

ANTIBODY VARIABLE DOMAINS THAT BIND IL-31

FIELD OF THE INVENTION

[0001] The present invention relates to an antibody variable domain, which specifically binds to IL-31, to multispecific antibodies comprising one or two of said antibody variable domains and at least one further binding domain that specifically binds to a target different from IL-31. The present invention further relates to a nucleic acid or two nucleic acids encoding said antibody variable domain or said multispecific antibody, vector(s) comprising said nucleic acids or said nucleic acids, host cell(s) comprising said nucleic acid or said nucleic acids or said vector(s), and a method of producing said antibody variable domain or said multispecific antibody. Additionally, the present invention relates to pharmaceutical compositions comprising said antibody variable domain or said multispecific antibody and to methods of use thereof.

BACKGROUND OF THE INVENTION

[0002] Interleukin 31 (IL-31) is an inflammatory cytokine that helps trigger cell-mediated immunity against pathogens. IL-31 is preferentially produced by Th2-cells. IL-31 sends signals through a heterodimeric receptor complex (IL-31R or IL31R) comprising the interleukin 31 receptor alpha (IL-31RA or IL31RA) and the oncostatin M receptor β (OSMR β), expressed in immune and epithelial cells. Binding of IL-31 to this receptor complex results in activation of the JAK/STAT and PI3K/AKT signal transduction pathways, and also activates different MAPK pathways (ERK, p38, and JNK).

[0003] IL-31 is implicated in various chronic inflammatory diseases. For example, it has been found that IL-31 over-expression in mice results in dermatitis-like symptoms, see, Dillon, et al, Nature Immunol. 5 (2004):752-760. Furthermore, in many chronic inflammatory diseases, such as for example in atopic dermatitis (AD), IL-31 mediates activation of nerve fibers within the skin of the patients resulting in an aggressive itch-phenotype, which exacerbates the symptoms of these diseases upon patient scratching, see for example Oetjen et al., Cell 171 (2017) 217–228.

Scratching can lead to skin barrier disruption, access of microbial pathogens into the skin and further promotes inflammation at the site.

[0004] Atopic dermatitis (AD) is a chronic inflammatory skin disease characterized by intense pruritus (*i. e.* severe itch) and by scaly and dry eczematous lesions.

Severe disease can be extremely disabling due to major psychological problems, significant sleep loss, and impaired quality of life, leading to high socioeconomic costs. AD often begins in childhood before age 5 and may persist into adulthood.

[0005] The pathophysiology of AD is influenced by a complex interplay between immunoglobulin E (IgE)-mediated sensitization, the immune system, and environmental factors. The primary skin defect may be an immunological disturbance that causes IgE-mediated sensitization, with epithelial-barrier dysfunction that is the consequence of both genetic mutations and local inflammation.

[0006] Also, it has been found that IL-31 is implicated in allergic asthma, allergic rhinitis, inflammatory bowel diseases, malignancies and osteoporosis, see Bagci et al., J Allergy Clin Immunol. 141 (2018):858-866.

[0007] Blockage of IL-31/IL-31RA-signaling by anti-IL31RA antibodies, such as for example by the anti-IL-31RA antibody nemolizumab, is clinically proven to be effective at reducing itch in patients suffering from AD, see Ruzicka et al., N Engl J Med. 376 (2017):2092-2093.

[0008] Furthermore, the IL-31-neutralizing antibody BMS-981164 was developed to provide an effective targeted therapy for the treatment of chronic pruritic skin conditions, see Lewis et al, J Eur Acad of Dermatol Venereol. 31 (2017)142-150.

[0009] While these anti-IL-31 therapies appear to be effective in treating itch symptoms occurring in pruritus-causing diseases, such as for example in AD, they typically do not address the underlying cause of these diseases. Even for allergic, inflammatory and autoimmune disorders that have been associated with an imbalanced IL-31 signaling, the efficacy of these anti-IL-31 therapies is often limited and/or the response rates are low to moderate, indicating that imbalanced IL-31 signaling is often not the sole cause of these diseases. Thus, in order to increase the response rates and/or efficacy of these therapies, other signaling pathways have to be addressed as well. Thus, there is a critical need for additional IL-31-based treatment options for patients living with such allergic, inflammatory and autoimmune disorders.

[0010] More specifically, it is desirable to have a stable and potent anti-IL-31 antibody building block at hand that can readily be incorporated into multispecific antibody formats, which additionally interfere in other signaling pathways. Said anti-IL-31 building blocks should have a high potency in inhibiting IL-31-mediated signaling. Furthermore, said building blocks should have superior biophysical properties, such as in particular a high stability, in order to facilitate their efficient incorporation into multispecific antibodies being suitable for pharmaceutical development.

[0011] In particular, said anti-IL-31 building block, *i. e.* antibody binding domain, should exhibit the following minimum features:

- it should bind to *human* IL-31 with a monovalent dissociation constant (K_D) of 5 nM or less, as measured by surface plasmon resonance (SPR);
- it should inhibit the *human* IL-31-induced signaling with an IC_{50} of 30 ng/ml or less, as measured in a Path Hunter IL-31RA/OSMRb dimerization assay;
- it should have a loss in monomer content, after storage for at least four weeks at 4°C or 40°C of 5 % or less, when being at a starting concentration of 10 mg/ml, and when formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4.

[0012] Furthermore, it is desirable that said anti-IL-31 building block has a melting temperature (T_m), determined by differential scanning fluorimetry, of 65°C or higher, when formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4.

[0013] While strategies are known in the prior art how to identify anti-IL-31 antibody variable domains that fulfill one or two of the abovementioned criteria, the identification of such antibody variable domains that fulfill all of these criteria, let alone most or all of the criteria mentioned in item 7 below, is challenging and the outcome is unpredictable.

SUMMARY OF THE INVENTION

[0014] It is an object of the present invention to provide novel antibody variable domains, which specifically bind IL-31, that are able to efficiently reduce or eliminate IL-31-mediated activity and that are at the same time highly stable so that they can be readily incorporated into multispecific antibody formats.

[0015] The inventors have now surprisingly found that scFvs based on the monoclonal rabbit antibody clone 50-09-D07 are able to potently block IL-31 signaling while exhibiting excellent stability. This antibody clone is one of a limited number of monoclonal rabbit antibody clones from a broad immunization campaign that have been identified to bind to IL-31 with high affinity. In particular, the scFvs derived from clone 50-09-D07 bind to IL-31 with a dissociation constant (KD) of well below 1 nM, can neutralize the IL-31-induced signaling with an IC₅₀ of below 30 ng/ml and can be stored at a concentration of 10 mg/ml over a period of 4 weeks at 4°C and 40°C without significant loss in protein content and monomeric content. This is particularly surprising in view of the fact that none of the scFvs produced from the other clones exhibit a good pharmacological activity and at the same time a high stability. Optimization of the pharmacological activity of these scFvs almost exclusively resulted in a worsening of the stability and *vice versa*.

[0016] Thus, the scFvs that are based on clone 50-09-D07 represent suitable building blocks that can readily be incorporated into multispecific antibody formats such as Morrison formats.

[0017] Accordingly, in a first aspect, the present invention relates to an antibody variable domain, which specifically binds to IL-31, comprising:

- a) a VH chain having a sequence selected from SEQ ID NOs: 5, 6 and 7, and
- b) a VL chain having a sequence selected from SEQ ID NO: 12 and 37.

[0018] In a second aspect, the present invention relates to a multispecific antibody comprising:

- a) one or two antibody variable domains as defined herein;
- b) at least one binding domain, which specifically binds to a target different from IL-31.

[0019] In a third aspect, the present invention relates to a nucleic acid or two nucleic acids encoding the antibody variable domain or the multispecific antibody of the present invention.

[0020] In a fourth aspect, the present invention relates to a vector or two vectors comprising the nucleic acid or the two nucleic acids of the present invention.

[0021] In a fifth aspect, the present invention relates to a host cell or host cells comprising the vector or the two vectors of the present invention.

[0022] In a sixth aspect, the present invention relates to a method for producing the antibody variable domain or the multispecific antibody of the present invention, comprising (i) providing the nucleic acid or the two nucleic acids of the present invention, or the vector or the two vectors of the present invention, expressing said nucleic acid or said two nucleic acids, or said vector or vectors, and collecting said antibody variable domain or said multispecific antibody from the expression system, or (ii) providing a host cell or host cells of the present invention, culturing said host cell or said host cells; and collecting said antibody variable domain or said multispecific antibody from the cell culture.

[0023] In a seventh aspect, the present invention relates to a pharmaceutical composition comprising the antibody variable domain of the multispecific antibody of the present invention and a pharmaceutically acceptable carrier.

[0024] In an eighth aspect, the present invention relates to the antibody variable domain or the multispecific antibody of the present invention for use as a medicament.

[0025] In a ninth aspect, the present invention relates to the antibody variable domain or the multispecific antibody of the present invention for use in the treatment of a disease, particularly a human disease, more particularly a human disease selected from allergic, inflammatory and autoimmune diseases, particularly from inflammatory and autoimmune diseases.

[0026] In a tenth aspect, the present invention relates to a method for the treatment of a disease, particularly a human disease, more particularly a human disease selected from allergic, inflammatory and autoimmune diseases, particularly from inflammatory and autoimmune diseases, comprising the step of administering the antibody variable domain or the multispecific antibody of the present invention to a patient in need thereof.

[0027] The aspects, advantageous features and preferred embodiments of the present invention summarized in the following items, respectively alone or in combination, further contribute to solving the object of the invention:

1. An antibody variable domain, which specifically binds to IL-31, comprising:
 - a) variable heavy chain (VH),

wherein the variable heavy chain comprises, from N-terminus to C-terminus, the regions HFW1-HCDR1-HFW2-HCDR2-HFW3-HCDR3-HFW4, wherein each HFW designates a heavy chain framework region, and each HCDR designates a heavy chain complementarity-determining region, and wherein said HCDR1 has the sequence of SEQ ID NO: 1;
said HCDR2 has a sequence selected from SEQ ID NO: 2 or 3; and
said HCDR3 has the sequence of SEQ ID NO: 4;

b) variable light chain (VL),

wherein the variable light chain comprises, from N-terminus to C-terminus, the regions LFW1-LCDR1-LFW2-LCDR2-LFW3-LCDR3-LFW4, wherein each LFW designates a light chain framework region, and each LCDR designates a light chain complementarity-determining region, and wherein said LCDR1 has a sequence selected from SEQ ID NO: 9 or 36;
said LCDR2 has the sequence of SEQ ID NO: 10; and
said LCDR3 has the sequence of SEQ ID NO: 11.

2. The antibody variable domain of item 1, wherein said variable heavy chain is a VH3 chain, and/or wherein said variable light chain is a Vk1 light chain.
3. The antibody variable domain of item 1, wherein
 - said variable heavy chain is a VH3 chain,
 - the LFW1, LFW2 and LFW3 are of the Vk1 light chain subtype, and
 - the LFW4 has a human Vλ sequence selected from SEQ ID NOs: 16 to 23.
4. The antibody variable domain of any one of the preceding items, wherein said antibody variable domain is selected from a Fab, an Fv, an scFv, dsFv, and an scAB, preferably from a Fab, an Fv, an scFv and a dsFv, in particular from a Fab, an scFv and a dsFv.
5. The antibody variable domain of any one of the preceding items, wherein said antibody variable domain comprises:

- a) a VH chain having a sequence at least 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 percent identical to any one of the amino acid sequences selected from SEQ ID NOs: 5, 6 and 7; and
 - b) a VL chain having a sequence at least 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 percent identical to any one of the amino acid sequences selected from SEQ ID NO: 12 and 37.
6. The antibody variable domain of any one of the items 1 to 5, wherein said antibody variable domain blocks the binding of IL-31 to the interleukin 31 receptor alpha (IL-31RA)/oncostatin M receptor (OSMR) complex (IL-31RA/OSMR complex).
7. The antibody variable domain of any one of the items 1 to 5, wherein said antibody variable domain, when being in an scFv format, exhibits at least 2 of the following features a. to d.:
- a. binds to *human* IL-31 with a monovalent dissociation constant (K_D) of 5 nM or less, particularly with a monovalent K_D of 5 pM to 5 nM, particularly of 5 pM to 2 nM, particularly of 5 to 1000 pM, as measured by surface plasmon resonance (SPR);
 - b. is cross-reactive with *Macaca fascicularis* (Cynomolgus) IL-31, in particular bind to Cynomolgus IL-31 with a monovalent K_D of 5 nM or less, particularly with a monovalent K_D of 5 pM to 5 nM, particularly of 5 pM to 2 nM, particularly of 5 to 1000 pM, as measured by SPR;
 - c. inhibits the human IL-31-induced signaling with an IC_{50} of 0.1 to 30 ng/ml, particularly with an IC_{50} of 0.1 to 20 ng/ml, particularly with an IC_{50} of 0.1 to 10 ng/ml, as measured in a Path Hunter IL-31RA/OSMRb dimerization assay;
 - d. blocks the binding of human IL-31 to human IL-31R with an IC_{50} of 0.1 to 20 ng/ml, particularly with an IC_{50} of 0.1 to 10 ng/ml, particularly with an IC_{50} of 0.1 to 6 ng/ml, as measured in a competition ELISA;
- and wherein wherein said antibody variable domain, when being in an scFv format, further exhibits at least 2 of the following features e. to i.:
- e. has a melting temperature (T_m), determined by differential scanning fluorimetry, of at least 65°C, preferably of at least 67°C, more preferably at

- least 69°C, in particular wherein said scFv is formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
- f. has a loss in monomer content, after storage for four weeks at 4°C of less than 5 %, *e. g.* less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFv is at a starting concentration of 10 mg/ml, and in particular wherein said scFv is formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
 - g. has a loss in monomer content, after storage for four weeks at 40°C of less than 5 %, *e. g.* less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFv is at a starting concentration of 10 mg/ml, and in particular wherein said scFv is formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
 - h. has a loss in monomer content, after 3 freeze-thawing cycles, of less than 5 %, *e. g.* less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFv is at a starting concentration of 10 mg/ml, and in particular wherein said scFv is formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
 - i. has a loss in protein content, after storage for four weeks at 4°C or 40°C of less than 5 %, *e. g.* less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFv is at a starting concentration of 10 mg/ml, and in particular wherein said scFv is formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4.
8. The antibody variable domain of item 7, wherein said antibody variable domain, when being in an scFv format, exhibits at least the features a., c., f. and g.
9. The antibody variable domain of item 7, wherein said antibody variable domain, when being in an scFv format, exhibits at least the features a., c., e., f. and g., in particular at least the features a., c., d., e., f. and g., in particular all features a. to i.
10. The antibody variable domain of any one of the preceding items, wherein said antibody variable domain comprises:

- a) a VH chain having a sequence selected from SEQ ID NOs: 5, 6 and 7, and
 - b) a VL chain having a sequence selected from SEQ ID NO: 12 and 37.
11. The antibody variable domain of any one of the preceding items, wherein said antibody variable domain comprises:
- a) a VH chain having the sequence of SEQ ID NO: 5 and a VL chain having the sequence of SEQ ID NO: 12; or
 - b) a VH chain having the sequence of SEQ ID NO: 6 and a VL chain having the sequence of SEQ ID NO: 12; or
 - c) a VH chain having the sequence of SEQ ID NO: 7 and a VL chain having the sequence of SEQ ID NO: 12; or
 - d) a VH chain having the sequence of SEQ ID NO: 5 and a VL chain having the sequence of SEQ ID NO: 37.
12. The antibody variable domain of any one of the preceding items, which is an scFv antibody having a sequence selected from SEQ ID NOs: 27 to 29 and 31.
13. A multispecific antibody comprising:
- a) one or two antibody variable domains as defined in any one of items 1 to 12;
 - b) at least one binding domain, which specifically binds to a target different from IL-31.
14. The multispecific antibody of item 13, wherein the multispecific antibody does not comprise an immunoglobulin Fc region.
15. The multispecific antibody of item 14, wherein the multispecific antibody is in a format selected from the group consisting of: a tandem scDb (Tandab), a linear dimeric scDb (LD-scDb), a circular dimeric scDb (CD-scDb), a tandem tri-scFv, a tribody (Fab-(scFv)₂), a Fab-Fv₂, atriabody, an scDb-scFv, a tetrabody, a di-diabody, a tandem-di-scFv and a MATCH.
16. The multispecific antibody of item 14, wherein said antibody does not comprise CH1 and/or CL regions.

17. The multispecific antibody of item 16, wherein said antibody is in a scDb-scFv, a triabody, a tetrabody or a MATCH format, in particular wherein said multispecific antibody is in a MATCH or scDb-scFv format, more particularly wherein said multispecific antibody is in a MATCH format, more particularly a MATCH3 or a MATCH4 format.
18. The multispecific antibody of item 13, wherein the multispecific antibody comprises an immunoglobulin Fc region.
19. The multispecific antibody of item 18, wherein the immunoglobulin Fc region is selected from an IgG subclass, particularly from IgG subclasses IgG1 and IgG4, particularly from IgG4.
20. The multispecific antibody of item 19, wherein the format of said multispecific antibody is selected from bivalent bispecific IgG formats, trivalent bispecific IgG formats and tetravalent bispecific IgG formats;
more particularly wherein the format of said multispecific antibody is selected from KiH-based IgGs; DVD-Ig; CODV-IgG and Morrison (IgG CH₃-scFv fusion (Morrison-H) or IgG CL-scFv fusion (Morrison-L)), even more particularly from DVD-Ig and Morrison (IgG CH₃-scFv fusion (Morrison-H) or IgG CL-scFv fusion (Morrison-L)).
21. The multispecific antibody of item 20, wherein the format of said multispecific antibody is selected from a Morrison-H and Morrison-L format.
22. The multispecific antibody of any one of items 13 to 21, wherein said multispecific antibody comprises two antibody variable domains as defined in any one of items 1 to 12 and two binding domains, which specifically bind to a second target different from IL-31.
23. A nucleic acid or two nucleic acids encoding the antibody variable domain of any one of items 1 to 12 or the multispecific antibody of any one of items 13 to 22.

24. A vector or two vectors comprising the nucleic acid or the two nucleic acids of item 23.
25. A host cell or host cells comprising the vector or the two vectors of item 24.
26. A method for producing the antibody variable domain of items 1 to 12 or the multispecific antibody of items 13 to 22, comprising (i) providing the nucleic acid or the two nucleic acids of item 23, or the vector or the two vectors of item 24, expressing said nucleic acid or said two nucleic acids, or said vector or said two vectors, and collecting said antibody variable domain or said multispecific antibody from the expression system, or (ii) providing a host cell or host cells according to item 25, culturing said host cell or said host cells; and collecting said antibody variable domain or said multispecific antibody from the cell culture.
27. A pharmaceutical composition comprising the antibody variable domain of items 1 to 12 or the multispecific antibody of any one of items 13 to 22 and a pharmaceutically acceptable carrier.
28. The antibody variable domain of any one of items 1 to 12 or the multispecific antibody of any one of items 13 to 22 for use as a medicament.
29. The antibody variable domain of any one of items 1 to 12 or the multispecific antibody of any one of items 13 to 22 for use in the treatment of a disease, particularly a human disease, more particularly a human disease selected from allergic, inflammatory and autoimmune diseases, particularly from pruritus-causing allergic diseases, pruritus-causing inflammatory diseases and pruritus-causing autoimmune diseases.
30. The antibody variable domain or the multispecific antibody for use according to item 29, wherein said disease is selected from atopic dermatitis, acute allergic contact dermatitis, chronic spontaneous urticaria, bullous pemphigoid, alopecia areata, dermatomyositis, prurigo nodularis, psoriasis and atopic asthma; particularly wherein said disease is atopic dermatitis.

31. A method for the treatment of a disease, particularly a human disease, more particularly a human disease selected from allergic, inflammatory and autoimmune diseases, particularly from inflammatory and autoimmune diseases, comprising the step of administering the antibody variable domain of any one of items 1 to 12 or the multispecific antibody of any one of items 13 to 22 to a patient in need thereof.
32. The method of item 31, wherein said disease is selected from atopic dermatitis, acute allergic contact dermatitis, chronic spontaneous urticaria, bullous pemphigoid, alopecia areata, dermatomyositis, prurigo nodularis, psoriasis and atopic asthma; particularly wherein said disease is atopic dermatitis.

BRIEF DESCRIPTION OF THE DRAWINGS

[0028] **FIG. 1** shows the potency of three scFvs to neutralize IL-31-induced signaling in the IL-31RA/OSMR dimerization assay. (A) PRO1641 (50-03-H07-sc03), (B) PRO1643 (50-09-D07-sc03) and (C) PRO1650 (50-35-B03-sc03) are potent inhibitors with IC_{50} values comparable to BMS-981164 for neutralization of IL-31 induced signaling.

[0029] **FIG. 2** shows the potencies of three scFvs to inhibit the interaction between IL-31 and IL-31RA in the competitive ELISA. (A) PRO1641 (50-03-H07-sc03), (B) PRO1643 (50-09-D07-sc03) and (C) PRO1650 (50-35-B03-sc03) are potent inhibitors of the IL-31 / IL-31R interaction with IC_{50} values comparable to BMS-981164.

[0030] **FIG. 3** shows the potency of the optimized scFvs based on PRO1643 (50-09-D07-sc03) to neutralize IL-31-induced signaling in the IL-31RA/OSMR dimerization assay. (A) PRO1900 (50-09-D07-sc04) and PRO1901 (50-09-D07-sc05), as well as (C) PRO1903 (50-09-D07-sc07) are potent inhibitors with IC_{50} values comparable to BMS-981164 for neutralization of IL-31-induced signaling. (B) PRO1902 (50-09-D07-sc06) lost inhibition potency due to the optimization process.

DETAILED DESCRIPTION OF THE INVENTION

[0031] Although anti-IL-31 therapies appear to be effective in treating itch symptoms occurring in pruritus causing diseases, they typically do not address the underlying cause of these diseases. Furthermore, the efficacy of these anti-IL-31 therapies is often limited and/or the response rates are low to moderate in patients suffering from allergic, inflammatory and autoimmune disorders, even in cases where these disorders have been associated with an imbalanced IL-31 signaling. Thus, there is a critical need for additional IL-31-based treatment options for patients living with said allergic, inflammatory and autoimmune disorders.

[0032] The present invention provides novel anti-IL-31 antibody variable domains comprising specific VL and VH chains. Said variable domains are based on the monoclonal rabbit antibody clone 50-09-D07. This clone was selected from a limited number of monoclonal rabbit antibodies that were identified in a broad immunization campaign and were found to bind to IL-31 with high affinity. The scFvs derived from said monoclonal rabbit antibody clone 50-09-D07 bind to IL-31 with a dissociation constant (K_D) of well below 1 nM, can neutralize the IL-31-induced signaling with an IC_{50} of below 30 ng/ml and can be stored at a concentration of 10 mg/ml over a period of 4 weeks at 4°C and 40°C without significant loss in protein content and monomeric content.

[0033] To the best knowledge of the inventors, there exist no anti-IL-31 antibody variable domains in the prior art that have such advantageous properties.

[0034] The antibody variable domain of the present invention could be successfully incorporated in a multispecific antibody format that additionally targets IL-4R. These anti-IL-4R x IL-31 multispecific antibodies are able to bind to IL-31 with high affinity and to potently inhibit IL-31-mediated signaling, while exhibiting very advantageous biophysical properties, in particular an outstanding formulation and storage stability at antibody concentrations well above 100 mg/ml. This demonstrates that the antibody variable domains of the present invention also provide advantageous biological and biophysical properties when incorporated in multispecific antibody formats.

[0035] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which this invention pertains.

[0036] The terms “comprising” and “including” are used herein in their open-ended and non-limiting sense unless otherwise noted. With respect to such latter embodiments, the term “comprising” thus includes the narrower term “consisting of”.

[0037] The terms “a” and “an” and “the” and similar references in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. For example, the term “a cell” includes a plurality of cells, including mixtures thereof. Where the plural form is used for compounds, salts, and the like, this is taken to mean also a single compound, salt, or the like.

[0038] In one aspect, the present invention relates to an antibody variable domain, which specifically binds to IL-31, comprising:

- a) a VH chain having a sequence selected from SEQ ID NOs: 5, 6 and 7, and
- b) a VL chain having a sequence selected from SEQ ID NO: 12 and 37.

[0039] The term “antibody” and the like, as used herein, includes whole antibodies or single chains thereof; and any antigen-binding fragment (*i. e.*, “antigen-binding portion”) or single chains thereof; and molecules comprising antibody CDRs, VH regions or VL regions (including without limitation multispecific antibodies). A naturally occurring “whole antibody” is a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as VL) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), flanked by regions that are more conserved, termed framework regions (FRs). Each VH and VL is composed of three CDRs and four FRs arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions

of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (*e. g.*, effector cells) and the first component (C1q) of the classical complement system.

[0040] The term “antibody variable domain”, as used herein, refers to one or more portions of an intact antibody that have the ability to specifically bind to a given antigen (*e. g.*, IL-31). This can be any antigen-binding fragment (*i. e.*, “antigen-binding portion”) of an intact antibody or single chains thereof; and molecules comprising antibody CDRs, VH regions or VL regions. Specifically, in case of the multispecific antibodies of the present invention, the term “antibody variable domain”, as used herein, refers to a Fab fragment, *i. e.* a monovalent fragment consisting of the VL, VH, CL and CH1 domains; an Fv fragment consisting of the VL and VH domains of a single arm of an antibody (Fv); a disulfide stabilized Fv fragment (dsFv); a single chain Fv fragment (scFv); and a single chain Fv fragment having an additional light chain constant domain (CL) fused to it (scAB). Preferably, the antibody variable domain of the present invention is selected from a Fab fragment, an Fv fragment, a disulfide stabilized Fv fragment (dsFv) and an scFv fragment. More preferably, the antibody variable domain of the present invention is selected from a Fab fragment, a disulfide stabilized Fv fragment (dsFv) and an scFv fragment. In particular embodiments, the antibody variable domain of the present invention is a single-chain Fv fragment (scFv). In other particular embodiments, the VL and VH domains of the scFv fragment are stabilized by an interdomain disulfide bond, in particular said VH domain comprises a single cysteine residue in position 51 (Aho numbering) and said VL domain comprises a single cysteine residue in position 141 (Aho numbering).

[0041] The term “Complementarity Determining Regions” (“CDRs”) refers to amino acid sequences with boundaries determined using any of a number of well-known schemes, including those described by Kabat et al. (1991), “Sequences of Proteins of Immunological Interest,” 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (“Kabat” numbering scheme); Al-Lazikani et al., (1997) JMB 273, 927-948 (“Chothia” numbering scheme); ImMunoGenTics (IMGT) numbering (Lefranc, M.-P., The Immunologist, 7, 132-136 (1999); Lefranc, M.-P. et al., Dev. Comp. Immunol., 27, 55-77 (2003)) (“IMGT” numbering scheme); and the numbering scheme described in Honegger & Plückthun, J. Mol. Biol. 309 (2001) 657-670 (“Aho”

numbering). For example, for classic formats, under Kabat, the CDR amino acid residues in the heavy chain variable domain (VH) are numbered 31-35 (HCDR1), 50-65 (HCDR2), and 95-102 (HCDR3); and the CDR amino acid residues in the light chain variable domain (VL) are numbered 24-34 (LCDR1), 50-56 (LCDR2), and 89-97 (LCDR3). Under Chothia the CDR amino acids in the VH are numbered 26-32 (HCDR1), 52-56 (HCDR2), and 95-102 (HCDR3); and the amino acid residues in VL are numbered 24-34 (LCDR1), 50-56 (LCDR2), and 89-97 (LCDR3). By combining the CDR definitions of both Kabat and Chothia, the CDRs consist of amino acid residues 26-35 (HCDR1), 50-65 (HCDR2), and 95-102 (HCDR3) in human VH and amino acid residues 24-34 (LCDR1), 50-56 (LCDR2), and 89-97 (LCDR3) in human VL. Under IMGT the CDR amino acid residues in the VH are numbered approximately 26-35 (HCDR1), 51-57 (HCDR2) and 93-102 (HCDR3), and the CDR amino acid residues in the VL are numbered approximately 27-32 (LCDR1), 50-52 (LCDR2), and 89-97 (LCDR3) (numbering according to "Kabat"). Under IMGT, the CDRs of an antibody can be determined using the program IMGT/DomainGap Align. [0042] In the context of the present invention, the numbering system suggested by Honegger & Plückthun ("AHO") is used (Honegger & Plückthun, J. Mol. Biol. 309 (2001) 657-670), unless specifically mentioned otherwise. In particular, the following residues are defined as CDRs according to AHO numbering scheme: LCDR1 (also referred to as CDR-L1): L24-L42; LCDR2 (also referred to as CDR-L2): L58-L72; LCDR3 (also referred to as CDR-L3): L107-L138; HCDR1 (also referred to as CDR-H1): H27-H42; HCDR2 (also referred to as CDR-H2): H57-H76; HCDR3 (also referred to as CDR-H3): H108-H138. For the sake of clarity, the numbering system according to Honegger & Plückthun takes the length diversity into account that is found in naturally occurring antibodies, both in the different VH and VL subfamilies and, in particular, in the CDRs, and provides for gaps in the sequences. Thus, in a given antibody variable domain usually not all positions 1 to 149 will be occupied by an amino acid residue.

[0043] The term "binding specificity" as used herein refers to the ability of an individual antibody to react with one antigenic determinant and not with a different antigenic determinant. As used herein, the term "specifically binds to" or is "specific for" refers to measurable and reproducible interactions such as binding between a target and an antibody, which is determinative of the presence of the target in the

presence of a heterogeneous population of molecules including biological molecules. For example, an antibody that specifically binds to a target (which can be an epitope) is an antibody that binds this target with greater affinity, avidity, more readily, and/or with greater duration than it binds to other targets. In its most general form (and when no defined reference is mentioned), "specific binding" is referring to the ability of the antibody to discriminate between the target of interest and an unrelated molecule, as determined, for example, in accordance with specificity assay methods known in the art. Such methods comprise, but are not limited to Western blots, ELISA, RIA, ECL, IRMA, SPR (Surface plasmon resonance) tests and peptide scans. For example, a standard ELISA assay can be carried out. The scoring may be carried out by standard color development (e. g. secondary antibody with horseradish peroxidase and tetramethyl benzidine with hydrogen peroxide). The reaction in certain wells is scored by the optical density, for example, at 450 nm. Typical background (= negative reaction) may be about 0.1 OD; typical positive reaction may be about 1 OD. This means the ratio between a positive and a negative score can be 10-fold or higher. In a further example, an SPR assay can be carried out, wherein at least 10-fold, particularly at least 100-fold difference between a background and signal indicates on specific binding. Typically, determination of binding specificity is performed by using not a single reference molecule, but a set of about three to five unrelated molecules, such as milk powder, transferrin or the like. [0044] In a further aspect, the present invention relates to a multispecific antibody comprising:

- a) one or two antibody variable domains as defined herein;
- b) at least one binding domain, which specifically binds to a target different from IL-31, in particular wherein said at least one binding domain is an hSA-BD and/or an IL4R-BD.

[0045] In particular embodiments, the multispecific antibodies of the invention do not comprise an immunoglobulin Fc region.

[0046] In these particular embodiments, the multispecific antibody is preferably in a format selected from the group consisting of: a tandem scDb (Tandab), a linear dimeric scDb (LD-scDb), a circular dimeric scDb (CD-scDb), a tandem tri-scFv, a tribody (Fab-(scFv)₂), a Fab-Fv₂, a triabody, an scDb-scFv, a tetrabody, a di-diabody, a tandem-di-scFv and a MATCH (described in WO 2016/0202457; Egan T., et al.,

MABS 9 (2017) 68-84). In particular, the multispecific antibody of the invention is in a MATCH format. More particularly, the multispecific antibody of the invention is in a MATCH3, MATCH4 or a MATCH5 format.

[0047] The term “immunoglobulin Fc region” or “Fc region”, as used herein, is used to define a C-terminal region of an immunoglobulin heavy chain, *i. e.* the CH2 and CH3 domains of the heavy chain constant regions. The term “Fc region” includes native-sequence Fc regions and variant Fc regions, *i. e.* Fc regions that are engineered to exhibit certain desired properties, such as for example altered Fc receptor binding function and/or reduced or suppressed Fab arm exchange. An example of such an engineered Fc region is the knob-into-hole (KiH) technology (see for example Ridgway et al., Protein Eng. 9:617-21 (1996) and Spiess et al., J Biol Chem. 288(37):26583-93 (2013)). Native-sequence Fc regions include human IgG1, IgG2 (IgG2A, IgG2B), IgG3 and IgG4. “Fc receptor” or “FcR” describes a receptor that binds to the Fc region of an antibody. Particularly, the FcR is a native sequence human FcR, which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors, FcγRII receptors including FcγRIIA (an “activating receptor”) and FcγRI IB (an “inhibiting receptor”), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain, (see M. Daeron, Annu. Rev. Immunol. 5:203-234 (1997). FcRs are reviewed in Ravetch and Kinet, Annu. Rev. Immunol. 9: 457-92 (1991); Capet et al, Immunomethods 4: 25-34 (1994); and de Haas et al, J. Lab. Clin. Med. 126: 330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term “FcR” herein. The term “Fc receptor” or “FcR” also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus. Guyer et al., J. Immunol. 117: 587 (1976) and Kim et al., J. Immunol. 24: 249 (1994). Methods of measuring binding to FcRn are known (see, *e. g.*, Ghetie and Ward, Immunol. Today 18: (12): 592-8 (1997); Ghetie et al., Nature Biotechnology 15 (7): 637-40 (1997); Hinton et al., J. Biol. Chem. TJI (8): 6213-6 (2004); WO 2004/92219 (Hinton et al). Binding to FcRn *in vivo* and serum half-life of human FcRn high-affinity binding

polypeptides can be assayed, *e. g.*, in transgenic mice or transfected human cell lines expressing human FcRn, or in primates to which the polypeptides having a variant Fc region are administered. WO 2004/42072 (Presta) describes antibody variants which improved or diminished binding to FcRs. See also, *e. g.*, Shields et al., J. Biol. Chem. 9(2): 6591-6604 (2001).

[0048] In other particular embodiments, the multispecific antibodies of the invention comprise an immunoglobulin Fc region.

[0049] In further particular embodiments, the multispecific antibodies of the invention comprise an IgG region.

[0050] The term "IgG region", as used herein, refers to the heavy and light chain of an immunoglobulin G, *i. e.* the Fc region, as defined above, and the Fab region, consisting of the VL, VH, CL and CH1 domains. The term "IgG region" includes native-sequence IgG regions, such as human IgG1, IgG2 (IgG2A, IgG2B), IgG3 and IgG4, as well as engineered IgG regions, which exhibit certain desired properties, as for example the properties defined above for the Fc region.

[0051] In particular embodiments, the multispecific antibodies of the invention comprise an IgG region, wherein the IgG region is selected from the IgG subclasses IgG1 and IgG4, in particular from IgG4.

[0052] The terms "binding domain", "antigen-binding fragment thereof", "antigen-binding portion" of an antibody, and the like, as used herein, refer to one or more parts of an intact antibody that have the ability to specifically bind to a given antigen. Antigen-binding functions of an antibody can be performed by fragments of an intact antibody. Specifically, in case of the multispecific antibodies of the present invention, the terms "binding domain", "antigen-binding fragment thereof", "antigen-binding portion", and the like, as used herein, refer to a Fab fragment, *i. e.* a monovalent fragment consisting of the VL, VH, CL and CH1 domains; an Fv fragment consisting of the VL and VH domains of a single arm of an antibody; a disulfide stabilized Fv fragment (dsFv); and a single chain Fv fragment (scFv). Preferably, the binding domains of the multispecific antibodies of the present invention are independently of each other selected from a Fab fragment, an Fv fragment, an scFv fragment and a single-chain Fv fragment (scFv). In particular embodiments, the binding domains of the antibodies of the present invention are independently of each other selected from a Fab fragment and a single-chain Fv fragment (scFv). In other particular

embodiments, the VL and VH domains of the scFv fragment are stabilized by an interdomain disulfide bond, in particular said VH domain comprises a single cysteine residue in position 51 (AHo numbering) and said VL domain comprises a single cysteine residue in position 141 (AHo numbering).

[0053] Suitably, the antibody variable domain of the invention is an isolated variable domain. Likewise, the multispecific antibodies of the invention are isolated antibodies. The term “isolated variable domain” or “isolated antibody”, as used herein, refers to a variable domain or an antibody that is substantially free of other variable domains or other antibodies having different antigenic specificities (e. g., an isolated antibody variable domain that specifically binds IL-31 is substantially free of antibody variable domains that specifically bind antigens other than IL-31).

Moreover, an isolated antibody variable domain or isolated antibody may be substantially free of other cellular material and/or chemicals.

[0054] Suitably, the antibody variable domains and multispecific antibodies of the invention are monoclonal antibody variable domains and antibodies. The term “monoclonal antibody variable domains” or “monoclonal antibody” as used herein refers to variable domains or antibodies that have substantially identical amino acid sequences or are derived from the same genetic source. A monoclonal variable domain or antibody displays a binding specificity and affinity for a particular epitope, or binding specificities and affinities for specific epitopes.

[0055] The antibody variable domains and multispecific antibodies of the invention include, but are not limited to, chimeric, human and humanized antibody variable domains and antibodies.

[0056] The term “chimeric antibody” or “chimeric antibody variable domain”, as used herein, refers to an antibody molecule or antibody variable domain, in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen-binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity. For example, a mouse antibody can be modified by replacing its constant region with the constant region from a human immunoglobulin. Due to the replacement with a human constant region, the chimeric antibody can

retain its specificity in recognizing the antigen while having reduced antigenicity in human as compared to the original mouse antibody.

[0057] The term “human antibody” or “human antibody variable domain”, as used herein, is intended to include antibodies or antibody variable domains having variable regions in which both the framework and CDR regions are derived from sequences of human origin. Furthermore, if the antibody or antibody variable domain contains a constant region, the constant region also is derived from such human sequences, *e. g.*, human germline sequences, or mutated versions of human germline sequences. The human antibodies and antibody variable domains of the invention may include amino acid residues not encoded by human sequences (*e. g.*, mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*). This definition of a human antibody or antibody variable domain specifically excludes a humanized antibody or antibody variable domain comprising non-human antigen-binding residues. Human antibodies and antibody variable domains can be produced using various techniques known in the art, including phage-display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1992); Marks et al, *J. Mol. Biol.*, 222:581 (1991)). Also available for the preparation of human monoclonal antibodies and human monoclonal antibody variable domains are methods described in Cole et al, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985); Boemer et al, *J. Immunol.*, 147(l):86-95 (1991). See also van Dijk and van de Winkel, *Curr. Opin. Pharmacol.*, 5: 368-74 (2001). Human antibodies and human antibody variable domains can be prepared by administering the antigen to a transgenic animal that has been modified to produce such antibodies and antibody variable domains in response to antigenic challenge, but whose endogenous loci have been disabled, *e. g.*, immunized xenomice (see, *e. g.*, U.S. Pat. Nos. 6,075,181 and 6,150,584 regarding XENOMOUSE™ technology). See also, for example, Li et al, *Proc. Natl. Acad. Sci. USA*, 103:3557- 3562 (2006) regarding human antibodies generated via a human B-cell hybridoma technology.

[0058] The term “humanized” antibody or “humanized” antibody variable domain, as used herein, refers to an antibody or antibody variable domain that retains the reactivity of a non-human antibody or antibody variable domain while being less immunogenic in humans. This can be achieved, for instance, by retaining the non-human CDR regions and replacing the remaining parts of the antibody or antibody

variable domain with their human counterparts (*i. e.*, the constant region as well as the framework portions of the variable region). Additional framework region modifications may be made within the human framework sequences as well as within the CDR sequences derived from the germline of another mammalian species. The humanized antibodies and antibody variable domains of the invention may include amino acid residues not encoded by human sequences (*e. g.*, mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*, or a conservative substitution to promote stability or manufacturing). See, *e. g.*, Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855, 1984; Morrison and Oi, Adv. Immunol., 44:65-92, 1988; Verhoeyen et al., Science, 239: 1534-1536, 1988; Padlan, Molec. Immun., 28:489-498, 1991; and Padlan, Molec. Immun., 31: 169-217, 1994. Other examples of human engineering technology include but are not limited to the Xoma technology disclosed in U.S. Pat. No. 5,766,886.

[0059] The term “recombinant humanized antibody” or “recombinant humanized antibody variable domain” as used herein, includes all human antibodies and human antibody variable domains that are prepared, expressed, created or isolated by recombinant means, such as antibodies and antibody variable domains isolated from a host cell transformed to express the humanized antibody or humanized antibody variable domain, *e. g.*, from a transfectoma, and antibodies and antibody variable domains prepared, expressed, created or isolated by any other means that involve splicing of all or a portion of a human immunoglobulin gene, sequences to other DNA sequences.

[0060] Preferably, the antibody variable domains and multispecific antibodies of the invention are humanized. More preferably, the antibody variable domains and multispecific antibodies of the invention are humanized and comprise rabbit derived CDRs.

[0061] The term “multispecific antibody” as used herein, refers to an antibody that binds to two or more different epitopes on at least two or more different targets (*e. g.*, IL-31 and IL-4R). Preferably, the multispecific antibodies of the invention are bispecific. The term “bispecific antibody” as used herein, refers to an antibody that binds to at least two different epitopes on two different targets (*e. g.*, IL-31 and IL-4R).

[0062] The term “epitope” means a protein determinant capable of specific binding to an antibody. Epitopes usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three-dimensional structural characteristics, as well as specific charge characteristics.

“Conformational” and “linear” epitopes are distinguished in that the binding to the former but not the latter is lost in the presence of denaturing solvents.

[0063] The term “conformational epitope” as used herein refers to amino acid residues of an antigen that come together on the surface when the polypeptide chain folds to form the native protein.

[0064] The term “linear epitope” refers to an epitope, wherein all points of interaction between the protein and the interacting molecule (such as an antibody) occurring linearly along the primary amino acid sequence of the protein (continuous).

[0065] The term “recognize” as used herein refers to an antibody or antigen-binding portion thereof that finds and interacts (*e. g.*, binds) with its conformational epitope.

[0066] Suitably, the multispecific antibodies of the invention comprise one or two antibody variable domains that specifically bind IL-31, as defined herein. Particularly, the multispecific antibodies of the invention comprise two antibody variable domains that specifically bind IL-31, as defined herein.

[0067] The term “IL-31” or “IL31” refers in particular to human IL-31 with UniProt ID number Q6EBC2. The antibody variable domains of the invention target *human* IL-31. Particularly, the antibody variable domains of the invention target *human* and *cynomolgus* (*Macaca fascicularis*) IL-31.

[0068] The antibody variable domains of the invention, when being in scFv format, are characterized by the following parameters:

- a. bind to human IL-31 with a monovalent dissociation constant (K_D) of 5 nM or less, particularly with a monovalent K_D of 5 pM to 5 nM, particularly of 5 pM to 2 nM, particularly of 5 to 1000 pM, as measured by surface plasmon resonance (SPR);
- b. inhibit the human IL-31 induced signaling with an IC_{50} of 0.1 to 30 ng/ml, particularly with an IC_{50} of 0.1 to 20 ng/ml, particularly with an IC_{50} of 0.1 to 10 ng/ml, as measured in a Path Hunter IL-31RA/OSMRb dimerization assay;
- c. have a loss in monomer content, after storage for four weeks at 4°C of less than 5 %, *e. g.* less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %,

when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4; and

- d. have a loss in monomer content, after storage for four weeks at 40°C of less than 5 %, *e. g.* less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4.

[0069] In specific embodiments, the antibody variable domains of the invention, when being in scFv format, are characterized by the following parameters:

- a. bind to human IL-31 with a monovalent dissociation constant (K_D) of 5 nM or less, particularly with a monovalent K_D of 5 pM to 5 nM, particularly of 5 pM to 2 nM, particularly of 5 to 1000 pM, as measured by surface plasmon resonance (SPR);
- b. inhibit the human IL-31 induced signaling with an IC_{50} of 0.1 to 30 ng/ml, particularly with an IC_{50} of 0.3 to 20 ng/ml, particularly with an IC_{50} of 0.1 to 10 ng/ml, as measured in a Path Hunter IL-31RA/OSMRb dimerization assay;
- c. have a melting temperature (T_m), determined by differential scanning fluorimetry, of at least 65°C, preferably of at least 67°C, more preferably at least 69°C, in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
- d. have a loss in monomer content, after storage for four weeks at 4°C of less than 5 %, *e. g.* less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4; and
- e. have a loss in monomer content, after storage for four weeks at 40°C of less than 5 %, *e. g.* less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4.

[0070] In more specific embodiments, the antibody variable domains of the invention, when being in scFv format, are characterized by the following parameters:

- a. bind to *human* IL-31 with a monovalent dissociation constant (K_D) of 5 nM or less, particularly with a monovalent K_D of 5 pM to 5 nM, particularly of 5 pM to 2 nM, particularly of 5 to 1000 pM, as measured by surface plasmon resonance (SPR);
- b. inhibit the human IL-31 induced signaling with an IC_{50} of 0.1 to 30 ng/ml, particularly with an IC_{50} of 0.1 to 20 ng/ml, particularly with an IC_{50} of 0.1 to 10 ng/ml, as measured in a Path Hunter IL-31RA/OSMRb dimerization assay;
- c. block the binding of human IL-31 to human IL-31R with an IC_{50} of 0.1 to 20 ng/ml, particularly with an IC_{50} of 0.1 to 10 ng/ml, particularly with an IC_{50} of 0.1 to 6 ng/ml, as measured in a competition ELISA;
- d. have a melting temperature (T_m), determined by differential scanning fluorimetry, of at least 65°C, preferably of at least 67°C, more preferably at least 69°C, in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
- e. have a loss in monomer content, after storage for four weeks at 4°C of less than 5 %, e. g. less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4; and
- f. have a loss in monomer content, after storage for four weeks at 40°C of less than 5 %, e. g. less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4.

[0071] In more specific embodiments, the antibody variable domains of the invention, when being in scFv format, are characterized by the following parameters:

- a. bind to *human* IL-31 with a monovalent dissociation constant (K_D) of 5 nM or less, particularly with a monovalent K_D of 5 pM to 5 nM, particularly of 5 pM to 2 nM, particularly of 5 to 1000 pM, as measured by surface plasmon resonance (SPR);
- b. are cross-reactive with *Macaca fascicularis* (Cynomolgus) IL-31, in particular bind to Cynomolgus IL-31 with a monovalent K_D of 5 nM or less, particularly with

a monovalent K_D of 5 pM to 5 nM, particularly of 5 pM to 2 nM, particularly of 5 to 1000 pM, as measured by SPR;

- c. inhibit the human IL-31 induced signaling with an IC_{50} of 0.1 to 30 ng/ml, particularly with an IC_{50} of 0.1 to 20 ng/ml, particularly with an IC_{50} of 0.1 to 10 ng/ml, as measured in a Path Hunter IL-31RA/OSMRb dimerization assay;
- d. block the binding of human IL-31 to human IL-31R with an IC_{50} of 0.1 to 20 ng/ml, particularly with an IC_{50} of 0.1 to 10 ng/ml, particularly with an IC_{50} of 0.1 to 6 ng/ml, as measured in a competition ELISA;
- e. have a melting temperature (T_m), determined by differential scanning fluorimetry, of at least 65°C, preferably of at least 67°C, more preferably at least 69°C, in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
- f. have a loss in monomer content, after storage for four weeks at 4°C of less than 5 %, e. g. less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
- g. have a loss in monomer content, after storage for four weeks at 40°C of less than 5 %, e. g. less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
- h. have a loss in monomer content, after 3 freeze-thawing cycles, of less than 5 %, e. g. less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4;
- i. have a loss in protein content, after storage for four weeks at 4°C or 40°C of less than 5 %, e. g. less than 4 %, less than 3 %, less than 2 %, preferably less than 1 %, when said scFvs are at a starting concentration of 10 mg/ml, and in particular wherein said scFvs are formulated in 50 mM phosphate citrate buffer with 150 mM NaCl at pH 6.4.

[0072] The term “HEK-Blue cells” or “HEK-Blue”, as used herein, refers to commercially available human embryonic kidney cells that are transfected with and stably express an optimized secreted embryonic alkaline phosphatase (SEAP) reporter gene under the control of a promoter inducible by NF- κ B transcription factor. The level of SEAP protein released into the culture media is typically used as a measure of NF- κ B activation.

[0073] As used herein, the term “affinity” refers to the strength of interaction between the antibody or the antibody variable domain and the antigen at single antigenic sites. Within each antigenic site, the variable region of the antibody variable domain or the antibody “arm” interacts through weak non-covalent forces with antigen at numerous sites; the more interactions, the stronger the affinity.

[0074] “Binding affinity” generally refers to the strength of the total sum of non-covalent interactions between a single binding site of a molecule (*e. g.*, of an antibody or an antibody variable domain) and its binding partner (*e. g.*, an antigen or, more specifically, an epitope on an antigen). Unless indicated otherwise, as used herein, “binding affinity”, “bind to”, “binds to” or “binding to” refers to intrinsic binding affinity that reflects a 1:1 interaction between members of a binding pair (*e. g.*, an antibody variable domain and an antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_D). Affinity can be measured by common methods known in the art, including those described herein. Low-affinity antibodies and antibody variable domains generally bind antigens slowly and tend to dissociate readily, whereas high-affinity antibodies generally bind antigens faster and tend to remain bound longer. A variety of methods of measuring binding affinity are known in the art, any of which can be used for purposes of the present invention. Specific illustrative and exemplary embodiments for measuring binding affinity, *i. e.* binding strength are described in the following.

[0075] The term “ K_{assoc} ”, “ K_a ” or “ K_{on} ”, as used herein, are intended to refer to the association rate of a particular antibody-antigen interaction, whereas the term “ K_{dis} ”, “ K_d ” or “ K_{off} ”, as used herein, is intended to refer to the dissociation rate of a particular antibody-antigen interaction. In one embodiment, the term “ K_D ”, as used herein, is intended to refer to the dissociation constant, which is obtained from the ratio of K_d to K_a (*i. e.* K_d/K_a) and is expressed as a molar concentration (M). The “ K_D ”

or "K_D value" or "KD" or "KD value" according to this invention is in one embodiment measured by using surface plasmon resonance assays.

[0076] Affinity to recombinant *human* IL-31 and recombinant *Cynomolgus* IL-31 was determined by surface plasmon resonance (SPR) measurements, as described in the paragraphs [0189] (scFvs) and [0225] (multispecific molecules).

[0077] The antibody variable domain of the invention acts as an antagonist of IL-31. In other words, the antibody variable domain of the invention is an inhibitor of IL-31-mediated signaling. The term "blocker" or "inhibitor" or "antagonist", as used herein, refers to an antibody or antibody variable domain that inhibits or reduces a biological activity of the antigen it binds to. The antibody variable domains of the invention bind to the IL-31, thereby blocking the binding of IL-31 to IL-31R, which leads to reduced IL-31R function.

[0078] DSF is described earlier (Egan, et al., *MAbs*, 9(1) (2017), 68-84; Niesen, et al., *Nature Protocols*, 2(9) (2007) 2212-2221). The midpoint of transition for the thermal unfolding of the scFv constructs is determined by Differential Scanning Fluorimetry using the fluorescence dye SYPRO® Orange (see Wong & Raleigh, *Protein Science* 25 (2016) 1834-1840). Samples in phosphate-citrate buffer at pH 6.4 are prepared at a final protein concentration of 50 µg/ml and containing a final concentration of 5x SYPRO® Orange in a total volume of 100 µl. Twenty-five microliters of prepared samples are added in triplicate to white-walled AB gene PCR plates. The assay is performed in a qPCR machine used as a thermal cycler, and the fluorescence emission is detected using the software's custom dye calibration routine. The PCR plate containing the test samples is subjected to a temperature ramp from 25°C to 96°C in increments of 1°C with 30 s pauses after each temperature increment. The total assay time is about 2 h. The T_m is calculated by the software GraphPad Prism using a mathematical second derivative method to calculate the inflection point of the curve. The reported T_m is an average of three measurements.

[0079] The loss in monomer content is as determined by area under the curve calculation of SE-HPLC chromatograms. SE-HPLC is a separation technique based on a solid stationary phase and a liquid mobile phase as outlined by the US Pharmacopeia (USP), chapter 621. This method separates molecules based on their size and shape utilizing a hydrophobic stationary phase and aqueous mobile phase.

The separation of molecules is occurring between the void volume (V_0) and the total permeation volume (V_T) of a specific column. Measurements by SE-HPLC are performed on a Chromaster HPLC system (Hitachi High-Technologies Corporation) equipped with automated sample injection and a UV detector set to the detection wavelength of 280 nm. The equipment is controlled by the software EZChrom Elite (Agilent Technologies, Version 3.3.2 SP2) which also supports analysis of resulting chromatograms. Protein samples are cleared by centrifugation and kept at a temperature of 4-6°C in the autosampler prior to injection. For the analysis of scFv samples the column Shodex KW403-4F (Showa Denko Inc., #F6989202) is employed with a standardized buffered saline mobile phase (50 mM sodium-phosphate pH 6.5, 300 mM sodium chloride) at the recommended flow rate of 0.35 ml/min. The target sample load per injection was 5 µg. Samples are detected by an UV detector at a wavelength of 280 nm and the data recorded by a suitable software suite. The resulting chromatograms are analyzed in the range of V_0 to V_T thereby excluding matrix associated peaks with >10 min elution time.

[0080] Suitably, the antibody variable domains of the invention are binding domains provided in the present disclosure. They are derived from the rabbit antibody clone 50-09-D07, and include, but are not limited to, the humanized antibody variable domains whose sequences are listed in Table 1.

[0081] The term “multivalent antibody” refers to a single binding molecule with more than one valency, where “valency” is described as the number of antigen-binding moieties that binds to epitopes on target molecules. As such, the single binding molecule can bind to more than one binding site on a target molecule and/or to more than one target molecule due to the presence of more than one copy of the corresponding antigen-binding moieties. Examples of multivalent antibodies include, but are not limited to bivalent antibodies, trivalent antibodies, tetravalent antibodies, pentavalent antibodies, hexavalent antibodies, and the like.

[0082] The term “monovalent antibody”, as used herein, refers to an antibody that binds to a single target molecule, and more specifically to a single epitope on a target molecule. Also, the term “binding domain” or “monovalent binding domain”, as used herein, refers to a binding domain that binds to a single epitope on a target molecule.

[0083] In particular embodiments, the multispecific antibodies of the invention comprise one antibody variable domain that specifically binds IL-31, as defined herein, and one binding domain, which binds to a target different from IL-31, *i. e.* the multispecific antibodies of the invention are monovalent for both IL-31 and the target different from IL-31.

[0084] In further particular embodiments, the multispecific antibodies of the invention comprise one antibody variable domain that specifically binds IL-31, as defined herein, and two binding domains, which have the same binding specificity and specifically bind to a target different from IL-31, *i. e.* the multispecific antibodies of the invention are monovalent for IL-31 specificity and bivalent for the target different from IL-31.

[0085] In further particular embodiments, the multispecific antibodies of the invention comprise two antibody variable domains that specifically bind IL-31, as defined herein, and one binding domain, which binds to a target different from IL-31, *i. e.* the multispecific antibodies of the invention are bivalent for IL-31 specificity and monovalent for the target different from IL-31.

[0086] In preferred embodiments, the multispecific antibodies of the invention comprise two antibody variable domains that specifically bind IL-31, as defined herein, and two binding domains, which have the same binding specificity and specifically bind to a target different from IL-31, *i. e.* the multispecific antibodies of the invention are bivalent for IL-31 specificity and bivalent for the target different from IL-31.

[0087] In case the multispecific antibodies of the invention comprise two binding domains, which have the same binding specificity and specifically bind to a target different from IL-31, said two binding domains either bind the same epitope or different epitopes on the target molecules. Preferably, the two binding domains bind the same epitope on the target molecule.

[0088] The term "same epitope", as used herein, refers to an individual protein determinant on the protein capable of specific binding to more than one antibody, where that individual protein determinant is identical, *i. e.* consist of identical chemically active surface groupings of molecules such as amino acids or sugar side chains having identical three-dimensional structural characteristics, as well as identical charge characteristics for each of said antibodies.

[0089] The term “different epitope”, as used herein in connection with a specific protein target, refers to individual protein determinants on the protein, each capable of specific binding to a different antibody, where these individual protein determinants are not identical for the different antibodies, *i. e.* consist of non-identical chemically active surface groupings of molecules such as amino acids or sugar side chains having different three-dimensional structural characteristics, as well as different charge characteristics. These different epitopes can be overlapping or non-overlapping.

[0090] In particular embodiments, the multispecific antibodies of the invention are bispecific and bivalent.

[0091] In further particular embodiments, the multispecific antibodies of the invention are bispecific and trivalent.

[0092] Preferably, the multispecific antibodies of the invention are bispecific and tetravalent, *i. e.* bivalent for IL-31 and bivalent for a target different from IL-31.

[0093] In a particular aspect, the present invention relates to a multispecific antibody comprising:

- a) two antibody variable domains as defined herein;
- b) two binding domains, which have the same binding specificity and specifically bind to a target different from IL-31, in particular wherein said binding domains are hSA-BDs or IL4R-BDs.

wherein said multispecific antibody comprises an IgG region.

[0094] Other variable domains used in the invention include amino acid sequences that have been mutated, yet have at least 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 percent identity in the CDR regions with the CDR regions depicted in the sequences described in Table 1, provided that such other variable domains exhibit the functional features of section [0068], and optionally additionally of sections [0069] to [0071].

Other variable domains used in the invention include mutant amino acid sequences wherein no more than 1, 2, 3, 4 or 5 amino acids have been mutated in the CDR regions when compared with the CDR regions depicted in the sequence described in Table 1, provided that such other variable domains exhibit the functional features of section [0068], and optionally additionally of sections [0069] to [0071].

[0095] Suitably, the VH domains of the binding domains of the invention belong to a VH3 or VH4 family. In one embodiment, a binding domain used in the invention

comprises a VH domain belonging to the VH3 family. In the context of the present invention, the term “belonging to the VHx family (or VLx family)” means that the framework sequences FR1 to FR3 show the highest degree of homology to said VHx family (or VLx, respectively). Examples of VH and VL families are given in Knappik et al., J. Mol. Biol. 296 (2000) 57-86, or in WO 2019/057787. A specific example of a VH domain belonging to VH3 family is represented by SEQ ID NO: 13, and a specific example of a VH domain belonging to VH4 family is represented by SEQ ID NO: 14. In particular, framework regions FR1 to FR3 taken from SEQ ID NO: 13 belong to the VH3 family (Table 2, regions marked in non-bold). Suitably, a VH belonging to the VH3 family, as used herein, is a VH comprising FR1 to FR3 having at least 90 %, more particularly at least 95 %, at least 96%, at least 97%, at least 98%, at least 99%, sequence identity to FR1 to FR3 of SEQ ID NO: 13. Alternative examples of VH3 and VH4 sequences, and examples of other VHx sequences, may be found in Knappik et al., J. Mol. Biol. 296 (2000) 57-86 or in WO 2019/057787.

[0096] Suitably, the VL domains of the binding domains used in the invention comprise: Vk frameworks FR1, FR2 and FR3, particularly Vk1 or Vk3 frameworks, particularly Vk1 frameworks FR1 to FR3, and a framework FR4, which is selected from a Vk FR4. In the case where said binding domains are in an scFv-format, said binding domains comprise: Vk frameworks FR1, FR2 and FR3, particularly Vk1 or Vk3 frameworks, particularly Vk1 frameworks FR1 to FR3, and a framework FR4, which is selected from a Vk FR4 and a Vλ FR4, particularly a Vλ FR4.

[0097] Suitable Vk1 frameworks FR1 to FR3 as well as an exemplary Vλ FR4 are set forth in SEQ ID NO: 15 (Table 2, FR regions are marked in non-bold). Alternative examples of Vk1 sequences, and examples of Vk2, Vk3 or Vk4 sequences, may be found in Knappik et al., J. Mol. Biol. 296 (2000) 57-86. Suitable Vk1 frameworks FR1 to FR3 comprise the amino acid sequences having at least 80, 90, 95 percent identity to amino acid sequences corresponding to FR1 to FR3 and taken from SEQ ID NO: 15 (Table 2, FR regions are marked in non-bold). Suitable Vλ FR4 are as set forth in SEQ ID NO: 16 to SEQ ID NO: 22 and in SEQ ID NO: 23 comprising a single cysteine residue, particular in a case where a second single cysteine is present in the corresponding VH chain, particularly in position 51 (Aho numbering) of VH, for the formation of an inter-domain disulfide bond. In one embodiment, the VL domains of the binding domains of the invention, when being in scFv-format, comprises Vλ

FR4 comprising the amino acid sequence having at least 80, 90, 95 percent identity to an amino acid sequence selected from any of SEQ ID NO: 16 to SEQ ID NO: 23, particularly to SEQ ID NO: 16 or 23.

[0098] The antibody variable domains of the invention comprise a VH domain listed in Table 1. Suitably, the antibody variable domains of the invention comprise a VH amino acid sequence listed in Table 1, wherein no more than 5 amino acids, particularly no more than 4 amino acids, particularly no more than 3 amino acids, particularly no more than 2 amino acids, particularly no more than 1 amino acid in the framework sequences (*i. e.*, the sequence which is not CDR sequences) have been mutated (wherein a mutation is, as various non-limiting examples, an addition, substitution or deletion). Other binding domains used in the invention include amino acids that have been mutated, yet have at least 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 percent identity in the VH regions with the VH regions depicted in the corresponding sequences described in Table 1, including VH domains comprising at least positions 5 to 140 (AHO numbering), particularly at least positions 3 to 145 of one of the sequences shown in Table 1, provided that such other variable domains exhibit the functional features of section [0068], and optionally additionally of sections [0069] to [0071].

[0099] In particular, the antibody variable domains of the invention comprise a VL domain listed in Table 1. Suitably, the antibody variable domains of the invention comprise a VL amino acid sequence listed in Table 1, wherein no more than 5 amino acids, particularly no more than 4 amino acids, particularly no more than 3 amino acids, particularly no more than 2 amino acids, particularly no more than 1 amino acid in the framework sequences (*i. e.*, the sequence which is not CDR sequences) have been mutated (wherein a mutation is, as various non-limiting examples, an addition, substitution or deletion). Other binding domains used in the invention include amino acids that have been mutated, yet have at least 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 percent identity in the VL regions with a VL region depicted in the sequences described in Table 1, including VL domains comprising at least positions 5 to 140 (AHO numbering), particularly at least positions 3 to 145 of one of the sequences shown in Table 1, provided that such other variable domains exhibit the functional features of section [0068], and optionally additionally of sections [0069] to [0071].

[0100] Specific but non-limiting examples of the antibody variable domains of the invention are the scFvs PRO1643, PRO1900, PRO1901 and PRO1903, whose sequences are listed in Table 3.

[0101] Suitably, the at least one binding domains of the multispecific antibodies of the invention are selected from the group consisting of: a Fab, an Fv, a dsFv and an scFv.

[0102] The antibody variable domains and the binding domains comprised in the multispecific antibodies of the invention are capable of binding to their respective antigens or receptors simultaneously. The term “simultaneously”, as used in this connection refers to the simultaneous binding of at least one of the antibody variable domains that specifically bind to IL-31 and at least one of the binding domains that have specificity for a target different from IL-31.

[0103] Suitably, the antibody variable domains and the binding domains comprised in the multispecific antibodies of the invention are operably linked.

[0104] The term “operably linked”, as used herein, indicates that two molecules (e. g., polypeptides, domains, binding domains) are attached in a way that each molecule retains functional activity. Two molecules can be “operably linked” whether they are attached directly or indirectly (e. g., via a linker, via a moiety, via a linker to a moiety). The term “linker” refers to a peptide or other moiety that is optionally located between binding domains or antibody variable domains used in the invention. A number of strategies may be used to covalently link molecules together. These include, but are not limited to, polypeptide linkages between N- and C-termini of proteins or protein domains, linkage via disulfide bonds, and linkage via chemical cross-linking reagents. In one aspect of this embodiment, the linker is a peptide bond, generated by recombinant techniques or peptide synthesis. Choosing a suitable linker for a specific case where two polypeptide chains are to be connected depends on various parameters, including but not limited to the nature of the two polypeptide chains (e. g., whether they naturally oligomerize), the distance between the N- and the C-termini to be connected if known, and/or the stability of the linker towards proteolysis and oxidation. Furthermore, the linker may contain amino acid residues that provide flexibility.

[0105] In the context of the present invention, the term “polypeptide linker” refers to a linker consisting of a chain of amino acid residues linked by peptide bonds that is

connecting two domains, each being attached to one end of the linker. The polypeptide linker should have a length that is adequate to link two molecules in such a way that they assume the correct conformation relative to one another so that they retain the desired activity. In particular embodiments, the polypeptide linker has a continuous chain of between 2 and 30 amino acid residues (e. g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acid residues). In addition, the amino acid residues selected for inclusion in the polypeptide linker should exhibit properties that do not interfere significantly with the activity of the polypeptide. Thus, the linker peptide on the whole should not exhibit a charge that would be inconsistent with the activity of the polypeptide, or interfere with internal folding, or form bonds or other interactions with amino acid residues in one or more of the monomers that would seriously impede the binding of receptor monomer domains. In particular embodiments, the polypeptide linker is non-structured polypeptide. Useful linkers include glycine-serine, or GS linkers. By "Gly-Ser" or "GS" linkers is meant a polymer of glycines and serines in series (including, for example, (Gly-Ser)_n, (GSGGS)_n (GGGGS)_n and (GGGS)_n, where n is an integer of at least one), glycine-alanine polymers, alanine-serine polymers, and other flexible linkers such as the tether for the shaker potassium channel, and a large variety of other flexible linkers, as will be appreciated by those in the art. Glycine-serine polymers are preferred since oligopeptides comprising these amino acids are relatively unstructured, and therefore may be able to serve as a neutral tether between components. Secondly, serine is hydrophilic and therefore able to solubilize what could be a globular glycine chain. Third, similar chains have been shown to be effective in joining subunits of recombinant proteins such as single-chain antibodies. [0106] In one group of embodiments, the multispecific antibody of the invention comprises an immunoglobulin Fc region and is in a format selected from (scFv)₂-Fc-(scFv)₂ fusion (ADAPTIR); DVD-Ig; a DARTTM and a TRIDENTTM. The term " DARTTM " refers to an antibody format developed by MacroGenics that comprises an immunoglobulin Fc region polypeptide and one or two bispecific Fv binding domains fused to the N-terminus of one heavy chain of the Fc region or to both N-termini of the heavy chains of the Fc region. The term " TRIDENTTM " refers to an antibody format developed by MacroGenics that comprises an immunoglobulin Fc region polypeptide, one bispecific Fv binding domain and one Fab fragment. Both

the bispecific Fv binding domain and the Fab fragment are fused to the respective N-termini of the two heavy chains of the Fc region polypeptide.

[0107] In another group of embodiments, the format of the multispecific antibodies of the present invention is selected from bivalent bispecific IgG formats, trivalent bispecific IgG formats and tetravalent bispecific IgG formats. In particular, the format of said multispecific antibodies is selected from KiH-based IgGs, such as DuoBodies (bispecific IgGs prepared by the Duobody technology) (MAbs. 2017 Feb/Mar;9(2):182-212. doi: 10.1080/19420862.2016.1268307); DVD-Ig; IgG-scFv fusions, such as CODV-IgG, Morrison (IgG CH₃-scFv fusion (Morrison-H) or IgG CL-scFv fusion (Morrison-L)), bsAb (scFv linked to C-terminus of light chain), Bs1Ab (scFv linked to N-terminus of light chain), Bs2Ab (scFv linked to N-terminus of heavy chain), Bs3Ab (scFv linked to C-terminus of heavy chain), Ts1Ab (scFv linked to N-terminus of both heavy chain and light chain) and Ts2Ab (dsScFv linked to C-terminus of heavy chain). More particularly, the format of said multispecific antibody is selected from KiH-based IgGs, such as DuoBodies; DVD-Ig; CODV-IgG and Morrison (IgG CH₃-scFv fusion (Morrison-H) or IgG CL-scFv fusion (Morrison-L)), even more particularly from DVD-Ig and Morrison (IgG CH₃-scFv fusion (Morrison-H) or IgG CL-scFv fusion (Morrison-L)).

[0108] In particular embodiments of the invention, the format of said multispecific antibodies is selected from a Morrison format, *i. e.* a Morrison-L and a Morrison-H format. The Morrison-L and Morrison-H format used in the present invention are tetravalent and bispecific molecular formats bearing an IgG Fc region, in particular an IgG4 Fc region. Two highly stable scFv binding domains, wherein the light chain comprises Vk FR1 to FR3 in combination with a Vλ FR4 (λ-cap), herein also called λ-cap scFv, are fused via a linker L1 to the heavy chain (Morrison-H) or light chain (Morrison-L) C-termini.

[0109] The linker L1 is a peptide of 2-30 amino acids, more particularly 5-25 amino acids, and most particularly 10-20 amino acids. In particular embodiments, said linker L1 comprises one or more units of four (4) glycine amino acid residues and one (1) serine amino acid residue (GGGGS)_n, wherein n=1, 2, 3, 4 or 5, particularly n=2.

[0110] In a special embodiment of the invention, the multispecific antibodies have a Morrison-L format, as defined above. In another special embodiment of the invention, the multispecific antibodies have a Morrison-H format, as defined above.

[0111] In case the antibody variable domains comprised in the multispecific antibodies of the invention are in the form of scFv fragments, these scFv fragments comprise a variable heavy chain domain (VH) and a variable light chain domain (VL) connected by a linker L2.

[0112] The linker L2 is a peptide of 10-40 amino acids, more particularly 15-30 amino acids, and most particularly 20-25 amino acids. In particular embodiments, said linker L2 comprises one or more units of four (4) glycine amino acid residues and one (1) serine amino acid residue (GGGGS)_n, wherein n=1, 2, 3, 4, 5, 6, 7 or 8, particularly n=4.

[0113] Specific but non-limiting examples of multispecific antibodies of the invention, where the antibody variable domains comprised therein are Fab fragments, are the Morrison-H antibodies PRO2198, PRO2199, whose sequences are listed in Table 4.

[0114] The antibody variable domains and multispecific antibodies of the invention can be produced using any convenient antibody-manufacturing method known in the art (see, e. g., Fischer, N. & Leger, O., Pathobiology 74 (2007) 3-14 with regard to the production of bispecific constructs; Hornig, N. & Färber-Schwarz, A., Methods Mol. Biol. 907 (2012) 713-727, and WO 99/57150 with regard to bispecific diabodies and tandem scFvs). Specific examples of suitable methods for the preparation of the bispecific construct further include, inter alia, the Genmab (see Labrijn et al., Proc. Natl. Acad. Sci. USA 110 (2013) 5145-5150) and Merus (see de Kruif et al., Biotechnol. Bioeng. 106 (2010) 741-750) technologies. Methods for production of bispecific antibodies comprising a functional antibody Fc part are also known in the art (see, e. g., Zhu et al., Cancer Lett. 86 (1994) 127-134); and Suresh et al., Methods Enzymol. 121 (1986) 210-228).

[0115] These methods typically involve the generation of monoclonal antibodies or monoclonal antibody variable domains, for example by means of fusing myeloma cells with the spleen cells from a mouse that has been immunized with the desired antigen using the hybridoma technology (see, e. g., Yokoyama et al., Curr. Protoc. Immunol. Chapter 2, Unit 2.5, 2006) or by means of recombinant antibody

engineering (repertoire cloning or phage display/yeast display) (see, *e. g.*, Chames & Baty, FEMS Microbiol. Letters 189 (2000) 1-8), and the combination of the antigen-binding domains or fragments or parts thereof of two or more different monoclonal antibodies to give a bispecific or multispecific construct using known molecular cloning techniques.

[0116] The multispecific antibodies of the invention can be prepared by conjugating the constituent binding specificities, using methods known in the art. For example, each binding specificity of the bispecific molecule can be generated separately and then conjugated to one another. When the binding specificities are proteins or peptides, a variety of coupling or cross-linking agents can be used for covalent conjugation. Examples of cross-linking agents include protein A, carbodiimide, N-succinimidyl-5-acetyl-thioacetate (SATA), 5,5'-dithiobis (2-nitrobenzoic acid) (DTNB), o-phenylenedimaleimide (oPDM), N-succinimidyl-3-(2-pyridyldithio)propionate (SPDP), and sulfosuccinimidyl 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (sulfo-SMCC) (see *e. g.*, Karpovsky et al., 1984 J. Exp. Med. 160: 1686; Liu, M A et al., 1985 Proc. Natl. Acad. Sci. USA 82:8648). Other methods include those described in Paulus, 1985 Behring Ins. Mitt. No. 78, 118-132; Brennan et al., 1985 Science 229:81-83, and Glennie et al., 1987 J. Immunol. 139: 2367-2375. Conjugating agents are SATA and sulfo-SMCC, both available from Pierce Chemical Co. (Rockford, Ill, USA).

[0117] Alternatively, two or more binding specificities can be encoded in the same vector and expressed and assembled in the same host cell. This method is particularly useful where the bispecific molecule is a mAb x Fab, a mAb x scFv, a mAb x dsFv or a mAb x Fv fusion protein. Methods for preparing multispecific antibodies and molecules are described for example in Methods for preparing multispecific antibodies and molecules are described for example in US 5,260,203; US 5,455,030; US 4,881,175; US 5,132,405; US 5,091,513; US 5,476,786; US 5,013,653; US 5,258,498; and US 5,482,858.

[0118] Binding of the antibody variable domains and multispecific antibodies to their specific targets can be confirmed by, for example, enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (REA), FACS analysis, bioassay (*e. g.*, growth inhibition), or Western Blot assay. Each of these assays generally detects the

presence of protein-antibody complexes of particular interest by employing a labeled reagent (e. g., an antibody) specific for the complex of interest.

[0119] In a further aspect, the invention provides a nucleic acid or two nucleic acids encoding the antibody variable domain or the multispecific antibody of the invention. Such nucleic acids can be optimized for expression in mammalian cells.

[0120] The term “nucleic acid” is used herein interchangeably with the term “polynucleotide(s)” and refers to one or more deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphorates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs). Unless otherwise indicated, a particular nucleic acid also implicitly encompasses conservatively modified variants thereof (e. g., degenerate codon substitutions) and nucleic acids having complementary sequences, as well as the sequence explicitly indicated. Specifically, as detailed below, degenerate codon substitutions may be achieved by generating nucleic acids in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al., *Nucleic Acid Res.* 19:5081, 1991; Ohtsuka et al., *J. Biol. Chem.* 260:2605-2608, 1985; and Rossolini et al., *Mol. Cell. Probes* 8:91-98, 1994).

[0121] The invention provides substantially purified nucleic acid molecules which encode polypeptides comprising segments or domains of the antibody variable domain or multispecific antibody described above. When expressed from appropriate expression vectors, polypeptides encoded by these nucleic acid molecules are capable of exhibiting antigen-binding capacities of the multispecific antibody of the present invention.

[0122] The polynucleotide sequences can be produced by *de novo* solid-phase DNA synthesis or by PCR mutagenesis of an existing sequence (e. g., sequences as described in the Examples below) encoding the multispecific antibody of the invention or variable domains thereof or binding domains thereof. Direct chemical

synthesis of nucleic acids can be accomplished by methods known in the art, such as the phosphotriester method of Narang et al., 1979, Meth. Enzymol. 68:90; the phosphodiester method of Brown et al., Meth. Enzymol. 68: 109, 1979; the diethylphosphoramidite method of Beaucage et al., Tetra. Lett., 22: 1859, 1981; and the solid support method of U.S. Pat. No. 4,458,066. Introducing mutations to a polynucleotide sequence by PCR can be performed as described in, *e. g.*, PCR Technology: Principles and Applications for DNA Amplification, H. A. Erlich (Ed.), Freeman Press, NY, N.Y., 1992; PCR Protocols: A Guide to Methods and Applications, Innis et al. (Ed.), Academic Press, San Diego, Calif, 1990; Mattila et al., Nucleic Acids Res. 19:967, 1991; and Eckert et al., PCR Methods and Applications 1:17, 1991.

[0123] Also provided in the invention are expression vectors and host cells for producing the antibody variable domain or multispecific antibody of the invention.

[0124] The term “vector” is intended to refer to a polynucleotide molecule capable of transporting another polynucleotide to which it has been linked. One type of vector is a “plasmid”, which refers to a circular double stranded DNA loop into which additional DNA segments may be ligated. Another type of vector is a viral vector, wherein additional DNA segments may be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e. g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e. g.*, non-episomal mammalian vectors) can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome.

[0125] Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as “recombinant expression vectors” (or simply, “expression vectors”). In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, “plasmid” and “vector” may be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e. g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions. In this particular context, the term “operably linked” refers to a functional relationship between two or more

polynucleotide (e. g., DNA) segments. Typically, it refers to the functional relationship of a transcriptional regulatory sequence to a transcribed sequence. For example, a promoter or enhancer sequence is operably linked to a coding sequence if it stimulates or modulates the transcription of the coding sequence in an appropriate host cell or other expression system. Generally, promoter transcriptional regulatory sequences that are operably linked to a transcribed sequence are physically contiguous to the transcribed sequence, *i. e.*, they are *cis*-acting. However, some transcriptional regulatory sequences, such as enhancers, need not be physically contiguous or located in close proximity to the coding sequences whose transcription they enhance.

[0126] Various expression vectors can be employed to express the polynucleotides encoding the antibody variable domain or multispecific antibody chain(s). Both viral-based and non-viral expression vectors can be used to produce the antibodies or antibody variable domains in a mammalian host cell. Non-viral vectors and systems include plasmids, episomal vectors, typically with an expression cassette for expressing a protein or RNA, and human artificial chromosomes (see, e. g., Harrington et al., *Nat Genet.* 15:345, 1997). For example, non-viral vectors useful for expression of the IL-31-binding polynucleotides and polypeptides in mammalian (e. g., human) cells include pThioHis A, B and C, pcDNA3.1/His, pEBVHis A, B and C, (Invitrogen, San Diego, CA, USA), MPS V vectors, and numerous other vectors known in the art for expressing other proteins. Useful viral vectors include vectors based on retroviruses, adenoviruses, adeno-associated viruses, herpes viruses, vectors based on SV40, papilloma virus, HBP Epstein Barr virus, vaccinia virus vectors and Semliki Forest virus (SFV). See, Brent et al., *supra*; Smith, *Annu. Rev. Microbiol.* 49:807, 1995; and Rosenfeld et al., *Cell* 68: 143, 1992.

[0127] The choice of expression vector depends on the intended host cells in which the vector is to be expressed. Typically, the expression vectors contain a promoter and other regulatory sequences (e. g., enhancers) that are operably linked to the polynucleotides encoding a multispecific antibody chain or a variable domain. In one embodiment, an inducible promoter is employed to prevent expression of inserted sequences except under inducing conditions. Inducible promoters include, e. g., arabinose, lacZ, metallothionein promoter or a heat shock promoter. Cultures of transformed organisms can be expanded under non-inducing conditions without

biasing the population for coding sequences whose expression products are better tolerated by the host cells. In addition to promoters, other regulatory elements may also be required or desired for efficient expression of a multispecific antibody chain or a variable domain. These elements typically include an ATG initiation codon and adjacent ribosome binding site or other sequences. In addition, the efficiency of expression may be enhanced by the inclusion of enhancers appropriate to the cell system in use (see, e. g., Scharf et al., *Results Probl. Cell Differ.* 20: 125, 1994; and Bittner et al., *Meth. Enzymol.*, 153:516, 1987). For example, the SV40 enhancer or CMV enhancer may be used to increase expression in mammalian host cells.

[0128] Vectors to be used typically encode the antibody variable domain or multispecific antibody light and heavy chain including constant regions or parts thereof, if present. Such vectors allow expression of the variable regions as fusion proteins with the constant regions thereby leading to production of intact antibodies and antibody variable domains thereof. Typically, such constant regions are human.

[0129] The term "recombinant host cell" (or simply "host cell") refers to a cell into which a recombinant expression vector has been introduced. It should be understood that such terms are intended to refer not only to the particular subject cell but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein.

[0130] The host cells for harboring and expressing the antibody variable domain or multispecific antibody of the invention can be either prokaryotic or eukaryotic. *E. coli* is one prokaryotic host useful for cloning and expressing the polynucleotides of the present invention. Other microbial hosts suitable for use include bacilli, such as *Bacillus subtilis*, and other enterobacteriaceae, such as *Salmonella*, *Serratia*, and various *Pseudomonas* species. In these prokaryotic hosts, one can also make expression vectors, which typically contain expression control sequences compatible with the host cell (e. g., an origin of replication). In addition, any number of a variety of well-known promoters will be present, such as the lactose promoter system, a tryptophan (trp) promoter system, a beta-lactamase promoter system, or a promoter system from phage lambda. The promoters typically control expression, optionally with an operator sequence, and have ribosome binding site sequences and the like,

for initiating and completing transcription and translation. Other microbes, such as yeast, can also be employed to express the antibody variable domain or multispecific antibodies of the invention. Insect cells in combination with baculovirus vectors can also be used.

[0131] In one embodiment, mammalian host cells are used to express and produce the antibody variable domain or multispecific antibody of the invention. For example, they can be either a hybridoma cell line expressing endogenous immunoglobulin genes or a mammalian cell line harboring an exogenous expression vector. These include any normal mortal or normal or abnormal immortal animal or human cell. For example, a number of suitable host cell lines capable of secreting intact immunoglobulins have been developed including the CHO cell lines, various COS cell lines, HeLa cells, myeloma cell lines, transformed B-cells and hybridomas. The use of mammalian tissue cell culture to express polypeptides is discussed generally in, *e. g.*, Winnacker, FROM GENES TO CLONES, VCH Publishers, N.Y., N.Y., 1987. Expression vectors for mammalian host cells can include expression control sequences, such as an origin of replication, a promoter, and an enhancer (see, *e. g.*, Queen, et al., Immunol. Rev. 89:49-68, 1986), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. These expression vectors usually contain promoters derived from mammalian genes or from mammalian viruses. Suitable promoters may be constitutive, cell type-specific, stage-specific, and/or modulatable or regulatable. Useful promoters include, but are not limited to, the metallothionein promoter, the constitutive adenovirus major late promoter, the dexamethasone-inducible MMTV promoter, the SV40 promoter, the MRP polIII promoter, the constitutive MPS V promoter, the tetracycline-inducible CMV promoter (such as the human immediate-early CMV promoter), the constitutive CMV promoter, and promoter-enhancer combinations known in the art.

[0132] Methods for introducing expression vectors containing the polynucleotide sequences of interest vary depending on the type of cellular host. For example, calcium chloride transfection is commonly utilized for prokaryotic cells, whereas calcium phosphate treatment or electroporation may be used for other cellular hosts. (See generally Green, M. R., and Sambrook, J., Molecular Cloning: A Laboratory Manual (Fourth Edition), Cold Spring Harbor Laboratory Press (2012)). Other

methods include, *e. g.*, electroporation, calcium phosphate treatment, liposome-mediated transformation, injection and microinjection, ballistic methods, virosomes, immunoliposomes, polycation-nucleic acid conjugates, naked DNA, artificial virions, fusion to the herpes virus structural protein VP22 (Elliot and O'Hare, Cell 88:223, 1997), agent-enhanced uptake of DNA, and *ex vivo* transduction. For long-term, high-yield production of recombinant proteins, stable expression will often be desired. For example, cell lines which stably express the antibody variable domain or multispecific antibody of the invention can be prepared using expression vectors of the invention which contain viral origins of replication or endogenous expression elements and a selectable marker gene. Following the introduction of the vector, cells may be allowed to grow for 1 to 2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth of cells which successfully express the introduced sequences in selective media. Resistant, stably transfected cells can be proliferated using tissue culture techniques appropriate to the cell type. The present invention thus provides a method of producing the antibody variable domain or multispecific antibody of the invention, wherein said method comprises the step of culturing a host cell comprising a nucleic acid or a vector encoding the antibody variable domain or multispecific antibody of the invention, whereby said antibody variable domain or said multispecific antibody of the disclosure is expressed.

[0133] In one aspect, the present invention relates to a method of producing the antibody variable domain multispecific antibody of the invention, the method comprising the step of culturing a host cell expressing a nucleic acid encoding the antibody variable domain or multispecific antibody of the invention. In particular, the present invention relates to a method of producing the antibody variable domain or multispecific antibody of the invention, the method comprising (i) providing a nucleic acid or two nucleic acids encoding the antibody variable domain or multispecific antibody of the invention or one or two vectors encoding the antibody variable domain or multispecific antibody of the invention, expressing said nucleic acid or nucleic acids, or said vector or vectors, and collecting said antibody variable domain or multispecific antibody from the expression system, or (ii) providing a host cell or host cells expressing a nucleic acid or two nucleic acids encoding the antibody

variable domain or multispecific antibody of the invention, culturing said host cell or said host cells; and collecting said antibody variable domain or said multispecific antibody from the cell culture.

[0134] In a further aspect, the present invention relates to a pharmaceutical composition comprising the multispecific antibody of the invention, and a pharmaceutically acceptable carrier. "Pharmaceutically acceptable carrier" means a medium or diluent that does not interfere with the structure of the antibodies. Pharmaceutically acceptable carriers enhance or stabilize the composition, or facilitate preparation of the composition. Pharmaceutically acceptable carriers include solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible.

[0135] Certain of such carriers enable pharmaceutical compositions to be formulated as, for example, tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspension and lozenges for the oral ingestion by a subject. Certain of such carriers enable pharmaceutical compositions to be formulated for injection, infusion or topical administration. For example, a pharmaceutically acceptable carrier can be a sterile aqueous solution.

[0136] The pharmaceutical composition of the invention can be administered by a variety of methods known in the art. The route and/or mode of administration vary depending upon the desired results. Administration can be intravenous, intramuscular, intraperitoneal, or subcutaneous, or administered proximal to the site of the target. In particular embodiments, the administration is intramuscular, or subcutaneous, particularly subcutaneous. The pharmaceutically acceptable carrier should be suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (*e. g.*, by injection or infusion), particularly for intramuscular or subcutaneous administration. Depending on the route of administration, the active compound, *i. e.*, the multispecific antibody of the invention, may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound.

[0137] The pharmaceutical compositions of the invention can be prepared in accordance with methods well known and routinely practiced in the art. See, *e. g.*, Remington: The Science and Practice of Pharmacy, Mack Publishing Co., 20th ed.,

2000; and Sustained and Controlled Release Drug Delivery Systems, J. R. Robinson, ed., Marcel Dekker, Inc., New York, 1978. Pharmaceutical compositions are preferably manufactured under GMP conditions. Typically, a therapeutically effective dose or efficacious dose of the multispecific antibody of the invention is employed in the pharmaceutical compositions of the invention. The multispecific antibodies of the invention are formulated into pharmaceutically acceptable dosage forms by conventional methods known to those of skill in the art. Dosage regimens are adjusted to provide the optimum desired response (*e. g.*, a therapeutic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

[0138] Actual dosage levels of the active ingredients in the pharmaceutical compositions of the invention can be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. The selected dosage level depends upon a variety of pharmacokinetic factors including the activity of the particular compositions of the present invention employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors.

[0139] The multispecific antibody of the invention is usually administered on multiple occasions. Intervals between single dosages can be weekly, monthly or yearly. Intervals can also be irregular as indicated by measuring blood levels of the multispecific antibody of the invention in the patient. Alternatively, the multispecific

antibody of the invention can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the antibody in the patient. In general, humanized antibodies show longer half-life than that of chimeric antibodies and nonhuman antibodies. The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, a relatively low dosage is administered at relatively infrequent intervals over a long period of time. Some patients continue to receive treatment for the rest of their lives. In therapeutic applications, a relatively high dosage at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, and preferably until the patient shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regime.

[0140] In one aspect, the present invention relates to the multispecific antibody of the invention or the pharmaceutical composition of the invention for use as a medicament. In a suitable embodiment, the present invention provides the multispecific antibody or the pharmaceutical composition for use in the treatment of a disease selected from allergic, inflammatory and autoimmune diseases, particularly from inflammatory and autoimmune diseases.

[0141] In another aspect, the present invention provides the pharmaceutical composition for use in the manufacture of a medicament for the treatment of an allergic, inflammatory or autoimmune disease, particularly of an inflammatory or autoimmune disease.

[0142] In another aspect, the present invention relates to the use of the multispecific antibody or the pharmaceutical composition for treating an allergic, inflammatory or autoimmune disease, particularly for treating an inflammatory or autoimmune disease, in a subject in need thereof.

[0143] In another aspect, the present invention relates to a method of treating a subject comprising administering to the subject a therapeutically effective amount of the multispecific antibody of the present invention. In a suitable embodiment, the present invention relates to a method for the treatment of an allergic, inflammatory or autoimmune disease, particularly for treating an inflammatory or autoimmune disease, in a subject comprising administering to the subject a therapeutically effective amount of the multispecific antibody of the present invention.

[0144] The term “subject” includes human and non-human animals.

[0145] The term “animals” include all vertebrates, *e. g.*, non-human mammals and non-mammals, such as non-human primates, sheep, dog, cow, chickens, amphibians, and reptiles. Except when noted, the terms “patient” or “subject” are used herein interchangeably.

[0146] The terms “treatment”, “treating”, “treat”, “treated”, and the like, as used herein, refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be therapeutic in terms of a partial or complete cure for a disease and/or adverse effect attributable to the disease or delaying the disease progression.

“Treatment”, as used herein, covers any treatment of a disease in a mammal, *e. g.*, in a human, and includes: (a) inhibiting the disease, *i. e.*, arresting its development; and (b) relieving the disease, *i. e.*, causing regression of the disease.

[0147] The term “therapeutically effective amount” or “efficacious amount” refers to the amount of an agent that, when administered to a mammal or other subject for treating a disease, is sufficient to affect such treatment for the disease. The “therapeutically effective amount” will vary depending on the agent, the disease and its severity and the age, weight, etc., of the subject to be treated.

[0148] In one embodiment, the allergic, inflammatory and autoimmune diseases are selected from pruritus-causing allergic diseases, pruritus-causing inflammatory diseases and pruritus-causing autoimmune diseases, particularly from pruritus-causing inflammatory diseases and pruritus-causing autoimmune diseases. The terms “pruritus” and “itch”, which are herein used synonymously, refers to a sensation that causes the desire or reflex to scratch. Scratching can be problematic particularly in the case of chronic skin diseases that induce itching, such as atopic dermatitis, dermatomycoses, psoriasis or urticaria, as the permanent itching stimulates patients to scratch the affected skin areas constantly and/or excessively, which often leads to skin injuries and further deterioration of the skin surface.

[0149] The term “allergic diseases” or “allergies” as used herein refers to a large number of conditions caused by hypersensitivity of the immune system to typically harmless substances in the environment.

[0150] The term “inflammatory diseases” as used herein refers to a vast number of inflammatory disorders, *i. e.* inflammatory abnormalities, which are often characterized by prolonged inflammation, known as chronic inflammation. The term

“inflammation” refers to the complex biological response of body tissues to harmful stimuli, such as pathogens, damaged cells, or irritants. It is a protective response involving immune cells, blood vessels, and molecular mediators. While regular inflammation reactions are essential for the body to eliminate the initial cause of cell injury, clear out necrotic cells and tissues damaged from the original insult and the inflammatory process, and to initiate tissue repair, inflammatory disorders are generally characterized by persistent inflammation in the absence of harmful stimuli.

[0151] The term “autoimmune diseases” as used herein refers to a condition arising from an abnormal immune response to a functioning body part. It is the result of autoimmunity, *i. e.* the presence of self-reactive immune response (*e. g.*, autoantibodies, self-reactive T cells), with or without damage or pathology resulting from it, which is typically restricted to certain organs or involve a particular tissue in different places.

[0152] In particular embodiments, the pruritus-causing inflammatory or autoimmune disease is selected from atopic dermatitis, acute allergic contact dermatitis, chronic spontaneous urticaria, bullous pemphigoid, alopecia areata, dermatomyositis, prurigo nodularis, psoriasis and atopic asthma, in particular from atopic dermatitis.

[0153] In another aspect, the allergic, inflammatory and autoimmune diseases are selected from atopic dermatitis, acute allergic contact dermatitis, chronic spontaneous urticaria, bullous pemphigoid, alopecia areata, dermatomyositis, prurigo nodularis, psoriasis and atopic asthma, in particular from atopic dermatitis.

[0154] In another embodiment, the allergic, inflammatory and autoimmune diseases are selected from allergic asthma, allergic rhinitis, inflammatory airway disease, recurrent airway obstruction, airway hyperresponsiveness, chronic obstruction pulmonary disease, Crohn disease, chronic non-histamine related urticaria, antihistamine-unresponsive mastocytosis, lichen simplex chronicus, seborrhoeic dermatitis, xeroderma, Dermatitis herpetiformis, lichen planus and ulcerative colitis.

[0155] In another embodiment, the present invention provides the multispecific antibody or the pharmaceutical composition, as defined herein, for use in the treatment of a disease, which is a neuropathic pruritus disease selected from post-herpetic neuralgia, post-herpetic itch, notalgia paresthetica, multiple sclerosis and brachioradial pruritus.

[0156] In another embodiment, the present invention provides the multispecific antibody or the pharmaceutical composition for use in an antipruritic agent for the treatment of an systemic disease with itching, which disease is selected from Cholestasis, chronic kidney disease, Hodgkin's disease, cutaneous T-cell lymphoma and other lymphomas or leukemias associated with chronic itch, polycythemia vera, hyperthyroidism, chronic post-arthropod itch (Id reaction), pregnancy-induced chronic itch (e. g. PUPPP), eosinophilic pustular folliculitis, drug hypersensitivity reactions, chronic pruritus of the elderly or dry skin itch (local, generalized), and pruritus at the scar portion after burn (post-burn itch), genetic or nevoid chronic itches (e. g. Netherton syndrome, Darier's disease (Morbus Darier), Hailey-Hailey disease, inflammatory linear verrucous epidermal nevus (ILVEN), familial primary cutaneous amyloidosis, Olmsted syndrome), aquagenic pruritus, fiberglass dermatitis, mucous chronic itch, chemotherapy-induced itch and HIV.

Sequence listing (mutations designated according to AHo numbering scheme; the CDRs defined according to Numab CDR definition, unless specified otherwise)

Table 1. Examples of IL-31 binding domains as used in the present invention (CDR residues shown in bold and italic letters).

SEQ ID NUMBER	Ab region	Sequence
50-09-D07		
SEQ ID NO: 1	HCDR1 (H27-H42; AHo numbering)	<i>GFSFSANYWIC</i>
SEQ ID NO: 2	HCDR2 (H57-H76; AHo numbering)	<i>CYIGSRADTYYPWAKG</i>
SEQ ID NO: 3	HCDR2 (H57-H76; AHo numbering)	<i>CISIGSRADTYYPWAKG</i>
SEQ ID NO: 4	HCDR3 (H108-H138; AHo numbering)	<i>RFSSGIYDLDRFFL</i>
SEQ ID NO: 5	VH (50-09-D07-sc03/50-09-D07-sc07)	QSQLVESGGGLVQPGGSLRLSCAAS <i>GFSFSANYWICWVRQAPGKGLEWIVCIYIGSRADTYYPWAKG</i> GRFTISKDNSKNTVYQLQMNSLRAEDTAVYFC <i>ARFSSGIYDLDRFFLWGQGTQVTVSS</i>
SEQ ID NO: 6	VH (50-09-D07-sc04)	QSQLVESGGGRVQPGGSLRLSCAAS <i>GFSFSANYWICWVRQAPGKGLEWIVCIYIGSRADTYYPWAKG</i> GRFTISKDNSKNTVYQLQMNSLRAEDTATYFC <i>ARFSSGIYDLDRFFLWGQGTQVTVSS</i>
SEQ ID NO: 7	VH (50-09-D07-sc05)	QSQLVESGGGSVQPGGSLRLSCAAS <i>GFSFSANYWICWVRQAPGKGLEWIVCIYIGSRADTYYPWAKG</i> GRFTISKDNSKNTVYQLQMNSLRAEDTATYFC <i>ARFSSGIYDLDRFFLWGQGTQVTVSS</i>
SEQ ID NO: 8	VH (50-09-D07-sc06)	QSQLVESGGGLVQPGGSLRLSCAAS <i>GFSFSANYWICWVRQAPGKGLEWIVCISIGSRADTYYPWAKG</i> GRFTISKDNSKNTVYQLQMNSLRAEDTAVYFC <i>ARFSSGIYDLDRFFLWGQGTQVTVSS</i>
SEQ ID NO: 9	LCDR1 (L24-L42; AHo numbering)	<i>QASQSIDSWLA</i>
SEQ ID NO: 36	LCDR1	<i>QASQSIESWLA</i>

SEQ ID NO: 10	(L24-L42; AHo numbering) LCDR2	<i>QASKLAS</i>
SEQ ID NO: 11	(L58-L72; AHo numbering) LCDR3	<i>QTYYGGGHHIGWG</i>
SEQ ID NO: 12	(L107-L138; AHo numbering) VL	AFQLTQSPSSLSASVGDRVTITC <i>QASQSIDSWLAWYQQKPGKPPKLLIYQASKL</i> ASGVPSRFSGSGGTDTYTLTISSLQPEDFATYYC <i>QTYYGGGHHIGWG</i> FGGTGTVT VLG
SEQ ID NO: 37	VL	AFQLTQSPSSLSASVGDRVTITC <i>QASQSIDSWLAWYQQKPGKPPKLLIYQASKL</i> ASGVPSRFSGSGGTDTYTLTISSLQPEDFATYYC <i>QTYYGGGHHIGWG</i> FGGTGTVT VLG

Table 2. Other sequences related to the present invention.

SEQ ID NUMBER	Ab region	Sequence
SEQ ID NO: 13	VH3	EVQLVESGGGLVQPGGSLRLSCAASGFSANYYPCWVRQAPGKLEWIGCTY GGSSDITYDANWTKGRFTISRDNKNTVYLMNSLRAEDTAVYYCAR <i>RS4WYS</i> GWGGDLWGQGLVTVSS
SEQ ID NO: 14	VH4	QVQLQESGPGLVKPSSETLSLTCKVSGFSFNSYWCWIRQPPGKLEWIGCTFV GSSDSTYYANWAKGRVTISVDSSKNQFSLKLSSTVAADTAVYYCAR <i>RHPSDAVY</i> GYANLWGQGLVTVSS
SEQ ID NO: 15	Vkappa1	DIQMTQSPSSLSASVGDRVTITC <i>QASQSIDSWLAWYQQKPGKAPKLLIYR4STL</i> ASGVPSRFSGSGGTDFTLTISSLQPEDFATYYC <i>QSSYGNYGDF</i> FGGTGTVTLG
SEQ ID NO: 16	Vλ germline-based FR4 (Sk17)	FGTGTKVTVLG
SEQ ID NO: 17	Vλ germline-based FR4 (Sk12)	FGGGTKLTVLG
SEQ ID NO: 18	Vλ germline-based FR4	FGGGTQLIILG
SEQ ID NO: 19	Vλ germline-based FR4	FGEGTELTVLG
SEQ ID NO: 20	Vλ germline-based FR4	FGSGTKVTVLG

SEQ ID NO: 21	Vλ germline-based FR4	FGGGTQLTVLG
SEQ ID NO: 22	Vλ germline-based FR4	FGGGTQLTALG
SEQ ID NO: 23	Vλ germline-based FR4 G141C	FGCGTKVTVLG
SEQ ID NO: 24	Linker	GGGSGGGSGGGSGGGGS
SEQ ID NO: 25	Linker	GGGS
SEQ ID NO: 26	Linker	GGGSGGGGS

Table 3. Examples of scFv antibody variable domains of the present invention (Linkers are shown in bold).

SEQ ID NUMBER	Ab name and description	Sequence
SEQ ID NO: 27	PRO1643; scFv (VL-linker-VH) (50-09-D07-sc03)	AFQLTQSPSSLASVGDRTVTITCQASQSIDSWLAWYQQKPKGKPPKLLIYQASKLASGVP SRFSGSGGTDTYTLTISSLQPEDFATYYCQTYGGGHIGWGFGTGTGVTVLGGGGSG GGSGGGSGGGSGGSQSQLVESGGGLVQPGGSLRLSCAASGFSFSANYWICWVRQAP GKGLEWIVCIYIGSRADTYAPWAKGRFTISKDNSKNTVYLMNSLRAEDTATYFCAR FSSGIYDLDRFFLWGQGTQVTVSS
SEQ ID NO: 28	PRO1900; scFv (VL-linker-VH) (50-09-D07-sc04)	AFQLTQSPSSLASVGDRTVTITCQASQSIDSWLAWYQQKPKGKPPKLLIYQASKLASGVP SRFSGSGGTDTYTLTISSLQPEDFATYYCQTYGGGHIGWGFGTGTGVTVLGGGGSG GGSGGGSGGGSGGSQSQLVESGGGRVQPGGSLRLSCAASGFSFSANYWICWVRQAP GKGLEWIVCIYIGSRADTYAPWAKGRFTISKDNSKNTVYLMNSLRAEDTATYFCAR FSSGIYDLDRFFLWGQGTQVTVSS
SEQ ID NO: 29	PRO1901; scFv (VL-linker-VH) (50-09-D07-sc05)	AFQLTQSPSSLASVGDRTVTITCQASQSIDSWLAWYQQKPKGKPPKLLIYQASKLASGVP SRFSGSGGTDTYTLTISSLQPEDFATYYCQTYGGGHIGWGFGTGTGVTVLGGGGSG GGSGGGSGGGSGGSQSQLVESGGSVQPGGSLRLSCAASGFSFSANYWICWVRQAP GKGLEWIVCIYIGSRADTYAPWAKGRFTISKDNSKNTVYLMNSLRAEDTATYFCAR FSSGIYDLDRFFLWGQGTQVTVSS
SEQ ID NO: 30	PRO1902; scFv (VL-linker-VH) (50-09-D07-sc06)	AFQLTQSPSSLASVGDRTVTITCQASQSIDSWLAWYQQKPKGKPPKLLIYQASKLASGVP SRFSGSGGTDTYTLTISSLQPEDFATYYCQTYGGGHIGWGFGTGTGVTVLGGGGSG GGSGGGSGGGSGGSQSQLVESGGGLVQPGGSLRLSCAASGFSFSANYWICWVRQAP

		GKGLEWIVCISIGSRADTYAPWAKGRFTISKDNSKNTVYLQMNSLRAEDTAVYFCAR FSSGIYDLDRFFLWGQGTIVTVSS
SEQ ID NO: 31	PRO1903; scFv (VL-linker-VH) (50-09-D07-sc07)	AFQLTQSPSSLASVGDRTITCQASQIESWLAWYQQKPGKPPKLLIYQASKLASGVPS RFSGSGGTDTYTLTISSLQPEDFATYQCYYGGGHIGWGFGTKVTVLGGGGSGG GGSGGGSGGGG SQLVESGGGLVQPGGSLRLSCAASGFSFANYWICWVRQAPG KGLEWIVCIYIGSRADTYAPWAKGRFTISKDNSKNTVYLQMNSLRAEDTAVYFCARF SSGIYDLDRFFLWGQGTIVTVSS

Table 4. Examples of multispecific antibodies of the present invention (Linkers are shown in bold).

SEQ ID NUMBER	Ab Format	Sequence
PRO2198		
SEQ ID NO: 32	Morrison-H, LC	DIQMTQSPSSLARVGDRTITCQASEDIESYLAWYQQKPGKAPKLLIYRASTLAYGVP SRFSGSGGRDFTLTISLQPEDFATYCLGSSYSTGSIQFGQTKVEIKRTVAAPSVFIFP PSDEQLKSGTASVCLLNINFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS TLTLISKADYEKHKVYACEVTHQGLSPVTKSFNRGEC
SEQ ID NO: 33	Morrison-H, HC	EVQLVESGGGLVQPGGSLRLSCAASGFSSTSAHYMCWVRQAPGKGLIEWIGCIYAGSRG STYYASWAKGRFTISRDNKNTVYLQMNSLRAEDTAVYYCARAAFNRGVSWIWPYY FSLWGQGTIVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVSVLTVQLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKG QPREPVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD DGSEFLYSRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSLGGGGSGGGGSA FQLTQSPSSLASVGDRTITCQASQSIDSWLAWYQQKPGKPPKLLIYQASKLASGVPSR FSGSGGTDTYTLTISSLQPEDFATYQCYYGGGHIGWGFGTKVTVLGGGGSGGGG GSGGGSGGGG SQLVESGGGLVQPGGSLRLSCAASGFSFANYWICWVRQAPGK GLEWIVCIYIGSRADTYAPWAKGRFTISKDNSKNTVYLQMNSLRAEDTAVYFCARFSS GIYDLDRFFLWGQGTIVTVSS

PRO2199		
SEQ ID NO: 34	Morrison-H, LC	DIQMTQSPSSLSASVGDRVTITCQASEDIESYLAWYQQKPGKAPKLLIYRASTLAYGVPS RFGSGSGTDFTLTISSLQPEDFATYYCLGSSYSTGSIIFGQGTVEIKRTVAAPSVFIFPP SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 35	Morrison-H, HC	EVQLVESGGGRVQPGGSLRLSCAASGFSSTSAHYMCWVRQAPGKGLEWIGCIYAGSRG STYYASWAKGRFTISKASSTTVYLMNSLRAEDTATYYCARAAAFVNRGVSWIWPYYFS LWGQGTQVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPPC PPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLGSGGGSGGGGSAFQ LTQSPSSLASVGDRVTITCQASQSIDSWLAWYQQKPGKPKLLIYQASKLASGVPSRFS GSGGTDYTLTISSLQPEDFATYYCQYYGGGHIGWFGGTGKVTVLGSGGGSGGGG SGGGSGGGGSQSQLVESGGGRVQPGGSLRLSCAASGFSFSANYWICWVRQAPGKGL EWIVCIYIGSRADTYYPAPWAKGRFTISKDNSKNTVYLMNSLRAEDTATYFCARFSSGI YDLDRFFLWGQGTQVTVSS

[0157] Throughout the text of this application, should there be a discrepancy between the text of the specification (e. g., Tables 1 to 4) and the sequence listing, the text of the specification shall prevail.

[0158] It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments pertaining to the invention are specifically embraced by the present invention and are disclosed herein just as if each and every combination was individually and explicitly disclosed. In addition, all sub-combinations of the various embodiments and elements thereof are also specifically embraced by the present invention and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

[0159] The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are intended to fall within the scope of the appended claims.

[0160] To the extent possible under the respective patent law, all patents, applications, publications, test methods, literature, and other materials cited herein are hereby incorporated by reference.

[0161] The following Examples illustrates the invention described above, but is not, however, intended to limit the scope of the invention in any way. Other test models known as such to the person skilled in the pertinent art can also determine the beneficial effects of the claimed invention.

Examples

Example 1: Generation and testing of anti-IL-31 molecules:

Aim of the project

[0162] The goal of the project is to identify humanized monoclonal antibody variable domains that specifically bind to and neutralize the biological effect of human IL-31.

1.1. Immunization

[0163] Two different immunization protocols were applied to a total of six rabbits to obtain an optimal immune response against human IL-31. Rabbits were immunized with recombinantly produced and purified IL-31 (Sino Biological, Cat. No.11557-H08H). Prior to immunization, the quality of recombinant human IL-31 was analyzed by the manufacturer 1) for purity by SDS-page, and 2) for biological activity by measuring the ability to induce STAT3 activation in U87 cells. The first group of three rabbits (protocol 1) received 4 injections of 200 µg each throughout 70 days. The second group of three rabbits (protocol 2) received 5 injections of 200 µg each through a period of 112 days. During the course of the immunization, the strength of the humoral immune response against the antigen was qualitatively assessed by determining the maximal dilution (titer) for the serum of each rabbit that still results in detectable binding of the polyclonal serum antibodies to the antigen. Serum antibody titers against the immobilized antigen (recombinant human IL-31) were assessed using an enzyme-linked immunosorbent assay (ELISA). All six rabbits immunized with purified human IL-31 showed high titers with EC₅ up to 3 x 10⁷.

1.2. Sorting

[0164] Prior to the hit identification procedure, two flow-cytometry-based sorting campaigns with protein G beads were performed in the presence R-Phycoerythrin (RPE)-labelled IL-31, which allows the specific detection and isolation of high-affinity IL-31-binding B-cells. A total of 4.58 x 10⁷ and 4.53 x 10⁷ lymphocytes respectively, derived from four rabbits were analyzed in these two sorting campaigns. Of these, a total of 3,520 and 3,696 B-cells, respectively, expressing IL-31-specific antibodies (IgG) were isolated and individually cultured as single clones for three to four weeks

1.3. Hit identification

General remarks

[0165] For hit identification, direct ELISA screens were performed to assess binding to recombinant human IL-31. 618 clones were found to bind to human IL-31. Binding to cynomolgus IL-31 and mouse IL-31 was evaluated by SPR only. All supernatants were further analyzed for their potential to neutralize the biological activity of IL-31-induced signaling in the cell-based IL-31RA/OSMR dimerization assay and for blockage of the interaction of human IL-31RA and human IL-31 in a competition ELISA. Due to the lack of cross-reactivity to mouse IL-31 no further analyses were done with regard to mouse IL-31.

Binding to human IL-31 by ELISA

[0166] For hit identification, *i. e.* the identification of B cell clones that produce antibodies binding to IL-31, cell culture supernatants of the above 3,520 and 3,696 B-cells clones of the two sorts were screened for the presence of antibodies that bind to human IL-31 by ELISA, as described in section 1.3. Supernatants from 618 B cell clones produced a signal that was above background.

Determination of binding affinity to human IL-31

[0167] In a secondary hit identification procedure, information on the binding affinities to human IL-31 of the 618 monoclonal rabbit antibodies that were qualified as positive during the primary screening were determined by surface plasmon resonance (SPR).

[0168] For these affinity screening by SPR, an antibody specific for the Fc region of rabbit IgGs was immobilized on a sensor chip (SPR-2 Affinity Sensor, High Capacity Amine, Sierra Sensors) using a standard amine-coupling procedure. Rabbit monoclonal antibodies in B cell supernatants were captured by the immobilized anti-rabbit IgG antibody. A minimal IgG concentration in the B cell supernatants is required to allow sufficient capture. After capturing of the monoclonal antibodies, human IL-31 was injected into the flow cells for 3 min at a concentration of 90 nM, and dissociation of the protein from the IgG captured on the sensor chip was allowed to proceed for 5 min. The apparent dissociation (k_d) and association (k_a) rate constants and the apparent dissociation equilibrium constant (K_D) were calculated with the MASS-2 analysis software (Analyzer, Sierra Sensors) using the 1:1 Langmuir binding model.

[0169] For 584 anti-IL-31 antibodies binding affinities to human IL-31 could be measured. They showed dissociation constants (K_D) ranging from below 2.17×10^{-12} M to 2.11×10^{-5} M. 2.7 % of the antibodies displayed a K_D below 0.5 nM.

Neutralization of IL-31 in the IL-31RA/OSMR dimerization assay and in a competition ELISA

[0170] To assess potency, a cell-based IL-31RA/OSMR dimerization assay (PathHunter assay) and a receptor ligand competition-ELISA were developed and adapted for use with B cell supernatant. The cell-based assay allows to evaluate the blockage of IL-31-induced signaling, whereas in the competition ELISA, only the interaction of IL-31RA and IL-31 is assessed. Since the assays could be performed with B cell supernatant as matrix and were sensitive and precise enough, both assays were used for screening. The inhibitory activity of each B cell supernatant was tested using single well analysis (no dose-responses were performed). Therefore, the extent of inhibition observed is not only dependent on the IgG properties, but also on the concentration of rabbit IgGs in the B cell supernatant.

[0171] Analysis in the blocking ELISA led to a high number of neutralizing clones. 116 out of 618 clones inhibited the interaction of human IL-31 and human IL-31RA by more than 90 % and 143 clones by more than 80 %. 103 clones inhibited IL-31-induced signaling in the PathHunter assay, based on a threshold of > 30 % inhibition.

Species cross-reactivity (binding to cynomolgus monkey IL-31 by SPR)

[0172] All 618 hits identified in the primary screening, were analyzed for species cross-reactivity to cynomolgus monkey IL-31 by SPR. Binding affinities were determined by surface plasmon resonance (SPR) using a MASS-2 SPR device (Sierra Sensors) similarly as described above for human IL-31 with the exception that 90 nM cynomolgus monkey IL-31 were used instead of human IL-31.

[0173] 498 (80.5 %) clones showed binding to cynomolgus monkey IL-31. In terms of affinity, the exact K_D values could not be determined for five antibodies since their off-rates were below or close to the detection limit of the SPR instrument. 120 clones did not show binding to cynomolgus IL-31. Binding antibodies showed equilibrium dissociation constants (K_D) ranging from 4.73×10^{-12} M to 3.39×10^{-5} M. 3.8 % of all

antibodies analyzed displayed a K_D below 500 pM. 75.7 % of rabbit monoclonal antibodies binding to human IL-31 showed less than 10-fold difference in affinities to cynomolgus monkey. The correlation between human and cynomolgus IL-31 was very good.

1.4. Hit selection and hit confirmation

Hit selection and RT-PCR

[0174] As a prerequisite for Hit Confirmation, gene sequence analysis and subsequent humanization of the rabbit antibodies, the genetic information encoding the rabbit antibody variable domain needs to be retrieved. This was achieved by reverse transcription (RT) of the respective messenger RNA into the complementary DNA (cDNA), followed by amplification of the double-stranded DNA by the polymerase chain reaction (PCR). The selection of B cell clones subjected to RT-PCR was primarily based on affinities to human IL-31 below 500 pM and on neutralizing activity in the IL-31/IL-31RA competition ELISA. A few clones with affinities above 500 pM but with good neutralization properties were also included in the selection.

[0175] 94 sets of rabbit CDRs, corresponding to 94 independent clones, were selected and identified. 43 sets of rabbit CDRs, corresponding to 43 independent clones, were identified. Rabbit CDR sequences of all 43 sequenced clones were clustered into a phylogenetic tree. 40 sequences were non-redundant based on CDR regions and three sequences contained a free cysteine. Three clones with identical sequence were excluded. As a result, a total of 40 clones were selected for expression as recombinant IgG.

Cloning and manufacture of monoclonal antibodies

[0176] Following the selection of clones for hit confirmation the rabbit antibodies were cloned, expressed and purified for further characterization. The cloning of the corresponding light and heavy chain variable domains entailed the *in vitro* ligation of the DNA fragments into a suitable mammalian expression vector. The expression vectors for the rabbit antibody heavy and light chains were transfected into a

mammalian suspension cell line for transient heterologous expression. Subsequently the secreted rabbit IgGs were affinity purified and the final products were analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), UV absorbance at 280 nm and size-exclusion high performance liquid chromatography (SE-HPLC) to verify identity, content and purity. 37 of the 40 clones could be cloned into a suitable mammalian expression vector and manufactured with a good too high expression titer (3 – 19 µg protein/ml) and with a high percentage of monomeric content (94.7 to 99.5 %).

1.5. Pharmacological characterization of monoclonal antibodies

Affinity to human and cynomolgus IL-31

[0177] Binding kinetics of the 37 purified monoclonal rabbit antibodies to human and cynomolgus IL-31 were determined by SPR (MASS-2) analysis. Cynomolgus IL-31 was manufactured on demand by Sino Biological since it was not available commercially. Each IgG was captured via an anti-rabbit IgG coupled to a carboxymethylated dextran surface and an analyte dose response was measured. All antibodies were confirmed to bind to human IL-31, except for two IgGs. 12 of the 35 target-binding antibodies exhibited K_D values below 500 pM. 31 out of 37 IgGs bound to cynomolgus IL-31 with high affinity, 23 IgGs showed K_D values below 500 pM. 9 IgGs out of these even displayed values below 10 pM.

IL-31RA/OSMR dimerization assay (blockage of human IL-31-induced signaling)

[0178] Furthermore, the effects of the 37 rabbit monoclonal antibodies on IL-31 induced signaling via the IL-31RA/OSMR receptor complex were tested in the PathHunter dimerization assay from DiscoveryX. The potency (IC_{50}) to neutralize signaling induced by 10 ng/ml IL-31 was analyzed for serial dilutions of all antibodies and compared to the potency of BMS-981164. For comparison of IgGs from different assay plates, relative IC_{50} values were used. These values were determined by calibrating the IC_{50} value of the IgGs against the reference molecule BMS-981164 included on each assay plate (relative IC_{50} : IC_{50} , BMS-981164/ IC_{50} , test antibody).

[0179] IgGs inhibited IL-31-induced signaling with potencies higher than BMS-981164 or not more than five-fold lower. Two IgGs showed superior potency to BMS-981164 and two further IgGs were very similar in terms of IC₅₀ values.

Competitive ELISA (inhibition of hIL-31 binding to hIL-31RA)

[0180] The inhibition of human IL-31 binding to human IL-31RA was assessed by competitive ELISA. For this purpose, IL-31RA was coated on the ELISA plate. Biotinylated IL-31 was preincubated with the rabbit monoclonal antibodies and the mixture was added to the ELISA plate to allow binding to IL-31RA. Bound biotinylated IL-31 was then detected using streptavidin-HRP.

[0181] The competitive ELISA was sensitive enough to differentiate the rabbit antibodies in terms of potencies, and antibodies with lower IC₅₀ values than BMS-981164 were found. Except for two IgGs, all the antibodies blocked the interaction between human IL-31 and IL-31RA, some with incomplete inhibition. In comparison with BMS-981164, 20 rabbit antibodies inhibited the interaction more potently and 12 antibodies showed similar potencies or IC₅₀ values not more than 5-fold lower.

Rabbit IgG selection for generation of humanized scFvs

[0182] Based on the pharmacodynamic properties of the 37 characterized rabbit monoclonal antibodies the best performing clones were selected for the humanization and lead candidate generation. The criteria for the selection of clones were i) complete blockage of IL-31-induced signaling in the IL-31RA/OSMR dimerization assay (with one exception), ii) high affinity to human IL-31, iii) neutralization of the interaction of human IL-31 with human IL-31RA in the competition ELISA, iv) cross-reactivity to cynomolgus IL-31 by SPR and v) sequence diversity. In addition to these criteria the primary sequences of all 37 clones were screened for the presence of unpaired cysteines in the complementary determining regions (CDRs). The identification of unpaired cysteines excluded the commonly occurring pair of cysteines in CDR-H1 and CDR-H2, which is coded in the rabbit's germline repertoire and is considered to form a disulfide bridge.

[0183] Since most of the neutralizing antibodies showed high affinities, the focus of the selection of rabbit antibodies for humanization was on the IL-31RA/OSMR

dimerization assay. Antibodies showing an IC₅₀ of 50 ng/ml or lower for neutralizing IL-31-induced signaling in the IL-31RA/OSMR dimerization assay were chosen for humanization. In total, five promising clones were selected for reformatting and humanization.

1.6. Humanization of scFvs

[0184] For the Lead Candidate generation five rabbit monoclonal antibody clones were selected. The humanization of these clones comprised the transfer of the rabbit CDRs onto one of Numab's proprietary human variable domain acceptor scaffolds. In this process, the amino acid sequences of the six CDR regions were identified using Numab CDR definitions (Table 5) and grafted into Numab's proprietary and highly stable, fully human Vk1/VH3 lambda-capped acceptor framework, resulting in the constructs termed "CDR graft".

Table 5: Numab CDR definition

Region	AHo numbering	Kabat numbering
CDR1-VL	24-42	24-34
CDR2-VL	58-72	50-56
CDR3-VL	107-138	89-97
CDR1-VH	27-42	26-35A/35B/...
CDR2-VH	57-76	50-65
CDR3-VH	108-138	94-102

[0185] Exclusive engraftment of rabbit CDRs onto a human acceptor framework is the most basic grafting strategy. However, occasionally particular CDR sets require mutation of particular rabbit framework residues in order to preserve their full functionality. Therefore, beside the "CDR graft", additional grafting variants containing defined patterns of rabbit framework residues were designed.

[0186] The humanized scFv constructs were designed and ordered in 1 mg scale as mammalian (CHO-S, pcDNA3.1) expression vectors from GeneUniversal (former General Biosystems). Plasmids were used for transient transfection of CHO-S cells as described below.

1.7. Manufacture of humanized scFv

[0187] Expression of mammalian constructs was performed in CHO-S cells using CHOgro transient transfection kit (Mirus). Cultures were harvested after 5-7 days (when cell viability <70 % was reached) expression at 37°C by centrifugation followed by filtration. Proteins were purified from clarified culture supernatants by Protein L affinity chromatography. None of the molecules needed polishing by size exclusion chromatography as all molecules exhibited at least one affinity chromatography fraction with a monomeric content >95 % post capture as assessed by SE-HPLC analysis. Samples were re-buffered to final buffer (50 mM phosphate-citrate buffer with 150 mM NaCl at pH 6.4) by dialysis. For quality control of the manufactured material standard analytical methods such as SE-HPLC, UV₂₈₀ and SDS-PAGE were applied. The manufacture characteristics of five sc03 constructs ("Full grafts") originating from the five clones that were deemed to be suitable for incorporation into multispecific antibody formats are summarized in Table 6. Manufacture characteristics of different grafts of clone 50-35-B03 are summarized in Table 7.

Table 6: scFv manufacture of 5 selected clones. Sc03: Full graft

Protein ID	Clone Id (scFv)	Expression volume [ml]	Yield post affinity chromatography purification [mg]	Yield/L post affinity chromatography purification [mg/l]	Final yield [mg]	Titer [mg/l]	Purity SE-HPLC [% monomer]	Purity SDS-PAGE
PRO1641	50-03-H07-sc03	30	1.3	43	0.6	20	97.8	identity confirmed°
PRO1643	50-09-D07-sc03	30	0.7	23	0.2	7	90.4	identity confirmed°
PRO1644	50-10-F09-sc03	100	0.2	2	0.8	8	97.1	identity confirmed°
PRO1645	50-25-H10-sc03	30	2.0	67	1.4	41	96.6	identity confirmed°
PRO1650	50-35-B03-sc03	30	3.2	107	1.8	57	97.0	identity confirmed°

°protein of interest detected only

Table 7: 50-35-B03 scFv manufacture. Sc08 and sc10: other grafting variants

Protein ID	Clone Id (scFv)	Expression volume [ml]	Yield post affinity chromatography purification [mg]	Yield/L post affinity chromatography purification [mg/l]	Final yield [mg]	Titer [mg/l]	Purity SE-HPLC [% monomer]	Purity SDS-PAGE
PRO1688	50-35-B03-sc08	100	4.7	47	3.7	37	99.4	identity confirmed°
PRO1690	50-35-B03-sc10	100	5.5	55	3.8	38	99.4	identity confirmed°

°protein of interest detected only

1.8. Pharmacodynamics characterization of suitable anti-IL-31 binding domains (scFv format)

[0188] The humanized scFv antibodies that were evaluated as suitable were characterized for primary pharmacodynamics properties.

Affinity to human and cynomolgus IL-31

[0189] Affinity of the seven humanized scFvs to human and cynomolgus IL-31 was determined by SPR analysis on a T200 device (Biacore, GE Healthcare). Cynomolgus IL-31 was manufactured on demand by Sino Biological since it was not available commercially. Human and cynomolgus IL-31-His was captured via an anti-His tag antibody coupled to a carboxymethylated dextran surface and the scFvs were injected as analyte. After each analyte injection cycle the sensor chip was regenerated and new antigen was captured. The scFvs were measured using a dose response multi-cycle kinetic assay in a high-throughput mode with two concentrations (30 and 10 nM) diluted in running buffer. Obtained sensorgrams were fitted using a 1:1 binding model.

[0190] As shown in Table 8, binding to human IL-31 was confirmed for all seven humanized scFvs.

Table 8: Affinity of scFvs to human and cynomolgus IL-31. Sc03: Full graft, sc08 and sc10: other grafting variants

Protein ID	scFv	Affinity to human IL-31				Affinity to cynomolgus IL-31			
		Clone ID	k_a ($M^{-1} s^{-1}$)	k_d (s^{-1})	K_D (M)	k_a ($M^{-1} s^{-1}$)	k_d (s^{-1})	K_D (M)	
PRO1641		50-03-H07-sc03	1.78E+06	5.81E-04	3.27E-10	1.20E+06	5.63E-04	4.69E-10	
PRO1643		50-09-D07-sc03	8.84E+05	4.47E-04	5.05E-10	7.61E+05	4.44E-04	5.83E-10	
PRO1644		50-10-F09-sc03	2.67E+06	1.17E-03	4.37E-10	2.01E+06	1.15E-03	5.73E-10	
PRO1645		50-25-H10-sc03	6.53E+05	4.69E-04	7.19E-10	7.74E+05	5.05E-04	6.53E-10	
PRO1650		50-35-B03-sc03	3.40E+06	9.66E-04	2.84E-10	1.68E+06	1.19E-03	7.09E-10	
PRO1688		50-35-B03-sc08	2.28E+06	1.14E-03	4.99E-10	9.29E+05	1.23E-03	1.32E-09	
PRO1690		50-35-B03-sc10	2.20E+06	1.13E-03	5.15E-10	8.88E+05	1.49E-03	1.68E-09	

IL-31RA/OSMR dimerization assay (blockage of human IL-31-induced signaling)

[0191] The IL-31RA/OSMR dimerization assay was used to test the ability of the humanized scFvs to inhibit IL-31-induced signaling via the IL-31RA/OSMR heterodimer. 10,000 cells per well were seeded in a 96-well plate. Serial dilutions of the scFvs and of the control antibody BMS-981164 were added to the plates on the next day in presence of 10 ng/ml IL-31. After 6 h incubation at 37°C and 5 % CO₂, detection solution was added, the plates were incubated for another hour and luminescence was measured.

[0192] The seven scFvs were tested in the cellular assay. As described above the potency of the analyzed molecules was compared to BMS-981164.

[0193] Relative IC₅₀ values were calculated in mass units (ng/ml) of BMS-981164 and the scFvs. The potency data are summarized in Table 9. Representative dose-response curves for PRO1641, PRO1643 and PRO1650 are shown in Figure 1.

Table 9: Potencies of scFvs to neutralize IL-31R- and IL-31-induced signaling in IL-31RA/OSMR dimerization assay. Sc03: Full graft, sc08 and sc10: other grafting variants

Protein ID	scFv	Neutralization of hIL-31-induced signaling in IL-31RA/OSMR dimerization assay	
		IC ₅₀ [ng/ml]	rel. IC ₅₀ *
PRO1641	50-03-H07-sc03	4.11	3.14
PRO1643	50-09-D07-sc03	11.14	1.16
PRO1644	50-10-F09-sc03	33.41	0.40
PRO1645	50-25-H10-sc03	11.65	1.16
PRO1650	50-35-B03-sc03	7.57	1.45
PRO1688	50-35-B03-sc08	24.00	0.36
PRO1690	50-35-B03-sc10	25.43	0.43

*: IC₅₀, BMS-981164/IC₅₀, test sample

Competitive ELISA (inhibition of hIL-31 binding to hIL-31RA)

[0194] Potency of the two humanized scFvs was further determined using a competitive ELISA. The potency of each scFv to inhibit the interaction between human IL-31 and human IL-31RA was assessed by an ELISA using the same procedure as described above. Comparably to the IL-31RA/OSMR dimerization assay, individual IC₅₀

values on each plate were calibrated against the IC₅₀ of the reference molecule BMS-981164. The Full graft scFv inhibited the interaction between human IL-31 and human IL-31RA with similar potency to BMS-981164. The potency data are summarized in Table 10. Representative dose-response curves for PRO1641, PRO1643 and PRO1650 are shown in Figure 2.

Table 10: Potencies of scFvs to inhibit the interaction between IL-31 and IL-31R. Sc03: Full graft, sc08 and sc10: other grafting variants

Protein ID	scFv	Potency in IL-31/IL-31RA ELISA	
	Clone ID	IC ₅₀ [ng/ml]	rel. IC ₅₀ *
PRO1641	50-03-H07-sc03	3.56	2.67
PRO1643	50-09-D07-sc03	4.58	2.04
PRO1644	50-10-F09-sc03	8.83	1.38
PRO1645	50-25-H10-sc03	5.25	1.81
PRO1650	50-35-B03-sc03	5.05	2.30
PRO1688	50-35-B03-sc08	6.19	1.90
PRO1690	50-35-B03-sc10	6.86	1.69

*: IC₅₀, BMS-981164/IC₅₀, test sample

Summary of pharmacological characterization of scFvs and molecule selection for detailed biophysical evaluation

[0195] Based on the above results of the pharmacological characterization, PRO1645 was excluded, since PRO1645 exhibited the lowest binding affinity. The other six scFvs were selected for detailed biophysical evaluation to judge their developability and suitability for incorporation into multispecific antibody formats.

1.9. Biophysical characterization of suitable anti-IL-31 binding domains (scFv format)

Manufacture of stability material for stability measurements

[0196] PRO1641, PRO1643, PRO1644 and PRO1650 were produced again using the same manufacturing process as described above at slightly larger scale (0.25 l expression volume) to generate sufficient material for stability assessment. For other proteins, which were selected for stability assessment, previously produced material amount was sufficient to perform stability assessment. Samples were formulated in 50 mM phosphate-citrate buffer with 150 mM NaCl at pH 6.4 (50 mM NaCiP, pH 6.4). The protein was concentrated to >10 mg/ml using centrifugal concentration tubes with 5MWCO after purification and dialysis.

[0197] Monomer loss upon concentration to 10 mg/ml was between 0.0 to 4.9 % as shown in Table 11.

Table 11: % monomer loss (SE-HPLC) upon concentration to 10 mg/ml. Sc03: Full graft, sc08 and sc10: other grafting variants

Protein ID	Clone ID (scFv)	Initial monomer content [%]	Monomer content post concentration to 10mg/ml [%]	% loss upon concentration to 10 mg/ml
PRO1641	50-03-H07-sc03	98.8	98.5	0.3
PRO1643	50-09-D07-sc03	98.3	98.2	0.1
PRO1644	50-10-F09-sc03	95.2	95.4	-0.2
PRO1650	50-35-B03-sc03	98.5	97.8	0.7
PRO1688	50-35-B03-sc08	99.4	94.5	4.9
PRO1690	50-35-B03-sc10	99.4	96.2	3.2

Storage stability study

[0198] Humanized scFvs were subjected to stability studies in a four-week stability study, in which the scFvs were formulated in an aqueous buffer (final buffer, 50 mM NaCiP, 150 mM NaCl, pH 6.4) at 10 mg/ml and stored at < -80°C, 4°C and 40°C for four weeks. The fractions of monomers and oligomers in the formulation were evaluated by integration of SE-HPLC peak areas at different time points of the study. Further, protein concentration was determined by UV₂₈₀ measurement at different time points. Table 12 compares d14 and endpoint measurements obtained at d28 of the study.

[0199] Three scFvs, *i. e.* PRO1641, PRO1643 and PRO1644, showed <5 % loss of monomeric content at 4°C and d28 of the study. PRO1643 was the only scFv that did not show considerable loss of monomeric content for d14 and d28 storage at 40°C. All other scFvs lost significantly more than 5 % of monomeric content already after 14d storage at 40°C. In summary, PRO1643, based on clone 50-09-D07, showed the best storage stability with no considerable loss of monomeric content as well as protein content at any temperature.

Freeze-thaw stability

[0200] In addition to the storage stability study described above, the compatibility of the six selected scFvs regarding freeze-thawing (F/T) cycles (colloidal stability) was assessed.

[0201] For the F/T stability assessment the same analytical methods (SE-HPLC, UV-Vis) and parameters (% monomer content and % monomer loss) as for the storage stability study were applied to monitor the quality of the molecules over three F/T cycles. Table 13 illustrates the course of monomer content in % and % monomer content loss over three F/T cycles. As no dedicated freeze-thaw study was performed, freeze-thaw data obtained with the -80°C samples of storage stability study which was acquired over 28 days is shown in the table below. As only three time points could be recorded per sample, freeze-thaw stability data is available for three F/T-cycles only.

Thermal unfolding

[0202] Thermal unfolding measurement of the six scFvs has been performed using Differential Scanning Fluorimetry (DSF). PRO1698 was excluded because of its bad storage stability. Resulting midpoint of thermal unfolding (T_m) and onset temperature of unfolding calculated at 10 % of maximal signal (T_{onset} 10%) values was determined by fitting of data to a Boltzmann equation. Table 14 summarizes calculated melting temperatures measured by DSF.

Table 12: 28d storage stability study at 10 mg/ml and temperatures of -80°C, 4°C and 40°C. Sc03: Full graft, sc08 and sc10: other grafting variants

Protein ID	Clone ID (scFv)	Temp. [°C]	monomer content [%]			% monomer change		protein concentration [mg/ml]			% protein content change	
			d0	d14	d28	d14	d28	d0	d14	d28	d14	d28
PRO1641	50-03-H07-sc03	-80	98.5	98.7	99.4	0.3	0.9	10.4	7.3	13.5	-25.9	36.1
		4	98.6	98.8	99.1	0.4	0.7	10.4	12.8	9.9	28.7	-0.1
		40	98.5	90.2	87.8	-8.4	-10.8	10.4	12.7	12.0	28.5	20.9
PRO1643	50-09-D07-sc03	-80	98.2	98.3	99.2	0.1	1.0	10.6	12.4	12.1	23.2	20.4
		4	98.2	98.2	99.0	-0.1	0.7	10.6	11.9	10.3	18.4	2.6
		40	98.2	97.2	97.8	-1.0	-0.4	10.6	12.1	13.0	20.6	29.1
PRO1644	50-10-F09-sc03	-80	95.4	95.7	95.8	0.3	0.5	10.1	10.6	10.7	3.8	5.1
		4	95.4	94.9	94.9	-0.5	-0.5	10.1	10.7	10.7	4.9	5.2
		40	95.4	85.1	82.3	-10.7	-13.7	10.1	11.6	12.8	14.2	25.7
PRO1650	50-35-B03-sc03	-80	97.8	97.6	97.3	-0.3	-0.5	10.0	7.5	11.5	-25.3	15.0
		4	97.8	92.3	89.8	-5.7	-8.2	10.0	10.5	8.3	4.3	-16.8
		40	97.8	89.1	88.6	-8.9	-9.4	10.0	10.5	11.2	4.9	11.4
PRO1688	50-35-B03-sc08	-80	94.5	91.0	90.7	-3.7	-4.0	10.4	9.6	11.5	-7.6	10.5
		4	94.5	87.0	85.4	-7.9	-9.6	10.4	12.0	12.0	15.4	15.4
		40	94.5	89.2	88.5	-5.6	-6.3	10.4	12.2	13.1	17.0	26.0
PRO1690	50-35-B03-sc10	-80	96.2	92.1	92.0	-4.3	-4.4	10.6	8.2	7.8	-23.0	-26.4
		4	96.2	86.4	83.8	-10.2	-12.9	10.6	9.8	7.9	-7.9	-25.5
		40	96.2	88.7	88.4	-7.9	-8.1	10.6	11.1	11.6	4.7	9.5

Table 13: F/T stability – monomer content in % and % monomeric change upon freeze thawing. Sc03: Full graft, sc08 and sc10: other grafting variants

Protein ID	Clone Id (scFv)	monomer content [%]			% monomer change		
		F/T 0	F/T 1	F/T 2	F/T 1	F/T 2	F/T 3
PRO1641	50-03-H07-sc03	98.5	98.7	98.7	0.2	0.3	0.9
PRO1643	50-09-D07-sc03	98.2	98.2	98.3	-0.1	0.1	1.0
PRO1644	50-10-F09-sc03	95.4	95.3	95.7	-0.1	0.3	0.5
PRO1650	50-35-B03-sc03	97.8	97.7	97.6	-0.1	-0.3	-0.5
PRO1688	50-35-B03-sc08	94.5	92.1	91.0	-2.5	-3.7	-4.0
PRO1690	50-35-B03-sc10	96.2	92.1	92.1	-4.3	-4.3	-4.4

Table 14: DSF measurement of selected scFv domains. Sc03: Full graft, sc08 and sc10: other grafting variants

Protein ID	Clone ID (scFv)	Purity SE-HPLC [% monomer]	T _m [°C]	T _{onset} 10% [°C]
PRO1641	50-03-H07-sc03	98.8	73.6	62.3
PRO1643	50-09-D07-sc03	90.4*	69.5	64.3
PRO1644	50-10-F09-sc03	95.2	75.0	68.0
PRO1650	50-35-B03-sc03	98.5	67.6	62.3
PRO1688	50-35-B03-sc08	99.4	64.8	59.0
PRO1690	50-35-B03-sc10	99.4	63.1	56.7

*initial material with 90.4 % mc used for measurement

Example 2: Selection and optimization of anti-IL-31 molecules for multispecific format:

2.1. General remarks on the selection of anti-IL-31 domains

[0203] The anti-IL-31 domain PRO1643 (50-09-D07-sc03) was selected in the first place for further development, since it exhibits the desired pharmacodynamic properties as well as an excellent stability. Nevertheless, the anti-IL-31 binding domain PRO1643 (50-09-D07-sc03) underwent further solubility improving as shown below in 2.2.

[0204] The anti-IL-31 binding domains applied in the final multispecific antibodies do cross-react with cynomolgus monkey IL-31.

2.2. Optimization of anti-IL-31 domains

[0205] The anti-IL-31 domain PRO1643 (50-09-D07-sc03) was further optimized for assembly into multispecific format.

Optimization of anti-IL-31 domain 50-09-D07-sc03

[0206] PRO1643 (50-09-D07-sc03) is a very stable anti-IL-31 scFv, however, efforts were nevertheless made to improve it with respect to solubility, long-term stability and concentration behavior. Therefore, new variants of this molecule were designed. These variants are described below. Briefly, hydrophobic patches in CDRs or in the former VH-CH interface have been analyzed in detail with the aim to design molecules with removed hydrophobic patches without compromising binding affinity and without introducing critical sequence liabilities (chemical and post-translational modifications), T cell epitopes etc.

[0207] In total, four variants were designed, which are summarized in Table 15.

Table 15: Optimization variants for 50-09-D07-sc03

Protein ID	Construct	Optimization Aim	Mutations VL	Mutations VH
PRO1900	50-09-D07-sc04	Solubility, stability	-	L12R, V103T, L144Q
PRO1901	50-09-D07-sc05	Solubility, stability	-	L12S, V103T, L144Q
PRO1902	50-09-D07-sc06	Solubility, stability	-	Y59S
PRO1903	50-09-D07-sc07	Solubility, stability, sequence liability (DS)	D32E	-

2.3. Biophysical characterization of optimized anti-IL-31 binding domains (scFv format)

Storage stability study

[0208] PRO1900, PRO1901, PRO1902 and PRO1903 were subjected to storage stability studies as described above in section 1.2.3. except that the last readout was taken at day 14 and F/T as well as that stability at -80°C was not assessed. The results are summarized in Table 16.

[0209] As summarized in Table 16, scFvs PRO1900, PRO1901, PRO1902 and PRO1903 exhibited excellent storage stability. The loss of monomeric content after storage at 4°C for 14 days was less than 0.2 % and <3 % after storage at 40°C for 14 days. Also, none of these molecules showed considerable loss of protein content at any temperature and data point.

Thermal unfolding

[0210] Thermal stability of PRO1900, PRO1901, PRO1902 and PRO1903 was analyzed by nano dynamic scanning fluorimetry (nDSF) using a NanoTemper, allowing the determination of the onset of unfolding (T_{onset}), midpoint of unfolding (T_{m1}) and scattering onset temperature. T_{m1} and T_{onset} results of duplicate/triplicate measurements are summarized in Table 17. As can be deduced from Table 17, PRO1900, PRO1901, PRO1902 and PRO1903 exhibited high melting temperatures.

Table 16: 14d storage stability study at 10 mg/mL at temperatures of 4°C and 40°C.

Protein ID	Clone ID (scFv)	Temp. [°C]	monomer content [%]			% monomer change		protein concentration [mg/ml]		% protein content change	
			d0	d1	d14	d1	d14	d0	d1	d14	d1
PRO1900	50-09-D07-sc04	4	99.8	NA	99.8	NA	0.0	9.8	NA	10.0	NA
		40	99.8	99.3	98.9	-0.5	-0.9	9.8	10.1	10.1	3.4
PRO1901	50-09-D07-sc05	4	97.0	NA	97.0	NA	-0.0	10.5	NA	10.9	NA
		40	97.0	96.9	96.3*	-0.1	-0.7*	10.5	10.1	10.9*	-3.7
PRO1902	50-09-D07-sc06	4	98.5	NA	98.4	NA	0.0	9.3	NA	9.4	NA
		40	98.5	97.2	95.8	-1.3	-2.7	9.3	9.3	9.4	0.7
PRO1903	50-09-D07-sc07	4	98.7	NA	98.7	NA	-0.1	9.6	NA	10.1	NA
		40	98.7	98.2	97.7	-0.5	-1.1	9.6	9.8	9.9	1.2

*sample incubated for first 7 days at 25°C instead of 40°C
NA: not analyzed

Table 17: nDSF of optimized anti-IL-31 binding domains (scFvs format).

Protein ID	Clone ID (scFv)	Purity SE-HPLC [% monomer]	T _{m1} [°C]	T _{onset} [°C]
PRO1900	50-09-D07-sc04	99.8	70.7	60.5
PRO1901	50-09-D07-sc05	97.7	69.0	52.3
PRO1902	50-09-D07-sc06	98.3	73.8	62.5
PRO1903	50-09-D07-sc07	98.9	71.1	55.6

Concentration stability study

[0211] PRO1643, PRO1900, PRO1901, PRO1902 and PRO1903 were concentrated to >10 mg/ml and >50 mg/ml using centrifugal concentration tubes with 5MWCO, as described herein.

[0212] There was virtually no loss in monomer content upon concentration to 10 mg/ml and 50 mg/ml respectively, as shown in Table 18.

Storage stability study

[0213] PRO1900, PRO1901, PRO1902 and PRO1903 were subjected to a two-week stability study, in which the scFvs were formulated in an aqueous buffer (final buffer, 50 mM NaCl, 150 mM NaCl, pH 6.4) at 50 mg/ml, and stored at 4°C and 40°C for two weeks. The fractions of monomers and oligomers in the formulation were evaluated by integration of SE-HPLC peak areas at different time points of the study. Further, protein concentration was determined by UV₂₈₀ measurement at different time points. Table 19 present the results of the d14 measurements of the study.

[0214] PRO1900, PRO1901, PRO1902 and PRO1903 exhibit excellent storage stability at 50 mg/ml with virtually no loss in monomeric content and protein content particularly at 4°C, but as well at 40°C.

2.4. Pharmacodynamics characterization of optimized anti-IL-31 binding domains (scFv format)

Affinity to human IL-31

[0215] Affinity of PRO1643 and of the optimized anti-IL-31 scFvs to human IL-31 was determined by SPR analysis on a T200 device (Biacore, GE Healthcare), as described above in section 1.8. The scFvs were measured using a dose response multi-cycle kinetic assay in a high-throughput mode with two concentrations (30 and 10 nM) diluted in running buffer. Obtained sensorgrams were fitted using a 1:1 binding model.

[0216] As shown in Table 20, binding to human IL-31 and cynomolgus IL-31 was confirmed for all optimized scFvs.

Table 18: % monomer loss (SE-HPLC) upon concentration to 10 mg/ml. Sc03: Full graft, sc04 to sc07: optimized variants

Protein ID	Clone ID (scFv)	Initial monomer content [%]	Monomer content post concentration to 10 mg/ml [%]	% loss upon concentration to 10 mg/ml	Monomer content post concentration to 50 mg/ml [%]	% loss upon concentration to 50 mg/ml
PRO1643	50-09-D07-sc03	99.9	99.8	-0.1	99.7	-0.1
PRO1900	50-09-D07-sc04	99.8	99.8	0.0	99.8	0.0
PRO1901	50-09-D07-sc05	97.2	97.0	-0.2	97.0	-0.2
PRO1902	50-09-D07-sc06	98.5	98.5	-0.1	98.4	-0.1
PRO1903	50-09-D07-sc07	98.9	98.7	-0.2	98.7	-0.2

Table 19: 14d storage stability study at 50 mg/ml and temperatures of 4°C and 40°C. Sc03: Full graft, sc04 to sc07: optimized variants

Protein ID	Clone ID (scFv)	Temp. [°C]	monomer content [%] d0	monomer content [%] d14	% monomer change d14	protein concentration [mg/ml] d0	protein concentration [mg/ml] d14	% protein content change d14
PRO1900	50-09-D07-sc04	4 40	100 100	100 96	0 -2	55 55	54 44	-3 -19
PRO1901	50-09-D07-sc05	4 40	97 97	97 95	0 -4	NA NA	NA NA	NA NA
PRO1902	50-09-D07-sc06	4 40	98 98	98 96	0 -3	56 56	63 58	11 3
PRO1903	50-09-D07-sc07	4 40	99 99	99 93	0 -23	52 52	68 56	30 8

Table 20: Affinity of scFvs to human and cynomolgus IL-31. Sc03: Full graft, sc04 to sc07: other grafting variants

Protein ID	scFv	Affinity to human IL-31			Affinity to cynomolgus IL-31			
		Clone ID	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)	K_D (M)	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)	K_D (M)
PRO1643		50-09-D07-sc03	5.79E+05	6.53E-04	1.13E-09	5.01E+05	5.87E-04	1.17E-09
PRO1900		50-09-D07-sc04	6.61E+05	5.99E-04	9.07E-10	5.54E+05	5.94E-04	1.07E-09
PRO1901		50-09-D07-sc05	5.91E+05	5.65E-04	9.56E-10	5.01E+05	5.69E-04	1.14E-09
PRO1902		50-09-D07-sc06	8.52E+05	2.46E-03	2.89E-09	7.31E+05	2.47E-03	3.38E-09
PRO1903		50-09-D07-sc07	5.24E+05	6.38E-04	1.22E-09	4.34E+05	6.05E-04	1.39E-09

Path Hunter IL-31RA/OSMR dimerization assay (blockage of human IL-31-induced signaling)

[0217] PRO1643 and the optimized scFvs were tested for their ability to inhibit IL-31-induced signaling via the IL-31RA/OSMR heterodimer by using an IL-31RA/OSMR dimerization assay. The assay was performed as described in section 1.8. The potency of the analyzed molecules was compared to BMS-981164.

[0218] Relative IC₅₀ values were calculated in mass units (ng/ml) of BMS-981164 and the scFvs. The potency data are summarized in Table 21. As can be depicted from Table 21, PRO1643 as well as the optimized variants PRO1900, PRO1901 and PRO1903 could potentially neutralize IL-31-induced signaling. The mutations introduced in the variant PRO1902 to optimize solubility and stability obviously resulted in the disruption of the ability to inhibit IL-31-induced signaling. Dose-response curves for the optimized scFvs PRO1900, PRO1901, PRO1902 and PRO1903 are shown in Figure 3.

Table 21: Potencies of scFvs to neutralize IL-31R- and IL-31-induced signaling in IL-31RA/OSMR dimerization assay. Sc03: Full graft, sc04 to sc07: other grafting variants

Protein ID	scFv	Neutralization of hIL-31-induced signaling in IL-31RA/OSMR dimerization assay	
		Clone ID	rel. IC ₅₀ *
PRO1643	50-09-D07-sc03	IC ₅₀ [ng/ml]	0.85
PRO1900	50-09-D07-sc04	8.209	0.73
PRO1901	50-09-D07-sc05	8.071	0.78
PRO1902	50-09-D07-sc06	371.3	0.03
PRO1903	50-09-D07-sc07	7.982	1.49

*: IC₅₀, BMS-981164/IC₅₀, test sample

Example 3: Anti-IL-4R x IL-31 bispecific antibodies based on Morrison-H IgG4

[0219] It was then further tested whether the anti-IL-31 antibody variable domains of the present invention also provides advantageous biological and biophysical properties when incorporated into multispecific antibody formats. Therefore, multispecific antibodies were designed based on Morrison-H IgG4 format comprising two anti-IL-31 antibody variable domains, as defined herein. For the binding domains, which specifically binds to a target different from IL-31, two IL-4R binding domains (IL4R-BDs) were selected.

3.1. Morrison format design

[0220] A series of anti-IL-4R x IL-31 bispecific antibodies were designed having a Morrison-H format, wherein the Fc region is derived from the IgG subclass IgG4.

[0221] Due to their cross-reactivity to cynomolgus monkey IL-31, their excellent potency in blocking IL-31-mediated signalling and their excellent biophysical properties, the anti-IL-31 scFv variable domain 50-09-D07-sc04 was selected for the scFv-domains that are fused to the C-terminus of the heavy chain of the Morrison-H antibodies.

Likewise, due to their excellent biological and biophysical properties, the anti-IL-4R scFv variable domains 44-34-C10-sc08 and 44-34-C10-sc09 were selected for the Fab-arm binding domains of the Morrison-H constructs.

[0222] The identification, humanization, production and final selection of the humanized anti-IL-4R binding domains 44-34-C10-sc08 and 44-34-C10-sc09 was performed using the same methodology as described above for the anti-IL-31 antibody variable domains.

[0223] Two IgG4-(scFv)₂ Morrison-H molecules were designed, *i. e.* PRO2198 and PRO2199, as shown in Table 22 (Morrison-H).

Table 22: IgG4 Morrison-H constructs

PRO ID	Fab-arm domain	Constant	scFv-domain
PRO2198	44-34-C10-sc08	IgG4 (S228P)	50-09-D07-sc04
PRO2199	44-34-C10-sc09	IgG4 (S228P)	50-09-D07-sc04

[0224] Expression of multispecific antibodies PRO2198 and PRO2199 was performed in FreeStyle CHO-S cells using the transient CHOgro expression system (Mirus). The genes of interest were optimized for mammalian expression, synthesized and cloned into a standard pcDNA3.1 vector. Expression cultures were cultivated in batch using shaking flasks for 6 to 7 days (cell viability < 70 %) at 37°C. The culture supernatants were separated from cells by centrifugation followed by a 0.22 µm sterile filtration. The target proteins were captured from the clarified culture supernatants by Protein L or A affinity chromatography followed by a size-exclusion chromatography polishing step (in case no fractions with a suitable monomeric content as assessed by SE-HPLC were available post capture already). For the quality control of the manufactured material standard analytical methods, such as SE-HPLC, SDS-PAGE, and UV₂₈₀ were used.

3.2. Affinity to human and cyno IL-31

[0225] Binding kinetics (including affinity) of the bispecific Morrison-H antibodies PRO2198, PRO2199 to recombinant human IL-31 protein (Peprotech) were determined by SPR analysis on a T200 device (Biacore, Cytiva). In this SPR experiment, Morrison antibodies were injected over a carboxymethylated dextran surface (CM5 sensorchip; Biacore, Cytiva) immobilized with human recombinant IL-4R protein (ECD with Fc Tag, R&D Systems) and a titration series of human IL-31 was injected as analyte. The affinity to human IL-31 was measured using a single-cycle kinetic assay with injections of five sequential analyte concentrations, ranging from 0.05 to 30 nM diluted in running buffer (HEPES buffered saline, 0.05 % Tween-20, pH 7.5), without regeneration of the sensorchip surface after injection of the analyte. The calculation of the kinetics and the apparent dissociation equilibrium constant (K_D) as well as the measurement for the quality of curve fitting were done as described above for IL-4R. The binding level was calculated as the maximum stability binding achieved normalized to the theoretical R_{max} . Cross-reactivity to cynomolgus monkey IL-31 was measured using the same setup as for the analysis of human IL-31 affinities, with the difference that recombinant cynomolgus monkey IL-31 (ECD with His Tag, Sino Biological) protein was used as analytes instead of human IL-31.

[0226] A prerequisite of the SPR setup employed to measure binding kinetics to recombinant IL-31 is the capture of Morrison antibodies via immobilized human IL-4R. All previously tested Morrison antibodies showed stable binding to immobilized human IL-4R, and thus the setup was proven valid. The rationale to use this SPR setup is to guarantee a homogeneous orientation of the captured Morrison molecules, while minimizing steric hindrance for the IL-31 binding site.

[0227] After having shown a stable capture of Morrison antibodies via recombinant human IL-4R protein, IL-31 was injected as analyte and the kinetics of the binding of IL-31 to captured Morrison molecules were calculated.

[0228] As shown in Table 23 high affinity binding to human IL-31 and cynomolgus IL-31 was demonstrated for the Morrison-H antibodies PRO2198 and PRO2199.

3.3. Potency assessment to inhibit human IL-31-induced receptor dimerization (PathHunter® eXpress IL31RA/OSMRb assay)

PathHunter IL-31RA/OSMRb dimerization assay

[0229] In the IL-31RA/OSMR dimerization assay the ability of the Morrison-H antibodies PRO2198 and PRO2199 to inhibit IL-31-induced signaling via the IL-31RA/OSMR heterodimer was assessed. 10,000 cells per well were seeded in a 96-well plate. 3-fold serial dilutions of the molecules and of the control antibody BMS-981164 at concentrations ranging from 1,000 to 0.2 ng/ml were added to the plates on the next day in presence of 10 ng/ml IL-31. After 6 h incubation at 37°C and 5 % CO₂, detection solution was added, the plates were incubated for another hour and luminescence was measured. All antibodies were also tested for inhibition of IL-31-induced signaling with an excess of IL-4R (at 50 nM) in the assay medium.

Table 23: Binding kinetics of Morrison antibodies to human IL-31 and cynomolgus monkey IL-31

Protein ID	Fab arm	scFv domain	Affinity by SPR measurement			
			Antigen	k_a ($M^{-1} s^{-1}$)	k_d (s^{-1})	K_D (M)
PRO2198	44-34-C10-sc08	50-09-D07-sc04	human IL-31	2.75E+05	1.60E-05	5.20E-11
PRO2199	44-34-C10-sc09	50-09-D07-sc04	human IL-31	2.51E+05	1.75E-05	6.97E-11
PRO2198	44-34-C10-sc08	50-09-D07-sc04	cynomolgus IL-31	9.92E+04	< 1.00E-05	1.03E-10
PRO2199	44-34-C10-sc09	50-09-D07-sc04	cynomolgus IL-31	8.10E+04	< 1.00E-05	1.23E-10

Table 24: Potencies of the Morrison-H molecules to neutralize human IL-31-induced signaling in IL-31RA/OSMR dimerization assay without and with IL-4R in the medium. n = number of repeated analyses.

PRO ID	Fab-arm domain	scFv-domain	Retained IC ₅₀ with and without IL-4R excess (n=1)		
			Mean IC ₅₀	Mean rel. IC ₅₀	[IC ₅₀ , no IL-4R/IC ₅₀ , with IL-4R] ng/ml values
PRO2198	44-34-C10-sc08	50-09-D07-sc04	198	0.70	1.02
PRO2199	44-34-C10-sc09	50-09-D07-sc04	142	0.61	0.90

* IC₅₀ or relative IC₅₀ (single analysis)/NA: not applicable

Inhibition of human IL-31

In Table 24, a summary of all potency data is shown. Mean relative IC₅₀ values from repeated analysis are indicated in pM. Both Morrison-H antibodies inhibited IL-31-induced signaling with similar potency as BMS-981164. Efficient blockage of the interaction of IL-31 with IL-31R was maintained when the anti-IL-4R domains were bound to IL-4R.

3.4. Biophysical characterization of PRO2198 and PRO2199:**3.4.1. Thermal stability**

[0230] PRO2198 and PRO2199 were analyzed for their thermal stability between pH 5 and pH 8.5. Both thermal unfolding as well as the onset of thermal aggregation were determined. During thermal unfolding, all molecules showed more than one transition due to the multi domain architecture of the molecules. For simplicity, only the first melting midpoint is shown. Table 25 summarizes the results.

Table 25: Thermal stability

pH	PRO2198	PRO2199
Onset of unfolding (T _{onset}) by nDSF [°C]		
5	55.4	55.1
7	60.5	59.3
8.5	59.7	58.3
Midpoint of the first unfolding transition (T _{m1}) by nDSF [°C]		
5	62.9	62.8
7	66.9	66.7
8.5	66.5	66.2
Onset of aggregation (T _{scattering}) by nDSF [°C]		
5	No aggregation observed	
7	73.5	71.6
8.5	71.4	68.4

[0231] The onset of unfolding (T_{onset}) as well as the first melting point (T_{m1}) was highest at pH 7 for all molecules. A change to pH 8.5 decreased the thermal stability only slightly. Towards acidic pH, the thermal stability decreased. However, at pH 5 all onsets of unfolding were above 55°C.

- 5 [0232] Thermal aggregation was only observed at pH 7 and pH 8.5. At pH 5.0, both Morrison antibodies did not form larger aggregates, even in the unfolded state. At neutral and basic pH, the aggregation onset was above the first melting point, suggesting a non-native aggregation mechanism.

10 **3.4.2. High concentration stability study**

[0233] For the high concentration stability tests PRO2198 was formulated in two formulation buffers:

Formulation buffer F1: 20 mM acetate at pH 5.5;

- 15 Formulation buffer F2: 20 mM citrate with 50 mM NaCl at pH 5.5.

Solubility - Protein concentration

- [0234] PRO2198 could be concentrated above 100 mg/ml, without signs of
20 precipitation or reaching the limit of solubility. Furthermore, PRO2198 showed no detectable decrease in protein concentration, *i. e.* PRO2198 was sufficiently soluble to reach and keep a target concentration of above 100 mg/ml for at least four weeks at 4°C and 25°C.

25 *Monomer stability at different temperatures*

- [0235] PRO2198 was formulated in F1 and F2 and concentrated to >100 mg/ml. The concentrated samples were stored at 4°C, 25°C and 40°C for up to 4 weeks. At different time points, the monomeric content was analyzed by means of SE-HPLC. The
30 results are summarized in Table 26.

Table 26: Monomer stability for PRO2198 at a concentration of >100 mg/ml

Storage temperature [°C]	time [weeks]	Formulation F1		Formulation F2	
		Monomer [rel. %]		Monomer [rel. %]	
		Absolut	Delta	Absolut	Delta
N/A	0	99.0	0.0	99.1	0.0
4.0	4	98.1	-0.9	98.3	-0.8
25.0	4	96.1	-2.9	96.2	-2.9
40.0	2	83.1	-15.9	82.0	-17.1
	4	72.4	-26.6	70.9	-28.2

3.5. General methods used in the biophysical characterization of PRO2198 and PRO2199

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Buffer exchange

[0236] Buffer exchange was carried out by dialysis. The antibodies were dialyzed in Spectra Pro 3 dialysis membranes (Spectrum Laboratories) with at least a 200-fold excess of dialysis buffer.

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Concentrating of the antibodies

[0237] Antibodies were concentrated using centrifugal concentrators with a molecular weight cut-off (MWCO) of 10 kDa or 30 kDa. Samples were centrifuged in 5 min steps at 22°C until target concentration was reached. In between steps, the samples are resuspended.

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Determination of protein concentration

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[0238] The concentration of the protein samples was determined using a Tecan plate reader and a NanoQuant Plate. The buffer was used as blank to be subtracted from the absorbance measured at 280 nm. Each measurement was corrected for scattering caused by visible particles determined at 310 nm. The corrected value was normalized

to a path length of 1 cm and the protein concentration calculated using the theoretical extinction coefficient of the corresponding protein. For protein samples with a concentration higher than 10 mg/ml, the sample was diluted in the corresponding buffer at least 10 times or to 1 mg/ml nominal concentration.

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Storage

[0239] To assess the protein stability at different temperatures, samples were incubated at 4°C, 25°C and 40°C. 4°C storage was carried out in a fridge at a nominal temperature of 4°C. For storage at 25°C and 40°C samples were placed in cabinets with controlled humidity of 65 % rH and 75 % rH, respectively.

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Dynamic Light Scattering

[0240] Dynamic Light Scattering is used to determine the diffusion coefficient of molecules and particles in solution. It allows to calculate the hydrodynamic radius (R_h) of the molecule in solution as well as provides a sensitive method to detect the formation of higher order oligomers.

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[0241] Within the high concentration stability study, R_h and the polydispersity were determined at the target concentration. This yielded information on self-association, oligomerization as well as potential increase in viscosity. Measurements were not corrected for buffer or sample viscosity, instead the viscosity of water was used to calculate the R_h of the samples.

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Thermal unfolding by nanoDSF

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[0242] Thermal unfolding using TSA was obtained by the change in fluorescence intensity of Sypro Orange. The fluorescence of the dye is sensitive to hydrophobic interactions. As the protein unfolds, hydro-phobic amino acids are exposed to the solvent leading to an increased fluorescence of Sypro Orange. The resulting midpoint of thermal unfolding (T_m) as well as the onset temperature calculated at 10 % of the

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maximal signal (T_{onset} is the temperature at: $\text{min. signal} + 0.1 * (\text{max. signal} - \text{min. signal})$) was determined by fitting the data to a Boltzmann equation.

Monomeric content by SE-HPLC

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[0243] The monomeric content was determined by analytical size-exclusion chromatography using a Shodex KW403-4F column running in 50 mM sodium phosphate, 300 mM NaCl, pH 6.5. For analysis, 5 μg of sample were injected and the absorption recorded at 280 nm. The quality of the sample is stated as relative

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percentages of monomer, HMWS, and LMWS.

CLAIMS

1. An antibody variable domain, which specifically binds to IL-31, comprising:
 - a) a VH chain having a sequence selected from SEQ ID NOs: 5, 6 and 7, and
 - 5 b) a VL chain having a sequence selected from SEQ ID NO: 12 and 37.
2. The antibody variable domain of claim 1, wherein said antibody variable domain comprises:
 - a) a VH chain having a sequence of SEQ ID NO: 5 and a VL chain having a
 - 10 sequence of SEQ ID NO: 12; or
 - b) a VH chain having a sequence of SEQ ID NO: 6 and a VL chain having a
 - sequence of SEQ ID NO: 12; or
 - c) a VH chain having a sequence of SEQ ID NO: 7 and a VL chain having a
 - sequence of SEQ ID NO: 12; or
 - 15 d) a VH chain having a sequence of SEQ ID NO: 5 and a VL chain having a
 - sequence of SEQ ID NO: 37.
3. The antibody variable domain of claim 1 or 2, wherein said antibody variable domain is selected from a FAB, an Fv, an scFv and a dsFv.
- 20 4. The antibody variable domain of claim 3, which is selected from the scFv antibodies of SEQ ID NOs: 27 to 29 and 31.
5. A multispecific antibody comprising:
 - 25 a) one or two antibody variable domains as defined in any one of claims 1 to 4;
 - b) at least one binding domain, which specifically binds to a target different from IL-31.
6. The multispecific antibody of claim 5, wherein the multispecific antibody does not
- 30 comprise an immunoglobulin Fc region.

7. The multispecific antibody of claim 6, wherein the multispecific antibody is in a format selected from the group consisting of: a tandem scDb (Tandab), a linear dimeric scDb (LD-scDb), a circular dimeric scDb (CD-scDb), a tandem tri-scFv, a tribody (Fab-(scFv)₂), a Fab-Fv₂, atriabody, an scDb-scFv, a tetrabody, a di-
5 diabody, a tandem-di-scFv and a MATCH.
8. The multispecific antibody of claim 5, wherein the multispecific antibody comprises an immunoglobulin Fc region that is selected from IgG subclasses IgG1 and IgG4, particularly from IgG4.
- 10 9. The multispecific antibody of claim 8, wherein the format of said multispecific antibody is selected from KiH-based IgGs; DVD-Ig; CODV-IgG and Morrison (IgG CH₃-scFv fusion (Morrison H) or IgG CL-scFv fusion (Morrison L)), in particular from Morrison H and Morrison L.
- 15 10. The multispecific antibody of any one of claims 5 to 9, wherein said multispecific antibody comprises two antibody variable domains as defined in any one of claims 1 to 4 and two binding domains, which specifically bind to a second target different from IL-31.
- 20 11. A nucleic acid or two nucleic acids encoding the antibody variable domain of any one of claims 1 to 4 or the multispecific antibody of any one of claims 5 to 10.
- 25 12. A vector or two vectors comprising the nucleic acid or the two nucleic acids of claim 11.
13. A host cell or host cells comprising the vector or the two vectors of claim 12.
- 30 14. A pharmaceutical composition comprising the antibody variable domains of any one of claims 1 to 4 or the multispecific antibody of any one of claims 5 to 10, and a pharmaceutically acceptable carrier.

15. The antibody variable domains of any one of claims 1 to 4 or the multispecific antibody of any one of claims 5 to 10 for use as a medicament.
- 5 16. The antibody variable domains of any one of claims 1 to 4 or the multispecific antibody of any one of claims 5 to 10 for use in the treatment of a disease, particularly a human disease, more particularly a human disease selected from allergic, inflammatory and autoimmune diseases, particularly from pruritus-causing allergic diseases, pruritus-causing inflammatory diseases and pruritus-causing
- 10 autoimmune diseases.