The binding reagent of any one of claims 18 to 32 wherein the patient has been selected for treatment on the basis of detecting an increase in the level of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells, levels of expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 and/or levels of cells with high expression of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 in a sample obtained from the patient.

34. The binding reagent of any one of claims 18 to 33 wherein 20-50% of the patient's blood is applied to the column in a single treatment.

35. A method of diagnosing, monitoring progression of, or monitoring treatment of inflammatory skin disease comprising determining
a) the levels of one or more of chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells
b) levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 ; and/or
c) levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23
in a sample obtained from a subject, wherein high levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, high levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 or high levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 or increased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells compared to control, increased levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 compared to a control or increased levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 compared to a control indicate the presence or progression of inflammatory skin disease.

36. The method of claim 35 wherein the inflammatory skin disease is selected from psoriasis and atopic dermatitis.

37. The method of claim 35 or 36 wherein the sample is a peripheral blood sample optionally wherein the CCR4 expressing cells comprise CCR4 expressing lymphocytes, in particular CCR4 expressing T cells or wherein the CXCR1 and/or CXCR2 expressing cells comprise neutrophils.

38. The method of any of claims 35 to 37 wherein higher levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 and/or levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 correlate with more active disease.

39. The method of any of claims 35 to 38 wherein low levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 and/or levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 correlate with a lack of active disease or less active disease.

40. The method of any of claims 35 to 39 wherein decreased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 and/or levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 correlate with successful treatment.

41. The method of claim 10 wherein the treatment is as claimed in any one of claims 1 to 17.

42. The method of any of claims 35 to 41 wherein increased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 and/or levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 indicate the progression of disease.

43. A method of selecting a suitable treatment for inflammatory skin disease comprising determining
a) the levels of one or more of the chemokine receptor CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells
b) levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 ; and/or
c) levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23
in a sample obtained from a subject, wherein high levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 expressing cells, high levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 or high levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 or increased levels of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 or ChemR23 expressing cells compared to control, increased levels of expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 compared to a control or increased levels of cells with high expression of one or more of CCR4, CXCR1, CXCR2, CCR2, CCR6, CCR3, CCR5, CCR1, CCR9 and ChemR23 compared to a control, result in selection of a treatment as defined in any one of claims 1 to 17 for treatment of the inflammatory skin disease.

44. The method of claim 43 wherein the inflammatory skin disease is selected from psoriasis and atopic dermatitis.

45. The method of claim 43 or 44 wherein the sample is a peripheral blood sample optionally wherein the CCR4 expressing cells comprise CCR4 expressing lymphocytes, in particular CCR4 expressing T cells or wherein the CXCR1 and/or CXCR2 expressing cells comprise neutrophils.

46. A modified MCP-1 chemokine comprising the amino acid sequence set forth as SEQ ID NO: 1, SEQ ID NO: 2 or SEQ ID NO: 3 in which one or more of the following modifications have been made:
a) the glutamine residue at position 1 of SEQ ID NO: 2 has been replaced with pyroglutamine
b) the C terminus is produced as an amide derivative
c) the lysine residue at position 98 of SEQ ID NO: 1 or position 75 of SEQ ID NO:2 or position 67 of SEQ ID NO: 3, which may be replaced by a suitable alternative amino acid such as diaminopropionic acid or ornithine, is biotinylated, optionally via a spacer group, in order to permit immobilization of the chemokine on a solid support
d) the methionine residue at position 87 of SEQ ID NO: 1 or position 64 of SEQ ID NO: 2 or position 56 of SEQ ID NO: 3 has been replaced with norleucine
e) the methionine residue at position 87 of SEQ ID NO: 1 or position 64 of SEQ ID NO: 2 or position 56 of SEQ ID NO: 3 has been replaced with norleucine

47. The modified MCP-1 chemokine of claim 30 wherein the lysine residue at position 98 of SEQ ID NO: 1 or position 75 of SEQ ID NO:2 or position 67 of SEQ ID NO: 3 is biotinylated via a polyethylene glycol (PEG) spacer group, in order to permit immobilization of the chemokine on a solid support.

48. The modified MCP-1 chemokine of claim 47 wherein the PEG spacer is 3,6-dioxo aminooctanoic acid.

49. The modified MCP-1 chemokine of any one of claims 46 to 48 having the structure shown in any one of figures 7 to 9.

50. The modified MCP-1 chemokine of any one of claims 46 to 49 which is an agonist or an antagonist of CCR2 activity.

51. A modified MCP-5 chemokine comprising the amino acid sequence set forth as SEQ ID NO: 4, SEQ ID NO: 5 or SEQ ID NO: 6 in which the isoleucine residue at position 97 of SEQ ID NO: 4 or at position 75 of SEQ ID NO: 5 or SEQ ID NO: 6 has been replaced with lysine or an alternative amino acid such as diaminopropionic acid or ornithine, which permits biotinylation.

52. The modified MCP-5 chemokine of claim 51 which comprises the amino acid sequence of SEQ ID NO: 7.

53. The modified MCP-5 chemokine of claim 51 or 52 which is biotinylated at the lysine residue at position 97 of SEQ ID NO: 4 or at position 75 of SEQ ID NO: 5 or SEQ ID NO: 6.

54. The modified MCP-5 chemokine of any one of claims 51 to 53 wherein biotinylation is via a spacer group.

55. The modified MCP-5 chemokine of claim 54 wherein the spacer group is a PEG spacer, optionally 3,6-dioxo aminooctanoic acid.

56. The modified MCP-5 chemokine of any one of claims 51 to 55 wherein the C terminus is produced as an amide derivative.

57. The modified MCP-5 chemokine of any one of claims 51 to 56 having the structure shown in figure 11.

58. The modified MCP-5 chemokine of any one of claims 51 to 57 which is an agonist or an antagonist of CCR2 activity.

59. An apheresis column loaded with a solid support comprising a binding reagent capable of specifically binding to a chemokine receptor immobilized directly or indirectly on the support to permit removal of a cell expressing the chemokine receptor from the peripheral blood of a patient, wherein the binding reagent is not a chemokine.

60. The column of claim 59 wherein the binding reagent capable of specifically binding to the chemokine receptor is an agonist or an antagonist of the chemokine receptor.

61. The column of any preceding claim wherein the binding reagent capable of specifically binding to the chemokine receptor is selected from an antibody and a chemical compound.

62. The column of any preceding claim as further defined by any one or more of the features of claims 1 to 58.

63. A method for treating an inflammatory condition comprising applying peripheral blood from a patient to an apheresis column as defined in any one of claims 59 to 62 thus removing chemokine receptor expressing cells from the peripheral blood of the patient.

64. The method of claim 63 as further defined by any one or more of the features of claims 1 to 58.

65. A binding reagent capable of specifically binding to a chemokine receptor for use in the treatment of an inflammatory condition, wherein the binding reagent is immobilized on a solid support contained within an apheresis column as claimed in any one of claims 59 to 62,

to which is applied peripheral blood from a patient thus removing chemokine receptor expressing cells from the peripheral blood of the patient.

66. The binding reagent of claim 65 as further defined by any one or more of the features of claims 1 to 58.

67. A modified CCL8 (MCP-2) chemokine comprising the amino acid sequence set forth as SEQ ID NO: 18.

68. The modified CCL8 chemokine of claim 67 wherein the residue at position 75 of SEQ ID NO: 18 is biotinylated via a polyethylene glycol (PEG) spacer group, in order to permit immobilization of the chemokine on a solid support.

69. The modified CCL8 chemokine of claim 68 wherein the PEG spacer is 3,6-dioxo aminooctanoic acid.

70. The modified CCL8 chemokine of any one of claims 67 to 69 comprising the amino acid sequence of SEQ ID NO: 20.

71. The modified CCL8 chemokine of any one of claims 67 to 70 which is an agonist or an antagonist of CCR5 activity.

72. A modified CCL5 chemokine comprising the amino acid sequence set forth as SEQ ID NO: 17 or 15

73. The modified CCL5 chemokine of claim 72 wherein the residue at position 67 is biotinylated.

74. The modified CCL5 chemokine of claim 73 wherein the residue at position 67 is biotinylated via a PEG spacer.

75. The modified CCL5 chemokine of any one of claims 72 to 74 which is an agonist or an antagonist of CCR5 activity.

76. A modified CCL20 chemokine comprising the amino acid sequence set forth as SEQ ID NO: 29.

77. The modified CCL20 chemokine of claim 76 wherein the amino acid residue at position 68 is biotinylated, optionally via a spacer group, in order to permit immobilization of the chemokine on a solid support.

78. The modified CCL20 chemokine of claim 77 wherein the residue at position 68 of SEQ ID NO: 29 is biotinylated via a polyethylene glycol (PEG) spacer group, in order to permit immobilization of the chemokine on a solid support.

79. The modified CCL20 chemokine of claim 78 wherein the PEG spacer is 3,6-dioxo aminooctanoic acid.

80. The modified CCL20 chemokine of any one of claims 76 to 79 which is an agonist or an antagonist of CCR6 activity.

81. A modified CCL22 chemokine comprising the amino acid sequence set forth as SEQ ID NO: 32.

82. The modified CCL22 chemokine of claim 81 wherein the amino acid residue at position 66 is biotinylated, optionally via a spacer group, in order to permit immobilization of the chemokine on a solid support.

83. The modified CCL22 chemokine of claim 82 wherein the residue at position 66 of is biotinylated via a polyethylene glycol (PEG) spacer group, in order to permit immobilization of the chemokine on a solid support.

84. The modified CCL22 chemokine of claim 83 wherein the PEG spacer is 3,6-dioxo aminooctanoic acid.

85. The modified CCL22 chemokine of any one of claims 81 to 84 which is an agonist or an antagonist of CCR4 activity.

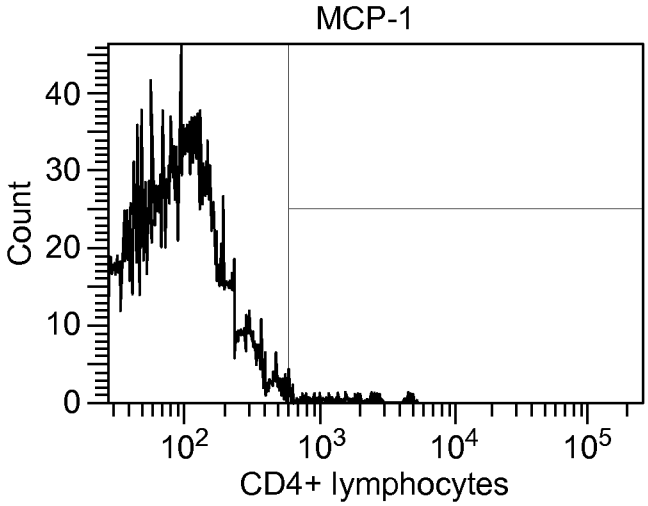

FIG. 1a

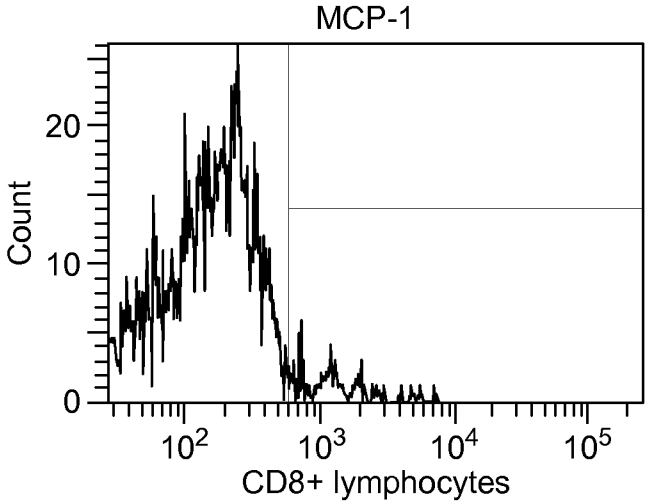

FIG. 1b

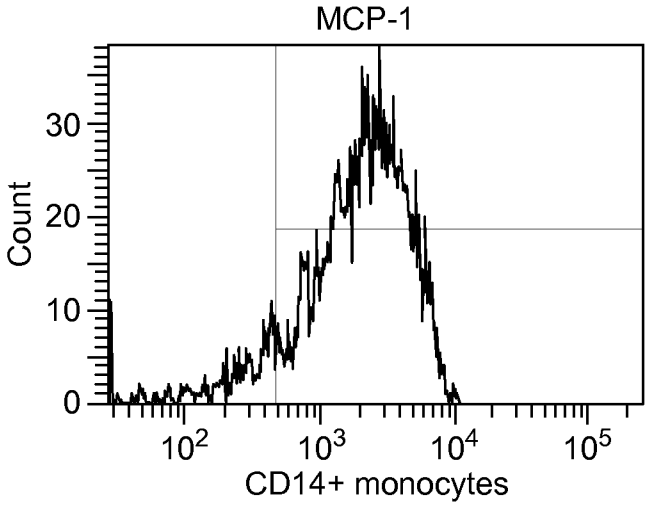

FIG. 1c

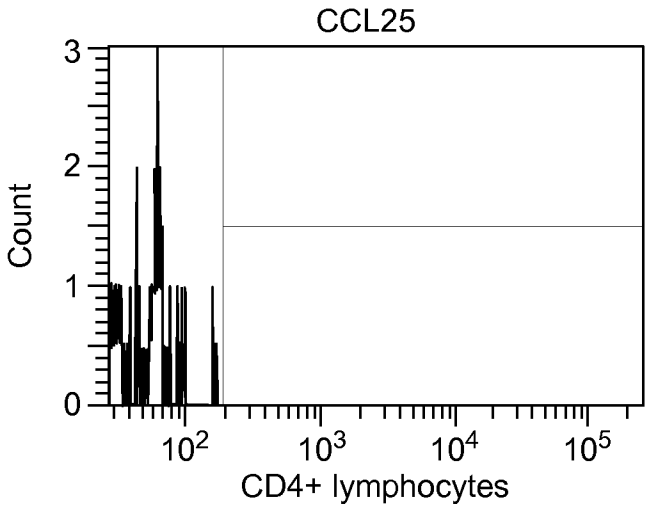

FIG. 1d

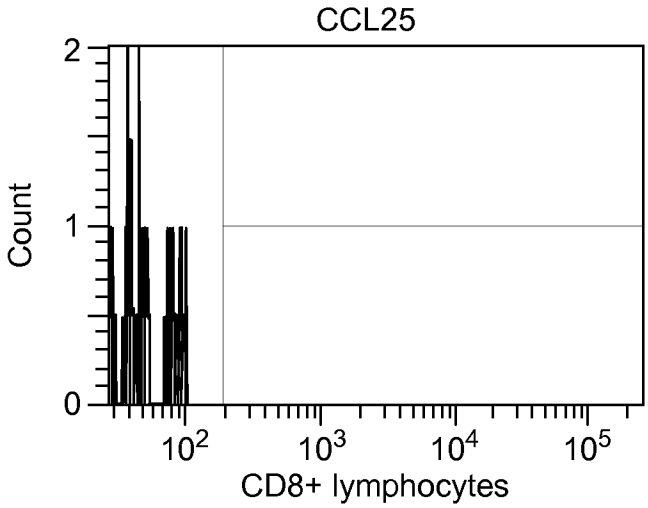

FIG. 1e

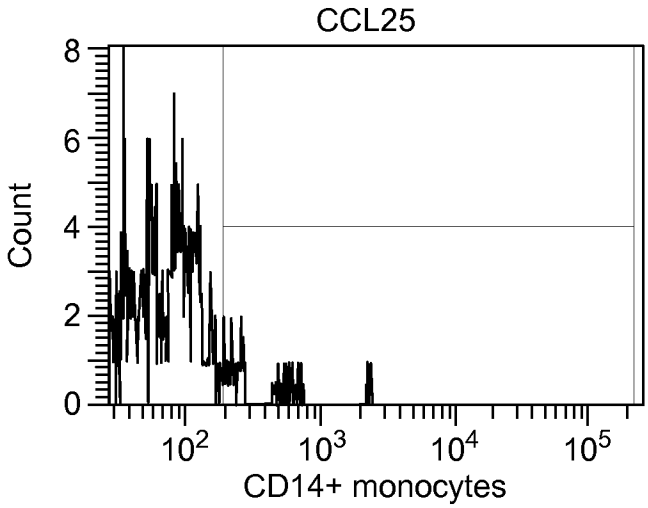

FIG. 1f

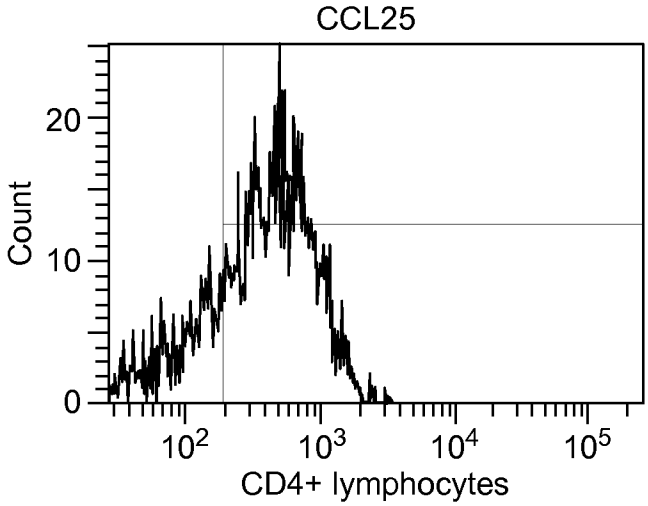

FIG. 1g

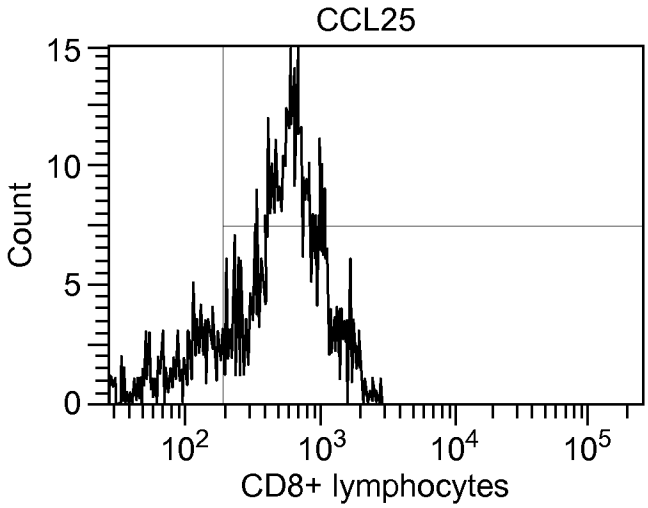

FIG. 1h

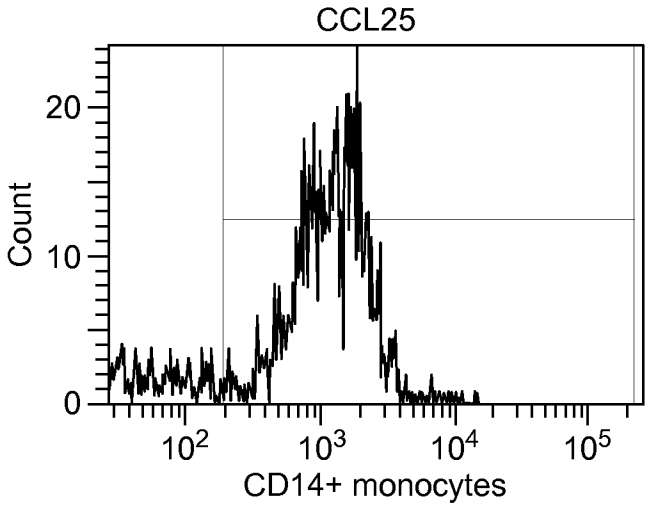

FIG. 1i

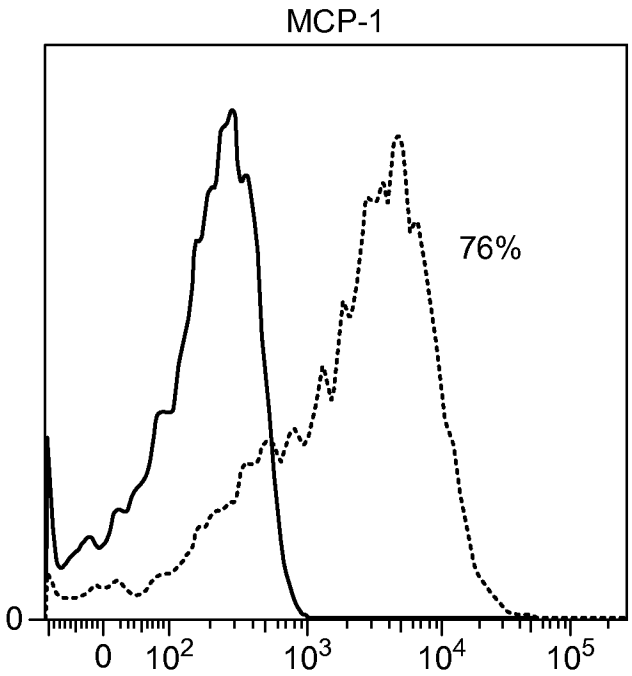

FIG. 2a

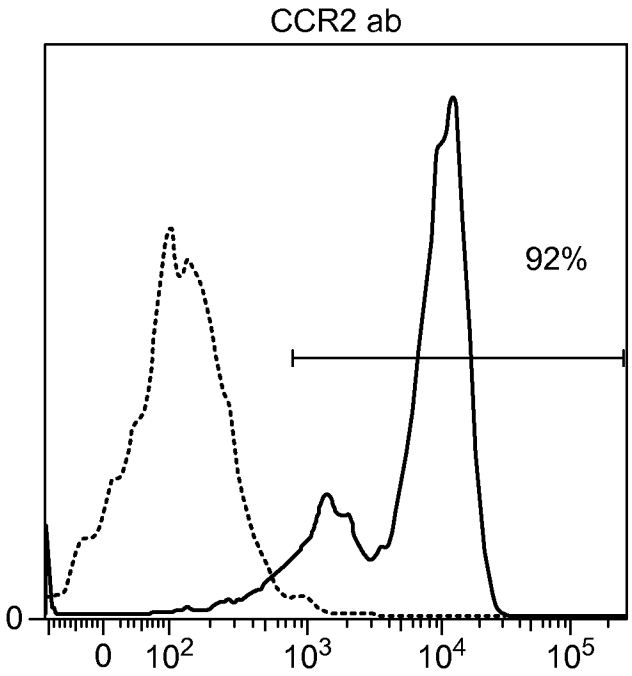

FIG. 2b

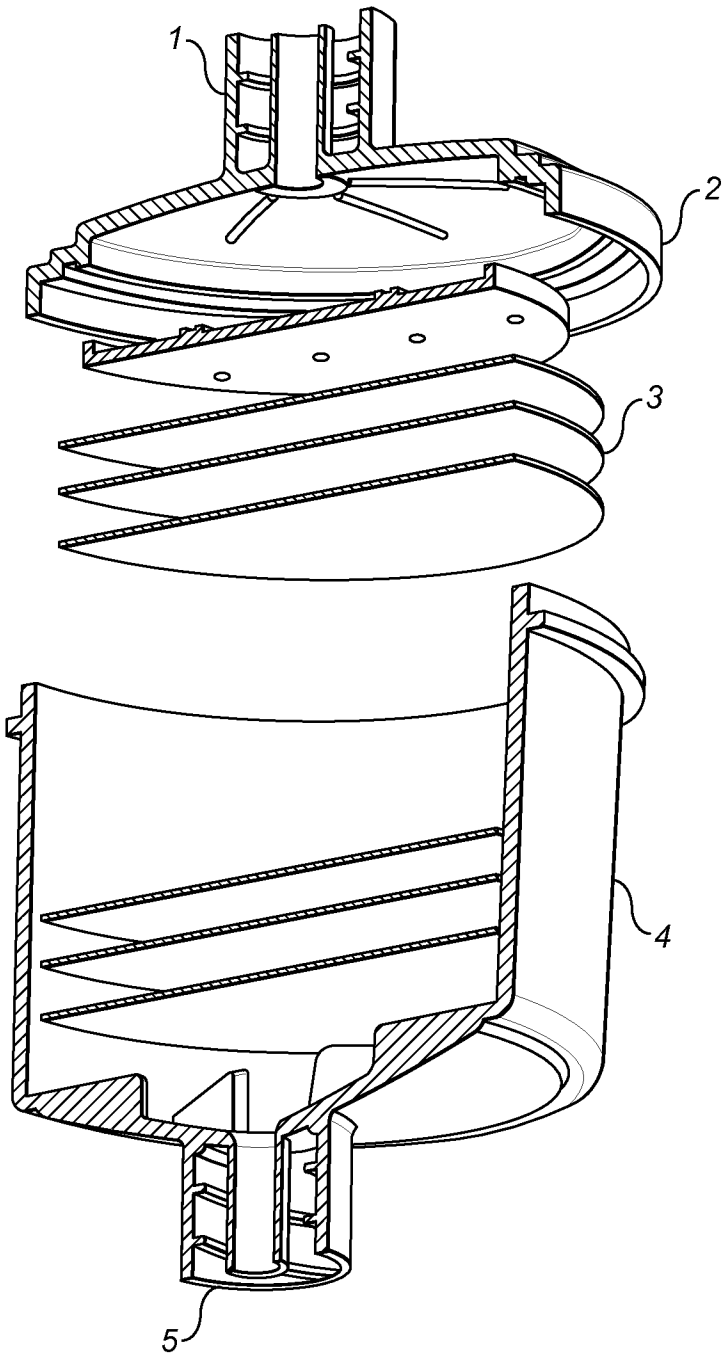

FIG. 3

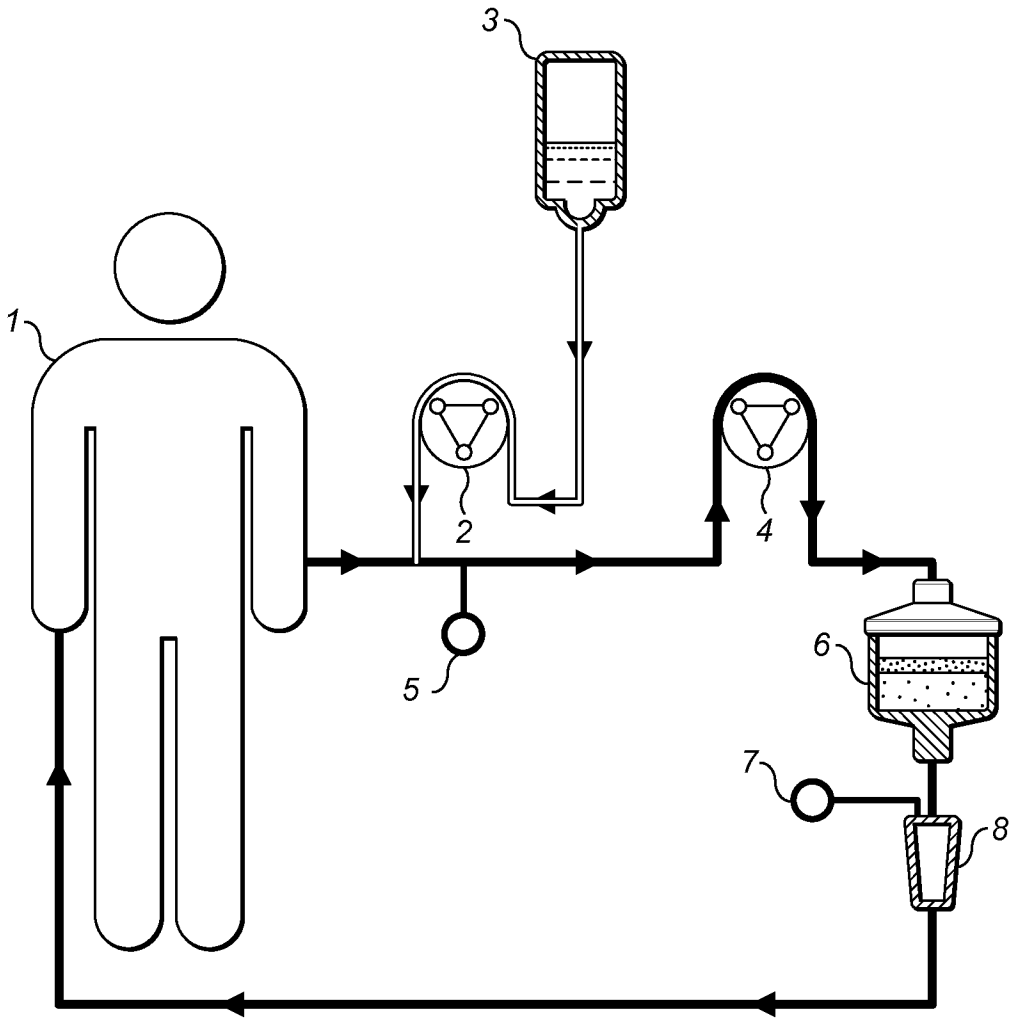

FIG. 4

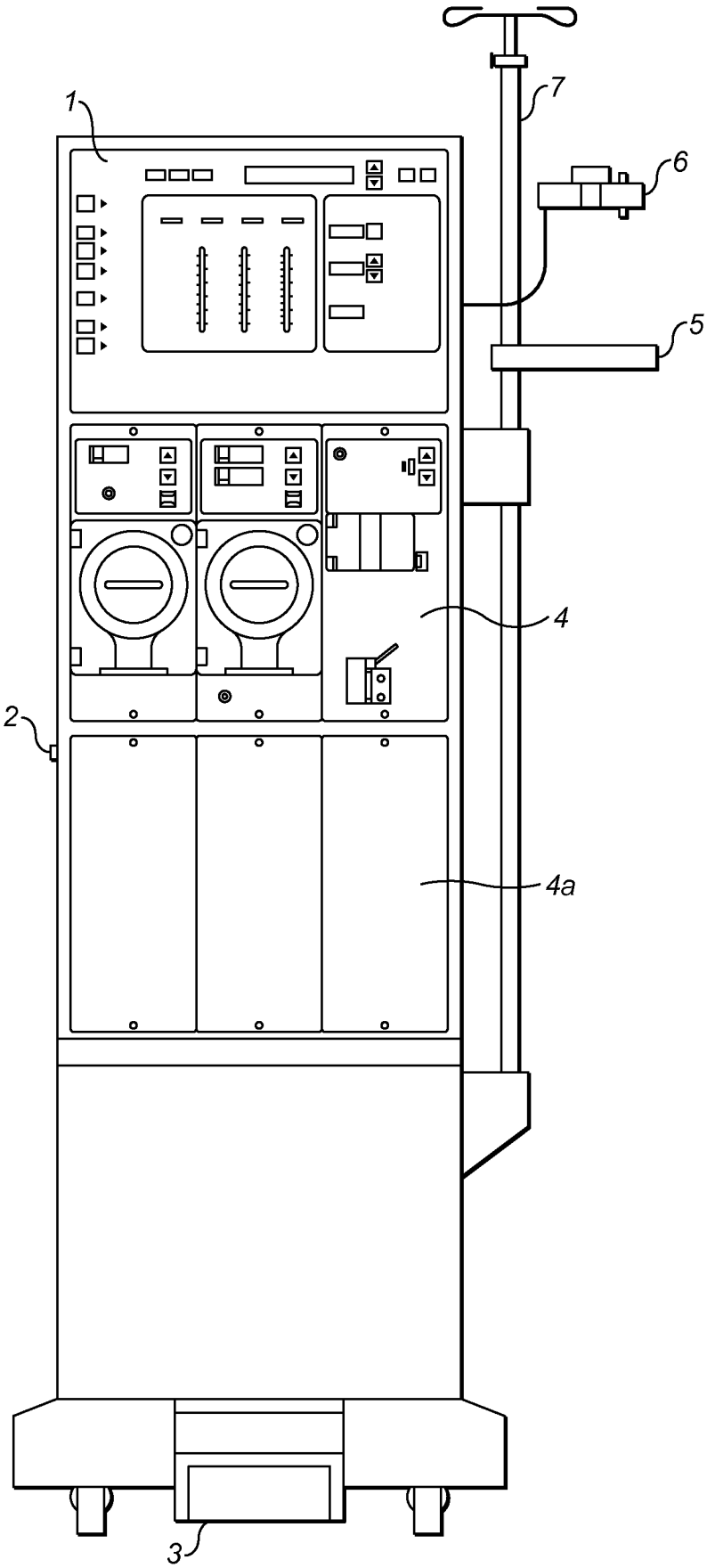

FIG. 5

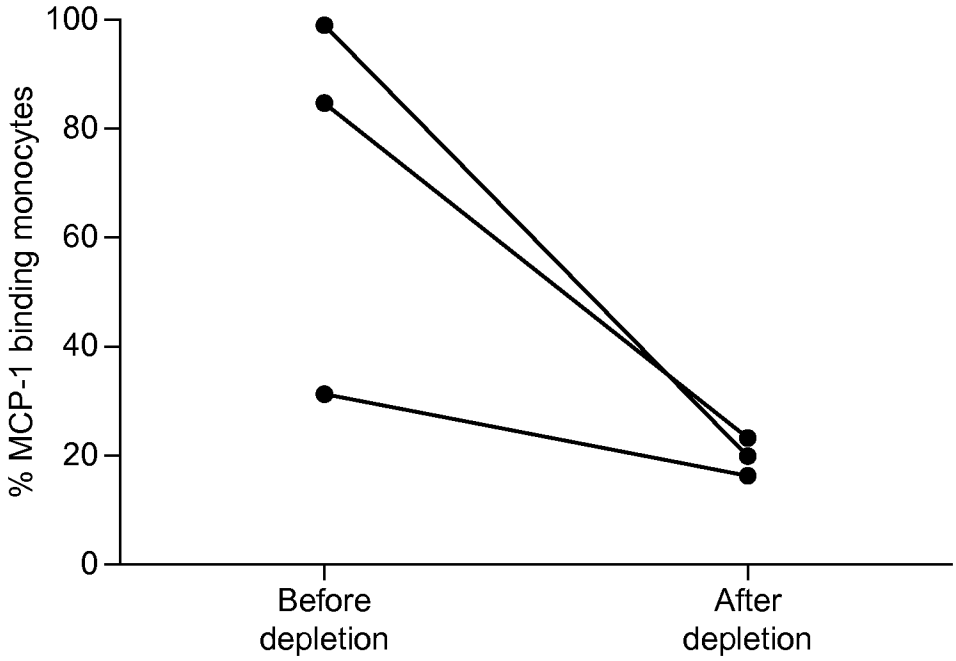
100
80
60
40
20
0
% MCP-1 binding monocytes
Before depletion
After depletion

FIG. 6a

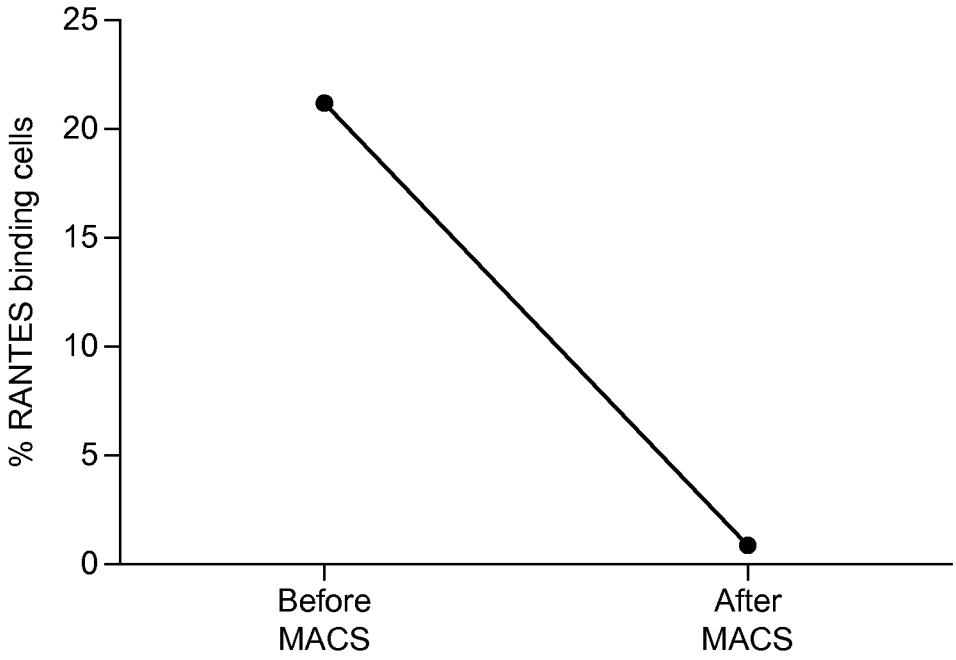
25
20
15
10
5
0
% RANTES binding cells
Before MACS
After MACS

FIG. 6b

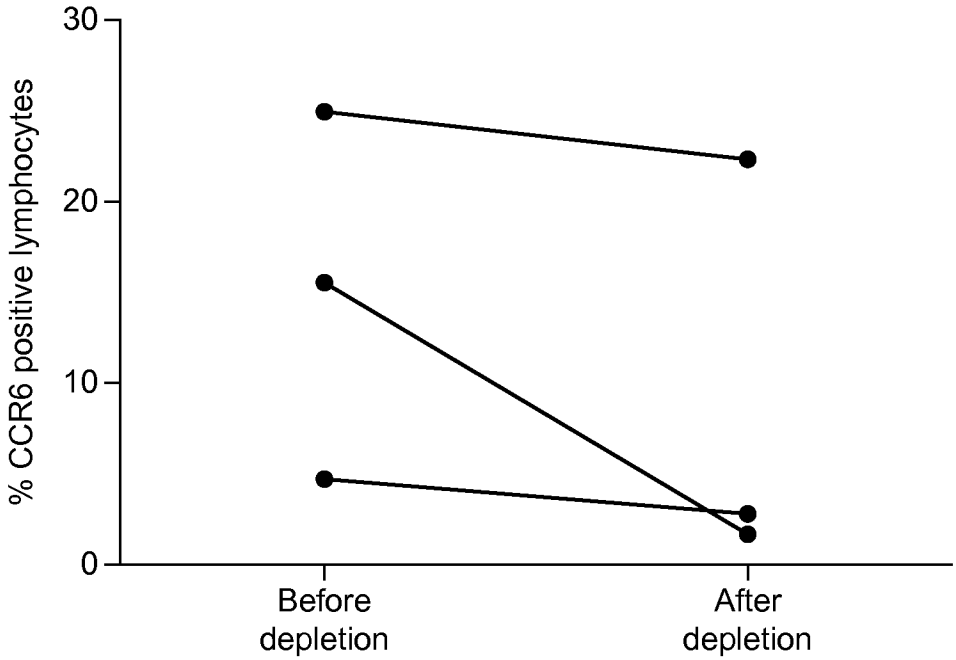
30
20
10
0
% CCR6 positive lymphocytes
Before depletion
After depletion

FIG. 6c

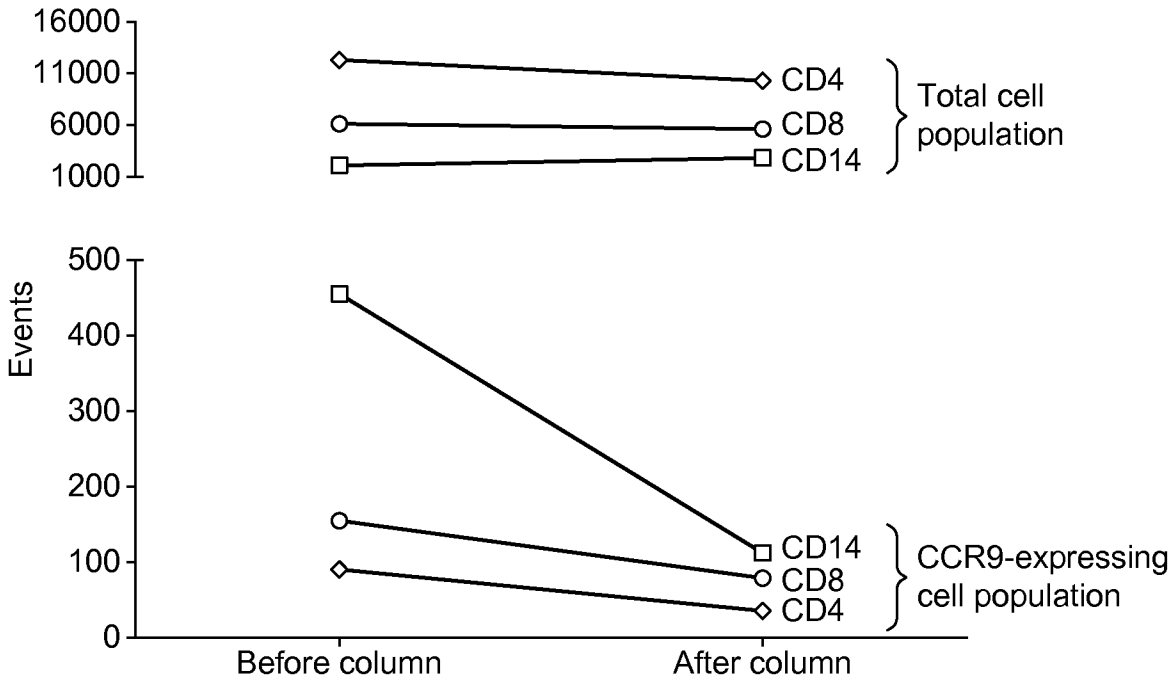
16000
11000
6000
1000
CD4
CD8
CD14
Total cell population
500
400
300
200
100
0
Events
CD14
CD8
CD4
CCR9-expressing cell population
Before column
After column

FIG. 6d

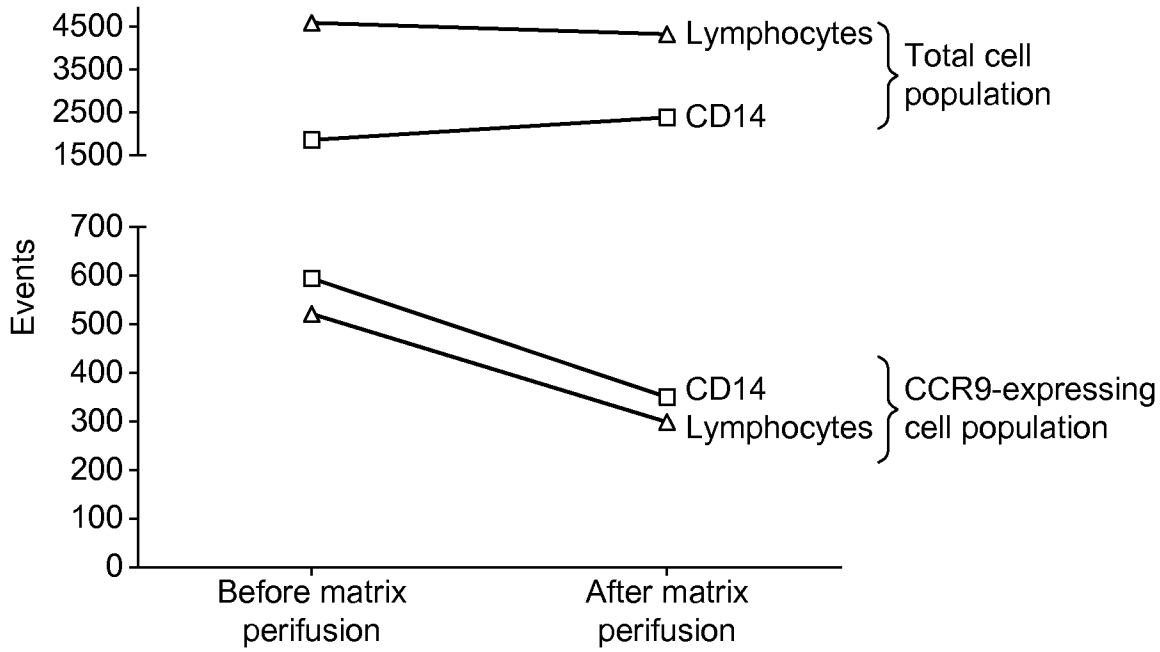
4500
3500
2500
1500
Lymphocytes
CD14
Total cell population
Events
700
600
500
400
300
200
100
0
CD14
Lymphocytes
CCR9-expressing cell population
Before matrix perifusion
After matrix perifusion

FIG. 6e

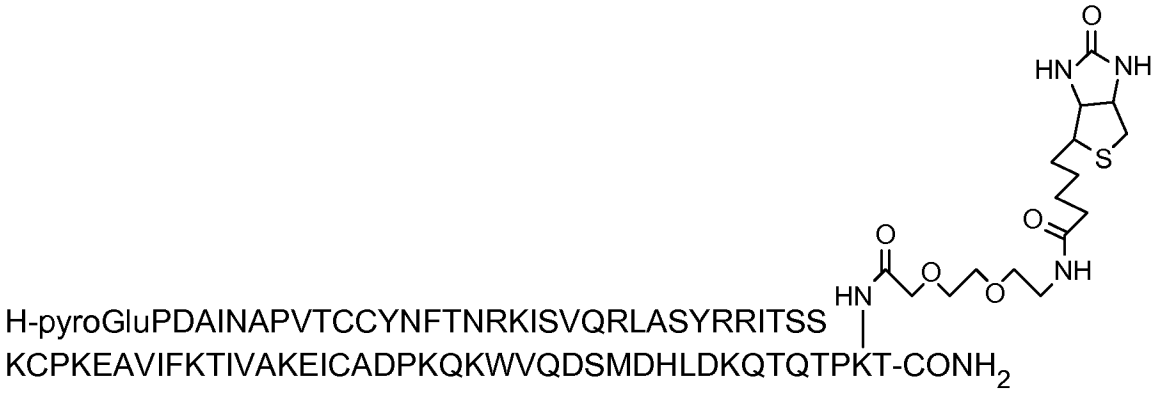

FIG. 7

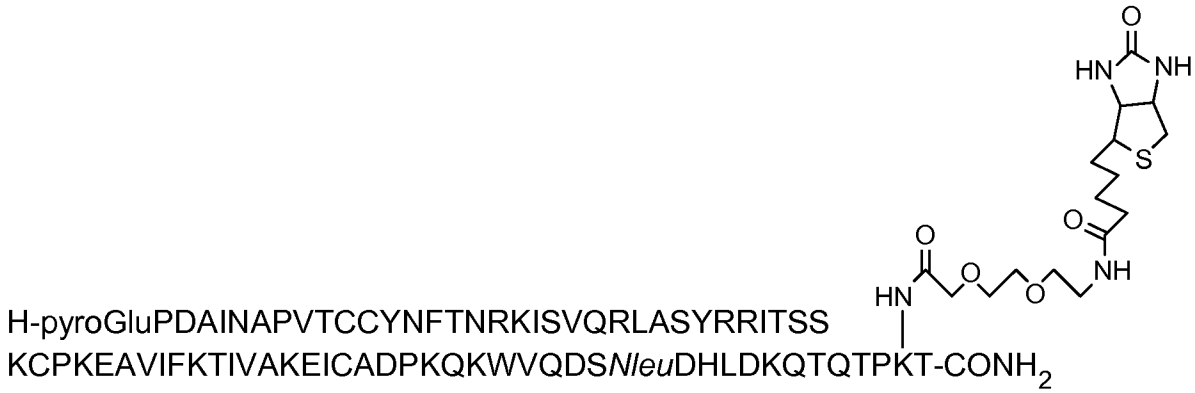

FIG. 8

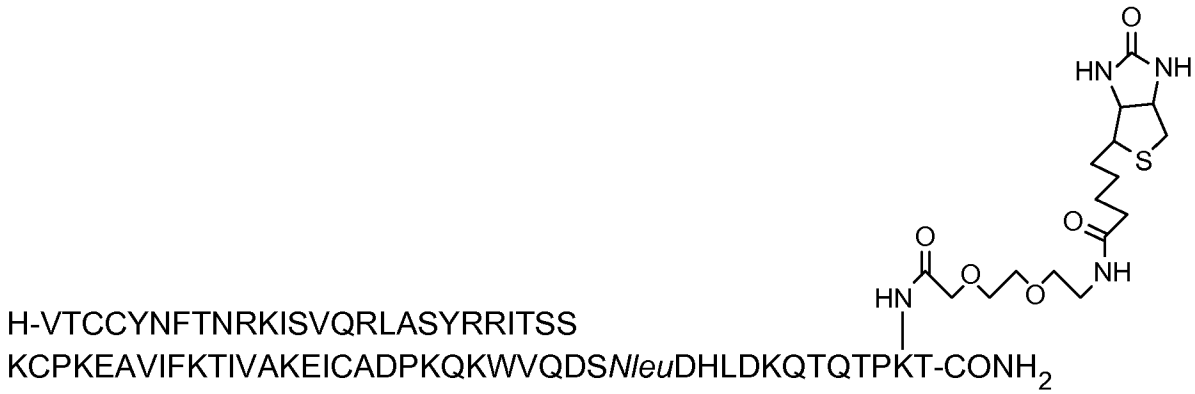

FIG. 9

ulimit -t 30; /usr/molbio/bin/lalign -f -14 -g -4 -K 3 ./wwwtmp/.11134.1.seq ./wwwtmp/.11134.2.seq > ./wwwtmp/.11134.out LALIGN finds the best local alignments between two sequences version 2.1u09 December 2006 Please cite: X. Huang and W. Miller (1991) Adv. Appl. Math. 12:373-381 alignments < E(0.05):score: 38 (3 max)

```
 Comparison of:
(A) ./wwwtmp/.11134.1.seq MCP1 (human) 76 bp
- 76 aa
(B) ./wwwtmp/.11134.2.seq MCP-5 (mouse) 82 bp
- 82 aa
 using matrix file: BL50 (15/-5), gap-open/ext: -14/-4 E(limit)
0.05

  68.1% identity in 72 aa overlap (2-73:2-73); score:  370 E(10000):
1.6e-31

               10        20        30        40        50        60
MCP1    PDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQ
        :::..:::::::: ..::: :..: :::::::.::.:::::.::. :::::::::.:::.
MCP-5   PDAVSTPVTCCYNVVKQKIHVRKLKSYRRITSSQCPREAVIFRTILDKEICADPKEKWVK
               10        20        30        40        50        60

               70
MCP1    DSMDHLDKQTQTPKT
        .:..:::: .::
MCP-5   NSINHLDKTSQTFILEPSCLG
              70
```

FIG. 10

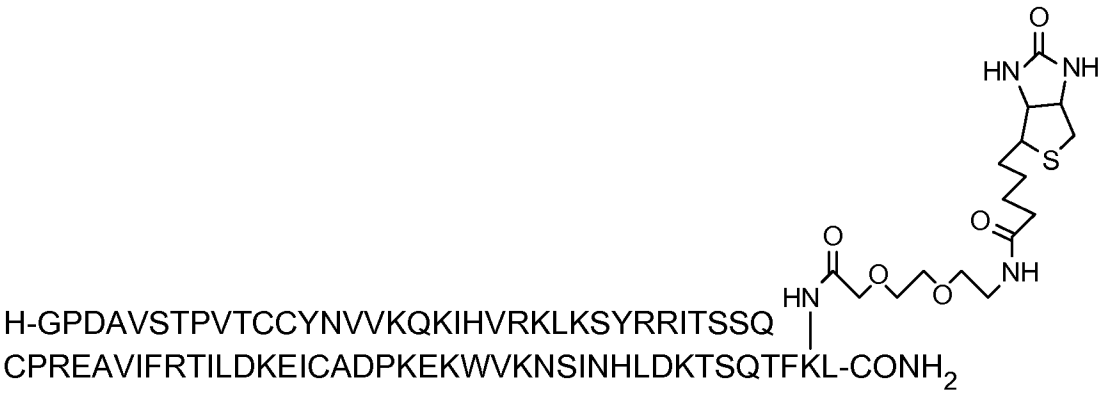
O
HN
NH
S
O
O
NH
HN
O
O
H-GPDAVSTPVTCCYNVVKQKIHVRKLKSYRRITSSQ
CPREAVIFRTILDKEICADPKEKWVKNSINHLDKTSQTFKL-CONH2

FIG. 11

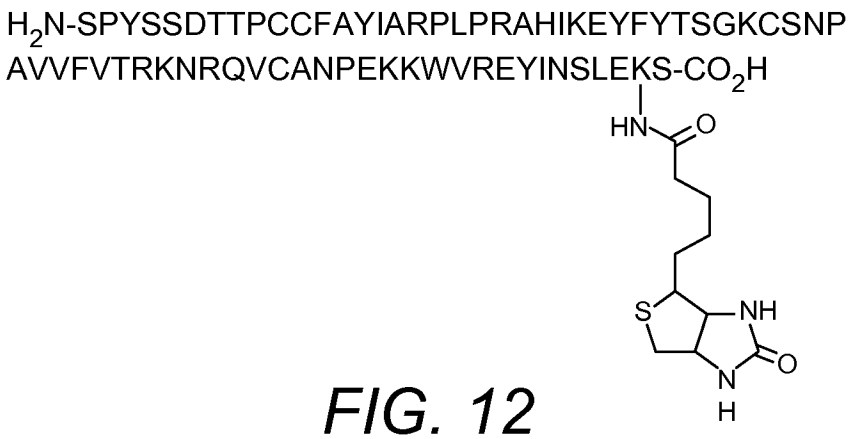
H2N-SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP
AVVFVTRKNRQVCANPEKKWVREYINSLEKS-CO2H
HN
O
S
NH
O
N
H

FIG. 12

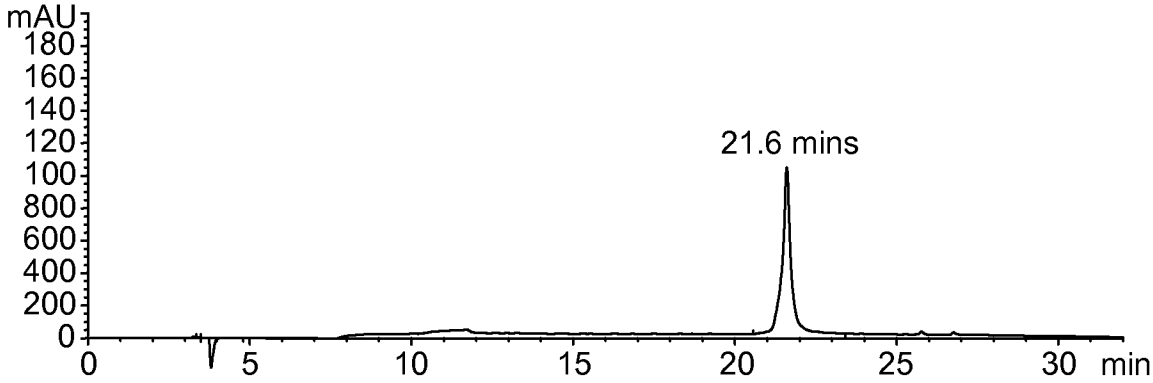
mAU
180
160
140
120
100
800
600
400
200
0
21.6 mins
0
5
10
15
20
25
30
min

FIG. 13

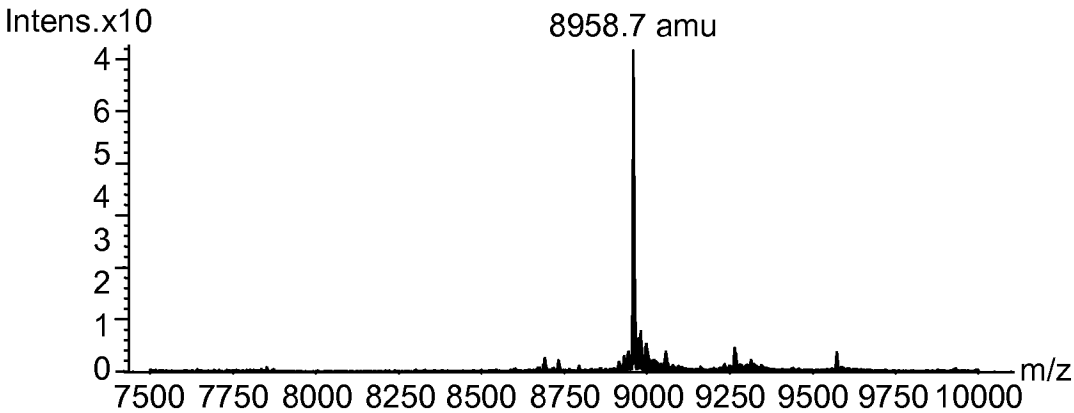
Intens.x10
4
6
5
4
3
2
1
0
8958.7 amu
m/z
7500 7750 8000 8250 8500 8750 9000 9250 9500 9750 10000

FIG. 14

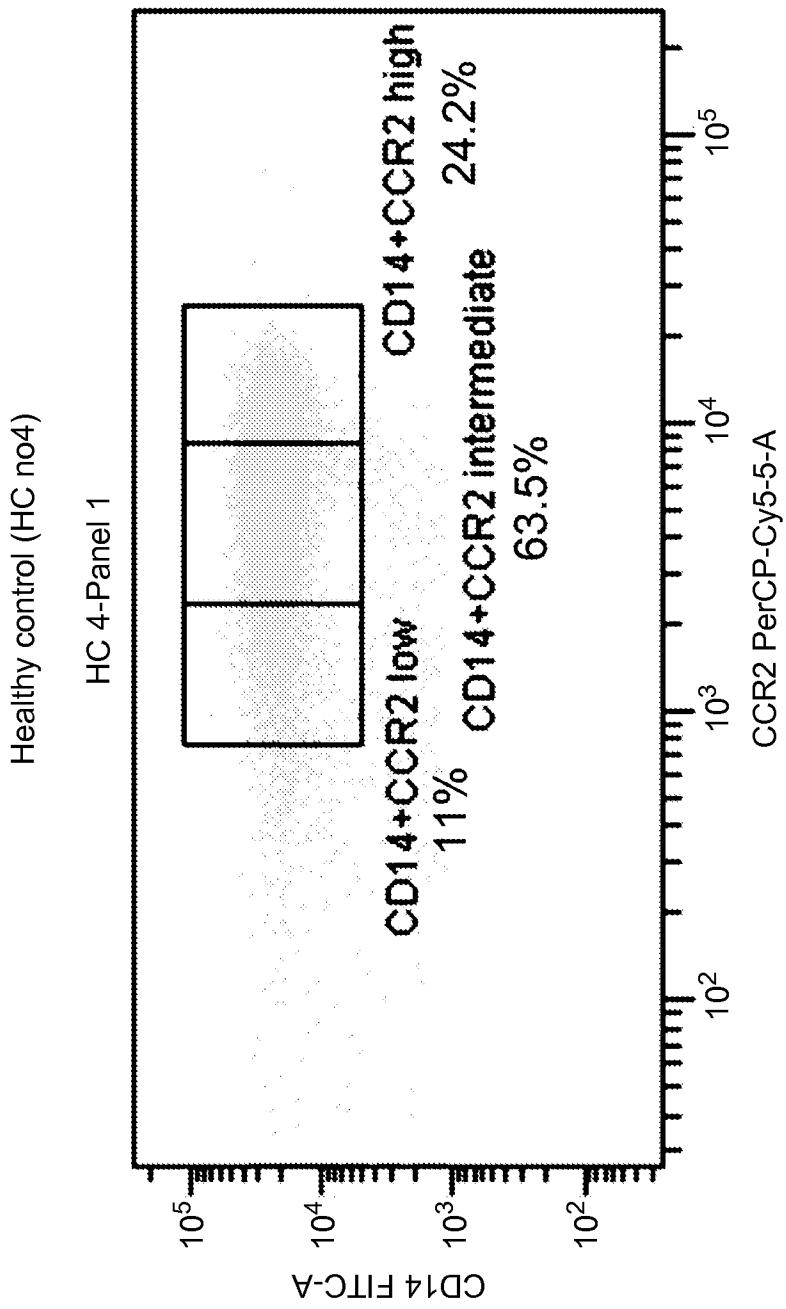
Healthy control (HC no4)
HC 4-Panel 1
CD14+CCR2 high
24.2%
CD14+CCR2 intermediate
63.5%
CD14+CCR2 low
11%
CD14 FITC-A
CCR2 PerCP-Cy5-5-A
10^2
10^3
10^4
10^5

FIG. 15

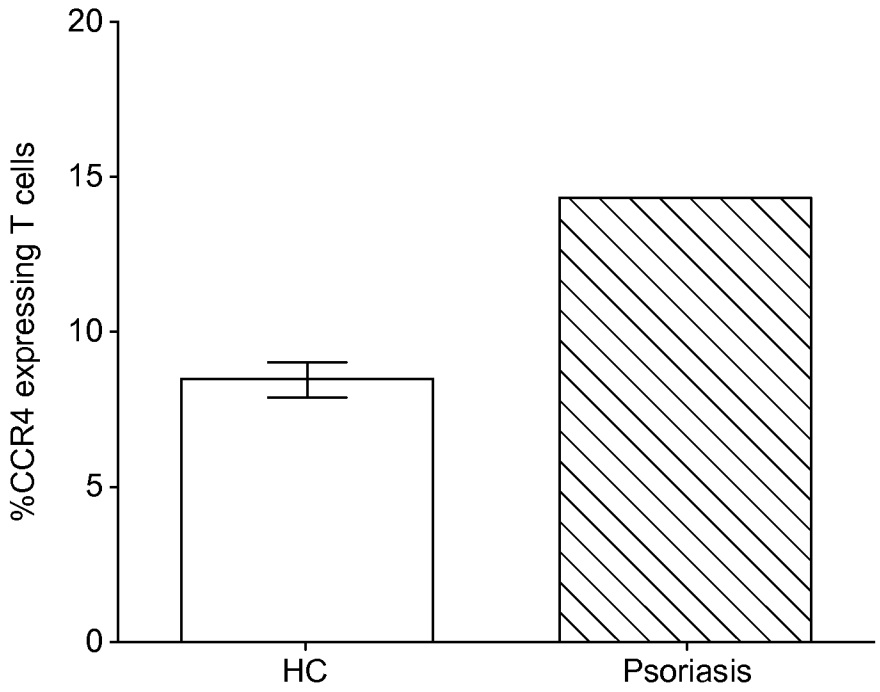
20
15
10
5
0
%CCR4 expressing T cells
HC
Psoriasis

FIG. 16

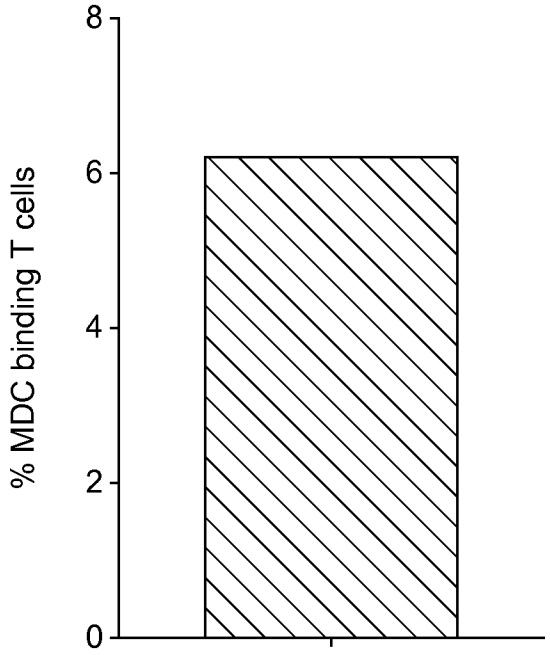
8
6
4
2
0
% MDC binding T cells

FIG. 17

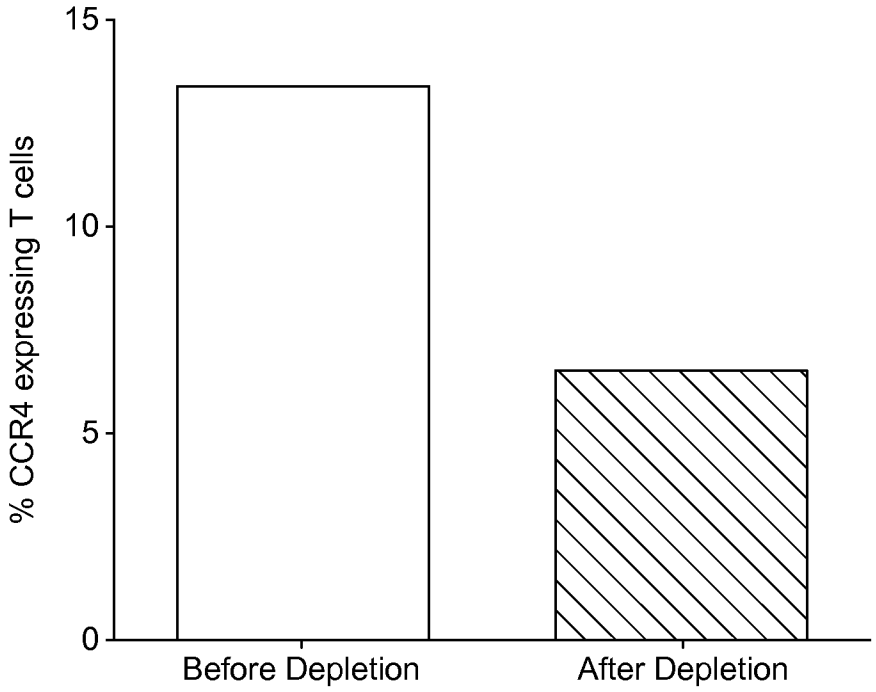
15
10
5
0
% CCR4 expressing T cells
Before Depletion
After Depletion

FIG. 18

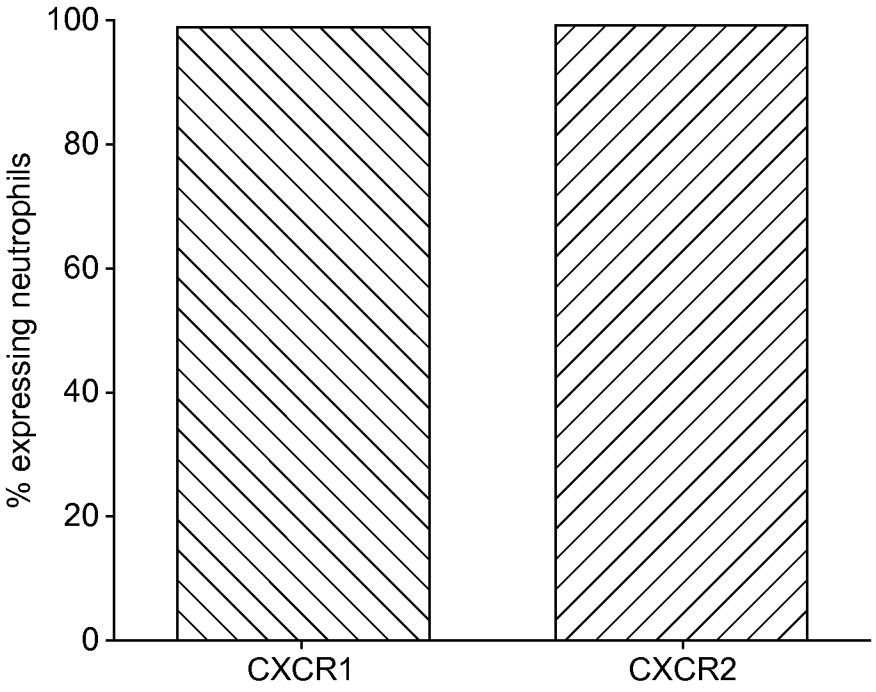
100
80
60
40
20
0
% expressing neutrophils
CXCR1
CXCR2

FIG. 19

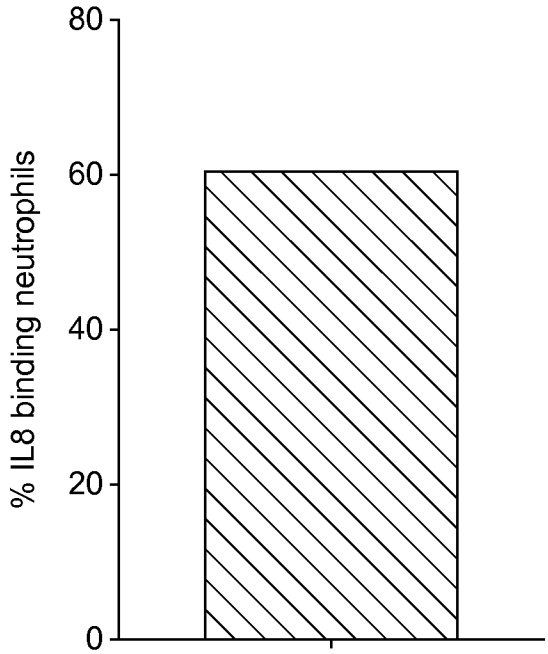
80
60
40
20
0
% IL8 binding neutrophils

FIG. 20

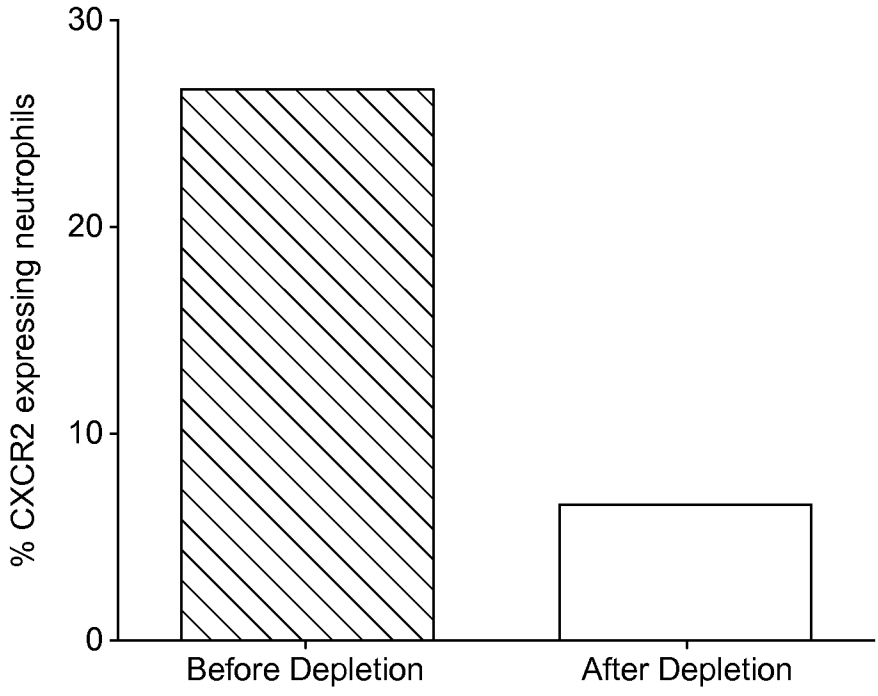
30
20
10
0
% CXCR2 expressing neutrophils
Before Depletion
After Depletion

FIG. 21