HUMAN ANTIBODY MOLECULES FOR IL-13

The present invention relates to specific binding members, in particular human anti-IL-13 antibody molecules and especially those which neutralise IL-13 activity. It further relates to methods for using anti-IL-13 antibody molecules in diagnosis or treatment of IL-13 related disorders, including asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel disease and Hodgkin's lymphoma.

Preferred embodiments of the present invention employ the antibody VH and/or VL domain of the antibody molecule herein termed BAK502G9 and other antibody molecules of the BAK502G9 lineage and of the BAK278D6 lineage, as herein defined. Further preferred embodiments employ complementarity determining regions (CDRs) of the BAK278D6 lineage, and preferably BAK502G9, especially VH CDR3 in other antibody framework regions. Further aspects of the present invention provide for compositions containing specific binding members of the invention, and their use in methods of inhibiting or neutralising IL-13, including methods of treatment of the human or animal body by therapy.

The present invention provides antibody molecules of particular value in binding and neutralising IL-13, and thus of use in any of a variety of therapeutic treatments, as indicated by the experimentation contained herein and further by the supporting technical literature.

Interleukin (IL)-13 is a 114 amino acid cytokine with an unmodified molecular mass of approximately 12 kDa [1,2]. IL-13 is most closely related to IL-4 with which it shares 30% sequence similarity at the amino acid level. The human IL-13 gene is located on chromosome 5q31 adjacent to the IL-4 gene

[1][2]. This region of chromosome 5q contains gene sequences for other Th2 lymphocyte derived cytokines including GM-CSF and IL-5, whose levels together with IL-4 have been shown to correlate with disease severity in asthmatics and rodent models of allergic inflammation [3][4][5][6][7][8].

Although initially identified as a Th2 CD4+ lymphocyte derived cytokine, IL-13 is also produced by Th1 CD4+ T-cells, CD8+ T lymphocytes NK cells, and non-T-cell populations such as mast cells, basophils, eosinophils, macrophages, monocytes and airway smooth muscle cells.

IL-13 is reported to mediate its effects through a receptor system that includes the IL-4 receptor α chain (IL-4Rα), which itself can bind IL-4 but not IL-13, and at least two other cell surface proteins, IL-13Rα1 and IL-13Rα2 [9][10]. IL-13Rα1 can bind IL-13 with low affinity, subsequently recruiting IL-4Rα to form a high affinity functional receptor that signals [11][12]. The Genbank database lists the amino acid sequence and the nucleic acid sequence of IL-13Rα1 as NP_001551 and Y10659 respectively. Studies in STAT6 (signal transducer and activator of transcription 6) -deficient mice have revealed that IL-13, in a manner similar to IL-4, signals by utilising the JAK-STAT6 pathway [13][14]. IL-13Rα2 shares 37% sequence identity with IL-13Rα1 at the amino acid level and binds IL-13 with high affinity [15][16]. However, IL-13Rα2 has a shorter cytoplasmic tail that lacks known signalling motifs. Cells expressing IL-13Rα2 are not responsive to IL-13 even in the presence of IL-4Rα [17]. It is postulated, therefore, that IL-13Rα2 acts as a decoy receptor regulating IL-13 but not IL-4 function. This is supported by studies in IL-13Rα2 deficient mice whose phenotype was consistent with increased responsiveness to IL-13 [18][19]. The Genbank database lists

the amino acid sequence and the nucleic acid sequence of IL-13Rα2 as NP_000631 and Y08768 respectively.

The signalling IL-13Rα1/IL-4Rα receptor complex is expressed on human B-cells, mast cells, monocyte/macrophages, dendritic cells, eosinophils, basophils, fibroblasts, endothelial cells, airway epithelial cells and airway smooth muscle cells.

Bronchial asthma is a common persistent inflammatory disease of the lung characterised by airways hyper-responsiveness, mucus overproduction, fibrosis and raised serum IgE levels. Airways hyper-responsiveness (AHR) is the exaggerated constriction of the airways to non-specific stimuli such as cold air. Both AHR and mucus overproduction are thought to be responsible for the variable airway obstruction that leads to the shortness of breath characteristic of asthma attacks (exacerbations) and which is responsible for the mortality associated with this disease (around 2000 deaths/year in the United Kingdom).

The incidence of asthma, along with other allergic diseases, has increased significantly in recent years [20][21]. For example, currently, around 10% of the population of the United Kingdom (UK) has been diagnosed as asthmatic.

Current British Thoracic Society (BTS)and Global Initiative for Asthma (GINA) guidelines suggest a stepwise approach to the treatment of asthma [22, 23]. Mild to moderate asthma can usually be controlled by the use of inhaled corticosteroids, in combination with beta-agonists or leukotriene inhibitors. However, due to the documented side effects of corticosteroids, patients tend not to comply with the treatment regime which reduces the effectiveness of treatment [24-26].

There is a clear need for new treatments for subjects with more severe disease, who often gain very limited benefit from either higher doses of inhaled or oral corticosteroids recommended by asthma guidelines. Long term treatment with oral corticosteroids is associated with side effects such as osteoporosis, slowed growth rates in children, diabetes and oral candidiasis [88]. As both beneficial and adverse effects of corticosteroids are mediated via the same receptor, treatment is a balance between safety and efficacy. Hospitalisation of these patients, who represent around 6% of the UK asthma population, as a result of severe exacerbations accounts for the majority of the significant economic burden of asthma on healthcare authorities [89].

It is believed that the pathology of asthma is caused by ongoing Th2 lymphocyte mediated inflammation that results from inappropriate responses of the immune system to harmless antigens. Evidence has been accrued which implicates IL-13, rather than the classical Th2 derived cytokine IL-4, as the key mediator in the pathogenesis of established airway disease.

Administration of recombinant IL-13 to the airways of naïve non-sensitised rodents caused many aspects of the asthma phenotype including airway inflammation, mucus production and AHR [27][28][29][30]. A similar phenotype was observed in a transgenic mouse in which IL-13 was specifically overexpressed in the lung. In this model more chronic exposure to IL-13 also resulted in fibrosis [31].

Further, in rodent models of allergic disease many aspects of the asthma phenotype have been associated with IL-13. Soluble murine IL-13Rα2, a potent IL-13 neutraliser, has been shown to

inhibit AHR, mucus hypersecretion and the influx of inflammatory cells which are characteristics of this rodent model [27][28][30]. In complementary studies, mice in which the IL-13 gene had been deleted, failed to develop allergen-induced AHR. AHR could be restored in these IL-13 deficient mice by the administration of recombinant IL-13. In contrast, IL-4 deficient mice developed airway disease in this model [32][33].

Using a longer-term allergen-induced pulmonary inflammation model, Taube *at al.* demonstrated the efficacy of soluble murine IL-13Rα2 against established airway disease [34]. Soluble murine IL-13Rα2 inhibited AHR, mucus overproduction and to a lesser extent airway inflammation. In contrast, soluble IL-4Rα, which binds and antagonises IL-4, had little effect on AHR or airway inflammation in this system [35]. These findings were supported by Blease *et al.* who developed a chronic fungal model of asthma in which polyclonal antibodies against IL-13 but not IL-4 were able to reduce mucus overproduction, AHR and subepithelial fibrosis [36].

A number of genetic polymorphisms in the IL-13 gene have also been linked to allergic disease. In particular, a variant of the IL-13 gene in which the arginine residue at amino acid 130 is substituted with glutamine (Q130R) has been associated with bronchial asthma, atopic dermatitis and raised serum IgE levels [37][38][39][40]. This particular IL-13 variant is also referred to as the Q110R variant (arginine residue at amino acid 110 is substituted with glutamine) by some groups who exclude the 20 amino acid signal sequence from the amino acid count. Arima et al, [41] report that this variant is associated with raised levels of IL-13 in serum. The IL-13 variant (Q130R) and antibodies to this variant are discussed in WO 01/62933. An IL-13 promoter polymorphism, which alters

IL-13 production, has also been associated with allergic asthma [42].

Raised levels of IL-13 have also been measured in human subjects with asthma, atopic rhinitis (hay fever), allergic dermatitis (eczema) and chronic sinusitis. For example levels of IL-13 were found to be higher in bronchial biopsies, sputum and broncho-alveolar lavage (BAL) cells from asthmatics compared to control subjects [43][44][45][46]. Further, levels of IL-13 in BAL samples increased in asthmatic individuals upon challenge with allergen [47][48]. The IL-13 production capacity of CD4(+) T cells has further been shown to be useful marker of risk for subsequent development of allergic disease in newborns [49].

Li et al [114] have recently reported affects of a neutralising anti-mouse IL-13 antibody in a chronic mouse model of asthma. Chronic asthma-like response (such as AHR, severe airway inflammation, hyper mucus productions) was induced in OVA sensitised mice. Li et al report that administration of an IL-13 antibody at the time of each OVA challenge suppresses AHR, eosinophil infiltration, serum IgE levels, proinflammatory cytokine/chemokine levels and airway remodelling [14].

In summary, these data provide indication that IL-13 rather than IL-4 is a more attractive target for the treatment of human allergic disease.

IL-13 may play a role in the pathogenesis of inflammatory bowel disease. Heller et al.[116] report that neutralisation of IL-13 by administration of soluble IL-13Rα2 ameliorated colonic inflammation in a murine model of human ulcerative colitis [116]. Correspondingly, IL-13 expression was higher in

rectal biopsy specimens from ulcerative colitis patients when compared to controls [117].

Aside from asthma, IL-13 has been associated with other fibrotic conditions. Increased levels of IL-13, up to a 1000 fold higher than IL-4, have been measured in the serum of patients with systemic sclerosis [50] and in BAL samples from patients affected with other forms of pulmonary fibrosis [51]. Correspondingly, overexpression of IL-13 but not IL-4 in the mouse lung resulted in pronounced fibrosis [52][53]. The contribution of IL-13 to fibrosis in tissues other than the lung has been extensively studied in a mouse model of parasite-induced liver fibrosis. Specific inhibition of IL-13 by administration of soluble IL-13Rα2 or IL-13 gene disruption, but not ablation of IL-4 production prevented fibrogenesis in the liver [54][55][56].

Chronic Obstructive Pulmonary Disease (COPD) includes patient populations with varying degrees of chronic bronchitis, small airway disease and emphysema and is characterised by progressive irreversible lung function decline that responds poorly to current asthma based therapy [90].
The incidence of COPD has risen dramatically in recent years to become the fourth leading cause of death worldwide (World Health Organisation). COPD therefore represents a large unmet medical need.

The underlying causes of COPD remain poorly understood. The "Dutch hypothesis" proposes that there is a common susceptibility to COPD and asthma and therefore, that similar mechanisms may contribute to the pathogenesis of both disorders [57].

Zheng et al [58] have demonstrated that overexpression of IL-13 in the mouse lung caused emphysema, elevated mucus production and inflammation, reflecting aspects of human COPD. Furthermore, AHR, an IL-13 dependent response in murine models of allergic inflammation, has been shown to be predictive of lung function decline in smokers [59]. A link has also been established between an IL-13 promoter polymorphism and susceptibility to develop COPD [60].

The signs are therefore that IL-13 plays an important role in the pathogenesis of COPD, particularly in patients with asthma-like features including AHR and eosinophilia. mRNA levels of IL-13 have been shown to be higher in autopsy tissue samples from subjects with a history of COPD when compared to lung samples from subjects with no reported lung disease (J. Elias, Oral communication at American Thoracic Society Annual Meeting 2002). In another study, raised levels of IL-13 were demonstrated by immunohistochemistry in peripheral lung sections from COPD patients [91].

Hodgkin's disease is a common type of lymphoma, which accounts for approximately 7,500 cases per year in the United States. Hodgkin's disease is unusual among malignancies in that the neoplastic Reed-Sternberg cell, often derived from B-cells, make up only a small proportion of the clinically detectable mass. Hodgkin's disease-derived cell lines and primary Reed-Sternberg cells frequently express IL-13 and its receptor [61]. As IL-13 promotes cell survival and proliferation in normal B-cells, it was proposed that IL-13 could act as a growth factor for Reed-Sternberg cells. Skinnider et al. have demonstrated that neutralising antibodies against IL-13 can inhibit the growth of Hodgkin's disease-derived cell lines *in vitro* [62]. This finding suggested that Reed-Sternberg cells might enhance their own survival by an IL-13 autocrine and

paracrine cytokine loop. Consistent with this hypothesis, raised levels of IL-13 have been detected in the serum of some Hodgkin's disease patients when compared to normal controls [63]. IL-13 inhibitors may therefore prevent disease progression by inhibiting proliferation of malignant Reed-Sternberg cells.

Many human cancer cells express immunogenic tumour specific antigens. However, although many tumours spontaneously regress, a number evade the immune system (immunosurveillance) by suppressing T-cell mediated immunity. Terabe *et al.*[64] have demonstrated a role of IL-13 in immunosuppression in a mouse model in which tumours spontaneously regress after initial growth and then recur. Specific inhibition of IL-13, with soluble IL-13Rα2, protected these mice from tumour recurrence. Terabe *et al* [64] went on to show that IL-13 suppresses the differentiation of tumour specific CD8+ cytotoxic lymphocytes that mediate anti-tumour immune responses.

IL-13 inhibitors may, therefore, be used therapeutically to prevent tumour recurrence or metastasis. Inhibition of IL-13 has been shown to enhance anti-viral vaccines in animal models and may be beneficial in the treatment of HIV and other infectious diseases [65].

It should be noted that generally herein reference to interleukin-13 or IL-13 is, except where context dictates otherwise, reference to human IL-13. This is also referred to in places as "the antigen". The present invention provides antibodies to human IL-13, especially human antibodies, that are cross-reactive with non-human primate IL-13, including cynomolgus and rhesus monkey IL-13. Antibodies in accordance with some embodiments of the present invention recognise a

variant of IL-13 in which the arginine residue at amino acid position 130 is replaced by glutamine. In other aspects and embodiments the present invention provides specific binding members against murine IL-13, specifically mouse IL-13.

Brief Description of Figures

Figure 1 shows neutralisation potency (% inhibition) of BAK167A11 (closed squares) and its derivative BAK615E3 (open squares) as scFv against 25 ng/ml human IL-13 in the TF-1 cell proliferation assay. The triangles represent an irrelevant scFv. Data represent the mean with standard error bars of triplicate determinations within the same experiment.

Figure 2 shows the neutralisation potency (% inhibition) of BAK278D6 (closed squares) and its derivative BAK502G9 (open squares) as scFv against 25 ng/ml human IL-13 in the TF-1 cell proliferation assay. The triangles represent an irrelevant scFv. Data represent the mean with standard error bars of triplicate determinations within the same experiment.

Figure 3 shows the neutralisation potency (% inhibition) of BAK209B11 (closed squares) as a scFv against 25 ng/ml murine IL-13 in the TF-1 cell proliferation assay. The triangles represent an irrelevant scFv. Data represent the mean with standard error bars of triplicate determinations within the same experiment.

Figure 4 shows the neutralisation potency (% inhibition) of BAK278D6 (closed squares) as a scFv against IL-13 in the TF-1 cell proliferation assay. The triangles represent an irrelevant scFv. Data represent the mean with standard error bars of triplicate determinations within the same experiment.

Figure 4A show potency against 25 ng/ml human IL-13.

Figure 4B shows potency against 25 ng/ml human variant IL-13.

Figure 4C shows potency against 50 ng/ml non-human primate IL-13.

Figure 5 shows a comparison of the potency of anti-human IL-13 antibodies in the TF-1 proliferation assay. Data represent the mean neutralisation potency with standard error bars over 5-7 experiments against 25 ng/ml human IL-13. The performance relative to the commercially available antibody, B-B13, was evaluated statistically by performing a one-way ANOVA with Dunnett's test. * $P<0.05$, ** $P<0.01$ compared to B-B13.

Figure 6 shows the neutralisation potency (% inhibition) of BAK502G9 (closed squares), BAK1167F2 (closed triangles) and BAK1183H4 (closed inverted triangles) as human IgG4 against tagged IL-13 in the TF-1 cell proliferation assay. Open triangles represent an irrelevant IgG4. Data represent the mean with standard error bars of three separate experiments.

Figure 6A shows potency against 25 ng/ml human IL-13.

Figure 6B shows potency against 25 ng/ml human variant IL-13.

Figure 6C shows potency against 50 ng/ml non-human primate IL-13.

Figure 7 shows the neutralisation potency (% inhibition) of BAK502G9 (closed squares), BAK1167F2 (closed triangles), BAK1183H4 (closed inverted triangles) as human IgG4 and commercial anti-human IL-13 antibodies (B-B13 - open squares; JES10-5A2 - open inverted triangles) in the native IL-13 dependent HDLM-2 cell proliferation assay. Open triangles represent an irrelevant IgG4. Data represent the mean with standard error bars of triplicate determinations within the same experiment.

Figure 8 shows a comparison of the potency of anti-human IL-13 antibodies in the NHLF assay. Data represent the mean neutralisation potency (IC_{50} pM) with standard error bars over 4-5 experiments against 10 ng/ml human IL-13 in the NHLF eotaxin release assay. The performance relative to the commercially available antibody, B-B13, was evaluated statistically by performing a one-way ANOVA with Dunnett's test. * $P<0.05$, ** $P<0.01$ compared to B-B13.

Figure 9 shows the neutralisation potency (% inhibition) of BAK502G9 (closed squares), BAK1167F2 (closed triangles), BAK1183H4 (closed inverted triangles) as human IgG4 against VCAM-1 upregulation on the surface of HUVEC in response to 10ng/ml human IL-13. Open triangles represent irrelevant IgG4. Data represent the mean with standard error bars of triplicate determinations within the same experiment.

Figure 10 shows the neutralisation potency (% inhibition) of BAK502G9 (closed squares), BAK1167F2 (closed triangles), BAK1183H4 (closed inverted triangles) as human IgG4 against eotaxin release from VCAM-1 upregulation on the surface of HUVEC in response to either 1ng/ml human IL-4 (Figure 10A) or 0.5ng/ml human IL-1β (Figure 10B). Open triangles represent an irrelevant IgG4. Data represent the mean with standard error bars of triplicate determinations within the same experiment.

Figure 11 shows the neutralisation potency (% inhibition) of BAK209B11 (squares) as a human IgG4 against 1 ng/ml murine IL-13 in the factor dependent B9 cell proliferation assay. Open triangles represent an irrelevant IgG4. Data represent the mean with standard error bars of triplicate determinations within the same experiment.

Figure 12 shows the relative level of IL-13 in lung homogenates from sensitised (s) (right-hand bar) and non-sensitised (ns) (left-hand bar) mice post challenge in a murine model of acute pulmonary allergic inflammation. The effect of sensitisation was statistically evaluated by performing Student's t-test using quantity of IL-13 data. *<0.05. **<0.01 compared to non-sensitised control animals (n=5-6 mice). Data represent the mean with standard error bars.

Figure 13 illustrates the effects of i.v. administration of BAK209B11 as human IgG4 in different amounts compared to an isotype matched IgG4 irrelevant control antibody on ovalbumin induced leukocyte recruitment to the lung in ovalbumin sensitised mice. The number of leukocytes is shown (x 10^4). The effect of antibody treatment was statistically evaluated by performing one way ANOVA with Dunnett's test using differential cell count data. *<0.05. **<0.01 compared to ovalbumin challenged PBS control animals (=0% inhibition; n=5-8 mice). Data represent the mean with standard error bars.

Figure 14 illustrates the effects of i.v. administration of BAK209B11 as human IgG4 in different amounts compared to an isotype matched IgG4 irrelevant control antibody on ovalbumin induced eosinophil recruitment to the lung in ovalbumin sensitised mice. The number of eosinophils is shown (x 10^4). The effect of antibody treatment was statistically evaluated by performing one way ANOVA with Dunnett's test using differential cell count data. *<0.05. **<0.01 compared to ovalbumin challenged PBS control animals (=0% inhibition; n=5-8 mice). Data represent the mean with standard error bars.

Figure 15 illustrates the effects of i.v. administration of BAK209B11 as human IgG4 in different amounts compared to an isotype matched IgG4 irrelevant control antibody on ovalbumin

induced neutrophil recruitment to the lung in ovalbumin sensitised mice. The number of neutrophils is shown (x 10^4). The effect of antibody treatment was statistically evaluated by performing one way ANOVA with Dunnett's test using differential cell count data. *<0.05. **<0.01 compared to ovalbumin challenged PBS control animals (=0% inhibition; n=5-8 mice). Data represent the mean with standard error bars.

Figure 16 illustrates the effects of i.v. administration of BAK209B11 as human IgG4 in different amounts compared to an isotype matched IgG4 irrelevant control antibody on ovalbumin induced lymphocyte recruitment to the lung in ovalbumin sensitised mice. The induction of lymphocytes was dose dependently inhibited by BAK209B11 with maximal inhibition at 3μg/ml of BAK209B11. The effect of antibody treatment was statistically evaluated by performing one way ANOVA with Dunnett's test using differential cell count data. *<0.05. **<0.01 compared to ovalbumin challenged PBS control animals (=0% inhibition; n=5-8 mice). Data represent the mean with standard error bars.

Figure 17 illustrates the effects of i.v. administration of BAK209B11 as human IgG4 in different amounts compared to an isotype matched IgG4 irrelevant control antibody on ovalbumin induced monocyte/macrophage recruitment to the lung in ovalbumin sensitised mice. There was no significant increase in the levels of monocytes/macrophages of sensitised animals when compared with control animals. However, such background levels of these cells were depressed by ≥36μg/ml BAK209B11 in sensitised animals. The effect of antibody treatment was statistically evaluated by performing one way ANOVA with Dunnett's test using differential cell count data. *<0.05. **<0.01 compared to ovalbumin challenged PBS control animals

(=0% inhibition; n=5-8 mice). Data represent the mean with standard error bars.

Figure 18 shows the effects of a commercial anti-IL-13 neutralising antibody JES10-5A2 on the influx of cells (number of leukocytes is shown (x 10^4)) into the murine airpouch elicited by administration of bacterially derived recombinant human IL-13. The effect of antibody treatment was statistically evaluated by performing one way ANOVA with Dunnett's test using differential cell count data. *<0.05. **<0.01 compared to CMC control animals (=0% inhibition; n=11-13 mice). Data represent the mean with standard error bars.

Figure 19 shows an sequence alignment of cynomolgus IL-13 against human IL-13 amino acid sequences. The seven amino acid residues that differ between human and cynomolgus IL-13 are shaded. Rhesus and cynomolgus IL-13 have an identical amino acid sequence.

Figure 20 illustrates the effects of single 10mg/kg i.v bolus dose of BAK502G9 as human IgG4 on serum IgE levels in 4 allergic but non-challenged cynomolgus primates (2 male/2 female) over 29 days. Serum IgE concentration is significantly reduced from 100 % (predose) to 66 ± 10% of control values ($p<0.05$), at 4 and 5 days after dosing. This lowering of serum IgE concentration recovers to 88 ± 8 % of control levels by day 22. * = $p<0.05$ as compared to predose IgE levels, repeated measures ANOVA followed by Dunnett's multiple comparisons test (n=4 animals).

Figure 20B shows relative serum IgE levels of male and female cynomolgus primates versus time following a single 10mg/kg intravenous dose of BAK502G9. Relative serum IgE data are

expressed as arithmetic mean ± SEM percentage of baseline value.

Figure 21 illustrates the effects of intraperitoneal administration of BAK209B11 in different amounts (H=237μg/day, M=23.7μg/day and L=2.37μg/day) compared with an isotype matched IgG1 irrelevant control antibody on the lung function of ovalbumin sensitised and challenged mice. In Figure 21A lung function is represented by log PC_{50}s (log methacholine concentration required to increase baseline PenH by 50%) before any treatment (day 0) and post sensitisation, challenge and drug treatment (day 25). Figure 21A shows the raw data used to calculate the study endpoint, shown in figure 21B (Delta log PC_{50}). Data represent the mean with standard error bars of n=8.

In Figure 21B changing lung function is shown by a change in an individual mouse's log PC_{50} (delta log PC_{50}). Delta log PC_{50} is defined as an individuals change in log PC_{50} at day 25 verus day 0. Data represent group mean delta log PC_{50} (individual changes averaged within treatment groups) with standard error bars. The effect of antibody treatment was statistically evaluated by performing one way ANOVA with Dunnett's test using delta log PC_{50} data. **$p<0.01$ compared to ovalbumin sensitised and challenged control animals (n=8 mice).

Figure 22 illustrates the effects of local (i.po.) and systemic (i.v.) administration of BAK502G9 as human IgG4 in different amounts compared to an isotype matched IgG4 irrelevant control antibody on the total leukocyte recruitment (Figure 22A) and eosinophil recruitment (Figure 22B) into the air pouch of BALB/C mice. Data represent the mean with standard error bars of n=10. The effect of antibody treatment was statistically evaluated by performing one way ANOVA with

Dunnett's test using log-transformed data. *p<0.05, **p<0.01 compared to huIL-13 challenged mice (n=10).

Figure 23: illustrates the effects of i.p. administration of BAK502G9 as human IgG4 compared to an isotype matched IgG4 irrelevant control antibody on the development of AHR following intratracheal administration of human IL-13 to the airways of mice. The effect of antibody treatment was statistically evaluated by performing one way ANOVA with Dunnett's test using PC_{200} Methacholine data. *<0.05. **<0.01 compared to the human IL-13 positive control group (n=6-8 mice). Data represent the mean with standard error bars.

Figure 24 shows the neutralisation potency (% maximal response) of BAK502G9 (closed squares) as IgG4 against 30ng/ml IL-13 in a human B cell IgE production assay. Open squares represent an irrelevant IgG4. Data represent the mean with standard error bars of six donors from separate experiments.

Figure 25 shows the effects of BAK502G9 on IL-13 induced potentiation of agonist induced Ca^{2+} signalling in bronchial smooth muscle cells. The area under the curve (AUC) of the Ca^{2+} signalling response to histamine was determined for each antibody +/- IL-13 pre-treatment condition. Combined data from three independent experiments are shown for irrelevant antibody CAT-001 (a) and BAK502G9 (b) as the percentage difference versus untreated cells of AUC±SD (ns=not significant (p>0.05), *p<0.05, **p<0.01). The results were statistically evaluated utilising a one-way analysis of variance (ANOVA) with Bonferroni's multiple comparisons post-test.

Figure 26 shows effects of phase II administered BAK502G9.

Figure 26A shows effect on AHR as measured by change in area under the histamine dose response curve (n=14).

Figure 26B shows effect on AHR as measured by change in PC_{30} (n=18).

Figure 26C shows effect on antigen priming (n=20).

Figure 26D shows effect on BAL inflammation (n=21).

Figure 27 shows effect of BAK502G9 on IL-13-induced CD23 expression. Data are presented as a percentage of the response to IL-13 alone (100%) and expressed as mean ± SEM % control of 6 separate experiments from 6 individual donors (performed in triplicate).

Figure 28 shows effect of BAK502G9 and irrelevant IgG4 on IL-13 and/or IL-4 induced PBMC CD23 expression. Data are presented as a percentage of the response to IL-4 alone (100%) and expressed as mean ± SEM % control of 4 separate experiments from 4 individual donors (performed in triplicate).

Figure 29A shows effect of BAK502G9 on NHLF eotaxin-1 production induced by 48h culture with IL-13/ TNF-α/ TGF-β1 containing media. Data are shown as an arithmetic mean ± SEM from triplicate determinations of the media used in this study to induce leukocyte shape change.

Figure 29B shows effect of BAK502G9 on shape change of human eosinophils induced by 1:16 diultion of conditioned media. Data points represented are mean ± SEM %blank media shape change from separate experiments from four individual donors.

Figure 30 shows alignment of human IL-13 against murine IL13 highlighting the mutations that were introduced into human IL-

13 to produce the first panel of IL-13 chimaeras. The four alpha helices are highlighted in boxes and loop 1 and loop 3 are labelled. Five chimeric proteins were produced where helices B, C and D, and loops 1 and loop 3 were replaced with the murine sequence. Four further chimeric proteins were produced and numbered according to the amino acid in the human pre-protein (not to the numbering of the multiple aligment above) where arginine at residue 30 (position 34 above) was mutated, residues 33 and 34 (position 37 and 38 above) were mutated, residues 37 and 38 (VH) were mutated (position 41 and 42 above), and residues 40 and 41 (TQ) were mutated (position 44 and 45 above).

Figure 31 shows alignment of human IL-13 against murine IL-13 highlighting the mutations that were introduced into human IL-13 to produce the second panel of IL-13 chimaeras. Six chimaeras were produced where the human residue(s) were substituted for the murine residue(s) (highlighted with boxes). Four further chimeric proteins were produced (numbering is according to the amino acid position in the human pre-protein) where leucine at residue 58 (62 in above figure) was mutated, leucine at residue 119 (residue 123 above) was mutated, lysine at position 123 (residue 127 above) was mutated, and arginine at residue 127 (residue 132 above was mutated.

Figure 32 shows mutations made to human IL-13. Mutations in dark grey reduced binding to BAK502G9, mutations in light grey did not alter binding. Linear sequence of pre-human IL-13 with the mutated residues indicated.

In various aspects and embodiments of the invention there is provided the subject-matter of the claims included below.

In a first aspect, there is provided an isolated specific binding member for human IL-13,
comprising an antibody antigen-binding site which is composed of a human antibody VH domain and a human antibody VL domain and which comprises a set of CDR's HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, wherein the VH domain comprises HCDR 1, HCDR2 and HCDR3 and the VL domain comprises LCDR1, LCDR2 and LCDR3, wherein the set of CDR's consists of a set of CDR's selected from the group consisting of:

the BAK278D6 set of CDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 1, the HCDR2 has the amino acid sequence of SEQ ID NO: 2, the HCDR3 has the amino acid sequence of SEQ ID NO: 3, the LCDR1 has the amino acid sequence of SEQ ID NO: 4, the LCDR2 has the amino acid sequence of SEQ ID NO: 5, and the LCDR3 has the amino acid sequence of SEQ ID NO: 6,

a set of CDR's which contains one or two amino acid substitutions compared with the BAK278D6 set of CDR's, and

each set of CDR's as shown for individual clones in Table 1.

In a second aspect, there is provided an isolated antibody VH domain of a specific binding member as defined in the first aspect.

In a third aspect, there is provided an isolated antibody VL domain of a specific binding member as defined in the first aspect.

In a fourth aspect, there is provided a composition comprising a specific binding member, antibody VH domain or antibody VL as defined in the first to third aspects and at least one additional component.

In a fifth aspect, there is provided an isolated nucleic acid which comprises a nucleotide sequence encoding a specific

binding member or antibody VH or VL domain of a specific binding member as defined in the first to third aspects.

In a sixth aspect, there is provided a host cell in vitro transformed with nucleic acid as defined in the fifth aspect.

In a seventh aspect, there is provided a method of producing a specific binding member or antibody VH or VL domain, the method comprising culturing host cells as defined in the sixth aspect under conditions for production of said specific binding member or antibody VH or VL domain.

In an eighth aspect, there is provided a method for producing an antibody antigen-binding domain specific for human IL-13, the method comprising

providing, by way of addition, deletion, substitution or insertion of one or more amino acids in the amino acid sequence of a parent VH domain comprising HCDR 1, HCDR2 and HCDR3, wherein the parent VH domain HCDR1, HCDR2 and HCDR3 are the BAK278D6 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 1, the HCDR2 has the amino acid sequence of SEQ ID NO: 2, the HCDR3 has the amino acid sequence of SEQ ID NO: 3, or the BAK502G9 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 7, the HCDR2 has the amino acid sequence of SEQ ID NO: 8, the HCDR3 has the amino acid sequence of SEQ ID NO: 9, a VH domain which is an amino acid sequence variant of the parent VH domain; and

testing said VH domain which is an amino acid sequence variant of the parent VH domain to identify an antibody antigen binding domain specific for human IL-13, or

combining said VH domain with one or more VL domains to provide one or more VH/VL combinations and testing the VH/VL combination or combinations to identify an antibody antigen binding domain specific for human IL-13.

In a ninth aspect, there is provided a method for producing an antibody antigen-binding domain specific for human IL-13, the method comprising

providing, by way of addition, deletion, substitution or insertion of one or more amino acids in the amino acid sequence of a parent VH domain comprising HCDR 1, HCDR2 and HCDR3, wherein the parent VH domain HCDR1, HCDR2 and HCDR3 are the BAK167A11 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 55, the HCDR2 has the amino acid sequence of SEQ ID NO: 56, the HCDR3 has the amino acid sequence of SEQ ID NO: 57, the BAK615E3 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 153, the HCDR2 has the amino acid sequence of SEQ ID NO: 154, the HCDR3 has the amino acid sequence of SEQ ID NO: 155, the BAK582F7 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 141, the HCDR2 has the amino acid sequence of SEQ ID NO: 142, the HCDR3 has the amino acid sequence of SEQ ID NO: 143, or the BAK612B5 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 147, the HCDR2 has the amino acid sequence of SEQ ID NO: 148, the HCDR3 has the amino acid sequence of SEQ ID NO: 149, a VH domain which is an amino acid sequence variant of the parent VH domain; and

testing said VH domain which is an amino acid sequence variant of the parent VH domain to identify an antibody antigen binding domain specific for human IL-13, or

combining said VH domain with one or more VL domains to provide one or more VH/VL combinations and testing the VH/VL combination or combinations to identify an antibody antigen binding domain specific for human IL-13.

In a tenth aspect, there is provided a method of producing a specific binding member that binds human IL-13, which method comprises:

providing starting nucleic acid encoding a VH domain or a starting repertoire of nucleic acids each encoding a VH domain, wherein the VH domain or VH domains either comprise a HCDR1, HCDR2 and/or HCDR3 to be replaced or lack a HCDR1, HCDR2 and/or HCDR3 encoding region;

combining said starting nucleic acid or starting repertoire with donor nucleic acid or donor nucleic acids encoding or produced by mutation of the amino acid sequence of the HCDR1 (SEQ ID NO: 1) or HCDR1 (SEQ ID NO: 7), HCDR2 (SEQ ID NO: 2) or HCDR2 (SEQ ID NO: 8) and/or HCDR3 (SEQ ID NO: 3) or HCDR3 (SEQ ID NO: 9) such that said donor nucleic acid is or donor nucleic acids are inserted into the CDR1, CDR2 and/or CDR3 region in the starting nucleic acid or starting repertoire, so as to provide a product repertoire of nucleic acids encoding VH domains;

expressing the nucleic acids of said product repertoire to produce product VH domains;

selecting a specific binding member specific for human IL-13, which specific binding member comprises a product VH domain or

combining said product VH domains with one or more VL domains and selecting a specific binding member specific for human IL-13, which specific binding member comprises a product VH domain and a VL domain; and

recovering said specific binding member or nucleic acid encoding it.

In an eleventh aspect, there is provided a method comprising in vitro binding a specific binding member that binds IL-13 as defined in the first aspect to human IL-13 or a fragment of human IL-13.

In a twelfth aspect, there is provided the use of a specific binding member as defined in the first aspect in the manufacture of a medicament for treatment of a disease or disorder selected from the group consisting of asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel disease and Hodgkin's lymphoma.

In a thirteenth aspect, there is provided an isolated specific binding member for human Il-13,
comprising an antibody antigen-binding domain site which is composed of a human antibody VH domain and a human antibody VL domain and which comprises a set of CDR's, HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, wherein the VH domain comprises HCDR1, HCDR2 and HCDR3 and the VL domain comprises LCDR1, LCDR2 and LCDR3, wherein

HCDR1 is of amino acid sequence which has the formula

HX_1 HX_2 G HX_3 S

wherein

HX_1 is selected from the group consisting of N, Q, D, L, G and E,

HX_2 is selected from the group consisting of Y and T,

HX_3 is selected from the group consisting of V, I, F and L,

HCDR2 is of amino acid sequence which has the formula

W I HX_4 HX_5 HX_6 HX_7 G HX_8 T HX_9 Y HX_{10} HX_{11} HX_{12} F HX_{13} HX_{14}

wherein

HX_4 is selected from the group consisting of S, D, N, A, R, G and E,

HX_5 is selected from the group consisting of A, D, G, T, P, N and Y,

HX_6 is selected from the group consisting of N, D, L, A, P, T, S, I and R,

HX_7 is selected from the group consisting of N, S, T, D, G, K and I,

HX_8 is selected from the group consisting of D, T, E, Q, L, Y, N, V, A, M and G,

HX_9 is selected from the group consisting of N, I, L, Q, S, M, H, D and K,

HX_{10} is selected from the group consisting of G and R,

HX_{11} is selected from the group consisting of Q and R,

HX_{12} is selected from the group consisting of E, K and G,

HX_{13} is selected from the group consisting of Q and R,

HX_{14} is selected from the group consisting of G and K,

HCDR3 is of amino acid sequence which has the formula

D HX_{15} HX_{16} HX_{17} HX_{18} W A R W HX_{19} F HX_{20} L

wherein

HX_{15} is selected from the group consisting of S, R and D,

HX_{16} is selected from the group consisting of S, N, D, T and P,

HX_{17} is selected from the group consisting of S and R,

HX_{18} is selected from the group consisting of S, N, A, I, R, P and K,

HX_{19} is selected from the group consisting of F and Y,

HX_{20} is selected from the group consisting of D and Y,

LCDR1 is of amino acid sequence which has the formula

G G LX_1 LX_2 LX_3 G LX_4 LX_5 L V H

wherein

LX_1 is selected from the group consisting of N, D and S,
LX_2 is selected from the group consisting of N, I, L, M, C, V, K, Y, F, R, T, S, A, H and G,
LX_3 is selected from the group consisting of I and V,
LX_4 is selected from the group consisting of S and G,
LX_5 is selected from the group consisting of K and R,
LCDR2 is of amino acid sequence which has the formula

D D G D R P LX_6

wherein

LX_6 is selected from the group consisting of S and T,

LCDR3 is of amino acid sequence which has the formula

Q V W D T G S LX_7 P V LX_8

wherein

LX_7 is selected from the group consisting of D and N,
LX_8 is selected from the group consisting of V and I.

In a fourteenth aspect, there is provided an isolated antibody VH domain of a specific binding member as defined in the thirteenth aspect.

In a fifteenth aspect, there is provided an isolated antibody VL of a specific binding member as defined in the thirteenth aspect.

In a sixteenth aspect, there is provided a composition comprising the specific binding member, antibody VH domain or antibody VL domain as defined in the thirteenth to fifteenth aspects and at least one additional component.

In a seventeenth aspect, there is provided an isolated nucleic acid which comprises a nucleotide sequence encoding a specific binding member or antibody VH or VL domain of a specific binding member as defined in the thirteenth to fifteenth aspects.

In an eighteenth aspect, there is provided a host cell in vitro transformed with nucleic acid as defined in the seventeenth aspect.

In a nineteenth aspect, there is provided a method of producing a specific binding member or antibody VH or VL domain, the method comprising culturing host cells as defined in the eighteenth aspect under conditions for production of said specific binding member or antibody VH or VL domain.

In a twentieth aspect, there is provided a method comprising in vitro binding a specific binding member that binds IL-13 as defined in the thirteenth aspect to human IL-13 or a fragment of human IL-13.

In a twenty-first aspect, there is provided the use of a specific binding member as defined in the thirteenth aspect in the manufacture of a medicament for treatment of a disease or disorder selected from the group consisting of asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel disease and Hodgkin's lymphoma.

The present invention provides specific binding members for IL-13, in particular human and/or primate IL-13 and/or variant IL-13 (Q130R), and murine IL-13. Preferred embodiments within the present invention are antibody molecules, whether whole antibody (e.g. IgG, such as IgG4) or antibody fragments (e.g. scFv, Fab, dAb). Antibody antigen binding regions are provided, as are antibody VH and VL domains. Within VH and VL domains are provided complementarity determining regions, CDR's, which may be provided within different framework regions, FR's, to form VH or VL domains as the case may be. An antigen binding site may consist of an antibody VH domain and/or a VL domain.

An antigen binding site may be provided by means of arrangement of CDR's on non-antibody protein scaffolds such as fibronectin or cytochrome B etc. [115, 116]. Scaffolds for engineering novel binding sites in proteins have been reviewed in detail by Nygren et al [116]. Protein scaffolds for antibody mimics are disclosed in WO/0034784 in which the inventors describe proteins (antibody mimics) which include a fibronectin type III domain having at least one randomised loop. A suitable scaffold into which to graft one or more CDR's, e.g. a set of HCDR's, may be provided by any domain member of the immunoglobulin gene superfamily.

Preferred embodiments of the present invention are in what is termed herein the "BAK278D6 lineage". This is defined with reference to a set of six CDR sequences of BAK278D6 as follows: HCDR1 (SEQ ID NO: 1), HCDR2 (SEQ ID NO: 2), HCDR3 (SEQ ID NO: 3), LCDR1 (SEQ ID NO: 4), LCDR2 (SEQ ID NO: 5) and LCDR3 (SEQ ID NO: 6). In one embodiment, the present invention provides a specific binding member for human IL-13, comprising an antibody antigen-binding site which is composed of a human antibody VH domain and a human antibody VL domain and which

comprises a set of CDR's, wherein the VH domain comprises HCDR 1, HCDR2 and HCDR3 and the VL domain comprises LCDR1, LCDR2 and LCDR3, wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 1, the HCDR2 has the amino acid sequence of SEQ ID NO: 2, the HCDR3 has the amino acid sequence of SEQ ID NO: 3, the LCDR1 has the amino acid sequence of SEQ ID NO: 4, the LCDR2 has the amino acid sequence of SEQ ID NO: 5, and the LCDR3 has the amino acid sequence of SEQ ID NO: 6; or wherein the set of CDR's contains one or two amino acid substitutions compared with the set of CDR's, wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 1, the HCDR2 has the amino acid sequence of SEQ ID NO: 2, the HCDR3 has the amino acid sequence of SEQ ID NO: 3, the LCDR1 has the amino acid sequence of SEQ ID NO: 4, the LCDR2 has the amino acid sequence of SEQ ID NO: 5, and the LCDR3 has the amino acid sequence of SEQ ID NO: 6.

The set of CDR's wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 1, the HCDR2 has the amino acid sequence of SEQ ID NO: 2, the HCDR3 has the amino acid sequence of SEQ ID NO: 3, the LCDR1 has the amino acid sequence of SEQ ID NO: 4, the LCDR2 has the amino acid sequence of SEQ ID NO: 5, and the LCDR3 has the amino acid sequence of SEQ ID NO: 6, are herein referred to as the "BAK278D6 set of CDR's". The HCDR1, HCDR2 and HCDR3 within the BAK278D6 set of CDR's are referred to as the "BAK278D6 set of HCDR's" and the LCDR1, LCDR2 and LCDR3 within the BAK278D6 set of CDR's are referred to as the "BAK278D6 set of LCDR's". A set of CDR's with the BAK278D6 set of CDR's, BAK278D6 set of HCDR's or BAK278D6 LCDR's, or one or two substitutions therein, is said to be of the BAK278D6 lineage.

As noted, in one embodiment the invention provides a specific binding member for human IL-13, comprising an antibody

antigen-binding site which is composed of a human antibody VH domain and a human antibody VL domain and which comprises a set of CDR's, wherein the set of CDR's is the BAK278D6 set of CDR's or a set of CDR's containing one or two substitutions compared with the BAK278D6 set of CDR's.

In preferred embodiments, the one or two substitutions are at one or two of the following residues within the CDRs of the VH and/or VL domains, using the standard numbering of Kabat [107].

31, 32, 34 in HCDR1

52, 52A, 53, 54, 56, 58, 60, 61, 62, 64, 65 in HCDR2

96, 97, 98, 99, 101 in HCDR3

26, 27, 28, 30, 31 in LCDR1

56 in LCDR2

95A, 97 in LCDR3

Preferred embodiments have two substitutions compared with the BAK278D6 set of CDR's, at HCDR3 residue 99 and LCDR1 residue 27. Of these embodiments, preferred embodiments have S substituted for N at HCDR3 residue 99 and/or I substituted for N at LCDR 1 residue 27. Still further embodiments have a substitution at HCDR3 residue 99 selected from the group consisting of S, A, I, R, P and K, and/or a substitution at LCDR1 residue 27 selected from the group consisting of I, L, M, C, V, K, Y, F, R, T, S, A, H and G.

In preferred embodiments one or two substitutions are made at one or two of the following residues within the BAK278D6 set of CDR's in accordance with the identified groups of possible substitute residues:

Position of substitution	Substitute Residue selected from the group consisting of
31 in HCDR1:	Q, D, L, G and E
32 in HCDR1:	T
34 in HCDR1:	V, I and F
52 in HCDR2:	D, N, A, R, G and E
52A in HCDR2:	D, G, T, P, N and Y
53 in HCDR2:	D, L, A, P, T, S, I and R
54 in HCDR2:	S, T, D, G, K and I
56 in HCDR2:	T, E, Q, L, Y, N, V, A, M and G
58 in HCDR2:	I, L, Q, S, M, H, D and K
60 in HCDR2:	R
61 in HCDR2:	R
62 in HCDR2:	K and G
64 in HCDR2:	R
65 in HCDR2:	K
96 in HCDR3:	R and D
97 in HCDR3:	N, D, T and P
98 in HCDR3:	R
99 in HCDR3:	S,A, I, R, P and K
101 in HCDR3:	Y
26 in LCDR1:	D and S

27 in LCDR1: I, L, M, C, V, K, Y, F, R, T, S, A, H and G
28 in LCDR1: V
30 in LCDR1: G
31 in LCDR1: R

56 in LCDR2: T

95A in LCDR3: N
97 in LCDR3: I

Preferred embodiments have the BAK278D6 set of CDR's with a substitution of S for N at residue 99 within HCDR3 and I for N at residue 27 within LCDR 1. The set of CDR's thus defined is as follows: HCDR1 - SEQ ID NO: 7; HCDR2 - SEQ ID NO: 8, HCDR3 - SEQ ID NO: 9; LCDR1 - SEQ ID NO: 10, LCDR2 - SEQ ID NO: 11; LCDR3 - SEQ ID NO: 12. This set of CDR's is herein referred to as the "BAK502G9 set of CDR's".

Further preferred embodiments have the BAK278D6 set of CDR's with one or two substitutions within the CDR's, with the proviso that the pair of substitutions of S for N at residue 99 within HCDR3 and I for N at residue 27 within LCDR 1 is excluded.

Other preferred embodiments are as follows: BAK 1166G2: HCDR1- SEQ ID NO: 67, HCDR2- SEQ ID NO: 68, HCDR3- SEQ ID NO: 69, LCDR1 - SEQ ID NO: 70, LCDR2 - SEQ ID NO: 71; LCDR3 - SEQ ID NO: 72.

BAK1167F2 HCDR1- SEQ ID NO: 61, HCDR2- SEQ ID NO:62, HCDR3- SEQ ID NO:63, LCDR1 - SEQ ID NO: 64, LCDR2 - SEQ ID NO: 65; LCDR3 - SEQ ID NO: 66.

BAK1184C8: HCDR1- SEQ ID NO:73, HCDR2: SEQ ID NO:74, HCDR3- SEQ ID NO:75. LCDR1 - SEQ ID NO: 76, LCDR2 - SEQ ID NO: 77; LCDR3 - SEQ ID NO: 78.

BAK1185E1: HCDR1- SEQ ID NO:79, HCDR2- SEQ ID NO:80, HCDR3- SEQ ID NO: 81. LCDR1 - SEQ ID NO: 82, LCDR2 - SEQ ID NO: 83; LCDR3 - SEQ ID NO: 84.

BAK1167F4: HCDR1- SEQ ID NO: 85, HCDR2- SEQ ID NO:86, HCDR3- SEQ ID NO:87. LCDR1 - SEQ ID NO: 88, LCDR2 - SEQ ID NO: 89; LCDR3 - SEQ ID NO: 90.

BAK1111D10: HCDR1- SEQ ID NO: 91, HCDR2- SEQ ID NO: 92, HCDR3- SEQ ID NO: 93. LCDR1 - SEQ ID NO: 94, LCDR2 - SEQ ID NO: 95; LCDR3 - SEQ ID NO: 96.

BAK1183H4: HCDR1- SEQ ID NO: 97, HCDR2- SEQ ID NO: 98, HCDR3- SEQ ID NO: 99. LCDR1 - SEQ ID NO: 100, LCDR2 - SEQ ID NO: 101; LCDR3 - SEQ ID NO: 102.

BAK1185F8: HCDR1- SEQ ID NO: 103, HCDR2- SEQ ID NO: 104, HCDR3- SEQ ID NO: 105. LCDR1 - SEQ ID NO: 106, LCDR2 - SEQ ID NO: 107; LCDR3 - SEQ ID NO: 108. All of these were derived from BAK502G9 by heavy chain CDR1 and CDR2 randomisation and are thus of the BAK502G9 lineage.

A VH domain comprising a set of CDR's HCDR1, HCDR2 and HCDR3 of any clone as shown in Table 1. Table 1 is also provided by the present invention, as is separately a VL domain comprising a set of CDR's LCDR1, LCDR2 and LCDR3 of the clones shown in Table 1. Preferably such a VH domain is paired with such a VL domain, and most preferably the VH and VL domain pairings are the same as in the clones as set out in Table 1.

Further provided by the present invention is a VH domain comprising a set of CDR's HCDR1, HCDR2 and HCDR3 wherein the set of CDR's corresponds to that for any clone shown in Table 1 with one or two amino acid substitutions.

Further provided by the present invention is a VL domain comprising a set of CDR's LCDR1, LCDR2 and LCDR3 wherein the set of CDR's corresponds to that for any clone shown in Table 1 with one or two amino acid substitutions.

A specific binding member comprising an antibody antigen-binding domain comprising such a VH and/or VL domain is also provided by the present invention.

The present inventors have identified the BAK278D6 lineage as providing human antibody antigen-binding domains against IL-13 which are of particular value. Within the lineage, BAK502G9 has been identified to be of special value. The BAK278D6 and BAK502G9 sets of CDR's have been identified already above.

Following the lead of computational chemistry in applying multivariate data analysis techniques to the structure/property-activity relationships [94], quantitative activity-property relationships of antibodies can be derived using well-known mathematical techniques such as statistical regression, pattern recognition and classification [95-100]. The properties of antibodies can be derived from empirical and theoretical models (for example, analysis of likely contact residues or calculated physicochemical property) of antibody sequence, functional and three-dimensional structures and these properties can be considered singly and in combination.

An antibody antigen-binding site composed of a VH domain and a VL domain is formed by six loops of polypeptide: three from

the light chain variable domain (VL) and three from the heavy chain variable domain (VH). Analysis of antibodies of known atomic structure has elucidated relationships between the sequence and three-dimensional structure of antibody combining sites[101,102]. These relationships imply that, except for the third region (loop) in VH domains, binding site loops have one of a small number of main-chain conformations: canonical structures. The canonical structure formed in a particular loop has been shown to be determined by its size and the presence of certain residues at key sites in both the loop and in framework regions [101,102].

This study of sequence-structure relationship can be used for prediction of those residues in an antibody of known sequence, but of an unknown three-dimensional structure, which are important in maintaining the three-dimensional structure of its CDR loops and hence maintain binding specificity. These predictions can be backed up by comparison of the predictions to the output from lead optimization experiments.

In a structural approach, a model can be created of the antibody molecule [103] using an freely available or commercial package such as WAM [104]. A protein visualisation and analysis software package such as Insight II [105] or Deep View [106] may then be used to evaluate possible substitutions at each position in the CDR. This information may then be used to make substitutions likely to have a minimal or beneficial effect on activity.

The present inventors analysed sequence data of the panel of clones for which the sets of CDR's are shown in Table 1.

The analysis tested the hypothesis that any binary combinations of listed amino acid variations in the CDR's from

the presented set of scFv variants leads to a scFv variant with at least the starting potency of the parent scFv BAK278D6.

All scFv variants in the panel shown in Table 1 have been selected for improved affinity and have been confirmed to display higher potency.

The observed amino acid variations can either be favourable, non-favourable or neutral in their effect on the starting potency of scFv BAK278D6 in the TF-1 assay of 44nM.

No linkage was observed between any two amino acid variations confirming that there was no synergy, either "positive" or "negative", between any two selected amino acid variations.

There are four scenarios where such binary combination will fulfil the hypothesis and three scenarios where the hypothesis will not be valid. Synergistic amino acid variants are not considered as no linkage was observed.

The hypothesis is valid where:

A1: mutation 1 is favourable and mutation 2 is favourable
A2 : mutation 1 is favourable and mutation 2 is neutral
A3: mutation 1 is neutral and mutation 2 is neutral
A4: mutation 1 is favourable and mutation 2 is non-favourable (with the effect of 1 outweighing the effect of 2) .

The hypothesis is not valid where:

B1: mutation 1 is non-favourable and mutation 2 is neutral
B2: mutation 1 is non-favourable and mutation 2 is non-favourable

B3: mutation 1 is favourable and mutation 2 is non-favourable (with the effect of 2 outweighing the effect of 1).

For A4 to be possible, mutation 1 needs to be highly favourable to counterbalance the negative effect of mutation 2 on potency. Since such highly favourable mutation would be present in the library of variants used for selection, it would be selected for and would therefore appear frequently in the panel of variants. Since synergy can be excluded, such mutation would be beneficial in any kind of sequence context and should therefore reappear in different scFv variants. An example for such frequent amino acid change is the change in the light chain CDR1 Asn27Ile. However, this mutation on its own (in clone BAK531E2) has only a modest 2-fold effect on potency (final IC50 of 23.2nM). On its own this mutation would not allow the scenario depicted in A4, as it is not a highly favourable mutation. This suggests that every clone in the presented set of IL-13 binding clones (Table 1) which has a light chain CDR1 Asn27Ile change along with one or more further mutations is at least as potent as the variant having the single light chain CDR1 Asn27Ile mutation. The other mutations are either neutral or positive but do not have a negative or detrimental affect.

A further example is in the heavy chain CDR3 Asn99Ser (see Table 1). As a clone carrying this particular single amino acid variation is not observed, the potency of such a clone has been estimated to be approximately 12.0nM by the following rationale:

BAK278D6 potency is 44nM. Alterations of VL CDR1 N27I + VH CDR3 N99S lead to BAK502G9 with potency 8nM, i.e. 5.5 fold improvement.

BAK278D6 potency is 44nM. Alteration of VL CDR1 N27I leads to BAK531E2 with potency 23 nM, i.e. 1.9 fold improvement

BAK278D6 potency is 44nM. Alteration VH CDR3 N99S to provide a possible clone with potency 12.2nM, i.e. 2.9 fold improvement (5.5/1.9 = 2.9).

The binary combination of heavy chain CDR3 Asn99Ser with light chain CDR1 Asn27Ile gives a scFv BAK0502G9 with a potency of 8nM. As synergy is excluded, the contribution of heavy chain CDR3 Asn99Ser change in BAK502G9 is therefore additive.

Therefore every clone in the presented set of IL-13 binding clones (Table 1) which has a heavy chain CDR3 AsnH99Ser change along with one or more further mutations would have a potency of at least 12nM or greater, within a permissive assay window of 2.5-fold for n=1-2.

Thus, the inventors note that a highly favourable amino acid variation which would be selected preferentially is not observed. As discussed above, two variations which were prominently represented in Table 1 of scFv variants were analysed closer. Any scFv variant in Table 1 with either of these mutations along with one or more further mutations displayed a potency which was at least as improved as a clone containing any one of these two single amino acid variations in the parent BAK278D6. There is therefore no evidence that a highly favourable amino acid variation, that would allow scenario A4, is present in the panel.

This observation led the inventors to conclude that there were no non-favourable mutations present in this set of scFv variants. This means scenarios A4 and B1 to B3 are not relevant and the hypothesis is valid.

Accordingly, as noted already, the present invention provides specific binding members comprising the defined sets of CDR's, in particular the set of CDR's of BAK278D6, and sets of CDR's of the BAK278D6 lineage, with one or two substitutions within the set of CDR's, e.g. the BAK502G9 set of CDR's.

The relevant set of CDR's is provided within antibody framework regions or other protein scaffold, e.g. fibronectin or cytochrome B [115, 116]. Preferably antibody framework regions are employed, and where they are employed they are preferably germline, more preferably the antibody framework region for the heavy chain may be DP14 from the VH1 family. The preferred framework region for the light chain may be λ3-3H. For the BAK502G9 set of CDR's it is preferred that the antibody framework regions are for VH FR1, SEQ ID NO: 27, for VH FR2, SEQ ID NO: 28, for VH FR3, SEQ ID NO 29, for light chain FR1, SEQ ID NO: 30, for light chain FR2, SEQ ID NO: 31, for light chain FR3, SEQ ID NO: 32. In a highly preferred embodiment, a VH domain is provided with the amino acid sequence of SEQ ID NO: 15, this being termed "BAK502G9 VH domain". In a further highly preferred embodiment, a VL domain is provided with the amino acid sequence of SEQ ID NO: 16, this being termed "BAK502G9 VL domain". A highly preferred antibody antigen-binding site provided in accordance with the present invention is composed of the BAK502G9 VH domain, SEQ ID NO: 15, and the BAK502G9 VL domain, SEQ ID NO: 16. This antibody antigen-binding site may be provided within any desired antibody molecule format, e.g. scFv, Fab, IgG, IgG4, dAb etc., as is discussed further elsewhere herein.

In a further highly preferred embodiment, the present invention provides an IgG4 antibody molecule comprising the

BAK502G9 VH domain, SEQ ID NO: 15, and the BAK502G9 VL domain, SEQ ID NO: 16. This is termed herein "BAK502G9 IgG4".

Other IgG4 or other antibody molecules comprising the BAK502G9 VH domain, SEQ ID NO: 15, and/or the BAK502G9 VL domain, SEQ ID NO: 16, are provided by the present invention, as are other antibody molecules comprising the BAK502G9 set of HCDR's (SEQ ID NO: 7, 8 and 9) within an antibody VH domain, and/or the BAK502G9 set of LCDR's (SEQ ID NO: 10, 11 and 12) within an antibody VL domain.

It is convenient to point out here that "and/or" where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. For example "A and/or B" is to be taken as specific disclosure of each of (i) A, (ii) B and (iii) A and B, just as if each is set out individually herein.

As noted, the present invention provides a specific binding member which binds human IL-13 and which comprises the BAK502G9 VH domain (SEQ ID NO: 15) and/or the BAK502G9 VL domain (SEQ ID NO: 16).

Generally, a VH domain is paired with a VL domain to provide an antibody antigen binding site, although as discussed further below a VH domain alone may be used to bind antigen. In one preferred embodiment, the BAK502G9 VH domain (SEQ ID NO: 15) is paired with the BAK502G9 VL domain (SEQ ID NO: 16), so that an antibody antigen binding site is formed comprising both the BAK502G9 VH and VL domains. In other embodiments, the BAK502G9 VH is paired with a VL domain other than the BAK502G9 VL. Light-chain promiscuity is well established in the art.

Similarly, any set of HCDR's of the BAK278D6 lineage can be provided in a VH domain that is used as a specific binding member alone or in combination with a VL domain. A VH domain may be provided with a set of HCDR's of a BAK278D6 lineage antibody, e.g. as shown in Table 1, and if such a VH domain is paired with a VL domain, then the VL domain may be provided with a set of LCDR's of a BAK278D6 lineage antibody, e.g. as shown in Table 1. A pairing of a set of HCDR's and a set of LCDR's may be as shown in Table 1, providing an antibody antigen-binding site comprising a set of CDR's as shown in Table 1. The framework regions of the VH and/or VL domains may be germline frameworks. Frameworks regions of the heavy chain domain may be selected from the VH-1 family, and a preferred VH-1 framework is DP-14 framework. Framework regions of the light chain may be selected from the λ3 family, and a preferred such framework is λ3 3H.

One or more CDRs may be taken from the BAK502G9 VH or VL domain and incorporated into a suitable framework. This is discussed further herein. BAK502G9 HCDR's 1, 2 and 3 are shown in SEQ ID NO: 7, 8 and 9, respectively. BAK502G9 LCDR's 1, 2 and 3 are shown in SEQ ID NO: 10, 11 and 12, respectively.

The same applies for other BAK278D6 lineage CDR's and sets of CDR's as shown in Table 1.

Further embodiments of the invention relate to a specific binding member comprising the VH and/or VL domain, or an antigen binding site comprising CDRs of the VH and/or VL domain of the antibody molecule disclosed herein as 167A11 (VH: SEQ ID NO: 23 and VL: SEQ ID NO: 24) and its derivatives 615E3 (VH:SEQ ID NO: 33 and VL: SEQ ID NO: 34) BAK582F7 (VH CDR's SEQ ID's 141-143) and BAK612B5 (VH CDR's

SEQ ID's 147-149). These recognise human IL-13. The derivatives of 167A11 from VH CDR3 randomisation are potent scFv molecules (5-6nM). The 167A11 lineage may be employed in any aspect and embodiment of the present invention as disclosed herein for other molecules, for instance methods of mutation and selection of antigen binding sites with improved potency.

Variants of the VH and VL domains and CDRs of the present invention, including those for which amino acid sequences are set out herein, and which can be employed in specific binding members for IL-13 can be obtained by means of methods of sequence alteration or mutation and screening. Such methods are also provided by the present invention.

Variable domain amino acid sequence variants of any of the VH and VL domains whose sequences are specifically disclosed herein may be employed in accordance with the present invention, as discussed. Particular variants may include one or more amino acid sequence alterations (addition, deletion, substitution and/or insertion of an amino acid residue), may be less than about 20 alterations, less than about 15 alterations, less than about 10 alterations or less than about 5 alterations, 4, 3, 2 or 1. Alterations may be made in one or more framework regions and/or one or more CDR's.

In accordance with further embodiments of the present invention there is provided a specific binding member which competes for binding to antigen with any specific binding member which both binds the antigen and comprises a specific binding member, VH and/or VL domain disclosed herein, or HCDR3 disclosed herein, or variant of any of these. Competition between binding members may be assayed easily *in vitro*, for example using ELISA and/or by tagging a specific reporter molecule to one

binding member which can be detected in the presence of other untagged binding member(s), to enable identification of specific binding members which bind the same epitope or an overlapping epitope.

Thus, a further embodiment of the present invention provides a specific binding member comprising a human antibody antigen-binding site which competes with a BAK502G9 antibody molecule, in particular BAK502G9 scFv and/or IgG4, for binding to IL-13. In further aspects the present invention provides a specific binding member comprising a human antibody antigen-binding site which competes with an antibody antigen-binding site for binding to IL-13, wherein the antibody antigen-binding site is composed of a VH domain and a VL domain, and wherein the VH and VL domains comprise a set of CDR's of the BAK278D6 lineage.

Various methods are available in the art for obtaining antibodies against IL-13 and which may compete with a BAK502G9 antibody molecule, an antibody molecule with a BAK502G9 set of CDR's, or an antibody molecule with a set of CDR's of BAK278D6 lineage, for binding to IL-13.

In a further aspect, the present invention provides a method of obtaining one or more specific binding members able to bind the antigen, the method including bringing into contact a library of specific binding members according to the invention and said antigen, and selecting one or more specific binding members of the library able to bind said antigen.

The library may be displayed on the surface of bacteriophage particles, each particle containing nucleic acid encoding the antibody VH variable domain displayed on its surface, and optionally also a displayed VL domain if present.

Following selection of specific binding members able to bind the antigen and displayed on bacteriophage particles, nucleic acid may be taken from a bacteriophage particle displaying a said selected specific binding member. Such nucleic acid may be used in subsequent production of a specific binding member or an antibody VH variable domain (optionally an antibody VL variable domain) by expression from nucleic acid with the sequence of nucleic acid taken from a bacteriophage particle displaying a said selected specific binding member.

An antibody VH variable domain with the amino acid sequence of an antibody VH variable domain of a said selected specific binding member may be provided in isolated form, as may a specific binding member comprising such a VH domain. Ability to bind IL-13 may be further tested, also ability to compete with BAK502G9 (e.g. in scFv format and/or IgG format, e.g. IgG4) for binding to IL-13. Ability to neutralise IL-13 may be tested, as discussed further below.

A specific binding member according to the present invention may bind IL-13 with the affinity of a BAK502G9 antibody molecule, e.g. scFv, or preferably BAK502G9 IgG4, or with an affinity that is better.

A specific binding member according to the present invention may neutralise IL-13 with the potency of a BAK502G9 antibody molecule, e.g. scFv, or preferably BAK502G9 IgG4, or with a potency that is better.

A specific binding member according to the present invention may neutralise naturally occurring IL-13 with the potency of a BAK502G9 antibody molecule, e.g. scFv, or preferably BAK502G9 IgG4, or with a potency that is better.

Binding affinity and neutralisation potency of different specific binding members can be compared under appropriate conditions.

The antibodies of the present invention have a number of advantages over existing commercial anti-IL-13 antibodies, in particular three commercial rodent anti-human IL-13 antibodies namely, JES10-5A2 (BioSource), B-B13 (Euroclone) and clone 321166 (R&D Systems). The potency of the antibodies of the present invention was compared with commercial antibodies JES10-A2 and B-B13. Clone 321166 was not evaluated as previous experiments revealed that this clone was considerably less potent than other known commercial antibodies.

The efficacy and use of the rodent commercial IL-13 antibodies in man is likely to be limited, because of their increased potential to induce immunogenic responses and therefore more rapid clearance from the body. Kinetic analysis of the antibodies of the present invention in non-human primates suggests that these antibodies have a clearance rate which is similar to that of other known human or humanised antibodies.

Antibodies provided by various embodiments of the present invention recognize non-human primate IL-13, including rhesus and cynomolgus IL-13. Determining efficacy and safety profiles of an antibody in non-human primates is extremely valuable as it provides a means for predicting the antibody's safety, pharmacokinetic and pharmacodynamic profile in humans.

Moreover, antibodies of various embodiments of the present invention further recognize the human IL-13 variant, Q130R, which is associated with asthma. Cross reactivity with variant IL-13 allows antibodies of the present invention and

compositions comprising antibodies of the present invention to be used for the treatment of patients with wild-type and variant IL-13.

A preferred embodiment of the present invention comprises antibodies that neutralise naturally occurring IL-13 with a potency that is equal to or better than the potency of a IL-13 antigen binding site formed by BAK502G9 VH domain (SEQ ID NO:15) and the BAK502G9 VL domain (SEQ ID NO: 16). For example, the inventors have demonstrated that representative clones such as BAK502G9, 1167F2 and 1183H4 are significantly more potent against naturally occurring IL-13 than known commercial antibodies (Figure 7).

In addition to antibody sequences, a specific binding member according to the present invention may comprise other amino acids, e.g. forming a peptide or polypeptide, such as a folded domain, or to impart to the molecule another functional characteristic in addition to ability to bind antigen. Specific binding members of the invention may carry a detectable label, or may be conjugated to a toxin or a targeting moiety or enzyme (e.g. via a peptidyl bond or linker).

In further embodiments, the invention provides an isolated nucleic acid which comprises a sequence encoding a specific binding member, VH domain and/or VL domains according to the present invention, and methods of preparing a specific binding member, a VH domain and/or a VL domain of the invention, which comprise expressing said nucleic acid under conditions to bring about production of said specific binding member, VH domain and/or VL domain, and recovering it.

Specific binding members according to the invention may be used in a method of treatment or diagnosis of the human or animal body, such as a method of treatment (which may include prophylactic treatment) of a disease or disorder in a human patient which comprises administering to said patient an effective amount of a specific binding member of the invention. Conditions treatable in accordance with the present invention include any in which IL-13 plays a role, especially asthma, atopic dermatitis, allergic rhinitis, fibrosis, chronic obstructive pulmonary disease, scleroderma, inflammatory bowel disease and Hodgkin's lymphoma. Further, the antibodies of the present invention may also be used in treating tumours and viral infections as these antibodies will inhibit IL-13 mediated immunosupression [64, 65].

A further embodiment of the present invention provides nucleic acid, generally isolated, encoding an antibody VH variable domain and/or VL variable domain disclosed herein.

Another embodiment of the present invention provides nucleic acid, generally isolated, encoding a VH CDR or VL CDR sequence disclosed herein, especially a VH CDR selected from SEQ ID NO's: 7, 8 and 9 or a VL CDR selected from SEQ ID NO's: 10, 11 and 12, most preferably BAK502G9 VH CDR3 (SEQ ID NO: 9). Nucleic acid encoding the BAK502G9 set of CDR's, nucleic acid encoding the BAK502G9 set of HCDR's and nucleic acid encoding the BAK502G9 set of LCDR's are also provided by the present invention, as are nucleic acids encoding individual CDR's, HCDR's, LCDR's and sets of CDR's, HCDR's, LCDR's of the BAK278D6 lineage.

A further embodiment provides a host cell transformed with nucleic acid of the invention.

A yet further embodiment provides a method of production of an antibody VH variable domain, the method including causing expression from encoding nucleic acid. Such a method may comprise culturing host cells under conditions for production of said antibody VH variable domain.

Analogous methods for production of VL variable domains and specific binding members comprising a VH and/or VL domain are provided as further embodiments of the present invention

A method of production may comprise a step of isolation and/or purification of the product.

A method of production may comprise formulating the product into a composition including at least one additional component, such as a pharmaceutically acceptable excipient.

These and other embodiments of the invention are described in further detail below.

TERMINOLOGY

Specific binding member

This describes a member of a pair of molecules which have binding specificity for one another. The members of a specific binding pair may be naturally derived or wholly or partially synthetically produced. One member of the pair of molecules has an area on its surface, or a cavity, which specifically binds to and is therefore complementary to a particular spatial and polar organisation of the other member of the pair of molecules. Thus the members of the pair have the property of binding specifically to each other. Examples of types of specific binding pairs are antigen-antibody, biotin-avidin, hormone-hormone receptor, receptor-ligand,

enzyme-substrate. The present invention is concerned with antigen-antibody type reactions.

Antibody molecule

This describes an immunoglobulin whether natural or partly or wholly synthetically produced. The term also covers any polypeptide or protein comprising an antibody binding domain. Antibody fragments which comprise an antigen binding domain are molecules such as Fab, scFv, Fv, dAb, Fd; and diabodies.

It is possible to take monoclonal and other antibodies and use techniques of recombinant DNA technology to produce other antibodies or chimeric molecules which retain the specificity of the original antibody. Such techniques may involve introducing DNA encoding the immunoglobulin variable region, or the complementarity determining regions (CDRs), of an antibody to the constant regions, or constant regions plus framework regions, of a different immunoglobulin. See, for instance, EP-A-184187, GB 2188638A or EP-A-239400, and a large body of subsequent literature. A hybridoma or other cell producing an antibody may be subject to genetic mutation or other changes, which may or may not alter the binding specificity of antibodies produced.

As antibodies can be modified in a number of ways, the term "antibody molecule" should be construed as covering any specific binding member or substance having an antibody antigen-binding domain with the required specificity. Thus, this term covers antibody fragments and derivatives, including any polypeptide comprising an immunoglobulin binding domain, whether natural or wholly or partially synthetic. Chimeric molecules comprising an immunoglobulin binding domain, or equivalent, fused to another polypeptide are therefore included. Cloning and expression of chimeric antibodies are

described in EP-A-0120694 and EP-A-0125023, and a large body of subsequent literature.

Further techniques available in the art of antibody engineering have made it possible to isolate human and humanised antibodies. For example, human hybridomas can be made as described by Kontermann et al [107]. Phage display, another established technique for generating specific binding members has been described in detail in many publications such as Kontermann et al [107] and WO92/01047 (discussed further below). Transgenic mice in which the mouse antibody genes are inactivated and functionally replaced with human antibody genes while leaving intact other components of the mouse immune system, can be used for isolating human antibodies to human antigens [108].

Synthetic antibody molecules may be created by expression from genes generated by means of oligonucleotides synthesized and assembled within suitable expression vectors, for example as described by Knappik et al. J. Mol. Biol. (2000) 296, 57-86 or Krebs et al. Journal of Immunological Methods 254 2001 67-84.

It has been shown that fragments of a whole antibody can perform the function of binding antigens. Examples of binding fragments are (i) the Fab fragment consisting of VL, VH, CL and CH1 domains; (ii) the Fd fragment consisting of the VH and CH1 domains; (iii) the Fv fragment consisting of the VL and VH domains of a single antibody; (iv) the dAb fragment (Ward, E.S. et al., Nature 341, 544-546 (1989), McCafferty et al (1990) Nature, 348, 552-554) which consists of a VH domain; (v) isolated CDR regions; (vi) F(ab')2 fragments, a bivalent fragment comprising two linked Fab fragments (vii) single chain Fv molecules (scFv), wherein a VH domain and a VL domain are linked by a peptide linker which allows the two domains to

associate to form an antigen binding site (Bird et al, Science, 242, 423-426, 1988; Huston et al, PNAS USA, 85, 5879-5883, 1988); (viii) bispecific single chain Fv dimers (PCT/US92/09965) and (ix) "diabodies", multivalent or multispecific fragments constructed by gene fusion (WO94/13804; P. Holliger et al, Proc. Natl. Acad. Sci. USA 90 6444-6448, 1993). Fv, scFv or diabody molecules may be stabilised by the incorporation of disulphide bridges linking the VH and VL domains (Y. Reiter et al, Nature Biotech, 14, 1239-1245, 1996). Minibodies comprising a scFv joined to a CH3 domain may also be made (S. Hu et al, Cancer Res., 56, 3055-3061, 1996).

Where bispecific antibodies are to be used, these may be conventional bispecific antibodies, which can be manufactured in a variety of ways (Holliger, P. and Winter G. Current Opinion Biotechnol. 4, 446-449 (1993)), e.g. prepared chemically or from hybrid hybridomas, or may be any of the bispecific antibody fragments mentioned above. Examples of bispecific antibodies include those of the BiTE™ technology in which the binding domains of two antibodies with different specificity can be used and directly linked via short flexible peptides. This combines two antibodies on a short single polypeptide chain. Diabodies and scFv can be constructed without an Fc region, using only variable domains, potentially reducing the effects of anti-idiotypic reaction.

Bispecific diabodies, as opposed to bispecific whole antibodies, may also be particularly useful because they can be readily constructed and expressed in *E.coli*. Diabodies (and many other polypeptides such as antibody fragments) of appropriate binding specificities can be readily selected using phage display (WO94/13804) from libraries. If one arm of the diabody is to be kept constant, for instance, with a

specificity directed against IL-13, then a library can be made where the other arm is varied and an antibody of appropriate specificity selected. Bispecific whole antibodies may be made by knobs-into-holes engineering (J. B. B. Ridgeway et al, Protein Eng., 9, 616-621, 1996).

Antigen-binding domain

This describes the part of an antibody molecule which comprises the area which specifically binds to and is complementary to part or all of an antigen. Where an antigen is large, an antibody may only bind to a particular part of the antigen, which part is termed an epitope. An antigen binding domain may be provided by one or more antibody variable domains (e.g. a so-called Fd antibody fragment consisting of a VH domain). Preferably, an antigen binding domain comprises an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH).

Specific

This may be used to refer to the situation in which one member of a specific binding pair will not show any significant binding to molecules other than its specific binding partner(s). The term is also applicable where e.g. an antigen binding domain is specific for a particular epitope which is carried by a number of antigens, in which case the specific binding member carrying the antigen binding domain will be able to bind to the various antigens carrying the epitope.

Comprise

This is generally used in the sense of include, that is to say permitting the presence of one or more features or components.

Isolated

This refers to the state in which specific binding members of the invention, or nucleic acid encoding such binding members, will generally be in accordance with the present invention. Isolated members and isolated nucleic acid will be free or substantially free of material with which they are naturally associated such as other polypeptides or nucleic acids with which they are found in their natural environment, or the environment in which they are prepared (e.g. cell culture) when such preparation is by recombinant DNA technology practised *in vitro* or *in vivo*. Members and nucleic acid may be formulated with diluents or adjuvants and still for practical purposes be isolated - for example the members will normally be mixed with gelatin or other carriers if used to coat microtitre plates for use in immunoassays, or will be mixed with pharmaceutically acceptable carriers or diluents when used in diagnosis or therapy. Specific binding members may be glycosylated, either naturally or by systems of heterologous eukaryotic cells (e.g. CHO or NS0 (ECACC 85110503) cells, or they may be (for example if produced by expression in a prokaryotic cell) unglycosylated.

Naturally occurring IL-13

This generally refers to a state in which the IL-13 protein or fragments thereof may occur. Naturally occurring IL-13 means IL-13 protein which is naturally produced by a cell, without prior introduction of encoding nucleic acid using recombinant technology. Thus, naturally occurring IL-13 may be as produced naturally by for example CD4+ T cells and/or as isolated from a mammal, e.g. human, non-human primate, rodent such as rat or mouse.

Recombinant IL-13

This refers to a state in which the IL-13 protein or fragments thereof may occur. Recombinant IL-13 means IL-13 protein or fragments thereof produced by recombinant DNA in a heterologous host. Recombinant IL-13 may differ from naturally occurring IL-13 by glycosylation.

Recombinant proteins expressed in prokaryotic bacterial expression systems are not glycosylated while those expressed in eukaryotic systems such as mammalian or insect cells are glycosylated. Proteins expressed in insect cells however differ in glycosylation from proteins expressed in mammalian cells.

By "substantially as set out" it is meant that the relevant CDR or VH or VL domain of the invention will be either identical or highly similar to the specified regions of which the sequence is set out herein. By "highly similar" it is contemplated that from 1 to 5, preferably from 1 to 4 such as 1 to 3 or 1 or 2, or 3 or 4, amino acid substitutions may be made in the CDR and/or VH or VL domain.

The structure for carrying a CDR or a set of CDR's of the invention will generally be of an antibody heavy or light chain sequence or substantial portion thereof in which the CDR or set of CDR's is located at a location corresponding to the CDR or set of CDR's of naturally occurring VH and VL antibody variable domains encoded by rearranged immunoglobulin genes. The structures and locations of immunoglobulin variable domains may be determined by reference to (Kabat, E.A. et al, Sequences of Proteins of Immunological Interest. 4th Edition. US Department of Health and Human Services. 1987, and updates thereof, now available on the Internet

(http://immuno.bme.nwu.edu or find "Kabat" using any search engine).

CDR's can also be carried by other scaffolds such as fibronectin or cytochrome B [115, 116].

Preferably, a CDR amino acid sequence substantially as set out herein is carried as a CDR in a human variable domain or a substantial portion thereof. The HCDR3 sequences substantially as set out herein represent preferred embodiments of the present invention and it is preferred that each of these is carried as a HCDR3 in a human heavy chain variable domain or a substantial portion thereof.

Variable domains employed in the invention may be obtained from any germ-line or rearranged human variable domain, or may be a synthetic variable domain based on consensus sequences of known human variable domains. A CDR sequence of the invention (e.g. CDR3) may be introduced into a repertoire of variable domains lacking a CDR (e.g. CDR3), using recombinant DNA technology.

For example, Marks *et al* (*Bio/Technology*, 1992, 10:779-783) describe methods of producing repertoires of antibody variable domains in which consensus primers directed at or adjacent to the 5' end of the variable domain area are used in conjunction with consensus primers to the third framework region of human VH genes to provide a repertoire of VH variable domains lacking a CDR3. Marks *et al* further describe how this repertoire may be combined with a CDR3 of a particular antibody. Using analogous techniques, the CDR3-derived sequences of the present invention may be shuffled with repertoires of VH or VL domains lacking a CDR3, and the shuffled complete VH or VL domains combined with a cognate VL

or VH domain to provide specific binding members of the invention. The repertoire may then be displayed in a suitable host system such as the phage display system of WO92/01047 or any of a subsequent large body of literature, including Kay, B.K., Winter, J., and McCafferty, J. (1996) Phage Display of Peptides and Proteins: A Laboratory Manual, San Diego: Academic Press, so that suitable specific binding members may be selected. A repertoire may consist of from anything from 10^4 individual members upwards, for example from 10^6 to 10^8 or 10^{10} members. Other suitable host systems include yeast display, bacterial display, T7 display, ribosome display and so on. For a review of ribosome display for see Lowe D and Jermutus L, 2004, Curr. Pharm, Biotech, 517-27, also WO92/01047.

Analogous shuffling or combinatorial techniques are also disclosed by Stemmer (*Nature*, 1994, 370:389-391), who describes the technique in relation to a β-lactamase gene but observes that the approach may be used for the generation of antibodies.

A further alternative is to generate novel VH or VL regions carrying CDR-derived sequences of the invention using random mutagenesis of one or more selected VH and/or VL genes to generate mutations within the entire variable domain. Such a technique is described by Gram *et al* (1992, *Proc. Natl. Acad. Sci., USA*, 89:3576-3580), who used error-prone PCR. In preferred embodiments one or two amino acid substitutions are made within a set of HCDR's and/or LCDR's.

Another method which may be used is to direct mutagenesis to CDR regions of VH or VL genes. Such techniques are disclosed by Barbas *et al*, (1994, *Proc. Natl. Acad. Sci., USA*, 91:3809-3813) and Schier *et al* (1996, *J. Mol. Biol.* 263:551-567).

All the above described techniques are known as such in the art and in themselves do not form part of the present invention. The skilled person will be able to use such techniques to provide specific binding members of the invention using routine methodology in the art.

A further aspect of the invention provides a method for obtaining an antibody antigen binding domain specific for IL-13 antigen, the method comprising providing by way of addition, deletion, substitution or insertion of one or more amino acids in the amino acid sequence of a VH domain set out herein a VH domain which is an amino acid sequence variant of the VH domain, optionally combining the VH domain thus provided with one or more VL domains, and testing the VH domain or VH/VL combination or combinations to identify a specific binding member or an antibody antigen binding domain specific for IL-13 antigen and optionally with one or more preferred properties, preferably ability to neutralise IL-13 activity. Said VL domain may have an amino acid sequence which is substantially as set out herein.

An analogous method may be employed in which one or more sequence variants of a VL domain disclosed herein are combined with one or more VH domains.

In a preferred embodiment, BAK502G9 VH domain (SEQ ID NO: 15) may be subject to mutation to provide one or more VH domain amino acid sequence variants, and/or BAK502G9 VL (SEQ ID NO: 16).

A further aspect of the invention provides a method of preparing a specific binding member specific for IL-13 antigen, which method comprises:

(a) providing a starting repertoire of nucleic acids encoding a VH domain which either include a CDR3 to be replaced or lack a CDR3 encoding region;

(b) combining said repertoire with a donor nucleic acid encoding an amino acid sequence substantially as set out herein for a VH CDR3 such that said donor nucleic acid is inserted into the CDR3 region in the repertoire, so as to provide a product repertoire of nucleic acids encoding a VH domain;

(c) expressing the nucleic acids of said product repertoire;

(d) selecting a specific binding member specific for a IL-13; and

(e) recovering said specific binding member or nucleic acid encoding it.

Again, an analogous method may be employed in which a VL CDR3 of the invention is combined with a repertoire of nucleic acids encoding a VL domain which either include a CDR3 to be replaced or lack a CDR3 encoding region.

Similarly, one or more, or all three CDRs may be grafted into a repertoire of VH or VL domains which are then screened for a specific binding member or specific binding members specific for IL-13.

In a preferred embodiment, one or more of BAK502G9 HCDR1 (SEQ ID NO: 7), HCDR2 (SEQ ID NO: 8) and HCDR3 (SEQ ID NO: 9), or the BAK502G9 set of HCDR's, may be employed, and/or one or more of BAK502G9 LCDR1 (SEQ ID NO: 10), LCDR2 (SEQ ID NO: 11), or the BAK502G9 set of LCDR's.

A substantial portion of an immunoglobulin variable domain will comprise at least the three CDR regions, together with

their intervening framework regions. Preferably, the portion will also include at least about 50% of either or both of the first and fourth framework regions, the 50% being the C-terminal 50% of the first framework region and the N-terminal 50% of the fourth framework region. Additional residues at the N-terminal or C-terminal end of the substantial part of the variable domain may be those not normally associated with naturally occurring variable domain regions. For example, construction of specific binding members of the present invention made by recombinant DNA techniques may result in the introduction of N- or C-terminal residues encoded by linkers introduced to facilitate cloning or other manipulation steps. Other manipulation steps include the introduction of linkers to join variable domains of the invention to further protein sequences including immunoglobulin heavy chains, other variable domains (for example in the production of diabodies) or protein labels as discussed in more detail elsewhere herein.

Although in a preferred aspect of the invention specific binding members comprising a pair of VH and VL domains are preferred, single binding domains based on either VH or VL domain sequences form further aspects of the invention. It is known that single immunoglobulin domains, especially VH domains, are capable of binding target antigens in a specific manner.

In the case of either of the single specific binding domains, these domains may be used to screen for complementary domains capable of forming a two-domain specific binding member able to bind IL-13.

This may be achieved by phage display screening methods using the so-called hierarchical dual combinatorial approach as

disclosed in WO92/01047, in which an individual colony containing either an H or L chain clone is used to infect a complete library of clones encoding the other chain (L or H) and the resulting two-chain specific binding member is selected in accordance with phage display techniques such as those described in that reference. This technique is also disclosed in Marks *et al, ibid.*

Specific binding members of the present invention may further comprise antibody constant regions or parts thereof. For example, a VL domain may be attached at its C-terminal end to antibody light chain constant domains including human Cκ or Cλ chains, preferably Cλ chains. Similarly, a specific binding member based on a VH domain may be attached at its C-terminal end to all or part (e.g. a CH1 domain) of an immunoglobulin heavy chain derived from any antibody isotype, e.g. IgG, IgA, IgE and IgM and any of the isotype sub-classes, particularly IgG1 and IgG4. IgG4 is preferred. IgG4 is preferred because it does not bind complement and does not create effector functions. Any synthetic or other constant region variant that has these properties and stabilizes variable regions is also preferred for use in embodiments of the present invention.

Specific binding members of the invention may be labelled with a detectable or functional label. Detectable labels include radiolabels such as ^{131}I or ^{99}Tc, which may be attached to antibodies of the invention using conventional chemistry known in the art of antibody imaging. Labels also include enzyme labels such as horseradish peroxidase. Labels further include chemical moieties such as biotin which may be detected via binding to a specific cognate detectable moiety, e.g. labelled avidin.

Specific binding members of the present invention are designed to be used in methods of diagnosis or treatment in human or animal subjects, preferably human.

Accordingly, further aspects of the invention provide methods of treatment comprising administration of a specific binding member as provided, pharmaceutical compositions comprising such a specific binding member, and use of such a specific binding member in the manufacture of a medicament for administration, for example in a method of making a medicament or pharmaceutical composition comprising formulating the specific binding member with a pharmaceutically acceptable excipient.

Clinical indications in which an anti-IL-13 antibody may be used to provide therapeutic benefit include asthma, atopic dermatitis, allergic rhinitis, fibrosis, chronic obstructive pulmonary disease, inflammatory bowel disease, scleroderma and Hodgkin's lymphoma . As already explained, anti-IL-13 treatment is effective for all these diseases.

Anti-IL-13 treatment may be given orally, by injection (for example, subcutaneously, intravenously, intraperitoneal or intramuscularly), by inhalation, or topically (for example intraocular, intranasal, rectal, into wounds, on skin). The route of administration can be determined by the physicochemical characteristics of the treatment, by special considerations for the disease or by the requirement to optimise efficacy or to minimise side-effects.

It is envisaged that anti-IL-13 treatment will not be restricted to use in the clinic. Therefore, subcutaneous injection using a needle free device is also preferred.

Combination treatments may be used to provide significant synergistic effects, particularly the combination of an anti-IL-13 specific binding member with one or more other drugs. A specific binding member according to the present invention may be provided in combination or addition to short or long acting beta agonists, corticosteroids, cromoglycate, leukotriene (receptor) antagonists, methyl xanthines and their derivatives, IL-4 inhibitors, muscarinic receptor antagonists, IgE inhibitors, histaminic inhibitors, IL-5 inhibitors, eotaxin/CCR3 inhibitors, PDE4 inhibitors, TGF-beta antagonists, interferon-gamma, perfenidone, chemotherapeutic agents and immunotherapeutic agents.

Combination treatment with one or more short or long acting beta agonists, corticosteroids, cromoglycate, leukotriene (receptor) antagonists, xanthines, IgE inhibitors, IL-4 inhibitors, IL-5 inhibitors, eotaxin/CCR3 inhibitors, PDE4 inhibitors may be employed for treatment of asthma. Antibodies of the present invention can also be used in combination with corticosteroids, anti-metabolites, antagonists of TGF-beta and its downstream signalling pathway, for treatment of fibrosis. Combination therapy of these antibodies with PDE4 inhibitors, xanthines and their derivatives, muscarinic receptor antagonists, short and long beta antagonists can be useful for treating chronic obstructive pulmonary disease. Similar consideration of combinations apply to the use of anti-IL-13 treatment for atopic dermatitis, allergic rhinitis, chronic obstructive pulmonary disease, inflammatory bowel disease, scleroderma and Hodgkin's lymphoma.

In accordance with the present invention, compositions provided may be administered to individuals. Administration is preferably in a "therapeutically effective amount", this being sufficient to show benefit to a patient. Such benefit

may be at least amelioration of at least one symptom. The actual amount administered, and rate and time-course of administration, will depend on the nature and severity of what is being treated. Prescription of treatment, e.g. decisions on dosage etc, is within the responsibility of general practitioners and other medical doctors. Appropriate doses of antibody are well known in the art; see Ledermann J.A. et al. (1991) Int. J. Cancer 47: 659-664; Bagshawe K.D. et al. (1991) Antibody, Immunoconjugates and Radiopharmaceuticals 4: 915-922.

The precise dose will depend upon a number of factors, including whether the antibody is for diagnosis or for treatment, the size and location of the area to be treated, the precise nature of the antibody (e.g. whole antibody, fragment or diabody), and the nature of any detectable label or other molecule attached to the antibody. A typical antibody dose will be in the range 100µg to 1 gm for systemic applications, and 1µg to 1mg for topical applications. Typically, the antibody will be a whole antibody, preferably the IgG4 isotype. This is a dose for a single treatment of an adult patient, which may be proportionally adjusted for children and infants, and also adjusted for other antibody formats in proportion to molecular weight. Treatments may be repeated at daily, twice-weekly, weekly or monthly intervals, at the discretion of the physician. In preferred embodiments of the present invention, treatment is periodic, and the period between administrations is about two weeks or more, preferably about three weeks or more, more preferably about four weeks or more, or about once a month.

Specific binding members of the present invention will usually be administered in the form of a pharmaceutical composition,

which may comprise at least one component in addition to the specific binding member.

Thus pharmaceutical compositions according to the present invention, and for use in accordance with the present invention, may comprise, in addition to active ingredient, a pharmaceutically acceptable excipient, carrier, buffer, stabiliser or other materials well known to those skilled in the art. Such materials should be non-toxic and should not interfere with the efficacy of the active ingredient. The precise nature of the carrier or other material will depend on the route of administration, which may be oral, or by injection, e.g. intravenous.

Pharmaceutical compositions for oral administration may be in tablet, capsule, powder or liquid form. A tablet may comprise a solid carrier such as gelatin or an adjuvant. Liquid pharmaceutical compositions generally comprise a liquid carrier such as water, petroleum, animal or vegetable oils, mineral oil or synthetic oil. Physiological saline solution, dextrose or other saccharide solution or glycols such as ethylene glycol, propylene glycol or polyethylene glycol may be included.

For intravenous injection, or injection at the site of affliction, the active ingredient will be in the form of a parenterally acceptable aqueous solution which is pyrogen-free and has suitable pH, isotonicity and stability. Those of relevant skill in the art are well able to prepare suitable solutions using, for example, isotonic vehicles such as Sodium Chloride Injection, Ringer's Injection, Lactated Ringer's Injection. Preservatives, stabilisers, buffers, antioxidants and/or other additives may be included, as required.

A composition may be administered alone or in combination with other treatments, either simultaneously or sequentially dependent upon the condition to be treated.

Specific binding members of the present invention may be formulated in liquid or solid forms depending on the physicochemical properties of the molecule and the route of delivery. Formulations may include excipients, or combinations of excipients, for example: sugars, amino acids and surfactants. Liquid formulations may include a wide range of antibody concentrations and pH. Solid formulations may be produced by lyophilisation, spray drying, or drying by supercritical fluid technology, for example. Formulations of anti-IL-13 will depend upon the intended route of delivery: for example, formulations for pulmonary delivery may consist of particles with physical properties that ensure penetration into the deep lung upon inhalation; topical formulations may include viscosity modifying agents, which prolong the time that the drug is resident at the site of action.

The present invention provides a method comprising causing or allowing binding of a specific binding member as provided herein to IL-13. As noted, such binding may take place *in vivo*, e.g. following administration of a specific binding member, or nucleic acid encoding a specific binding member, or it may take place *in vitro*, for example in ELISA, Western blotting, immunocytochemistry, immuno-precipitation, affinity chromatography, or cell based assays such as a TF-1 assay.

The amount of binding of specific binding member to IL-13 may be determined. Quantitation may be related to the amount of the antigen in a test sample, which may be of diagnostic interest.

A kit comprising a specific binding member or antibody molecule according to any aspect or embodiment of the present invention is also provided as an aspect of the present invention. In a kit of the invention, the specific binding member or antibody molecule may be labelled to allow its reactivity in a sample to be determined, e.g. as described further below. Components of a kit are generally sterile and in sealed vials or other containers. Kits may be employed in diagnostic analysis or other methods for which antibody molecules are useful. A kit may contain instructions for use of the components in a method, e.g. a method in accordance with the present invention. Ancillary materials to assist in or to enable performing such a method may be included within a kit of the invention.

The reactivities of antibodies in a sample may be determined by any appropriate means. Radioimmunoassay (RIA) is one possibility. Radioactive labelled antigen is mixed with unlabelled antigen (the test sample) and allowed to bind to the antibody. Bound antigen is physically separated from unbound antigen and the amount of radioactive antigen bound to the antibody determined. The more antigen there is in the test sample the less radioactive antigen will bind to the antibody. A competitive binding assay may also be used with non-radioactive antigen, using antigen or an analogue linked to a reporter molecule. The reporter molecule may be a fluorochrome, phosphor or laser dye with spectrally isolated absorption or emission characteristics. Suitable fluorochromes include fluorescein, rhodamine, phycoerythrin and Texas Red. Suitable chromogenic dyes include diaminobenzidine.

Other reporters include macromolecular colloidal particles or particulate material such as latex beads that are coloured,

magnetic or paramagnetic, and biologically or chemically active agents that can directly or indirectly cause detectable signals to be visually observed, electronically detected or otherwise recorded. These molecules may be enzymes which catalyse reactions that develop or change colours or cause changes in electrical properties, for example. They may be molecularly excitable, such that electronic transitions between energy states result in characteristic spectral absorptions or emissions. They may include chemical entities used in conjunction with biosensors. Biotin/avidin or biotin/streptavidin and alkaline phosphatase detection systems may be employed.

The signals generated by individual antibody-reporter conjugates may be used to derive quantifiable absolute or relative data of the relevant antibody binding in samples (normal and test).

The present invention also provides the use of a specific binding member as above for measuring antigen levels in a competition assay, that is to say a method of measuring the level of antigen in a sample by employing a specific binding member as provided by the present invention in a competition assay. This may be where the physical separation of bound from unbound antigen is not required. Linking a reporter molecule to the specific binding member so that a physical or optical change occurs on binding is one possibility. The reporter molecule may directly or indirectly generate detectable, and preferably measurable, signals. The linkage of reporter molecules may be directly or indirectly, covalently, e.g. via a peptide bond or non-covalently. Linkage via a peptide bond may be as a result of recombinant expression of a gene fusion encoding antibody and reporter molecule.

The present invention also provides for measuring levels of antigen directly, by employing a specific binding member according to the invention for example in a biosensor system.

The mode of determining binding is not a feature of the present invention and those skilled in the art are able to choose a suitable mode according to their preference and general knowledge.

As noted, in various aspects and embodiments, the present invention extends to a specific binding member which competes for binding to IL-13 with any specific binding member defined herein, e.g. BAK502G9 IgG4. Competition between binding members may be assayed easily *in vitro*, for example by tagging a specific reporter molecule to one binding member which can be detected in the presence of other untagged binding member(s), to enable identification of specific binding members which bind the same epitope or an overlapping epitope.

Competition may be determined for example using ELISA in which IL-13 is immobilised to a plate and a first tagged binding member along with one or more other untagged binding members is added to the plate. Presence of an untagged binding member that competes with the tagged binding member is observed by a decrease in the signal emitted by the tagged binding member.

In testing for competition a peptide fragment of the antigen may be employed, especially a peptide including an epitope of interest. A peptide having the epitope sequence plus one or more amino acids at either end may be used. Such a peptide may be said to "consist essentially" of the specified sequence. Specific binding members according to the present invention may be such that their binding for antigen is

inhibited by a peptide with or including the sequence given. In testing for this, a peptide with either sequence plus one or more amino acids may be used.

Specific binding members which bind a specific peptide may be isolated for example from a phage display library by panning with the peptide(s).

The present invention further provides an isolated nucleic acid encoding a specific binding member of the present invention. Nucleic acid may include DNA and/or RNA. In a preferred aspect, the present invention provides a nucleic acid which codes for a CDR or set of CDR's or VH domain or VL domain or antibody antigen-binding site or antibody molecule, e.g. scFv or IgG4, of the invention as defined above.

The present invention also provides constructs in the form of plasmids, vectors, transcription or expression cassettes which comprise at least one polynucleotide as above.

The present invention also provides a recombinant host cell which comprises one or more constructs as above. A nucleic acid encoding any CDR or set of CDR's or VH domain or VL domain or antibody antigen-binding site or antibody molecule, e.g. scFv or IgG4 as provided, itself forms an aspect of the present invention, as does a method of production of the encoded product, which method comprises expression from encoding nucleic acid therefor. Expression may conveniently be achieved by culturing under appropriate conditions recombinant host cells containing the nucleic acid. Following production by expression a VH or VL domain, or specific binding member may be isolated and/or purified using any suitable technique, then used as appropriate.

Specific binding members, VH and/or VL domains, and encoding nucleic acid molecules and vectors according to the present invention may be provided isolated and/or purified, e.g. from their natural environment, in substantially pure or homogeneous form, or, in the case of nucleic acid, free or substantially free of nucleic acid or genes origin other than the sequence encoding a polypeptide with the required function. Nucleic acid according to the present invention may comprise DNA or RNA and may be wholly or partially synthetic. Reference to a nucleotide sequence as set out herein encompasses a DNA molecule with the specified sequence, and encompasses a RNA molecule with the specified sequence in which U is substituted for T, unless context requires otherwise.

Systems for cloning and expression of a polypeptide in a variety of different host cells are well known. Suitable host cells include bacteria, mammalian cells, plant cells, yeast and baculovirus systems and transgenic plants and animals. Mammalian cell lines available in the art for expression of a heterologous polypeptide include Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney cells, NS0 mouse melanoma cells, YB2/0 rat myeloma cells, human embryonic kidney cells, human embryonic retina cells and many others. A common, preferred bacterial host is *E. coli*.

The expression of antibodies and antibody fragments in prokaryotic cells such as *E. coli* is well established in the art. For a review, see for example Plückthun, A. Bio/Technology 9: 545-551 (1991). Expression in eukaryotic cells in culture is also available to those skilled in the art as an option for production of a specific binding memberfor example Chadd HE and Chamow SM (2001) 110 Current Opinion in

Biotechnology 12: 188-194, Andersen DC and Krummen L (2002) Current Opinion in Biotechnology 13: 117, Larrick JW and Thomas DW (2001) Current opinion in Biotechnology 12:411-418.

Suitable vectors can be chosen or constructed, containing appropriate regulatory sequences, including promoter sequences, terminator sequences, polyadenylation sequences, enhancer sequences, marker genes and other sequences as appropriate. Vectors may be plasmids, viral e.g. 'phage, or phagemid, as appropriate. For further details see, for example, *Molecular Cloning: a Laboratory Manual*: 3rd edition, Sambrook and Russell, 2001, Cold Spring Harbor Laboratory Press. Many known techniques and protocols for manipulation of nucleic acid, for example in preparation of nucleic acid constructs, mutagenesis, sequencing, introduction of DNA into cells and gene expression, and analysis of proteins, are described in detail in *Current Protocols in Molecular Biology*, Second Edition, Ausubel et al. eds., John Wiley & Sons, 1988, *Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology*, Ausubel et al. eds., John Wiley & Sons, 4th edition 1999. The disclosures of Sambrook et al. and Ausubel et al. (both) are incorporated herein by reference.

Thus, a further aspect of the present invention provides a host cell containing nucleic acid as disclosed herein. Such a host cell may be *in vitro* and may be in culture. Such a host cell may be *in vivo*. *In vivo* presence of the host cell may allow intracellular expression of the specific binding members of the present invention as "intrabodies" or intracellular antibodies. Intrabodies may be used for gene therapy [112].

A still further aspect provides a method comprising introducing such nucleic acid into a host cell. The

introduction may employ any available technique. For eukaryotic cells, suitable techniques may include calcium phosphate transfection, DEAE-Dextran, electroporation, liposome-mediated transfection and transduction using retrovirus or other virus, e.g. vaccinia or, for insect cells, baculovirus. Introducing nucleic acid in the host cell, in particular a eukaryotic cell may use a viral or a plasmid based system. The plasmid system may be maintained episomally or may incorporated into the host cell or into an artificial chromosome [110,111]. Incorporation may be either by random or targeted integration of one or more copies at single or multiple loci. For bacterial cells, suitable techniques may include calcium chloride transformation, electroporation and transfection using bacteriophage.

The introduction may be followed by causing or allowing expression from the nucleic acid, e.g. by culturing host cells under conditions for expression of the gene.

In one embodiment, the nucleic acid of the invention is integrated into the genome (e.g. chromosome) of the host cell. Integration may be promoted by inclusion of sequences which promote recombination with the genome, in accordance with standard techniques.

The present invention also provides a method which comprises using a construct as stated above in an expression system in order to express a specific binding member or polypeptide as above.

Aspects and embodiments of the present invention will now be illustrated by way of example with reference to the following experimentation.

EXAMPLE 1

Isolation of anti-IL-13 scFv

ScFv antibody repertoire

A large single chain Fv (scFv) human antibody library derived from spleen lymphocytes from 20 donors and cloned into a phagemid vector was used for selections [66].

Selection of scFv

ScFv which recognised IL-13 were isolated from phage display libraries in a series of repeated selection cycles on recombinant bacterially derived human or murine IL-13 (Peprotech) essentially as described in [67]. In brief, following incubation with the library, the immobilised antigen, which had been pre-coupled to paramagnetic beads, and bound phage were recovered by magnetic separation whilst unbound phage were washed away. Bound phage was then rescued as described by Vaughan et al [67] and the selection process repeated. Different solid surfaces and capture methods were used at different rounds of selection to reduce non-specific binding. Antigen was either covalently coupled to beads (Dynabeads M-270 carboxylic acid) or modified by biotinylation prior to secondary capture by streptavidin-coated beads (Dynabeads M-280) according to manufacturer's protocols (Dynal). A representative proportion of clones from the output of selection rounds were subjected to DNA sequencing as described in Vaughan et al [67] and Osbourn et al [70]. Unique clones were assessed for their ability to neutralise IL-13 as purified scFv preparations in IL-13 dependent cell proliferation assays.

Ribosome display libraries were created and screened for scFv that specifically recognised recombinant, bacterially derived human or murine IL-13 (Peprotech), essentially as described in

Hanes *et al* [113]. Initially the BAK278D6 lead clone from the initial selections was converted to ribosome display format, and this template was subsequently used for library creation. On the DNA level, a T7 promoter was added at the 5'-end for efficient transcription to mRNA. On the mRNA level, the construct contained a prokaryotic ribosome-binding site (Shine-Dalgarno sequence). At the 3' end of the single chain, the stop codon was removed and a portion of gIII (gene III) was added to act as a spacer [113].

Ribosome display libraries derived from BAK278D6 were created by mutagenesis of antibody complementarity determining regions (CDRs) where PCR reactions were performed with non-proof reading *Taq* polymerase. Affinity-based selections were performed whereby, following incubation with the library, the biotinylated human-IL-13 was captured by streptavidin-coated paramagnetic beads (Dynal M280) and bound tertiary complexes (mRNA-ribosome-scFv-IL-13) were recovered by magnetic separation whilst unbound complexes were washed away. The mRNA encoding the bound scFvs were then recovered by RT-PCR as described in Hanes *et al* [113] and the selection process repeated with decreasing concentrations (100nM - 100pM over 5 rounds) of biotinylated human IL-13 present during the selection.

Error-prone PCR was also used to further increase library size. Three intensities of error were employed (2.0, 3.5 and 7.2 mutations per 1,000 bp after a standard PCR reaction, as described in manufacturer's protocol (Clontech)) during the selection regime. Initial error prone PCR reactions took place before round one selections commenced at 100nM. A subsequent round of error prone PCR was performed before round three selections at 10nM biotinylated human-IL-13. As above, a representative proportion of clones from the output of

selection rounds were subjected to DNA sequencing as described in Vaughan et al [67] and Osbourn et al [70]. Unique clones were assessed for their ability to neutralise IL-13 as purified scFv preparations in IL-13 dependent cell proliferation assays.

EXAMPLE 2

Neutralisation potency of anti-IL-13 scFv in the IL-13 dependent TF-1 cell proliferation assay

The neutralisation potency of purified scFv preparations against human and murine IL-13 bioactivity was assessed using TF-1 cell proliferation assay. Purified scFv preparations were prepared as described in Example 3 of WO01/66754. Protein concentrations of purified scFv preparations were determined using the BCA method (Pierce). TF-1 is a human premyeloid cell line established from a patient with erythroleukemia [68]. The TF-1 cell line is factor dependent for survival and proliferation. In this respect TF-1 cells responded to either human or murine IL-13 [69] and were maintained in media containing human GM-CSF (4 ng/ml, R&D Systems). Inhibition of IL-13 dependent proliferation was determined by measuring the reduction in incorporation of tritiated thymidine into the newly synthesized DNA of dividing cells.

TF-1 cell assay protocol

TF-1 cells were obtained from R&D Systems and maintained according to supplied protocols. Assay media comprised RPMI-1640 with GLUTAMAX I (Invitrogen) containing 5% foetal bovine serum (JRH) and 1% sodium pyruvate (Sigma). Prior to each assay, TF-1 cells were pelleted by centrifugation at 300 x *g* for 5 mins, the media removed by aspiration and the cells resuspended in assay media. This process was repeated twice with cells resuspended at a final concentration of 10^5 cells/ml

in assay media. Test solutions of antibody (in triplicate) were diluted to the desired concentration in assay media. An irrelevant antibody not directed at IL-13 was used as a negative control. Recombinant bacterially derived human or murine IL-13 (Peprotech) was added to a final concentration of 50 ng/ml when mixed with the appropriate test antibody in a total volume of 100 µl/well in a 96 well assay plate. The concentration of IL-13 used in the assay was selected as the dose that at final assay concentration gave approximately 80% of the maximal proliferative response. All samples were incubated for 30 minutes at room temperature. 100 µl of resuspended cells were then added to each assay point to give a total assay volume of 200 µl/well. Assay plates were incubated for 72 hours at 37°C under 5% CO_2. 25 µl of tritiated thymidine (10 µCi/ml, NEN) was then added to each assay point and assay plates were returned to the incubator for a further 4 hours. Cells were harvested on glass fibre filter plates (Perkin Elmer) using a cell harvester. Thymidine incorporation was determined using a Packard TopCount microplate liquid scintillation counter. Data were analysed using Graphpad Prism software.

Results

Despite alternating selection cycles between human and murine antigen no cross-reactive neutralising antibodies were obtained. Two distinct anti-human and one anti-murine IL-13 neutralising scFvs were obtained from selections. BAK278D6 (VH SEQ ID NO: 13; VL SEQ ID NO: 14) and BAK167A11 (VH SEQ ID NO: 23; VL SEQ ID NO: 24) recognised human IL-13 whilst BAK209B11 (VH SEQ ID NO: 25; VL SEQ ID NO: 26) recognised murine IL-13. BAK278D6 (Figure 2) and BAK167A11 (Figure 1) as scFv neutralised 25 ng/ml human IL-13 with an IC_{50} of 44nM and 111nM

respectively. BAK209B11 (Figure 3) as a scFv neutralised 25 ng/ml murine IL-13 with an IC_{50} of 185nM.

EXAMPLE 3

Neutralisation potency of lead clones from targeted optimisation of heavy chain CDR3 of parental clones in the IL-13 dependent TF-1 cell proliferation assay

Osbourn et al. [70] have demonstrated that targeted mutagenesis of residues within heavy chain CDR3 can significantly improve the affinity of antibodies. Selections were performed as described in Example 1, on scFv repertoires in which residues within the heavy chain CDR3 of BAK278D6 (SEQ ID NO: 6) BAK167A11 (SEQ ID NO: 57) had been randomised by mutagenesis. Unique clones from the selection output were identified by DNA sequencing and their neutralising potency assessed as scFv in the TF-1 cell proliferation assay, as described in Example 2.

Results

Significant gains in potency were achieved for both lineages. The most potent clones from the BAK167A11 lineage were BAK615E3, BAK612B5 and BAK582F7 which as scFv had IC_{50} of 3nM (Figure 1), 6.6nM, 6.65nM respectively against 25ng/ml human IL-13 in TF-1 cell proliferation assay. From the BAK278D6 lineage, the most potent clone was BAK502G9, which as scFv had IC_{50} of 8nM against 25 ng/ml human IL-13 in the TF-1 cell proliferation assay (Figure 2).

EXAMPLE 4

Neutralisation potency of BAK167A11 and BAK278D6 lineages against non-human primate IL-13 and an IL-13 variant associated with asthma in the TF-1 factor dependent cell proliferation assay

Neither of the BAK167A11 and BAK278D6 human IL-13 neutralising lineages were murine cross-reactive. The inventors therefore decided on the following criteria for the lineage selected for further optimisation and clinical development: should preferably be cross-reactive with non-human primate IL-13 and should recognise a variant of IL-13, in which arginine at amino acid at position 130 is substituted for by glutamine (Q130R). This variant has been genetically associated with asthma and other allergic diseases [37, 39, 41, 71]. Cross-reactivity was determined by the ability of purified scFv preparations to bind non-human primate IL-13 and IL-13 variant by surface plasmon resonance (BIAcore) analysis. Functional activity was determined using the TF-1 cell proliferation assay.

Production of wild-type, variant and non-human primate IL-13

A cDNA for wild-type human IL-13 was obtained from InvivoGen and modified by site-directed mutagenesis (Stratagene Quikchange® kit) to yield a cDNA encoding variant IL-13. The coding sequence for both rhesus and cynomolgus monkey IL-13 was obtained by PCR on genomic DNA template using degenerate primers based on the human IL-13 sequence. Both non-human primate (rhesus and cynomolgus) sequences were identical to each other but differed from human IL-13 by seven amino acids (Figure 19). Recombinant wild type, variant and non-human primate IL-13 were subsequently expressed using the baculovirus expression system (Invitrogen). Expression constructs added a carboxyl terminus affinity tag to the expressed protein that allowed purification from insect cell conditioned media to near homogeneity.

Qualitative binding assay using BIAcore

The binding affinity of purified scFv preparations to non-

human primate, variant and wild type IL-13 was determined by surface plasmon resonance measurements using a BIAcore 2000 Biosensor (BIAcore AB) as described in Karlsson et al [72]. In brief, IL-13 was coupled to CM5 sensorchips using an amine coupling kit (BIAcore) at a surface density of approximately 200Ru and three concentrations of test scFv (approximately 350nM, 175nM and 88nM) in HBS-EP buffer passed over the sensor chip surface. The resulting sensorgrams were evaluated using BIA evaluation 3.1 software to provide relative binding data.

TF-1 assay protocol

The assay was performed essentially as described in Example 2 with the following modifications: non-human primate IL-13, human variant IL-13 (Q130R) and wild type human IL-13 were used at concentrations of 50 ng/ml, 25 ng/ml and 25 ng/ml respectively.

Results

BIAcore binding assay data suggested that BAK278D6 but not BAK167A11 lineage had the required cross-reactivity profile for further therapeutic development (Table 2). This finding was supported by bioassay data demonstrating that BAK278D6 (Figure 4) and BAK502G9 (Figure 6) were able to neutralise human IL-13, the human IL-13 (Q130R) variant and non-human primate IL-13 in the TF-1 cell proliferation assay with near equivalent potency. In contrast, although BAK615E3 (VH SEQ ID NO: 33; VL SEQ ID NO: 34) had a significantly increased potency against human IL-13 over its parent BAK167A11 (VH SEQ ID NO: 23; VL SEQ ID NO: 24) in the TF-1 cell proliferation assay (Figure 1), neither clone bound non-human primate or variant IL-13 in the BIAcore binding assay.

Germlining framework regions of BAK278D6 and BAK502G9

The derived amino acid sequence of BAK278D6 VH (SEQ ID NO: 13) and VL (SEQ ID NO: 14) were aligned to the known human germline sequences in the VBASE database [73] and the closest germline identified by sequence similarity. The closest germline for the VH domain of BAK278D6 (SEQ ID NO: 14) and its derivatives, was identified as DP14, a member of the VH1 family. The BAK278D6 VH has 9 changes from the DP14 germline within framework regions. The closest germline for the VL of BAK278D6 was identified as $V_\lambda 3$ 3h. The BAK278D6 VL domain (SEQ ID NO: 14) has only 5 changes from the germline within framework regions. Framework regions of BAK278D6 and its derivatives were returned to germline by site directed mutagenesis (Stratagene Quikchange kit) to identically match native human antibodies.

EXAMPLE 5

Neutralisation potency of lead clones from targeted optimisation of heavy chain CDR1 and heavy chain CDR2 sequences of BAK502G9 in the human IL-13 dependent TF-1 cell proliferation assay

A second phase of optimisation was performed using BAK502G9 sequence, with germlined framework regions, as a template. Selections were performed essentially as described in Example 1 on scFv repertories in which either residues within the heavy chain CDR1 or heavy chain CDR2 of BAK502G9 had been randomised by mutagenesis. Unique clones from the selection output were identified by DNA sequencing and their neutralising potency assessed as purified scFv preparations in the TF-1 cell proliferation assay as described in Example 2. Vectors were constructed for the most potent scFv clones to allow re-expression as whole human IgG4 antibody as described by Persic et al. (1997 Gene 187; 9-18) with a few modifications. An oriP fragment was included in the vectors to

facilitate use with HEK-EBNA 293 cells and to allow episomal replication. The VH variable domain was cloned into the polylinker between the secretion leader sequence and the human gamma 4 constant domain of the expression vector pEU8.1(+). The VL variable domain was cloned into the polylinker between the secretion leader sequence and the human lambda constant domain of the expression vector pEU4.1(-).

Whole antibody was purified from conditioned media from EBNA-293 cells co-transfected with constructs expressing heavy and light chains by protein A affinity chromatography (Amersham Pharmacia). The purified antibody preparations were sterile filtered and stored at 4°C in phosphate buffered saline (PBS) prior to evaluation. Protein concentration was determined by measuring absorbance at 280nm using the BCA method (Pierce). Reformatted human IgG4 whole antibodies were compared to commercially available anti-human IL-13 antibodies in the TF-1 proliferation assay described in Example 2.

Results

As demonstrated in Figure 5, the commercial antibody B-B13, (mouse IgG1 -Euroclone 5) was shown to be significantly more potent against human IL-13 than the commercial antibody JES10-5A2 (rat IgG1 - Biosource) with IC_{50} of 1021pM and 471pM respectively. Eight clones, namely, BAK1111D10, BAK1166G02, BAK1167F02, BAK1167F04, BAK1183H4, BAK1184C8, BAK1185E1, BAK1185F8, derived from BAK502G9 (and so "BAK502G9 lineage"), in which the heavy chain CDR1 or CDR2 had been targeted, showed improved potency as scFv over the commercial antibodies. These improvements were maintained on conversion to whole antibody human IgG4. Each of these VH and VL domains individually and in the respective pairings of these claims represents an aspect or embodiment of the present invention, as do specific binding members for IL-13 that comprise one or

more of them, also specific binding members comprising one or more CDR's from the BAK502G9 lineage clones, preferably a VH domain comprising a BAK502G9 lineage set of HCDR's and/or a VL domain comprising a BAK502G9 lineage set of LCDR's. These may be employed in any and all aspects of the invention as disclosed elsewhere herein. Derivatives of BAK502G9 as whole antibodies (IgG4) had an IC_{50} ranging from 244pM to 283pM. BAK502G9 as a whole antibody IgG4 had an IC_{50} of 384pM. In summary, major improvements in potency could be obtained by targeting heavy chain CDR1 (SEQ ID NO:7) or CDR2 (SEQ ID NO: 8) of BAK502G9. Statistical comparisons to B-B13 were made using an ANOVA followed by a Dunnett's post test analysis (InStat software).

Further characterisation

Selected anti-human antibodies from the BAK278D6 lineage underwent further characterisation to determine their specificity. These included BAK502G9 (VH SEQ ID NO: 15; VL SEQ ID NO: 16) and its derivatives BAK1167F2 (VH SEQ ID NO: 35; VL SEQ ID NO: 36) and BAK1183H4 (VH SEQ ID NO: 37; VL SEQ ID NO: 38), which are representative examples of clones with modifications to heavy chain CDR1 and heavy chain CDR2 of BAK502G9 respectively.

EXAMPLE 6

Neutralisation potency of lead clones from targeted optimisation of heavy chain CDR1 and heavy chain CDR2 sequences of BAK502G9 against non-human primate IL-13 and an IL-13 variant associated with asthma in the TF-1 factor dependent cell proliferation assay

Cross-reactivity of anti-human IL-13 antibodies was determined by their ability to inhibit non-human primate IL-13 and IL-13

variant mediated TF-1 cell proliferation as described in Example 4.

Results

Optimised anti-human IL-13 antibodies BAK1167F2 (VH SEQ ID NO: 35; VL SEQ ID NO: 36) and BAK1183H4 (VH SEQ ID NO: 37; VL SEQ ID NO: 38) maintained the specificity of their parent BAK502G9 (VH SEQ ID NO: 15; VL SEQ ID NO: 16) (Figure 6). Potency gains against wild type IL-13 were reflected in their ability to neutralise non-human primate IL-13 and an IL-13 variant with substantially equivalent potency. The IC_{50} for BAK502G9 against human, human variant and non-human primate IL-13 were 1.4nM, 1.9nM and 2.0nM respectively. The IC_{50} for BAK1167F2 against human, human variant and non-human primate IL-13 were 1.0nM, 1.1nM and 1.3nM respectively. The IC_{50} for BAK1183H4 against human, human variant and non-human primate IL-13 were 0.9nM, 1.0nM and 1.6nM respectively. These clones are suitable for therapeutic use.

EXAMPLE 7

Neutralising potency of lead anti-human IL-13 antibodies against native human IL-13 in HDLM-2 cell proliferation assay

The human IL-13 sequence has four potential N-glycosylation sites. The inventors have demonstrated the ability of BAK278D6 and its derivatives to neutralise recombinant IL-13 expressed either in bacterial or baculovirus expression systems. Although, there is evidence that many processing events known in mammalian systems do also occur in insects there are key differences in protein glycosylation, particularly N-glycosylation [74].

The inventors investigated the ability of BAK278D6 derivatives to neutralise native IL-13 released from human cells.

HDLM-2 cells were isolated by Drexler et al [75] from a patient with Hodgkin's disease. Skinnider et al [76] demonstrated that HDLM-2 cell proliferation was in part dependent on autocrine and paracrine release of IL-13. Lead anti-human IL-13 antibodies were assessed for their ability to inhibit HDLM-2 cell proliferation mediated by the release of native (or naturally occurring) IL-13.

HDLM-2 cell assay protocol

HDLM-2 cells were obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) and maintained according to supplied protocols. Assay media comprised RPI-1640 with Glutamax I (Invitrogen) containing 20% foetal bovine serum. Prior to each assay, the cells were pelleted by centrifugation at 300x g for 5 min, the media removed by aspiration and the cells resuspended in fresh media. This process was repeated three times and the cells were finally resuspended to a final concentration of 2 x 10^5 cells/ml in assay media. 50µl of resuspended cells were added to each assay point in a 96 well assay plate. Test solutions of antibodies (in triplicate) were diluted to the desired concentration in assay media. An irrelevant isotype antibody not directed at IL-13 was used as a negative control. The appropriate test antibody in a total volume of 50µl / well were added to the cells, each assay point giving a total assay volume of 100µl / well. Assay plates were incubated for 72 hours at 37°C under 5% CO_2. 25 µl of tritiated thymidine (10 µCi/ml, NEN) was then added to each assay point and assay plates were returned to the incubator for a further 4 hours. Cells were harvested on glass fibre filter plates (Perkin Elmer) using a cell harvester. Thymidine incorporation was determined using a Packard TopCount microplate liquid

scintillation counter. Data were analysed using Graphpad Prism software.

Results

As demonstrated in Figure 7, BAK502G9 (VH SEQ ID NO: 15; VL SEQ ID NO: 16), and its derivatives BAK1183H4 (VH SEQ ID NO: 37; VL SEQ ID NO: 38) and BAK1167F2 (VH SEQ ID NO: 35; VL SEQ ID NO: 36) were able to cause a dose dependent inhibition of cell proliferation with relative potencies similar to those observed in other bioassays. IC_{50} for BAK502G9, BAK1183H4, BAK1167F2 as human IgG4 were 4.6nM, 3.5nM and 1.1nM respectively. IC_{50} for the commercial antibodies JES10-5A2 and B-B13 were 10.7nM and 16.7nM respectively.

EXAMPLE 8

Neutralising potency of lead anti-human IL-13 antibodies against IL-13 dependent responses in disease relevant primary cells

Secondary bioassays were performed using primary cells and readouts more relevant to airway disease. These included eotaxin release from normal human lung fibroblasts (NHLF) and vascular adhesion molecule 1 (VCAM-1) upregulation on the surface of human umbilical vein endothelial cells (HUVEC). Both IL-13 dependent responses could contribute to eosinophil recruitment, a feature of the asthma phenotype [92].

NHLF assay protocol

IL-13 has been shown to cause eotaxin release from lung fibroblasts[77] [78] [79]. Factor dependent eotaxin release from NHLF was determined by ELISA.

NHLF were obtained from Biowhittaker and maintained according to supplied protocols. Assay media was FGM-2 (Biowhittaker).

Test solutions of antibody (in triplicate) were diluted to the desired concentration in assay media. An irrelevant antibody not directed at IL-13 was used as a negative control. Recombinant bacterially-derived human IL-13 (Peprotech) was subsequently added to a final concentration of 10 ng/ml when mixed with the appropriate test antibody in a total volume of 200 µl. The concentration of IL-13 used in the assay was selected as the dose that gave an approximately 80% of the maximal response. All samples were incubated for 30 minutes at room temperature. Assay samples were then added to NHLF that had been preseeded at a density of 1 x 10^4 cells per well in 96-well assay plates. Assay plates were incubated at 37°C for 16-24 hours at 37°C under 5% CO_2. Assay plates were centrifuged at 300 x *g* for 5 minutes to pellet detached cells. Eotaxin levels in the supernatant were determined by ELISA using reagents and methods described by the manufacturer (R&D Systems). Data were analysed using Graphpad Prism software.

Results

BAK278D6 lineage clones were able to inhibit human IL-13 dependent eotaxin release from NHLF. Relative potency was similar to that observed in the TF-1 cell proliferation assay (Figure 8). BAK502G9 (VH SEQ ID NO: 15; VL SEQ ID NO: 16), BAK1183H4 (VH SEQ ID NO: 37; VL SEQ ID NO: 38), BAK1167F2 (VH SEQ ID NO: 35; VL SEQ ID NO: 36) had IC_{50} of 207pM, 118pM and 69pM respectively against 10 ng/ml human IL-13. Commercial antibodies JES10-5A2 and B-B13 had IC_{50} of 623pM and 219pM respectively.

HUVEC assay protocol

IL-13 has been shown to upregulate expression of VCAM-1 on cell surface of HUVECs [80, 81]. Factor dependent VCAM-1 expression was determined by detection of upregulation of

VCAM-1 receptor cellular expression using a time-resolved fluorescence read out.

HUVEC were obtained from Biowhittaker and maintained according to supplied protocols. Assay media was EGM-2 (Biowhittaker). Test solutions of antibody (in triplicate) were diluted to the desired concentration in assay media. An irrelevant antibody not directed at IL-13 was used as a negative control. Recombinant bacterially derived human IL-13 (Peprotech) was added to a final concentration of 10 ng/ml when mixed with the appropriate test antibody in a total volume of 200 µl. The concentration of IL-13 used in the assay was selected as the dose that gave approximately 80% of the maximal response. All samples were incubated for 30 minutes at room temperature. Assay samples were then added to HUVEC that had been preseeded at 4 x 10^4 cells per well in 96-well assay plates. Assay plates were incubated at 37°C for 16-20 hours under 5% CO_2. Assay media was then removed by aspiration and replaced with blocking solution (PBS containing 4% dried Marvel® milk powder). Assay plates were incubated at room temperature for 1 hour at room temperature. Wells were washed three times with PBST Tween before 100 µl (1:500 dilution in PBST/1% Marvel®) of biotinylated anti-VCAM-1 antibody (Serotec) was added to each well. Assay plates were incubated at room temperature for 1 hour. Wells were washed three times with Delfia wash buffer (Perkin Elmer) before 100 µl of Europium-labelled Streptavidin or anti-murine IgG1 (1:1000 dilution in Delfia assay buffer, Perkin Elmer) was added to each well. Assay plates were then incubated at RT for 1 hour. Wells were washed 7 times with Delfia wash buffer (Perkin Elmer). Finally, 100µl of enhancement solution (Perkin Elmer) was added to each well and fluorescence intensity was determined using the Wallac 1420

VICTOR2 plate reader (Standard Europium protocol). Data were analysed using Graphpad Prism software.

Results

Typical data for BAK502G9 (VH SEQ ID NO: 15; VL SEQ ID NO: 16), BAK1183H4 (VH SEQ ID NO: 37; VL SEQ ID NO: 38), BAK1167F2 (VH SEQ ID NO: 35; VL SEQ ID NO: 36) as whole antibody human IgG4 are shown in Figure 9. Relative potency was similar to the observed in the TF-1 cell proliferation assay. IC_{50} for BAK502G9, BAK1183H4 and BAK1167F2 were 235pM, 58pM and 55pM respectively against 10ng/ml human IL-13.

EXAMPLE 9

Neutralisation potency of anti-IL-13 antibodies against IL-1β and IL-4 dependent VCAM-1 upregulation

The specificity of the BAK278D6 lineage of clones was assessed in a modification of the HUVEC bioassay. Together with IL-13, both IL-4 and IL-1β have been shown to upregulate expression of VCAM-1 on cell surface of HUVECs [80, 81].

HUVEC assay protocol

The assay was performed essentially as described in Example 5 with the following modifications. Recombinant human IL-1β and IL-4 (R&D Systems) were used in place of human IL-13 at 0.5 ng/ml and 1 ng/ml respectively and represented the dose that gave approximately 80% of the maximal response.

Results

None of the clones evaluated from the BAK278D6 lineage neutralised VCAM-1 upregulation in response to either human IL-1β or IL-4 and thus demonstrated specificity for IL-13 (Figure 10). IL-4 is most closely related to IL-13, sharing 30% sequence identity at the amino acid level [82].

EXAMPLE 10

Neutralisation potency of BAK209B11 as a human IgG4 in a murine IL-13 dependent murine B9 cell proliferation assay

BAK209B11, identified as an anti-murine IL-13 neutralising clone as a scFv as described in Example 1, was reformatted as a whole antibody human IgG4 as described in Example 5 and its potency evaluated in the murine IL-13 dependent B9 cell proliferation assay. B9 is a murine B-cell hybridoma cell line [83]. B9 is factor dependent for survival and proliferation. In this respect B cells respond to murine IL-13 and are maintained in media containing human IL-6 (50pg/ml, R&D Systems). Inhibition of murine IL-13 dependent proliferation was determined by measuring the reduction in incorporation of tritiated thymidine into the newly synthesized DNA of dividing cells.

B9 cell assay protocol

B9 cells were obtained from European Collection of Animal Cell Culture ECACC and maintained according to supplied protocols. The assay was performed essentially as described for the TF-1 assay in Example 2 but with the following modifications. Assay media comprised RPMI-1640 with GLUTAMAX I (Invitrogen) containing 5% foetal bovine serum (Hyclone) and 50μM 2-mercaptoethanol (Invitrogen). Recombinant bacterially derived murine IL-13 (Peprotech) replaced human IL-13 with a final assay concentration of 1ng/ml.

Results

BAK209B11 (VH SEQ ID NO: 25; VL SEQ ID NO: 26) as a human IgG4 neutralised 1 ng/ml murine IL-13 with an IC_{50} of 776pM in the B9 assay (Figure 11). BAK209B11 therefore represents a useful tool to investigate the role of IL-13 in murine models

of disease. This is clearly demonstrated in Example 12, which demonstrates the efficacy of BAK209B11 in a murine model of acute pulmonary inflammation.

EXAMPLE 11

Affinity determination of anti-IL-13 antibodies by BIAcore analysis

The affinity of BAK502G9 (VH SEQ ID NO: 15; VL SEQ ID NO: 16), BAK1167F2 (VH SEQ ID NO: 35; VL SEQ ID NO: 36) and BAK1183H4 (VH SEQ ID NO: 37; VL SEQ ID NO: 38) for human IL-13 and BAK209B11 (VH SEQ ID NO: 25; VL SEQ ID NO: 26) for murine IL-13 as human IgG4 were determined by surface plasmon resonance measurements using a BIAcore 2000 Biosensor (BIAcore AB) essentially as described in [72]. In brief, antibodies were coupled to CM5 sensorchips using an amine coupling kit (BIAcore) at a surface density of approximately 500Ru and a serial dilution of IL-13 (between 50nM to 0.78nM) in HBS-EP buffer was passed over the sensorchip surface. The resulting sensorgrams were evaluated using BIA evaluation 3.1 software to provide kinetic data.

Results

BAK502G9, BAK1167F2 and BAK1183H4 IgG4 bound human IL-13 with high affinity with Kd of 178 pM, 136pM and 81pM respectively corresponding to their relative potency in cell based assays. BAK209B11 bound murine IL-13 with affinity of 5.1nM (Table 3).

EXAMPLE 12

Efficacy of BAK209B11 in a murine model of acute allergic pulmonary inflammation

Murine model of acute allergic pulmonary inflammation

The effect of BAK209B11 (VH SEQ ID NO: 25; VL SEQ ID NO: 26), an anti-murine IL-13 neutralising human IgG4 antibody, was investigated in a murine of acute allergic pulmonary inflammation. This model was performed essentially as described by Riffo-Vasquez et al [84] and is characterised at its endpoint by increased bronchial alveolar lavage (BAL) IL-13 (Figure 12), cellular infiltration into the lung and BAL (Figure 13), increased serum IgE levels and airways hyperresponsiveness (AHR).

Model protocol

Female Balb/C mice (Charles River UK) were treated with either anti-murine IL-13 antibody BAK209B11 (at 12, 36, 119 or 357 μg doses) or an isotype matched control antibody (357 μg dose). On days 0 and 7, mice in each group were sensitised by intraperitoneal injection of 10μg of ovalbumin (Ova) in 0.2 ml of the vehicle (saline containing 2% Al_2O_3 (Rehydragel) as an adjuvant). A separate control group of non-sensitised mice received an equal volume of the vehicle. Mice were challenged with ovalbumin on days 14, 15 and 16. Ovalbumin was diluted to 1% (w/v) in sterile saline prior to nebulisation. All inhalation challenges were administered in a Plexiglas exposure chamber. Ova was aerosolised using a deVilbiss Ultraneb 2000 nebuliser (Sunrise Medical) in a series of three exposures of 20 minutes separated by 1 hour intervals.

BAK209B11 or an irrelevant human IgG4 were administered intravenously, 1 day prior to first challenge and then 2 hours

prior to each subsequent challenge (4 doses in total). The model ended at day 17, 24 hours post final challenge. Blood (serum) and BAL were collected. Serum was assayed for total IgE. BAL was obtained by injecting 3 aliquots of saline (0.3ml, 0.3ml and 0.4ml) and pooling samples. Total leukocytes and differential cell counts were obtained from BAL cells.

Results

Ovalbumin challenge of sensitised mice caused a significant ($p<0.05$) increase in total BAL cell recruitment over non-sensitised but challenged animals. This recruitment was dose-dependently inhibited by BAK209B11; significant ($p<0.05$) inhibition was seen with ≥36µg BAK209B11, but not control antibody (Figure 13). Similar effects were also seen on eosinophils (Figure 14) and neutrophils (Figure 15) with significant ($p<0.05$) inhibition of cellular influx at a minimum BAK209B11 dose of 36µg. This inhibition was not seen with the control antibody. Lymphocytes were also induced in sensitised but not non-sensitised mice upon challenge. This induction was dose-dependently inhibited by BAK209B11, with maximal inhibition seen with 36µg BAK209B11. Control antibody had no effect (Figure 16). Although monocyte/macrophages were not induced in sensitised animals when compared to non-sensitised animals, background levels were depressed by ≥36µg BAK209B11, but not by control antibody (Figure 17). Serum IgE levels were significantly increased in sensitised animals when compared to non-sensitised after challenge ($p<0.05$). This increase was decreased after treatment with 36µg BAK209B11 but not by the control antibody.

In summary, systemic administration of BAK209B11, a murine IL-13 neutralising antibody, but not control antibody inhibited inflammatory cell influx and the upregulation of serum IgE

levels caused by sensitisation and subsequent challenge with ovalbumin in a murine model of allergic inflammation.

Examples 13 to 20 are prophetic.

EXAMPLE 13

Efficacy of BAK209B11 in the Lloyd murine model of acute pulmonary inflammation

Murine model of acute allergic pulmonary inflammation

The effect of BAK209B11 (VH SEQ ID NO: 25; VL SEQ ID NO: 26), an anti murine IL-13 neutralising antibody, was investigated in a second murine model of acute allergic pulmonary inflammation. This model was performed essentially as described by McMillan et al. [85] and is characterised at its endpoint by increased BAL and lung tissue IL-13, cellular infiltration into the lung and BAL, increased serum IgE levels and airways hyperresponsiveness (AHR).

Model protocol

Female Balb/C mice (Charles River UK) were administered with various doses of anti-murine IL-13 antibody BAK209B11 or an isotype matched control antibody, as follows. On days 0 and 12, mice in each group were sensitised (SN) by intraperitoneal injection of 10μg of ovalbumin (Ova) in 0.2 ml of the vehicle (saline containing 2mg $Al(OH)_3$ as an adjuvant [calculated as described in Example 12]). A separate control group of non-sensitised mice (NS) received an equal volume of the vehicle. Mice were challenged with ovalbumin for 20 minutes on days 19, 20, 21, 22, 23 and 24. Ovalbumin was diluted to 5% (w/v) in saline prior to nebulisation. All inhalation challenges were administered in a Plexiglas exposure chamber. Ova was aerosolised using a deVilbiss Ultraneb 2000 nebuliser (Sunrise Medical). On days 18,19,20,21,22,23 and 24 mice were

administered with various intraperitoneal doses (237µg, 23.7µg or 2.37µg; denoted in figure 21 by H,M and L) of anti-murine IL-13 antibody BAK209B11 muIgG1 or an isotype matched control antibody (237µg). Airway function was assessed on days 0 and 25 by increasing methacholine challenges and monitored using conscious plethysmography (Buxco). PC_{50} (concentration of methacholine required to increase baseline PenH by 50%) was estimated for individual mice at both day 0 and day 25 from 4 parameter unfixed curve fitting of methacholine dose-response curves.

The model ended at day 25, 24 hours post final challenge. Blood, serum, BAL and lung tissue were collected.

Results

Lung function was evaluated for individual animals at day 0 (pre-treatment) and at day 25 (post-challenge) and was quantitated by calculating PC_{50} values (concentration of methacholine required to increase baseline PenH by 50%) (Figure 21A). An individuals airways hyperresponsiveness (AHR) was determined by the change in log PC_{50} at day 25 versus day 0 (log day 25 PC_{50} - log day 0 PC_{50}). This delta logPC_{50} was the primary endpoint of the study; PC_{50} data log-transformed because of requirements of endpoint ANOVA. Individual changes were averaged within groups to generate group average delta log PC_{50} (as shown in Figure 21B).

Ovalbumin challenge of sensitised mice caused a significant AHR compared to non-sensitised and challenged mice ($p<0.01$). BAK209B11 caused a clear and dose-dependent decrease in AHR whereas the control antibody had no effect.

EXAMPLE 14

Efficacy of BAK209B11 in the Gerard murine model of acute pulmonary inflammation

Murine model of acute allergic pulmonary inflammation

The effect of BAK209B11 (VH SEQ ID NO: 25; VL SEQ ID NO: 26), an anti-murine IL-13 neutralising human IgG4 antibody, was investigated in a third murine model of acute allergic pulmonary inflammation. This model was performed essentially as described by Humbles *et al.* [86] and is characterised at its endpoint by increased BAL and lung tissue IL-13, cellular infiltration into the lung and BAL, increased serum IgE levels and airways hyperresponsiveness (AHR).

Model protocol

Female Balb/C mice (Charles River UK) were administered with various doses of anti-murine IL-13 antibody BAK209B11 or an isotype matched control antibody. On days 0, 7 and 14, mice in each group were sensitised (SN) by intraperitoneal injection of 10µg of ovalbumin (Ova) in 0.2 ml of the vehicle (saline containing 1.125mg $Al(OH)_3$ as an adjuvant [calculated as described in Example 12]). A separate control group of non-sensitised mice (NS) received an equal volume of the vehicle. Mice were challenged with ovalbumin for 20 minutes on days 21, 22, 23 and 24. Ovalbumin was diluted to 5% (w/v) in saline prior to nebulisation. All inhalation challenges were administered in a Plexiglas exposure chamber. Ova was aerosolised using a deVilbiss Ultraneb 2000 nebuliser (Sunrise Medical).

The model ended at day 25, 24 hours post challenge. Blood, serum, BAL and lung tissue were collected.

EXAMPLE 15

Efficacy of BAK209B11 in the Lloyd chronic model of pulmonary inflammation

Murine model of chronic allergic pulmonary inflammation

The effect of BAK209B11 (VH SEQ ID NO: 25; VL SEQ ID NO: 26), an anti murine IL-13 neutralising human IgG4 antibody, was investigated in a model of chronic allergic pulmonary inflammation. This model was performed essentially as described by Temelkovski *et al.* [87] and is characterised at its endpoint by cellular infiltration into the lung and BAL, increased serum IgE levels and airways hyperresponsiveness (AHR).

Model protocol

Female Balb/C mice (Charles River UK) were dosed with various doses of anti-murine IL-13 antibody BAK209B11 or an isotype matched control antibody. On days 0 and 11, mice in each group were sensitised (SN) by intraperitoneal injection of 10μg of ovalbumin (Ova) in 0.2 ml of the vehicle (saline containing 2mg $Al(OH)_3$ as an adjuvant [calculated as described in Example 12]). A separate control group of non-sensitised mice (NS) received an equal volume of the vehicle. Mice were challenged with ovalbumin for 20 minutes on days 18, 19, 20, 21, 22, 23, 28, 30, 32, 35, 37, 39, 42, 44, 46, 49 and 51. Ovalbumin was diluted to 5% (w/v) in saline prior to nebulisation. All inhalation challenges were administered in a Plexiglas exposure chamber. Ova was aerosolised using a deVilbiss Ultraneb 2000 nebuliser (Sunrise Medical).

The model ended at day 52, 24 hours post challenge. Blood, serum, BAL and lung tissue were collected.

EXAMPLE 16

Efficacy of anti-human IL-13 antibodies against exogenous human IL-13 administered to the murine air pouch model

The effect of anti-human IL-13 antibodies on the pro-inflammatory action of human IL-13 was investigated in a basic murine model. This model was performed essentially as described by Edwards et al [93] and was characterised at its endpoint by cellular infiltration into the airpouch.

Model protocol

An air pouch was created on the back of female Balb/C mice by subcutaneous injection of 2.5mL of sterile air at day 0. The air pouch was reinflated with another 2.5mL sterile air at day 3. 2µg huIL-13 in 0.75% CMC was injected directly into the pouch at day 6. 24 hours later the mice were killed and the air pouch lavaged with 1mL heparinised saline. Antibody treatments were either given with the huIL-13 (into the pouch) or given systemically.

Results

Human IL-13, injected into the airpouch (i.po.), caused a significantly increased infiltration of total leukocytes ($p<0.01$) and eosinophils ($p<0.01$) at 24 hours post-challenge versus vehicle (0.75% carboxymethyl cellulose (CMC) in saline i.po.) treated mice.

Locally administered BAK502G9 (200mg, 20mg or 2mg intrapouch) significantly and dose-dependently inhibited the total leukocyte ($p<0.01$) and eosinophil ($p<0.01$) infiltration into the air pouch caused by 2µg huIL-13 in 0.75% CMC.

Systemically administered BAK209B11 (30mg/kg, 10mg/kg and 1mg/kg) also signficantly and dose-dependently inhibited the total leukocyte ($p<0.01$) and eosinophil ($p<0.01$) infiltration into the air pouch caused by 2µg huIL-13 in 0.75% CMC.

EXAMPLE 17

Generation of human IL-13 knock-in / murine IL-13 knock out transgenic mice for the purposes of evaluating the efficacy of anti-human IL-13 antibodies in models of pulmonary allergic inflammation

The present inventors have generated mice which express human, rather than murine IL-13 by gene targeting. The mouse IL-13 gene has been replaced from start to stop codon with the relevant portion of the human IL-13 gene. This mouse strain expresses human IL-13, rather than mouse IL-13, in response to the same stimuli as in the wild-type mouse, as the endogenous IL-13 promoter and IL-13 pA tail remaining unchanged. It has been shown that human IL-13 can bind to and signal through mouse IL-13 receptors to generate the same physiological consequences as signalling caused by mouse IL-13 ligating mouse IL-13 receptors. For example exogenous human IL-13 caused inflammatory cell recruitment into the murine air pouch (Figure 18). These transgenic animals allow us to evaluate non-murine cross reactive anti-human IL-13 antibodies in established murine models of disease.

This mouse has been used in the acute allergic airway inflammation models (as described in examples 18 and 19) and chronic allergic airway inflammation models (as described in Example 20) allowing the evaluation of anti-human IL-13 antibody pharmacology in allergic airway disease.

EXAMPLE 18

Efficacy of anti-human IL-13 antibodies in the huIL-13-transgenic Lloyd murine model of acute pulmonary inflammation

Murine model of acute allergic pulmonary inflammation

The effect of anti human IL-13 neutralising human IgG4 antibodies were investigated in a murine model of acute allergic pulmonary inflammation using the transgenic mice generated in example 17. This model was performed essentially as described by McMillan *et al.* [85] and example 13. The model was characterised at its endpoint by increased BAL and lung tissue IL-13, cellular infiltration into the lung and BAL, increased serum IgE levels and airways hyperresponsiveness (AHR).

Model protocol

The protocol for this model was as described in Example 13 except that anti-human IL-13 antibodies were dosed instead of BAK209B11.

EXAMPLE 19

Efficacy of anti-human IL-13 antibodies in the huIL-13-transgenic Gerard murine model of acute pulmonary inflammation

Murine model of acute allergic pulmonary inflammation

The effect of anti human IL-13 neutralising human IgG4 antibodies were investigated in another murine model of acute allergic pulmonary inflammation using the transgenic mice generated in example 17. This model was performed essentially as described by Humbles et al, [86] and in example 14. The model is characterised at its endpoint by increased BAL and lung tissue IL-13, cellular infiltration into the lung and

BAL, increased serum IgE levels and airways hyperresponsiveness (AHR).

Model protocol

The protocol for this model was as described in Example 14 except that anti-human IL-13 antibodies were dosed instead of BAK209B11.

EXAMPLE 20

Efficacy of anti-human IL-13 antibodies in the huIL-13-transgenic Lloyd chronic model of pulmonary inflammation

The effect of anti human IL-13 neutralising human IgG4 antibodies were investigated in a model of chronic allergic pulmonary inflammation using the transgenic mice generated in example 17. This model was performed essentially as described by Temelkovski *et al.* [87] and in Example 15 and is characterised at its endpoint by cellular infiltration into the lung and BAL, increased serum IgE levels and airways hyperresponsiveness (AHR).

Model protocol

The protocol for this model was as described in Example 15 except that anti-human IL-13 antibodies were dosed instead of BAK209B11

EXAMPLE 21

Pharmacokinetics and pharmacodynamics of anti-human IL-13 antibodies in Ascaris.suum-allergic cynomolgus monkeys

The pharmacokinetics and pharmacodynamics of 502G9 were evaluated in 4 allergic but non-challenged cynomolgus primates (2 male/2 female) after a single 10mg/kg i.v bolus dose. The experiment ran for 29 days. The antibody's pharmacokinetic

parameters were determined from a geomean average serum-drug concentration curve and are detailed below in Table 4.

In the same study serum IgE concentrations were also followed using a human IgE ELISA kit (Bethyl laboratories, USA).

Results

Serum IgE concentrations were significantly reduced after a single 10mg/kg i.v bolus dose of BAK502G9, from 100 % control levels (predose) to 66 ± 10% of control values ($p<0.05$), at 4 and 5 days after dosing. This lowering of serum IgE concentration recovered to 88 ± 8 % of control levels by day 22 (see Figure 20). Again these data were derived by normalising each animals serum IgE concentration to predose levels, where predose concentrations was 100%, and then averaging the curves from the 4 animals tested.

The two male monkeys had relatively low predose total serum IgE (60ng/mL and 67ng/mL). These IgE levels did not change in a fashion suggesting a trend following treatment with BAK502G9 (Figure 20B). The two female monkeys had relatively high predose total serum IgE (1209ng/mL and 449ng/mL). These IgE levels were decreased following treatment with BAK502G9, maximally by 60% at 7 days, and returning to approximately predose levels by 28 days post-administration (Figure 20B). These data provide indication that BAK502G9 lowers serum IgE concentrations in animals with relatively high circulating IgE of IgE.

EXAMPLE 22

Efficacy of anti-human IL-13 antibodies in cynomolgus models of dermal allergy

The effects of anti-human IL-13 neutralising human IgG4

antibodies were investigated in a primate model of acute allergic dermal inflammation. This model was performed by injecting human IL-13 and *A.suum* antigen intradermally into cynomolgus monkeys. 24-96h later, dermal biopsies and serum samples were taken. The model was characterised at its endpoint by cellular infiltration into the skin.

EXAMPLE 23

Efficacy of anti-human IL-13 antibodies in cynomolgus models of pulmonary allergy

The effect of anti human IL-13 neutralising human IgG4 antibodies were investigated in a primate model of acute allergic pulmonary inflammation. This model was performed by exposing *a.suum*-allergic cynomolgus primates to nebulised *a.suum* antigen, thereby generating an allergic reaction. This allergy was characterized at its end point by cellular infiltration into the lung and BAL, increased serum IgE levels and airways hyper-responsiveness.

Pharmacodynamics were additionally evaluated *ex vivo* using a flow cytometric method. CD23 is the high affinity IgE receptor and can be expressed on peripheral human blood mononuclear cells. CD23 expression can be induced, in terms of the number of cells expressing CD23 and also in how much CD23 each cell expresses by both IL-13 and IL-4. The IL-13, but not IL-4, mediated response can be inhibited by anti-human IL-13 antibodies.

Animals were preselected for entry into this 2-phase study on the basis of previously established AHR following nebulised antigen (*ascaris suum* extract) challenge. In phase I airway function was assessed during intravenous histamine challenge on days 1 and 11. PC_{30}, the histamine dose required to

generate a 30% increase in lung resistance (R_L) above baseline, was determined from each histamine dose-response curve. On days 9 and 10, animals were challenged with individually tailored doses of nebulised antigen previously shown to generate a 40% increase in R_L as well as a 35% decrease in dynamic compliance (C_{DYN}). Historically in this model, a greater R_L has been observed following the second challenge with a given allergen dose than the first; this is antigen priming. The two antigen challenges caused AHR, as measured by an increased area under the histamine dose-response curve and/or a fall in PC_{30}, and BAL, as well as eosinophilia at day 11 compared to day 1. Animals displaying an AHR-phenotype were selected to enter phase II.

Phase II was run exactly as phase I except that all animals received a 30mg/kg BAK502G9 infusion on days 1, 5 and 9. The effects of BAK502G9 were assessed by comparing the changes seen in phase II with changes seen in phase I for individual animals.

Blood, serum, BAL and lung tissue were colleted. Serum IgE levels were monitored by ELISA. Serum from BAK502G9 treated cynomolgus monkeys was shown to inhibit the expression of CD23 on human peripheral blood mononuclear cells induced by IL-13 but not IL-4. The magnitude of this inhibition was consistent with the serum BAK502G9 levels predicted by PK ELISA.

Results

BAK502G9 significantly inhibited AHR as measured by R_L AUC ($p<0.05$) (Figure 26A; Table 7). An inhibitory effect of BAK502G9 on AHR, as measured by PC_{30}, was observed but did not reach statistical significance (Figure 26B; Table 7). BAK502G9 also significantly inhibited both antigen priming ($p<0.01$) (Figure 26C; Table 7) and BAL inflammation. BAK502G9

significantly inhibited total cell ($p<0.05$) and eosinophil ($p<0.05$) but not macrophage, lymphocyte or mast cell influx into the BAL (Figure 26D; Table 7).

EXAMPLE 24

Efficacy of anti-human IL-13 antibodies against the asthmatic phenotype that develops when human IL-13 is administered to the mouse lung

Murine model of airways hyperresponsiveness

The efficacy of the anti-human IL-13 neutralising antibody BAK502G9, against the development of airways hyper-responsiveness (AHR) following administration of human IL-13 to the mouse lung was investigated. This model was performed essentially as described by Yang *et al* [119] with the exception that human IL-13 was used in place of murine IL-13.

Model protocol

To develop the phenotype, male BALB/c mice were exposed to two doses of human IL-13 separated by a 48-hour interval. In brief, mice were anaesthetised with an intravenous injection of 100µl saffan solution (1:4 diluted in water). Mice were intubated with a 22-gauge catheter needle, through which human recombinant IL-13 (25 µg dissolved in 20µl phosphate-buffered saline (PBS)) or vehicle control (PBS) was instilled. Airway function was assessed 24 hours after the last administration of IL-13 by increasing methacholine challenges and monitored using conscious plethysmography (Buxco). PC_{200} (concentration of methacholine required to increase baseline penH by 200%) was determined from 4 parameter unfixed curve fitting of methacholine dose-response curves. Antibody treatments were administered by intra-peritoneal injection 24 hours prior to the each dose of IL-13.

Results

Intratracheal installation of human IL-13 into naïve wild-type mice resulted in development of significant ($p<0.05$) airways hyperresponsiveness relative to control animals as determined by PC_{200} methacholine concentrations. Systemically administered BAK502G9 (1mg/kg) significantly ($p<0.01$) inhibited the development of AHR whereas the null control antibody had no effect (Figure 23).

EXAMPLE 25

Neutralisation potency of BAK502G9 as a human IgG4 against human IL-13 dependent IgE release from human B cells.

B cell switching assay protocol

IL-13 has been shown to induce IgE synthesis in human B cells *in vitro* [120]. Factor dependent IgE release from human B cells was determined by ELISA. The neutralisation potency of BAK502G9 as a human IgG4 was assessed against human IL-13 dependent IgE release from human B cells.

Peripheral blood mononuclear cells (PBMC) were purified from human buffy coat (Blood Transfusion Service) by centrifugation over a 1.077g/L density gradient. B cells were purified from PBMC with a B cell isolation kit II (Miltenyi Biotec), using reagents and methods described by the manufacturer. Assay media comprised Iscoves modified dulbeccos medium (Life Technologies) containing 10% foetal bovine serum and 20µg/mL human transferrin (Serologicals Proteins Inc). Following purification, B cells were resuspended to a final concentration of 10^6/mL in assay media. 50µl of resuspended cells were added to each assay point in a 96 well assay plate. 50µl of 4µg/mL of the anti-CD40 antibody EA5 (Biosource) was added to assay wells as appropriate. Test solutions of

antibodies (six replicates) were diluted to the desired concentration in assay media. An irrelevant antibody not directed at IL-13 was used as a negative control. 50µl / well of the appropriate test antibody were added to the cells. Recombinant bacterially derived human IL-13 (Peprotech) was subsequently added to a final concentration of 30ng/ml to give a total assay volume of 200µl/well. The concentration of IL-13 used in the assay was selected to give a maximal response. Assay plates were incubated for 14 days at 37°C under 5% CO_2. IgE levels in the supernatant were determined by ELISA using reagents and protocols supplied by the manufacturer (BD Biosciences, Bethyl Laboratories). Data were analysed using Graphpad prism software.

Results

As demonstrated in Figure 24, BAK502G9 (VH SEQ ID NO: 15; VL SEQ ID NO: 16) was able to inhibit human IL-13 dependant IgE production by human B cells. BAK502G9 as human IgG4 had an IC_{50} of 1.8nM against 30ng/ml human IL-13.

EXAMPLE 26

Efficacy of BAK502G9 against IL-13 mediated potentiation of histamine induced Ca^{2+} signalling in primary human bronchial smooth muscle cells

IL-13 has been shown to directly modulate the contractility of airway smooth muscle [121, 122]. Intracellular calcium mobilization is a prerequisite for smooth muscle contraction. Recent studies have shown that IL-13's ability to alter smooth muscle contractility is mediated in part through modulation of contractile agonist induced Ca^{2+} signaling [123, 124].

The efficacy of BAK502G9, an anti-human IL-13 antibody formatted as an IgG4, against IL-13 mediated alterations in

primary human bronchial smooth muscle cells (BSMC) signalling responses to the contractile agonist, histamine, was investigated in a Ca^{2+} signalling assay.

BSMC Ca^{2+} signalling assay protocol

Human primary BSMC, Smooth Muscle Growth Medium-2 (SmGM-2) and Smooth Muscle Basal Medium (SmBM) were obtained from Bio Whittaker. The BSMC were maintained in SmGM-2 according to supplier's recommendations. BSMC were plated at 2 x 10^4 cells/well in a 96-well microtitre cell culture plate and were allowed to attach for 24 hours, then re-fed and incubated for a further 24 hours. Prior to the Ca^{2+} signalling experiment, the BSMC were stimulated with IL-13 (Peprotech) at 50ng/ml final concentration with or without antibody and incubated for 18-24 hours. BAK502G9 and an isotype matched irrelevant control monoclonal antibody, CAT-001, were evaluated at a final concentration of 10µg/ml. Changes in intracellular Ca^{2+} concentrations in response to histamine (Calbiochem), titrated from 20µM, were measured using standard techniques with the Ca^{2+} sensitive dye Fluo-4 (Molecular Probes) and a 96-well Fluorescence Imaging Plate Reader (FLIPR) (Molecular Devices). The area under the curve (AUC) of the Ca^{2+} signalling response to histamine was determined for each cell pre-treatment condition. Data analyses were performed using GraphPad Prism version 4 for Windows (GraphPad Software).

Results

Pre-incubation of BSMC with IL-13 significantly enhanced Ca^{2+} signalling in response to histamine. Pre-incubation of BAK502G9 (Figure 25B)(but not an irrelevant isotype control antibody (Figure 25A)) with IL-13 significantly inhibited the potentiation of Ca^{2+} signalling in response to histamine (Figure 25).

EXAMPLE 27

Neutralisation potency of anti-IL-13 antibodies in a human IL-13 dependent PBMC CD23 expression assay

The potency of a representative IL-13 antibody was evaluated in the human IL-13 dependent peripheral blood mononuclear cell (PBMC) CD23 expression assay. PBMC respond to both IL-13 and IL-4 by increasing cell surface expression of CD23 [120]. CD23 (FceRII) is the low-affinity receptor for IgE and is expressed on a variety of inflammatory cells, including monocytes. Inhibition of human IL-13 dependent CD23 expression upregulation was determined by measuring the reduction in binding of fluorescently labelled CD23 monoclonal antibody to PBMCs by flow cytometry.

Assay protocol

Human blood was obtained from the Blood Transfusion Service and erythrocytes depleted by 40 minute dextran-T500 (Pharmacia) sedimentation (0.6% final concentration). The leukocyte and platelet rich fraction was then separated by a 20 minute 1137*g* centrifugation over a discontinuous Percoll gradient of 3mL 64% and 5mL 80% (100% was 9 parts Percoll and 1 part 10x PBS). PBMCs were harvested from the top of the 64% layer, washed and resuspended in assay buffer (Invitrogen RPMI 1640, 10% FCS, 200IU/mL penicillin, 100µg/mL streptomycin, 2mM L-Glutamine). The assay was performed in 24 well plates with $2x10^6$ cells, ± 80pM recombinant human IL-13 (Peprotech) or 21pM recombinant human IL-4 (R&D Systems), ± BAK502G9 or irrelevant IgG4, in a final volume of 500mcL. Cells were cultured for 48h at 37C before being harvested and stained with CD23-PE (BD Pharmingen) for 20 minutes at 4C. Finally, cells were read on a flow cytometer. CD23 expression was determined by CD23 'score'; percent of CD23 positive cells multiplied by the 'brightness' of the stain (geomean

fluorescence). No stimulant CD23 'score' was subtracted and data presented as a percentage of the response to IL-13 alone (100%). Data has been expressed as the mean ± SEM drawn from 4-6 separate experiments, using cells from 4-6 individual donors, performed in triplicate for each point.

Results

Incubation of PBMC with 80pM IL-13 or 21pM IL-4 for 48 hours resulted in clear CD23 expression (Figure 27 and Figure 28). BAK502G9 dose-dependently inhibited IL-13-induced CD23 expression with a geometric mean of 120.2pM (Figure 27). In contrast, BAK502G9 was unable to inhibit the CD23 expression induced by 21.4pM IL-4 (n=4 from individual donors, Figure 28). Irrelevant IgG4 did not inhibit either IL-13 or IL-4 dependent CD23 expression on PBMC (Figure 27 and Figure 28). Co-stimulation of PBMC with 80pM IL-13 and 21.4pM IL-4, produced an additive CD23 response. BAK502G9, but not CAT-001, reduced CD23 expression levels to those seen with IL-4 stimulation alone (Figure 28).

EXAMPLE 28

Neutralisation potency of a human IL-13 antibody in a human IL-13 dependent eosinophil shape change assay

The aims of this study were to evaluate the effect of IL-13 antibodies on eosinophil shape change induced by mediators released from NHLF following stimulation with factors found in the lungs of asthmatics such as IL-13 [125,126], TNF-α [127], TGF-β1 [128]. IL-13 synergises with TNF-α [129] or TGF-β1 [130] to induce fibroblasts to produce eotaxin-1, which can then act to directly chemoattract eosinophils. Leukocyte shape change responses are mediated through rearrangements of the cellular cytoskeleton and are essential to the processes of leukocyte migration from the microcirculation into sites of

inflammation. Inhibition of IL-13-dependent shape-change-inducing factor release by NHLFs was determined by measuring the reduction in eotaxin-1secretion by ELISA and reduction in eosinophil shape change by flow cytometry.

Assay protocol

NHLF cells were cocultured with media alone or media containing stimulants (9.6nM IL-13, 285.7pM TNF-α (R&D Systems) and 160pM TGF-β1 (R&D Systems) in the absence or presence of BAK502G9 (concentration range 875nM - 6.84nM). Cells were then cultured for a further 48h at 37°C before the resulting conditioned media was aspirated and stored at -80°C. The concentration of eotaxin-1 in conditioned media was assessed using the R&D systems Duoset ELISA system (R&D Systems).

Human blood was obtained from the Blood Transfusion Service and erythrocytes depleted by 40 minute dextran-T500 (Pharmacia) sedimentation (0.6% final concentration). The leukocyte and platelet rich fraction was then separated by a 20 minute 1137*g* centrifugation over a discontinuous Percoll gradient of 3mL 64% and 5mL 80% (100% was 9 parts Percoll and 1 part 10x PBS). Granulocytes were harvested from the 64%:80% interface, washed and resuspended in assay buffer (Sigma PBS, 1mM CaCl2, 1mM MgCl2, 10mM HEPES, 10mM D-glucose, 0.1% Sigma BSA, pH 7.3). The assay was performed in FACS tubes with $5x10^5$ cells, ± 3nM recombinant human eotaxin-1 (R&D Systems) or conditioned media, in a final volume of 400µL. Cells were incubated for 8.5 minutes at 37C before being transferred to 4^0C and fixed with a fixing agent (CellFix, BD Biosciences) and finally read on a flow cytometer. Eosinophils were identified by their FL-2 autofluorescence and the forward scatter (FSC) parameter read. Eosinophil FSC changed in response to both eotaxin-1 and conditioned media providing

measurement of shape change. Tubes were sampled at high flow rate and acquisition was terminated after 1000 eosinophil events or 1 minute, whichever was the sooner. Shape change was calculated as a percentage of the FSC caused by shape change buffer alone (100% blank shape change). Data have been expressed as the mean % blank shape change ± SEM drawn from 4 separate experiments. Each experiment used cells from an individual buffy coat (and hence individual donor), performed in duplicate for each point.

Results

NHLF cells co-stimulated with 9.6nM IL-13, 285.7pM TNF- α and 160pM TGF-β1 and cultured for 48h secreted 9.6nM eotaxin-1 into the culture media. In contrast, NHLF cells cultured only with maintenance media secreted 0.1nM eotaxin-1 into the culture media. This eotaxin-1 production was IL-13 dependent as IL-13/TNF-α/TGF-β1 co-stimulated NHLF cell eotaxin-1 production was dose-dependently inhibited by BAK502G9 with an IC_{50} of 32.4nM (Figure 29A).

The primary aim of this part of the study was to examine eosinophil shape change. The magnitude of eosinophil shape change in response to 3nM eotaxin (positive control) was 122.2±2.1% (n=4). Eotaxin-1 induced shape change was completely inhibited by 100nM of an anti-eotaxin antibody CAT-213, mean shape change 101.0±1.0% (n=4).

Media from NHLF cells co-stimulated with 9.6nM IL-13, 285.7pM TNF-α and 160pM TGF-β1 and cultured for 48h (conditioned media), induced a clear eosinophil and shape change (Figure 29B). In contrast, media from NHLF cultured for 48h in NHLF maintenance media alone did not induce eosinophil shape change (Figure 29B).

The addition of anti-IL-13 antibody BAK502G9 to co-stimulated media prior to NHLF culture, resulted in a dose-dependent inhibition of eosinophil shape change, with a geometric mean IC_{50} of 16.8nM when assayed at 1:16 dilution (Figure 29B).

The ability of stimulants (IL-13, TNF-α and TGF-β1) not cultured with NHLF cells to induce eosinophil and neutrophil shape change was also investigated. 9.6nM IL-13, 285.7pM TNF-α and 160pM TGF-β1 did not induce a clear eosinophil shape change. This suggests that the eosinophil shape change ability of conditioned media develops during NHLF cell culture with the stimulants is not due to any of the stimulants alone or in combination (Figure 29B).

Example 29

Mapping of anti-IL-13 antibodies on Human IL-13

The epitope mapping of a representative IL-13 antibody BAK502G9 was performed using a molecular approach and standard peptide excision.

Molecular Approach

IL-13 chimaeras were engineered, where parts of the human IL-13 sequence were replaced with murine sequence. These chimeras were used in binding studies with representative IL-13 antibodies to help identify the specific epitope.

Two panels of IL-13 chimaeras were produced. The first panel contained nine chimaeras (Figure 30) and was used to locate the general position of the epitope. The second panel contained ten chimaeras (Figure 31) and was used to fine map the epitope.

The chimaeric IL-13 sequences were assembled using PCR and cloned into a Gateway® entry vector, which were then recombined with a destination vector pDEST8 (modified to code for a detection and affinity tag at the *C*-terminus of the recombinant protein). These expression vectors were used to transform DH10Bac™ chemically competent *E coli* allowing site-specific transposition of tagged chimeric IL-13, into the baculovirus shuttle vector (bacmid). Recombinant bacmid DNA was isolated for each IL-13 chimera and transfected into *Sf*9 (*Spodoptera frugiperda*) insect cells using Cellfectin® Reagent. Recombinant baculovirus was harvested 72 hours post-transfection and passaged through *Sf*9 insect cells twice more.

Insect 2000-500 ml culture supernatant was purified on an affinity column and eluted material was concentrated from 16 to 1 ml and loaded on a size exclusion Superdex 200 HR10/300GL column for final polishing and buffer exchange.

A homogenous competition assay using biotinylated human IL-13, streptavidin-anthophyocynate and Europium labelled BAK502G9 was developed. The assay is as follows: Eu-BAK502G9 binds biotinylated-human IL-13, the complex is then recognised by the streptavidin APC conjugate and when a flash of light is applied the energy is transferred from the APC label to the Europium by proximity, and time resolved florescence can be measured. Competition for this binding is introduced by way of the un-labelled human IL-13 (as control) and the chimeric constructs. This competition is quantified to calculate the relative affinities of the IL-13 mutants for IL-13 antibodies enabling mutations altering binding to be identified.

Results

Chimeric construct IL13-Helix D (Table 5) was found to be the weakest competitor against biotinylated human IL-13 for

binding BAK502G9, indicating that helixD within the IL-13 molecule was involved with BAK502G9 epitope binding (Table 5) Reduced activity was also seen for the 4041 and 3334 mutants where residues 40, 41, and 33, 34 of the parent sequence respectively were changed indicating potential involvement of helixA in the recognition of BAK502G9. The reduced activities of loop3 was discounted as this loop has a reduced number of amino acids in the mutant as compared to the human molecule and is likely to alter the overall structure of the protein. Other reductions in the ability of the chimeric IL-13 molecules to compete for BAK502G9 binding were not considered significant for such amino acid changes.

A more targeted set of mutations within helix D (Figure 26) were then tested. Results obtained are demonstrated in Table 6 and are as follows:

Results show that chimeric constructs 116117TK (where lysine at position 116 was replaced with threonine and the aspartate at position 117 was replaced with lysine), 123KA (where lysine at position 123 was replaced) and 127RA (where arginine at position 127 was replaced) are least able to compete for binding to BAK502G9 (123KA and 127RA do not compete at 1 μM). Other residues implicated in binding to BAK502G9 due to their reduced effectiveness in the competition assay include the helixD residues 124Q (here lysine has been replaced with glutamine) and 120121SY (a leucine histidine pair has been changed to a serine tyrosine pair). Mutation of leucine at position 58L also reduces binding and analysis of the 3D structures revealed that this residue packs against helixD and may either be directly contacted by BAK502G9 or may affect the alignment of helixD.

These experiments demonstrate that residues within helixD are critical for the binding of BAK502G9 to IL-13. In particular the lysine at position 123 and the arginine at position 127 are critical for this binding as mutation to either abolishes binding of BAK502G9.

Epitope Excision

The epitope mapping of BAK502G9 was also performed using the standard peptide excision procedure. Here IgG is immobilised onto solid phase and allowed to capture the IL-13 ligand. The formed complex is then subject to specific proteolytic digestion, during which accessible peptide bonds are cleaved, however those protected by the IgG: ligand interface remain intact. Thus, a peptide containing the epitope remains bound to the IgG. This can then be desorbed, collected and identified by mass spectrometry (ms).

Two complementary techniques were used, the first made use of the Ciphergen ProteinChip Reader MALDI-TOF mass spectrometer, where it was possible to covalently link the IgG to a mass spectrometer chip and then perform the digestion and extraction *in-situ*. The second technique used biotinylated BAK502G9 linked to streptavidin coated beads and allowed the collection of sufficient peptide for sequence confirmation by tandem mass spectrometry (ms/ms).

The two procedures although differing in absolute detail and scale involved essentially the same steps, coupling of the IgG, blocking of unreacted binding sites, washing, ligand capture, removal of unbound ligand, digestion and a final washing step.

The MALDI-TOF ms approach made use of proprietary ms chips activated with carbonyldiimidazole that covalently binds to

free primary amine groups to which the IgG at 1-2 mg/ml in PBS was coupled to overnight at 4°C. The chip was subsequently blocked with an ethanolamine solution at room temperature for 1 hour and then washed extensively with PBS or HBS plus a suitable detergent. A one picomole aliquot of IL-13 was then applied to the chip in either PBS or HBS and allowed to bind to the chemically immobilized IgG for 2 hours at room temperature. This was followed by further washes in PBS or HBS with and without detergent to remove any non-specifically bound IL-13. A solution of trypsin ranging from 200 to 3.1µg/ml in PBS or HBS was then applied to the IgG:ligand complex and digestion allowed to proceed for 30 minutes at room temperature after which the chip was washed in PBS or HBS plus detergent, PBS or HBS and finally water. After application of a suitable MALDI-TOF ms matrix the chip was then be placed directly in the mass spectrometer and analysed.

The bead based approach started with the biotinylation of the IgG, using an NHS biotin compound, at a molar ratio of 1 IgG to 4 biotin molecules. Removal of unbound biotin and the by-products of the reaction using gel filtration followed this. The biotinylated IgG was then allowed to bind to neutravidin coated agarose beads, where it was attempted to maximize the IgG capture. Aliquots of IgG coated beads were then dispensed into a concentrator spin columns and washed with Dulbecco's PBS + 0.05% Tween 20 followed by resuspension in Dulbecco's PBS + 0.05% Tween 20. A pulse of IL-13 was then applied to the resuspended IgG beads and binding allowed to proceed for 10 minutes after which the liquid phase was removed by centrifugation and the beads washed with Dulbecco's PBS + 0.05% Tween 20 followed by resuspension in Dulbecco's PBS + 0.05% Tween 20.

The bead:IgG:ligand complex was then subject to proteolysis with either trypsin or chymotrypsin with incubation at room temperature or 37°C. After which the beads were again washed in Dulbecco's PBS + 0.05% Tween 20 followed by a further washes in Dulbecco's PBS without detergent. The beads were then resuspended in a water, acetonitrile, trifluroacetic mix and the supernatant recovered. This was then variously analysed either by MALDI-TOF ms or by reverse phase HPLC mass spectrometry, including tandem (ms/ms) fragmentation using the ThermoQuest LCQ ESI ion-trap mass spectrometer. An attempt was then made to match the resulting fragmentation pattern to the human IL-13 sequence and the separate heavy and light chain sequence of BAK502G9 IgG.

During the experimental sequence a number of controls, primarily blank surfaces, IgG only and isotype controls were employed to demonstrate that the identified peptides were derived specifically from IgG captured IL-13 and not a product of BAK502G9 or non-specifically bound IL-13 digestion.

Results

The experimental series consistently gave single IL-13 specific peptides for each digestion. Data from the LCQ ion trap instrument revealed that the tryptic fragment had a monoisotopic mass of 3258Da (MH+) and the chymotrypsin fragment a monoisotopic mass of 3937Da (MH+).

A search of these masses against the appropriate in silico digestion of human IL-13 gave close matches to related peptides in the C-terminal portion of the molecule.

Match for trypsin peptide mass: 3258Da

At a tolerance of 1000ppm, 3258Da matches to the sequence from aspartic acid at position 106 to the C-terminal asparagine at position 132. There are no other matches at this tolerance. This region is highlighted in bold on the sequence of the precursor form of human IL-13 below.

MALLLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGM YCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVR**DTKIEVAQFVKDLLLHLKK LFREGRFN**

Match for chymotrypsin peptide mass: 3937Da

At a tolerance of 1000ppm, 3937Da matches to the sequence from serine at position 99 to the C-terminal asparagine at position 132. This region is highlighted in bold on the sequence of the precursor form of human IL-13 below.

MALLLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGM YCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQ**FSSLHVRDTKIEVAQFVKDLLLHLKK LFREGRFN**

Both these matches show that the BAK502G9 IgG retains the C-terminal portion of the IL-13 molecule during proteolysis of the antibody:ligand complex.

The identity of both peptides was successfully confirmed by the ms/ms, neither of which showed any significant sequence parallels with BAK502G9. The ms/ms fragment map tailored to identify either Y or B ions matched 26 of 104 possible ions in one charge state for the trypsin peptide and 19 of 128 possible ions for the chymotrypsin peptide. A review of all

charge states shows identification of 23 of the 27 amino acid residues for the trypsin fragment and 29 of the 33 residues for the chymotrypsin fragment. This is sufficient to confirm identity.

The experimental sequence as a whole has identified that part of the BAK502G9 epitope on human IL-13 as lying within the twenty-seven C-terminal amino acid residues. These findings corroborate the finding of the molecular approach detailed above.

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Table 1

		HCDR1					HCDR2																	HCDR3														LCDR1											LCDR2							LCDR3												
Kabat numbering		31	32	33	34	35	50	51	52	52A	53	54	55	56	57	58	59	60	61	62	63	64	65	95	96	97	98	99	100	100A	100B	100C	100D	100E	101	102	linker	24	25	26	27	28	29	30	31	32	33	34	50	51	52	53	54	55	56	89	90	91	92	93	94	95	95A	95B	96	97	Mean TF1 (nM)	TF1 reps
BAK0278D6		N	Y	G	L	S	W	I	S	A	N	H	G	D	T	N	Y	G	Q	E	F	Q	G	D	S	S	S	N	W	A	R	W	F	F	D	L		G	G	N	N	I	G	S	K	L	V	H	D	D	G	D	R	P	S	Q	V	W	D	T	G	S	D	P	V	V	44	
BAK0502G9																												S													I																											8	
BAK1167B4	PD								D	D	D	S		T		I												S													I																											0.1	2
BAK1167F2	PD	Q	T		V																							S													I																											0.2	2
BAK1105H3	PD									G	L			E		L												S													I																											0.2	3
BAK1185E1	PD								N	D	A	T				Q										N		S													I																											0.2	2
BAK1111D10	PD								A	T	P	D		Q		S												S													I																											0.2	2
BAK1184G5	PD								R	P	T	D		L		M												S													I																											0.2	2
BAK1166G2	PD		T		I																							S													I																											0.2	2
BAK1184C8	PD									G	S			Y		S												S													I																											0.2	2
BAK1185F8	PD	D							R	N	I	D		Y		I												S													I																											0.2	2
BAK1167F4	PD	D	T		V																							S													I																											0.2	2
BAK1109G06	PD								D	D	R	T		T		Q												S													I																											0.2	2
BAK1183H4	PD								N	Y	D	G		N		Q												S													I																											0.2	2
BAK1183D2	PD								R		S	D		Q		I												S													I																											0.3	2
BAK1184F9	PD									G	I	D		V		L												S													I																											0.3	2
BAK1103G08	PD								R		A	D		E		H												S													I																											0.3	3
BAK1157D08	PD	L	T		V																							S													I																											0.3	2
BAK1183B5	PD								G	N						L												S													I																											0.3	2
BAK1097H06	PD								G	P	S	K		E		S												S													I																											0.4	2
BAK1106F04	PD								R	F	R	D		T		H												S													I																											0.4	2
BAK1183G5	PD									G	R	S		A		L												S													I																											0.5	2
BAK1181H07	PD	G	T		V																							S													I																											0.6	1
BAK1182G04	PD	H	T		I																							S													I																											0.6	1
BAK1181D07	PD	D	T		I																							S													I																											0.8	1
BAK1182D09	PD	G	T		I																							S													I																											0.8	1
BAK1108F05	PD								E	G	S	T		N		I												S													I																											0.9	1
BAK1107F08	PD				F				G	P	I			M		H												S													I																											0.9	1
ALA_VL26L	O																											S													L																											1.4	1
ALA_VL26M	O																											S													M																											1.5	1
ALA_VL26C	O																											S													C																											2.5	1
ALA_VL26V	O																											S													V																											2.5	1
ALA_VL26K	O																											S													K																											2.9	1
ALA_VL26Y	O																											S													Y																											3.1	1
ALA_VL26F	O																											S													F																											3.6	1
ALA_VL26R	O																											S													R																											3.8	1
ALA_VL26T	O																											S													T																											3.9	1
BAK1001C10	RD																			K																					I																											4.3	1
BAK1018G7	RD															D												S																G																									4.5	2
BAK1008C3	RD															D																									S				R																								5.2	2
BAK1009A4	RD													G												N																																											5.3	2
BAK1010D2	RD																											S																G																									5.4	2
BAK1007F9	RD																																							D				G																									6.4	1
BAK1010H9	RD																	R										S																G																									6.8	2
BAK1008D2	RD																									N															S			G																									6.9	1
ALA_VL26A	O																											S													A																											7.2	1
BAK1007C4	RD								G																			S													S																											7.6	2
ALA_VL26H	O																											S													H																											7.7	1
BAK1054C8	RD																					R																						G																									9.3	1
BAK1050G7	RD	D																																										G																									9.5	2
BAK1016F8	RD																											S													T																						N				10.0	1
BAK1050D2	RD																									N															I																											10.0	1
BAK1063D10	RD															I																												G																									10.8	1
BAK1060F6	RD									T																																														T													11.7	1
BAK1021D5	RD															I		R																							I																											12.0	1
BAK1062E10	RD															S												S																																									14.4	1
ALA_VL26G	O																											S													G																											14.4	1
BAK1020C8	RD															K												S																G																								I	16.0	1
BAK1022G9	RD								G							D										N																																											17.0	1
BAK1063G4	RD											I																																G																									17.0	1

Table 1 (cont'd)

		HCDR1					HCDR2																	HCDR3												
Kabat numbering		31	32	33	34	35	50	51	52	52A	53	54	55	56	57	58	59	60	61	62	63	64	65	95	96	97	98	99	100	100A	100B	100C	100D	100E	101	102
BAK278D6		N	Y	G	L	S	W	I	S	A	N	N	G	D	T	N	Y	G	Q	E	F	Q	G	D	S	S	S	N	W	A	R	W	F	F	D	L
BAK502G9																												S								
BAK1063F1	RD																			G								S								
BAK0494B6	PD																									D		S								
BAK1010C5	RD																		R									S								
BAK0496H4	PD																																			
BAK0501B6	PD																									D		S								
BAK1049D7	RD																											S								
BAK0531E2	PD																																			
BAK0433C4	PD																									T		A								
BAK1008E9	RD									T									R																	
BAK0469C8	PD																									N		A								
BAK0442E6	PD																									N										
BAK1047E3	RD																											I								
BAK0472D7	PD																									T		R								
BAK1008A7	RD																																			
BAK1063H4	RD																						K													
BAK0495A4	PD																								D	P	R	P								
BAK0782D5	PD																																			
AK0502C3	PD																											K								
AK1007H6	RD																																			
BAK1004E6	RD																									N									Y	
BAK1049G1	RD	D																																		
BAK0464B2	PD																									N		S								
BAK0502D5	PD																								R	D		S								
Phage Display	PD																																			
Ribosome Display	RD	QDLGE	T		VIF				DNARGE	DGTPNY	DLAPTSIR	STDGKI		TEQLYNVAMG		ILQSMHDK		R	R	KG		R	K		RD	NDTP	R	SAIRPK							Y	
Point mutations	O																																			
Germlining	GL																																			

		LCDR1											LCDR2							LCDR3												
Kabat numbering	linker	24	25	26	27	28	29	30	31	32	33	34	50	51	52	53	54	55	56	89	90	91	92	93	94	95	95A	95B	96	97	Mean TF1 (nM)	TF1 reps
BAK278D6		G	G	N	N	I	G	S	K	L	V	H	D	D	G	D	R	P	S	Q	V	W	D	T	G	S	D	P	V	V	44	
BAK502G9					I																										8	
BAK1063F1					S																										20.0	1
BAK0494B6								G																							21.8	4
BAK1010C5																															22.0	1
BAK0496H4					Y																										22.0	3
BAK0501B6								G																							22.8	2
BAK1049D7				S				G																							23.0	1
BAK0531E2					I																										23.2	3
BAK0433C4																															25.3	4
BAK1008E9								G																							27.0	1
BAK0469C8																															28.2	5
BAK0442E6																															29.3	3
BAK1047E3								G																							30.0	1
BAK0472D7																															31.0	4
BAK1008A7						V		G																							32.0	1
BAK1063H4								G																							34.0	1
BAK0495A4																															34.6	5
BAK0782D5									R																						39.0	1
AK0502C3								G																							39.3	3
AK1007H6					S			G																							40.5	2
BAK1004E6																															45.0	1
BAK1049G1					S																										46.0	1
BAK0464B2																															28.6	5
BAK0502D5																															29.3	4
Phage Display PD																																
Ribosome Display RD				DS	ILMCVKYFRTSAHG	V		G	R										T								N			I		
Point mutations O																																
Germlining GL																																

Table 2

Binding specificity of anti-human IL-13 antibodies

	Human IL-13	Human IL-13 variant	Non-human primate IL-13
BAK278D6	+	+	+
BAK502G9	+	+	+
BAK615E3	+	-	-

Table 3a

Kinetic analysis of anti-human IL-13 antibodies

IgG	Off-rate (s^{-1})	On-rate (M^{-1} s^{-1})	KD (pM)
BAK278D6	$7.41e^{-3}$	$5.49e^{5}$	13500
BAK502G9	$4.09e^{-4}$	$2.49e^{6}$	178
BAK1167F2	$4.05e^{-4}$	$2.99e^{6}$	136
BAK1183H4	$3.00e^{-4}$	$3.7e^{6}$	81

Table 3b

Kinetic analysis of anti-murine IL-13 antibodies

IgG	Off-rate (s^{-1})	On-rate (M^{-1} s^{-1})	KD (pM)
BAK209B11	$1.98e^{-2}$	$3.9e^{6}$	5100

Table 4

Pharmacokinetics of BAK502G9 in 4 allergic but non-challenged cynomolgus primates (2 male/2 female) after a single 10mg/kg i.v bolus dose over 29 days. BAK502G9 levels in serum were measured by ELISA (mean data).

C_{max} (t=0.25h) (µg/mL)	349.04	
Vd_{inf} ($mL.kg^{-1}$)	75.03	<80mL/kg, infers no tissue binding.
Cl_{inf} ($mL.hr^{-1}.kg^{-1}$)	0.23	
AUC_{inf} ($mg.h.mL^{-1}$)	42.99	
AUC_{ext} (%)	17.34	<30% so clearance and vol. of distribution should be accurate.
$T_{0.5}$ (h)	223.55	

Vd_{inf} = volume of distribution over time 0 - infinity, calculated from the extrapolated AUC.

Cl_{inf} = clearance over time 0 - infinity, calculated from the extrapolated AUC.

AUC_{inf} = area under the curve (measure of total drug exposure) over time 0 - infinity, including an extrapolated term based on the elimination rate constant (k) and the last observed serum drug concentration.

AUC_{ext} = percentage of the total AUC that is extrapolated.

$T_{0.5}$ = Drug half-life in the terminal elimination phase.

Table 5

First set of Chimeric constructs

Chimeric constructs	**IC50 nM**
BAK502G9	0.17 ± 0.07
loop1	0.71 ± 0.35
hum-flag	1.30 ± 0.18
30R	1.76 ± 0.45
3738VN	1.89 ± 1.9
helixB	2.49 ± 0.88
helixC	4.11 ± 0.70
loop3	5.45 ± 3.96
4041	12.02 ± 1.3
3334	12.17 ± 1.2
helixD	110.07 ± 9.9

5

Table 6

Second Set of Chimeric Constructs

Chimeric Constructs	**IC50 nM**
BAK502G9	0.11± 0.04
113H	1.6 ± 0.5
128H	1.6± 1.0
119LA	1.96 ± 1.0
130P	2.22 ± 0.8
120121SY	4.73 ± 1.5
58LA	5.2 ± 2.0
124Q	18.7 ± 15.9
116117T	82 ±11.3
123KA	none
127RA	none

Table 7:

Effects of BAK502G9 on various predefined endpoints.

Parameter	Phase I change	N	Phase II change	N	Endpoint
AHR (R_L AUC)	0.020±0.003	14[a]	0.004±0.006	14[a]	-0.016±0.006*
AHR (PC_{30})	-1.343±0.318	18[b]	-1.061±0.244	18[b]	0.282±0.179
Antigen priming (R_L AUC)	0.159±0.033	20[c]	0.033±0.025	20[c]	-0.126±0.043**
BAL total cells	20.623±3.160	21[d]	14.597±1.951	21[d]	-6.026±2.194*
BAL eosinophils	18.453±3.009	21[d]	13.412±1.737	21[d]	-5.041±2.090*
BAL mononuclear cells	2.050±0.438	21[d]	1.176±0.481	21[d]	-0.874±0.506

21 animals displaying AHR (PC_{30}) in Phase I and an additional animal with an antigen priming phenotype were carried forward for testing in Phase II (22 in total). Not every animal had AHR as measured by both AUC and PC_{30}. Only animals which displayed AHR in phase I and whose AHR was assessed in both Phase I and Phase II were included in the AHR results. Statistical testing was performed using InStat. Testing was a 2-way student's *t*-test against the null hypothesis that the endpoint did include the number 0 (i.e. there was no change in phase II compared to phase I); *$p<0.05$, **$p<0.01$. Data are shown as arithmetic mean ± SEM (n=14-21).

[a]5 animals were excluded from the AUC analysis as they did not display AHR (increased AUC) in Phase I.
3 further animals were excluded due to a technical failure in Phase II airway function data collection.

[b]3 animals were excluded from PC_{30} analysis due to a technical failure in Phase II airway function data collection (same animals as in a). The additional animal with antigen priming phenotype was excluded as it did not display PC_{30} AHR in Phase I.

[c]2 animals were excluded from the antigen priming analysis as there was a technical failure in Phase I airway function data collection.

[d]1 animal was excluded from the BAL analysis due to marked BAL inflammation at study initiation.

BAK278D6
HEAVY CHAIN

CDR1- SEQ ID NO 1: NYGLS
CDR2- SEQ ID NO 2: WISANNGDTNYGQEFQG
CDR3- SEQ ID NO 3: DSSSNWARWFFDL

BAK278D6
LIGHT CHAIN

CDR1- SEQ ID NO 4: GGNNIGSKLVH
CDR2- SEQ ID NO 5: DDGDRPS
CDR3- SEQ ID NO 6: QVWDTGSDPVV

BAK502G9
HEAVY CHAIN

CDR1-SEQ ID NO 7: NYGLS
CDR2-SEQ ID NO 8: WISANNGDTNYGQEFQG
CDR3-SEQ ID NO 9: DSSSSWARWFFDL

LIGHT CHAIN

CDR1-SEQ ID NO 10: GGNIIGSKLVH
CDR2-SEQ ID NO 11: DDGDRPS
CDR3-SEQ ID NO 12: QVWDTGSDPVV

BAK278D6
HEAVY CHAIN DOMAIN

SEQ ID NO 13:
EVQLVQSGAEVKKPGASVKVSCKASGYTFRNYGLSWVRQAPGQGLEWMGWISANNGDTN
YGQEFQGRITMTTETSTNTAHMELRSLRSDDTAVYYCVRDSSSNWARWFFDLWGKGTMV
TVSS

BAK278D6
LIGHT CHAIN DOMAIN

SEQ ID NO 14:
SYVLTQPPSVSVAPGQTARIPCGGNNIGSKLVHWYQQKPGQAPVLVVYDDGDRPSGIPE
RFSGSNSGNTATLTISRIDAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK502G9
HEAVY CHAIN DOMAIN

SEQ ID NO 15:
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGLSWVRQAPGQGLEWMGWISANNGDTN
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK502G9
LIGHT CHAIN DOMAIN

SEQ ID NO 16:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK278D6
HEAVY CHAIN

FR1- SEQ ID NO 17: EVQLVQSGAEVKKPGASVKVSCKASGYTFR
FR2- SEQ ID NO 18: WVRQAPGQGLEWMG
FR3- SEQ ID NO 19: RITMTTETSTNTAHMELRSLRSDDTAVYYCVR

BAK278D6
LIGHT CHAIN

FR1- SEQ ID NO 20: SYVLTQPPSVSVAPGQTARIPC
FR2- SEQ ID NO 21: WYQQKPGQAPVLVVY
FR3- SEQ ID NO 22: GIPERFSGSNSGNTATLTISRIDAGDEADYYC

BAK167A11
HEAVY CHAIN DOMAIN

SEQ ID NO 23:
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVGAAGEGYYGYWGRGTLVTV
SS

BAK167A11
LIGHT CHAIN DOMAIN

SEQ ID NO 24:
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYDDNQRPSGV
PDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSNNDVFGGGTKVTVL

BAK209B11
HEAVY CHAIN DOMAIN

SEQ ID NO 25:
QVQLQESGGGGLVQPGGSLRLSCAASGFTFSSYGMSWVRQAPGKGLEWVSSISASGDST
FYADSVKGRFTISRDNNKNMVFLQVNSLRADDTAVYFCAKDWSQWLVGDAFDVWGRGTT
VTVSS

BAK209B11
LIGHT CHAIN DOMAIN

SEQ ID NO 26:
DIQLTQSPSTLSASVGDRVTITCRASQSVSLWVAWYQQRPGKAPKLLIYDGSTLQSGVP
ARFSGSGSGTEFTLTISSLQPDDFATYYCQQYKTFSTFGQGTKVEIKRA

BAK502G9
HEAVY CHAIN

FR1- SEQ ID NO 27: QVQLVQSGAEVKKPGASVKVSCKASGYTFT
FR2- SEQ ID NO 28: WYRQAPGQGLEWMG
FR3- SEQ ID NO 29: RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR

BAK502G9
LIGHT CHAIN

FR1- SEQ ID NO 30: SYVLTQPPSVSVAPGKTARITC
FR2- SEQ ID NO 31: WYQQKPGQAPVLVIY
FR3- SEQ ID NO 32: GIPERFSGSNSGNTATLTISRVEAGDEADYYC

BAK615E3
HEAVY CHAIN DOMAIN

SEQ ID NO 33:
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVGKATTEEGYYGYWGRGTLV
TVSS

BAK615E3
LIGHT CHAIN DOMAIN

SEQ ID NO 34:
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSAPTTVIYDDNQRPSGV
PDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSNNDVFGGGTKVTVL

BAK1167F2

HEAVY CHAIN DOMAIN

SEQ ID NO 35:
QVQLVQSGAEVKKPGASVKVSCKASGYTFEQTGVSWVRQAPGQGLEWMGWISANNGDTN
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1167F2
LIGHT CHAIN DOMAIN

SEQ ID NO 36:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1183H4
HEAVY CHAIN DOMAIN

SEQ ID NO 37:
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGLSWVRQAPGQGLEWMGWINYDGGNTQ
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1183H4
LIGHT CHAIN DOMAIN

SEQ ID NO 38:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1105H3
HEAVY CHAIN DOMAIN

SEQ ID NO 39:
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGLSWVRQAPGQGLEWMGWISGLNGETL
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1105H3
LIGHT CHAIN DOMAIN

SEQ ID NO 40:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1111D10
HEAVY CHAIN DOMAIN

SEQ ID NO 41:
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGLSWVRQAPGQGLEWMGWIATPDGQTS
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSNSSWARWFFDLWGRGTLV
TVSS

BAK1111D10

LIGHT CHAIN DOMAIN

SEQ ID NO 42:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1167F4
HEAVY CHAIN DOMAIN

SEQ ID NO 43:
QVQLVQSGAEVKKPGASVKVSCKASGYTFIDTGVSWVRQAPGQGLEWMGWISANNGDTN
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1167F4
LIGHT CHAIN DOMAIN

SEQ ID NO 44:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1184C8
HEAVY CHAIN DOMAIN

SEQ ID NO 45:

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGLSWVRQAPGQGLEWMGWISGSNGYTS
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1184C8
LIGHT CHAIN DOMAIN

SEQ ID NO 46:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1185E1
HEAVY CHAIN DOMAIN

SEQ ID NO 47:
QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGLSWVRQAPGQGLEWMGWINDATGDTQ
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1185E1
LIGHT CHAIN DOMAIN

SEQ ID NO 48:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1185F8
HEAVY CHAIN DOMAIN

SEQ ID NO 49:
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYGLSWVRQAPGQGLEWMGWIRNIDGYTI
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1185F8
LIGHT CHAIN DOMAIN

SEQ ID NO 50:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1187B4
HEAVY CHAIN DOMAIN

SEQ ID NO 51:

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGLSWVRQAPGQGLEWMGWIDDDSGTTI
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1187B4
LIGHT CHAIN DOMAIN

SEQ ID NO 52:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK1166G2
HEAVY CHAIN DOMAIN

SEQ ID NO 53:
QVQLVQSGAEVKKPGASVKVSCKASGYTFANTGISWVRQAPGQGLEWMGWISANNGDTN
YGQEFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSSSSWARWFFDLWGRGTLV
TVSS

BAK1166G2
LIGHT CHAIN DOMAIN

SEQ ID NO 54:
SYVLTQPPSVSVAPGKTARITCGGNIIGSKLVHWYQQKPGQAPVLVIYDDGDRPSGIPE
RFSGSNSGNTATLTISRVEAGDEADYYCQVWDTGSDPVVFGGGTKLTVL

BAK167A11
HEAVY CHAIN

CDR1- SEQ ID NO 55: SYAMS
CDR2- SEQ ID NO 56: AISGSGGSTYYADSVKG
CDR3- SEQ ID NO 57: VGAAGEGYYGY

BAK167A11
LIGHT CHAIN

CDR1- SEQ ID NO 58: TRSSGSIASNYVQ
CDR2- SEQ ID NO 59: DDNQRPS
CDR3- SEQ ID NO 60: QSYDSNNDV

BAK1167F2
HEAVY CHAIN

CDR1- SEQ ID NO 61: QTGVS
CDR2- SEQ ID NO 62: WISANNGDTNYGQEFQG

CDR3- SEQ ID NO 63: DSSSSWARWFFDL

BAK1167F2
LIGHT CHAIN

CDR1- SEQ ID NO 64: GGNIIGSKLVH
CDR2- SEQ ID NO 65: DDGDRPS
CDR3- SEQ ID NO 66: QVWDTGSDPVV

BAK1166G2
HEAVY CHAIN

CDR1- SEQ ID NO 67: NTGIS
CDR2- SEQ ID NO 68: WISANNGDTNYGQEFQG
CDR3- SEQ ID NO 69: DSSSSWARWFFDL

BAK1166G2
LIGHT CHAIN

CDR1- SEQ ID NO 70: GGNIIGSKLVH
CDR2- SEQ ID NO 71: DDGDRPS
CDR3- SEQ ID NO 72: QVWDTGSDPVV

BAK1184C8
HEAVY CHAIN

CDR1- SEQ ID NO 73: NYGLS
CDR2- SEQ ID NO 74: WISGSNGYTSYGQEFQG
CDR3- SEQ ID NO 75: DSSSSWARWFFDL

BAK1184C8
LIGHT CHAIN

CDR1- SEQ ID NO 76: GGNIIGSKLVH
CDR2- SEQ ID NO 77: DDGDRPS
CDR3- SEQ ID NO 78: QVWDTGSDPVV

BAK1185E1
HEAVY CHAIN

CDR1- SEQ ID NO 79: NYGLS
CDR2- SEQ ID NO 80: WINDATGDTQYGQEFQG
CDR3- SEQ ID NO 81: DSSSSWARWFFDL

BAK1185E1
LIGHT CHAIN

CDR1- SEQ ID NO 82: GGNIIGSKLVH
CDR2- SEQ ID NO 83: DDGDRPS
CDR3- SEQ ID NO 84: QVWDTGSDPVV

BAK1167F4
HEAVY CHAIN

CDR1- SEQ ID NO 85: DTGVS
CDR2- SEQ ID NO 86: WISANNGDTNYGQEFQG
CDR3- SEQ ID NO 87: DSSSSWARWFFDL

BAK1167F4
LIGHT CHAIN

CDR1- SEQ ID NO 88: GGNIIGSKLVH
CDR2- SEQ ID NO 89: DDGDRPS
CDR3- SEQ ID NO 90: QVWDTGSDPVV

BAK1111D10
HEAVY CHAIN

CDR1- SEQ ID NO 91: NYGLS
CDR2- SEQ ID NO 92: WIATPDGQTSYGQEFQG
CDR3- SEQ ID NO 93: DSNSSWARWFFDL

BAK1111D10
LIGHT CHAIN

CDR1- SEQ ID NO 94: GGNIIGSKLVH
CDR2- SEQ ID NO 95: DDGDRPS
CDR3- SEQ ID NO 96: QVWDTGSDPVV

BAK1183H4
HEAVY CHAIN

CDR1- SEQ ID NO 97: NYGLS
CDR2- SEQ ID NO 98: WINYDGGNTQYGQEFQG
CDR3- SEQ ID NO 99: DSSSSWARWFFDL

BAK1183H4
LIGHT CHAIN

CDR1- SEQ ID NO 100: GGNIIGSKLVH
CDR2- SEQ ID NO 101: DDGDRPS

CDR3- SEQ ID NO 102: QVWDTGSDPVV

BAK1185H8
HEAVY CHAIN

CDR1- SEQ ID NO 103: DYGLS
CDR2- SEQ ID NO 104: WRINDGYTIYGQEFQG
CDR3- SEQ ID NO 105: DSSSSWARWFFDL

BAK1185H8
LIGHT CHAIN

CDR1- SEQ ID NO 106: GGNIIGSKLVH
CDR2- SEQ ID NO 107: DDGDRPS
CDR3- SEQ ID NO 108: QVWDTGSDPVV

BAK278D6
HEAVY CHAIN- SEQ ID NO: 109

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAAATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTAATAATGGCGACACAAAT
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAACTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK278D6
LIGHT CHAIN- SEQ ID NO:110

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGTAAGACGGCCAGGAT
TACCTGTGGGGGAAACAACATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK502G9
HEAVY CHAIN- SEQ ID NO:111

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAAATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTAATAATGGCGACACAAAT
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG

ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK502G9
LIGHT CHAIN- SEQ ID NO:112

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK1105H03
HEAVY CHAIN- SEQ ID NO: 113

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAAATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCTCCGGCTTGAACGGCGAGACATTG
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK1105H03
LIGHT CHAIN- SEQ ID NO: 114

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK1111D10
HEAVY CHAIN- SEQ ID NO:115

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAAATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCGCAACCCCAGACGGCCAGACAAGC
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAACAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK1111D10
LIGHT CHAIN- SEQ ID NO:116

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK 1167F2
HEAVY CHAIN- SEQ ID NO: 117

CAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTGAGCAGACCGGCGTCTCCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTAATAATGGCGACACAAAT
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK 1167F2
LIGHT CHAIN- SEQ ID NO:118

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK 1167F04
HEAVY CHAIN- SEQ ID NO:119

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTATCGACACCGGGGTCTCCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTAATAATGGCGACACAAAT
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK 1167F04
LIGHT CHAIN- SEQ ID NO:120

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG

GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK 1183H4
HEAVY CHAIN- SEQ ID NO:121

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAAATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAACTACGACGGCGGCAACACACAG
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK 1183H4
LIGHT CHAIN- SEQ ID NO:122

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK1184C8
HEAVY CHAIN- SEQ ID NO:123

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAAATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGGGAGCAACGGCTACACATCT
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACGTCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK1184C8
LIGHT CHAIN- SEQ ID NO:124

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC

CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK1185E1
HEAVY CHAIN- SEQ ID NO:125

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAAATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAACGACGCCACCGGCGACACACAG
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK1185E1
LIGHT CHAIN- SEQ ID NO:126

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK1185F8
HEAVY CHAIN- SEQ ID NO:127

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAGATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTAGAGTGGATGGGATGGATCCGCAACATCGACGGCTACACAATT
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK1185F8
LIGHT CHAIN- SEQ ID NO:128

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK1187B4
HEAVY CHAIN- SEQ ID NO:129

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTACAAATTATGGTCTCAGCTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCGACGACGACAGCGGCACGACAATA
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGCCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK1187B4
LIGHT CHAIN- SEQ ID NO:130

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK1166G02
HEAVY CHAIN- SEQ ID NO: 131

CAAGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
CTCCTGCAAGGCTTCTGGTTACACCTTTGCGAACACCGGGATCTCGTGGGTGCGACAGG
CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTAATAATGGCGACACAAAT
TATGGACAGGAATTCCAGGGCAGAGTCACCATGACCACAGATACATCCACGAGCACAGC
CTACATGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTTTATTACTGTGCGAGAG
ACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTCTGGGGTCGGGGGACACTGGTC
ACCGTCTCCTCA

BAK1166G02
LIGHT CHAIN- SEQ ID NO:132

TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGAAAGACGGCCAGGAT
TACCTGTGGGGGAAACATCATTGGAAGTAAACTTGTACACTGGTACCAGCAGAAGCCAG
GCCAGGCCCCTGTGCTGGTCATCTATGATGATGGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGC
CGGGGATGAGGCCGACTATTATTGTCAGGTGTGGGATACTGGTAGTGATCCCGTGGTAT
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

BAK165E7
HEAVY CHAIN- SEQ ID NO: 133

EVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGLSWVRQAPGQGLEWMGWISANNGETN
YGQEFQGRVTMTTETPTNTAHMELRSLTSDDTAVYYCVRDSSSNWARWYFDLWGQGTLV
TVSS

BAK165E7
LIGHT CHAIN- SEQ ID NO: 134

SYVLTQPPSVSVAPGQTARIPCGGNNIGSKLVHWYQQKPGQAPVLVVYDDGDRPSGIPE
RFSGSNSGNTATLTISRIDAGDEADYYCQVWDTGSDPVVFGGGTKLTVLG

BAK165E7
HEAVY CHAIN

CDR1- SEQ ID NO:135 NYGLS
CDR2- SEQ ID NO:136 WISANNGETNYGQEFQG
CDR3- SEQ ID NO:137 DSSSNWARWYFDL

BAK165E7
LIGHT CHAIN

CDR1- SEQ ID NO:138 GGNNIGSKLVH
CDR2- SEQ ID NO:139 DDGDRPS
CDR3- SEQ ID NO:140 QVWDTGSDPVV

BAK582F7
HEAVY CHAIN

CDR1- SEQ ID NO 141: SYAMS
CDR2- SEQ ID NO 142: AISGSGGSTYYADSVKG
CDR3- SEQ ID NO 143: VGAAGEGYYGY

BAK582F7
LIGHT CHAIN

CDR1-SEQ ID NO 144: TRSSGSIASNYVE
CDR2-SEQ ID NO 145: DDNQRPS
CDR3-SEQ ID NO 146: QSYDSNNDV

BAK612B5
HEAVY CHAIN

CDR1- SEQ ID NO 147: SYAMS
CDR2- SEQ ID NO 148: AISGSGGSTYYADSVKG

CDR3- SEQ ID NO 149: VGRATTDEGYYGY

BAK612B5
LIGHT CHAIN

CDR1- SEQ ID NO 150: TRSSGSIASNYVQ
CDR2- SEQ ID NO 151: DDNQRPS
CDR3- SEQ ID NO 152: QSYDSNNDV

BAK615E3
HEAVY CHAIN

CDR1- SEQ ID NO 153: SYAMS
CDR2- SEQ ID NO 154: AISGSGGSTYYADSVKG
CDR3- SEQ ID NO 155: VGKATTEEGYY

BAK615E3
LIGHT CHAIN

CDR1- SEQ ID NO 156: TRSSGSIASNYVQ
CDR2- SEQ ID NO 157: DDNQRPS
CDR3- SEQ ID NO 158: QSYDSNNDV

BAK0278D6
HEAVY CHAIN

CDR1- SEQ ID NO 159: AATTATGGTCTCAGC
CDR2- SEQ ID NO 160: TGGATCAGCGCTAATAATGGCGACACAAATTAT
GGACAGGAATTCCAGGGC
CDR3- SEQ ID NO 161: GACTCCAGCAGCAACTGGGCCCGCTGGTTTTTC
GATCTC

BAK278D6
LIGHT CHAIN

CDR1- SEQ ID NO 162: GGGGGAAACAACATTGGAAGTAAACTTGTACAC

CDR2- SEQ ID NO 163: GATGATGGCGACCGGCCCTCA
CDR3- SEQ ID NO 164: CAGGTGTGGGATACTGGTAGTGATCCCGTGGTA

BAK502G9
HEAVY CHAIN

CDR1- SEQ ID NO 165: AATTATGGTCTCAGC

CDR2- SEQ ID NO 166:TGGATCAGCGCTAATAATGGCGACACAAATTATGGACA
GGAATTCCAGGGC
CDR3- SEQ ID NO 167:GACTCCAGCAGCAGCTGGGCCCGCTGGTTTTTCGATCTC

BAK502G9
LIGHT CHAIN

CDR1- SEQ ID NO 168: GGGGGAAACATCATTGGAAGTAAACTTGTACAC
CDR2- SEQ ID NO 169: GATGATGGCGACCGGCCCTCA
CDR3- SEQ ID NO 170: CAGGTGTGGGATACTGGTAGTGATCCCGTGGTA

CH Domains- SEQ ID NO: 171

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQE
EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKS
RWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

CL Domain- SEQ ID NO: 172
QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK
QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

CLAIMS:

1. An isolated specific binding member for human IL-13, comprising an antibody antigen-binding site which is composed of a human antibody VH domain and a human antibody VL domain and which comprises a set of CDR's HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, wherein the VH domain comprises HCDR 1, HCDR2 and HCDR3 and the VL domain comprises LCDR1, LCDR2 and LCDR3, wherein the set of CDR's consists of a set of CDR's selected from the group consisting of:

the BAK278D6 set of CDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 1, the HCDR2 has the amino acid sequence of SEQ ID NO: 2, the HCDR3 has the amino acid sequence of SEQ ID NO: 3, the LCDR1 has the amino acid sequence of SEQ ID NO: 4, the LCDR2 has the amino acid sequence of SEQ ID NO: 5, and the LCDR3 has the amino acid sequence of SEQ ID NO: 6,

a set of CDR's which contains one or two amino acid substitutions compared with the BAK278D6 set of CDR's, and

each set of CDR's as shown for individual clones in Table 1.

2. An isolated specific binding member according to claim 1 wherein the one or two substitutions are at one or two of the following residues within the CDRs, using the standard numbering of Kabat.

31, 32, 34 in HCDR1

52, 52A, 53, 54, 56, 58, 60, 61, 62, 64, 65 in HCDR2

96, 97, 98, 99, 101 in HCDR3

26, 27, 28, 30, 31 in LCDR1

56 in LCDR2

95A, 97 in LCDR3

3. An isolated specific binding member according to claim 2 wherein the one or two substitutions are made at the following positions from among the identified groups of possible substitute residues for each position:

Position of substitution	Substitute Residue selected from the group consisting of
31 in HCDR1:	Q, D, L, G and E
32 in HCDR1:	T
34 in HCDR1:	V, I and F
52 in HCDR2:	D, N, A, R, G and E
52A in HCDR2:	D, G, T, P, N and Y
53 in HCDR2:	D, L, A, P, T, S, I and R
54 in HCDR2:	S, T, D, G, K and I
56 in HCDR2:	T, E, Q, L, Y, N, V, A, M and G
58 in HCDR2:	I, L, Q, S, M, H,D and K
60 in HCDR2:	R
61 in HCDR2:	R
62 in HCDR2:	K and G
64 in HCDR2:	R
65 in HCDR2:	K
96 in HCDR3:	R and D

97 in HCDR3: N, D, T and P

98 in HCDR3: R

99 in HCDR3: S, A, I, R, P and K

101 in HCDR3: Y

26 in LCDR1: D and S

27 in LCDR1: I, L, M, C, V, K, Y, F, R, T, S, A, H and G

28 in LCDR1: V

30 in LCDR1: G

31 in LCDR1: R

56 in LCDR2: T

95A in LCDR3: N

97 in LCDR3: I.

4. An isolated specific binding member according to claim 3 wherein there are two substitutions compared with the BAK278D6 set of CDR's, at HCDR3 residue 99 and LCDR1 residue 27.

5. An isolated specific binding member according to claim 4 comprising the BAK278D6 set of CDR's with a substitution at HCDR3 residue 99 selected from the group consisting of S, A, I, R, P and K, and/or a substitution at LCDR1 residue 27 selected from the group consisting of I, L, M, C, V, K, Y, F, R, T, S, A, H and G.

6. An isolated specific binding member according to claim 4 comprising the BAK278D6 set of CDR's with S substituted for N at HCDR3 residue 99 and/or I substituted for N at LCDR 1 residue 27.

7. An isolated specific binding member according to any one of claims 1 to 6 wherein HCDR1, HCDR2 and HCDR3 of the VH domain are within a germ-line framework and/or LCDR1, LCDR2 and LCDR3 of the VL domain are within a germ-line framework.

8. An isolated specific binding member according to claim 7 wherein the HCDR1, HCDR2 and HCDR3 of the VH domain are within germ-line framework VH1 DP14.

9. An isolated specific binding member according to claim 7 or claim 8 wherein the HCDR1, HCDR2 and HCDR3 of the VH domain are within germ-line framework VL Vλ3 3h.

10. An isolated specific binding member according to any one of claims 1 to 9 which binds a human IL-13 variant in which arginine at position 130 is replaced by glutamine.

11. An isolated specific binding member according to any one of claims 1 to 10 which binds non-human primate IL-13.

12. An isolated specific binding member according to claim 11 wherein the non-human primate IL-13 is rhesus or cynomolgus.

13. A specific binding member according to any one of claims 8 to 12 comprising the BAK502G9 VH domain (SEQ ID NO: 15).

14. A specific binding member according to any one of claims 8 to 13 comprising the BAK502G9 VL domain (SEQ ID NO: 16).

15. A specific binding member according to any one of claims 1 to 14 that binds IL-13 with affinity equal to or better than the affinity of an IL-13 antigen-binding site formed by the

BAK502G9 VH domain (SEQ ID NO: 15) and the BAK502G9 VL domain (SEQ ID NO: 16), the affinity of the specific binding member and the affinity of the antigen-binding site being as determined under the same conditions.

16. A specific binding member according to any one of claims 1 to 15 that neutralizes human IL-13.

17. A specific binding member according to claim 16 that neutralizes human IL-13, with a potency equal to or better than the potency of a IL-13 antigen-binding site formed by the BAK502G9 VH domain (SEQ ID NO: 15) and the BAK502G9 VL domain (SEQ ID NO: 16), the potency of the specific binding member and the potency of the antigen-binding site being as determined under the same conditions.

18. A specific binding member according to any one of claims 1 to 17 that comprises an scFv antibody molecule.

19. A specific binding member according to any one of claims 1 to 17 that comprises an antibody constant region.

20. A specific binding member according to claim 19 that comprises a whole antibody.

21. A specific binding member according to claim 20 wherein the whole antibody is IgG4.

22. An isolated antibody VH domain of a specific binding member according to any one of claims 1 to 21.

23. An isolated antibody VL domain of a specific binding member according to any one of claims 1 to 21.

24. A composition comprising a specific binding member, antibody VH domain or antibody VL according to any one of claims 1 to 23 and at least one additional component.

25. A composition according to claim 24 comprising a pharmaceutically acceptable excipient, vehicle or carrier.

26. An isolated nucleic acid which comprises a nucleotide sequence encoding a specific binding member or antibody VH or VL domain of a specific binding member according to any one of claims 1 to 23.

27. A host cell *in vitro* transformed with nucleic acid according to claim 26.

28. A method of producing a specific binding member or antibody VH or VL domain, the method comprising culturing host cells according to claim 27 under conditions for production of said specific binding member or antibody VH or VL domain.

29. A method according to claim 28 further comprising isolating and/or purifying said specific binding member or antibody VH or VL variable domain.

30. A method according to claim 28 or claim 29 further comprising formulating the specific binding member or antibody VH or VL variable domain into a composition including at least one additional component.

31. A method for producing an antibody antigen-binding domain specific for human IL-13, the method comprising

providing, by way of addition, deletion, substitution or insertion of one or more amino acids in the amino acid sequence of a parent VH domain comprising HCDR 1, HCDR2 and HCDR3, wherein the parent VH domain HCDR1, HCDR2 and HCDR3 are the BAK278D6 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 1, the HCDR2 has the amino acid sequence of SEQ ID NO: 2, the HCDR3 has the amino acid sequence of SEQ ID NO: 3, or the BAK502G9 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 7, the HCDR2 has the amino acid sequence of SEQ ID NO: 8, the HCDR3 has the amino acid sequence of SEQ ID NO: 9, a VH domain which is an amino acid sequence variant of the parent VH domain; and

testing said VH domain which is an amino acid sequence variant of the parent VH domain to identify an antibody antigen binding domain specific for human IL-13, or

combining said VH domain with one or more VL domains to provide one or more VH/VL combinations and testing the VH/VL combination or combinations to identify an antibody antigen binding domain specific for human IL-13.

32. A method according to claim 31 wherein the parent VH domain amino acid sequence is selected from the group consisting of SEQ ID NO: 13 and SEQ ID NO: 15.

33. A method according to claim 31 or claim 32 wherein said one or more VL domains is provided by way of addition, deletion, substitution or insertion of one or more amino acids in the amino acid sequence of a parent VL domain comprising LCDR 1, LCDR2 and LCDR3, wherein the parent VL domain LCDR1, LCDR2 and LCDR3 are the BAK278D6 set of LCDR's, defined

wherein the LCDR1 has the amino acid sequence of SEQ ID NO: 4, the LCDR2 has the amino acid sequence of SEQ ID NO: 5, the LCDR3 has the amino acid sequence of SEQ ID NO: 6, or the BAK502G9 set of LCDR's, defined wherein the LCDR1 has the amino acid sequence of SEQ ID NO: 10, the LCDR2 has the amino acid sequence of SEQ ID NO: 11, the LCDR3 has the amino acid sequence of SEQ ID NO: 12, producing one or more VL domains each of which is an amino acid sequence variant of the parent VL domain.

34. A method according to claim 33 wherein the parent VL domain amino acid sequence is selected from the group consisting of SEQ ID NO: 14 and SEQ ID NO: 16.

35. A method for producing an antibody antigen-binding domain specific for human IL-13, the method comprising

providing, by way of addition, deletion, substitution or insertion of one or more amino acids in the amino acid sequence of a parent VH domain comprising HCDR 1, HCDR2 and HCDR3, wherein the parent VH domain HCDR1, HCDR2 and HCDR3 are the BAK167A11 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 55, the HCDR2 has the amino acid sequence of SEQ ID NO: 56, the HCDR3 has the amino acid sequence of SEQ ID NO: 57, the BAK615E3 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 153, the HCDR2 has the amino acid sequence of SEQ ID NO: 154, the HCDR3 has the amino acid sequence of SEQ ID NO: 155, the BAK582F7 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 141, the HCDR2 has the amino

acid sequence of SEQ ID NO: 142, the HCDR3 has the amino acid sequence of SEQ ID NO: 143, or the BAK612B5 set of HCDR's, defined wherein the HCDR1 has the amino acid sequence of SEQ ID NO: 147, the HCDR2 has the amino acid sequence of SEQ ID NO: 148, the HCDR3 has the amino acid sequence of SEQ ID NO: 149, a VH domain which is an amino acid sequence variant of the parent VH domain; and

testing said VH domain which is an amino acid sequence variant of the parent VH domain to identify an antibody antigen binding domain specific for human IL-13, or

combining said VH domain with one or more VL domains to provide one or more VH/VL combinations and testing the VH/VL combination or combinations to identify an antibody antigen binding domain specific for human IL-13.

36. A method according to claim 35 wherein the parent VH domain amino acid sequence is selected from the group consisting of SEQ ID NO: 55 and SEQ ID NO: 33.

37. A method according to claim 35 or claim 36 wherein said one or more VL domains is provided by way of addition, deletion, substitution or insertion of one or more amino acids in the amino acid sequence of a parent VL domain comprising LCDR 1, LCDR2 and LCDR3, wherein the parent VL domain LCDR1, LCDR2 and LCDR3 are the BAK167A11 set of LCDR's, defined wherein the LCDR1 has the amino acid sequence of SEQ ID NO: 58, the LCDR2 has the amino acid sequence of SEQ ID NO: 59, the LCDR3 has the amino acid sequence of SEQ ID NO: 60, the BAK615E3 set of LCDR's, defined wherein the LCDR1 has the amino acid sequence of SEQ ID NO: 156, the LCDR2 has the amino acid sequence of SEQ ID NO: 157, the LCDR3 has the amino acid sequence of SEQ ID NO: 158, the BAK582F7 set of LCDR's, defined wherein the LCDR1 has the amino acid sequence of SEQ

ID NO: 144, the LCDR2 has the amino acid sequence of SEQ ID NO: 145, the LCDR3 has the amino acid sequence of SEQ ID NO: 146, or the BAK612B5 set of LCDR's, defined wherein the LCDR1 has the amino acid sequence of SEQ ID NO: 150, the LCDR2 has the amino acid sequence of SEQ ID NO: 151, the LCDR3 has the amino acid sequence of SEQ ID NO: 152, producing one or more VL domains each of which is an amino acid sequence variant of the parent VL domain.

38. A method according to claim 37 wherein the parent VL domain amino acid sequence is selected from the group consisting of SEQ ID NO: 24 and SEQ ID NO: 34.

39. A method according to any one of claims 31 to 34 wherein said VH domain which is an amino acid sequence variant of the parent VH domain is provided by CDR mutagenesis.

40. A method according to any one of claims 35 to 38 wherein said VH domain which is an amino acid sequence variant of the parent VH domain is provided by CDR mutagenesis.

41. A method according to any one of claims 31 to 40 further comprising providing the antibody antigen binding site within an IgG, scFv or Fab antibody molecule.

42. A method of producing a specific binding member that binds human IL-13, which method comprises:

providing starting nucleic acid encoding a VH domain or a starting repertoire of nucleic acids each encoding a VH domain, wherein the VH domain or VH domains either comprise a HCDR1, HCDR2 and/or HCDR3 to be replaced or lack a HCDR1, HCDR2 and/or HCDR3 encoding region;

combining said starting nucleic acid or starting repertoire with donor nucleic acid or donor nucleic acids encoding or produced by mutation of the amino acid sequence of the HCDR1 (SEQ ID NO: 1) or HCDR1 (SEQ ID NO: 7), HCDR2 (SEQ ID NO: 2) or HCDR2 (SEQ ID NO: 8) and/or HCDR3 (SEQ ID NO: 3) or HCDR3 (SEQ ID NO: 9) such that said donor nucleic acid is or donor nucleic acids are inserted into the CDR1, CDR2 and/or CDR3 region in the starting nucleic acid or starting repertoire, so as to provide a product repertoire of nucleic acids encoding VH domains;

expressing the nucleic acids of said product repertoire to produce product VH domains;

selecting a specific binding member specific for human IL-13, which specific binding member comprises a product VH domain or

combining said product VH domains with one or more VL domains and selecting a specific binding member specific for human IL-13, which specific binding member comprises a product VH domain and a VL domain; and

recovering said specific binding member or nucleic acid encoding it.

43. A method according to claim 42 wherein the donor nucleic acids are produced by mutation of said HCDR1 and/or HCDR2.

44. A method according to claim 42 wherein the donor nucleic acid is produced by mutation of HCDR3.

45. A method according to claim 44 comprising providing the donor nucleic acid by mutation of nucleic acid encoding the amino acid sequence of HCDR3 (SEQ ID NO: 3) or HCDR3 (SEQ ID NO: 9).

46. A method according to claim 42 comprising providing the donor nucleic acid by random mutation of nucleic acid.

47. A method according to any one of claims 42 to 46 further comprising attaching a product VH domain that is comprised within the recovered specific binding member to an antibody constant region.

48. A method according to any one of claims 42 to 46 comprising providing an IgG, scFv or Fab antibody molecule comprising the product VH domain and a VL domain.

49. A method according to any one of claims 31 to 48, further comprising testing the antibody antigen-binding domain or specific binding member that binds human IL-13 for ability to neutralize human IL-13.

50. A method according to claim 49 wherein a specific binding member that comprises an antibody fragment that binds and neutralizes human IL-13 is obtained.

51. A method according to claim 50 wherein the antibody fragment is an scFv antibody molecule.

52. A method according to claim 50 wherein the antibody fragment is an Fab antibody molecule.

53. A method according to claim 51 or claim 52 further comprising providing the VH domain and/or the VL domain of the antibody fragment in a whole antibody.

54. A method according to any one of claims 31 to 53 further comprising formulating the specific binding member that binds IL-13, antibody antigen-binding site or an antibody VH or VL variable domain of the specific binding member or antibody antigen-binding site that binds IL-13, into a composition including at least one additional component.

55. A method according to any one of claims 31 to 54 further comprising *in vitro* binding a specific binding member that binds human IL-13 to IL-13 or a fragment of IL-13.

56. A method comprising *in vitro* binding a specific binding member that binds IL-13 according to any one of claims 1 to 21 to human IL-13 or a fragment of human IL-13.

57. A method according to claim 55 or claim 56 comprising determining the amount of binding of specific binding member to IL-13 or a fragment of IL-13.

58. A method according to any one of claims 31 to 57 further comprising use of the specific binding member in the manufacture of a medicament for treatment of a disease or disorder selected from the group consisting of asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel disease and Hodgkin's lymphoma.

59. Use of a specific binding member according to any one of claims 1 to 21 in the manufacture of a medicament for treatment of a disease or disorder selected from the group consisting of asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel disease and Hodgkin's lymphoma.

60. An isolated specific binding member for human IL-13, comprising an antibody antigen-binding domain site which is composed of a human antibody VH domain and a human antibody VL domain and which comprises a set of CDR's, HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, wherein the VH domain comprises HCDR1, HCDR2 and HCDR3 and the VL domain comprises LCDR1, LCDR2 and LCDR3, wherein

HCDR1 is of amino acid sequence which has the formula

$HX_1\ HX_2\ G\ HX_3\ S$

wherein

HX_1 is selected from the group consisting of N, Q, D, L, G and E,

HX_2 is selected from the group consisting of Y and T,

HX_3 is selected from the group consisting of V, I, F and L,

HCDR2 is of amino acid sequence which has the formula

$W\ I\ HX_4\ HX_5\ HX_6\ HX_7\ G\ HX_8\ T\ HX_9\ Y\ HX_{10}\ HX_{11}\ HX_{12}\ F\ HX_{13}\ HX_{14}$

wherein

HX_4 is selected from the group consisting of S, D, N, A, R, G and E,

HX_5 is selected from the group consisting of A, D, G, T, P, N and Y,

HX_6 is selected from the group consisting of N, D, L, A, P, T, S, I and R,

HX_7 is selected from the group consisting of N, S, T, D, G, K and I,

HX_8 is selected from the group consisting of D, T, E, Q, L, Y, N, V, A, M and G,

HX_9 is selected from the group consisting of N, I, L, Q, S, M, H, D and K,

HX_{10} is selected from the group consisting of G and R,
HX_{11} is selected from the group consisting of Q and R,
HX_{12} is selected from the group consisting of E, K and G,
HX_{13} is selected from the group consisting of Q and R,
HX_{14} is selected from the group consisting of G and K,

HCDR3 is of amino acid sequence which has the formula

D HX_{15} HX_{16} HX_{17} HX_{18} W A R W HX_{19} F HX_{20} L

wherein

HX_{15} is selected from the group consisting of S, R and D,
HX_{16} is selected from the group consisting of S, N, D, T and P,
HX_{17} is selected from the group consisting of S and R,
HX_{18} is selected from the group consisting of S, N, A, I, R, P and K,
HX_{19} is selected from the group consisting of F and Y,
HX_{20} is selected from the group consisting of D and Y,

LCDR1 is of amino acid sequence which has the formula

G G LX_1 LX_2 LX_3 G LX_4 LX_5 L V H

wherein

LX_1 is selected from the group consisting of N, D and S,
LX_2 is selected from the group consisting of N, I, L, M, C, V, K, Y, F, R, T, S, A, H and G,
LX_3 is selected from the group consisting of I and V,
LX_4 is selected from the group consisting of S and G,
LX_5 is selected from the group consisting of K and R,
LCDR2 is of amino acid sequence which has the formula

D D G D R P LX_6

wherein

LX_6 is selected from the group consisting of S and T,

LCDR3 is of amino acid sequence which has the formula

Q V W D T G S LX_7 P V LX_8

wherein

LX_7 is selected from the group consisting of D and N,

LX_8 is selected from the group consisting of V and I.

61. An isolated specific binding member according to claim 60, wherein

HX_1 is selected from the group consisting of D and N,

HX_2 is Y,

HX_3 is L,

HX_4 is selected from the group consisting of S and G,

HX_5 is selected from the group consisting of T and A,

HX_6 is N,

HX_7 is selected from the group consisting of N and I,

HX_8 is D,

HX_9 is selected from the group consisting of N, D and K,

HX_{10} is G,

HX_{12} is selected from the group consisting of E and G,

HX_{13} is Q,

HX_{19} is F,

LX_1 is selected from the group consisting of N and S,

LX_2 is selected from the group consisting of N, Y, T, S, and I,

LX_6 is S,

LX_7 is D.

62. An isolated specific binding member according to claim 60, wherein

HX_1 is selected from the group consisting of N and D,

HX_2 is Y,

HX_3 is L,

HX_4 is selected from the group consisting of S and G,

HX_5 is selected from the group consisting of A and T,

HX_6 is N,

HX_7 is N,

HX_8 is selected from the group consisting of D and G,

HX_9 is selected from the group consisting of I, S, N and D,

HX_{11} is Q,

HX_{12} is E and K,

HX_{14} is G,

HX_{15} is S,

HX_{16} is selected from the group consisting of S and N,

HX_{17} is S,

HX_{18} is selected from the group consisting of S and N,

HX_{19} is F,

HX_{20} is D,

LX_1 is selected from the group consisting of N and D,

LX_3 is I,

LX_8 is V.

63. An isolated specific binding member according to claim 60, wherein

HX_7 is selected from the group consisting of N, S, T, D, G and K,

HX_8 is selected from the group consisting of D, T, E, Q, L, Y, N, V, A, M,

HX_9 is selected from the group consisting of N, I, L, Q, S, M and H,

HX_{10} is G,

HX_{11} is Q,

HX_{12} is F,

HX_{13} is Q,

HX_{14} is G,

HX_{15} is S,

HX_{16} is selected from the group consisting of N and S,

HX_{17} is S,

HX_{18} is selected from the group consisting of N and S,

HX_{19} is F,

HX_{20} is D,

LX_1 is N,

LX_2 is selected from the group consisting of N and I,

LX_3 is I,

LX_4 is S,

LX_5 is K,

LX_6 is S,

LX_7 is D,

LX_8 is V.

64. An isolated specific binding member according to claim 63, wherein

HX_1 is selected from the group consisting of N, Q and D,

HX_3 is selected from the group consisting of L, V and I,

HX_4 is selected from the group consisting of S, N, A and

R,

HX_5 is selected from the group consisting of A, D, T, G, N and Y,

HX_6 is selected from the group consisting of N, A, P, S, D and I,

HX_7 is selected from the group consisting of N, T, D and G,

HX_8 is selected from the group consisting of D, Q, Y and N,

HX_9 is selected from the group consisting of N, Q, S and I.

65. A specific binding member according to any one of claims 60 to 64 that neutralizes human IL-13.

66. A specific binding member according to claim 65 that neutralizes human IL-13, with a potency equal to or better than the potency of a IL-13 antigen-binding site formed by the BAK502G9 VH domain (SEQ ID NO: 15) and the BAK502G9 VL domain (SEQ ID NO: 16), the potency of the specific binding member and the potency of the antigen-binding site being as determined under the same conditions.

67. A specific binding member according to any one of claims 60 to 66 that comprises an scFv antibody molecule.

68. A specific binding member according to any one of claims 60 to 66 that comprises an antibody constant region.

69. A specific binding member according to claim 68 that comprises a whole antibody.

70. A specific binding member according to claim 69 wherein the whole antibody is IgG4.

71. An isolated specific binding member according to any one of claims 60 to 70 which binds a human IL-13 variant in which arginine at position 130 is replaced by glutamine.

72. An isolated specific binding member according to any one of claims 60 to 70 which binds non-human primate IL-13.

73. An isolated specific binding member according to claim 72 wherein the non-human primate IL-13 is rhesus or cynomolgus.

74. An isolated antibody VH domain of a specific binding member according to any one of claims 60 to 73.

75. An isolated antibody VL domain of a specific binding member according to any one of claims 60 to 73.

76. A composition comprising the specific binding member, antibody VH domain or antibody VL domain of any one of claims 60 to 75 and at least one additional component.

77. A composition according to claim 76 comprising a pharmaceutically acceptable excipient, vehicle or carrier.

78. An isolated nucleic acid which comprises a nucleotide sequence encoding a specific binding member or antibody VH or VL domain of a specific binding member according to any one of claims 60 to 75.

79. A host cell *in vitro* transformed with nucleic acid according to claim 78.

80. A method of producing a specific binding member or antibody VH or VL domain, the method comprising culturing host cells according to claim 79 under conditions for production of said specific binding member or antibody VH or VL domain.

81. A method according to claim 80 further comprising isolating and/or purifying said specific binding member or antibody VH or VL variable domain.

82. A method according to claim 80 or claim 81 further comprising formulating the specific binding member or antibody VH or VL variable domain into a composition including at least one additional component.

83. A method according to any one of claims 80 to 82 further comprising *in vitro* binding a specific binding member that binds human IL-13 to IL-13 or a fragment of IL-13.

84. A method comprising *in vitro* binding a specific binding member that binds IL-13 according to any one of claims 60 to 73 to human IL-13 or a fragment of human IL-13.

85. A method according to claim 83 or claim 84 comprising determining the amount of binding of specific binding member to IL-13 or a fragment of IL-13.

86. A method according to any one of claims 80 to 82 further comprising use of the specific binding member in the manufacture of a medicament for treatment of a disease or disorder selected from the group consisting of asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel disease and Hodgkin's lymphoma.

87. Use of a specific binding member according to any one of claims 60 to 73 in the manufacture of a medicament for treatment of a disease or disorder selected from the group consisting of asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel disease and Hodgkin's lymphoma.