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(72) **Inventeurs/Inventors:**
LUTTERBUSE, RALF, DE;
MAYER, PETRA, DE;
SCHALLER, EVELYNE, DE;
RAU, DORIS, DE;
MANGOLD, SUSANNE, DE;
KUFER, PETER, DE;
...

(73) **Propriétaire/Owner:**
AMGEN RESEARCH (MUNICH) GMBH, DE

(74) **Agent:** GOWLING WLG (CANADA) LLP

(54) **Titre : PREPARATIONS PHARMACEUTIQUES COMPRENANT UN ANTICORPS A CHAINE UNIQUE BISPECIFIQUE A SPECIFICITE POUR LE CD3 HUMAIN ET L'ACE HUMAIN ET POSEDANT UNE RESISTANCE A L'ACE SOLUBLE**

(54) **Title: PHARMACEUTICAL COMPOSITIONS COMPRISING A BISPECIFIC SINGLE CHAIN ANTIBODY WITH SPECIFICITY FOR HUMAN CD3 AND HUMAN CEA AND HAVING RESISTANCE TO SOLUBLE CEA**

(57) **Abrégé/Abstract:**

The present invention relates to pharmaceutical compositions for the treatment of an epithelial tumor in a human, said pharmaceutical composition comprising a bispecific single chain antibody which has a first binding domain specifically binding to human CD3, and a second binding domain specifically binding to human CEA, wherein said second binding domain comprises at least a part of the CDR-H3 or the complete CDR-H3 of murine monoclonal antibody A5B7. Furthermore, processes for the production of said pharmaceutical compositions as well as medical/pharmaceutical uses for the specific bispecific single chain antibody molecules bearing specificities for the human CD3 antigen and the human CEA antigen are disclosed.

(72) **Inventeurs(suite)/Inventors(continued):** MURR, ALEXANDER, DE; WISSINGER, MONIKA, DE; RAUM, TOBIAS, DE

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(71) **Applicant** *(for all designated States except US)*: **MICROMET AG** [DE/DE]; Staffelseestrasse 2, 81477 München (DE).

(72) **Inventors; and**
(75) **Inventors/Applicants** *(for US only)*: **LUTTERBÜSE, Ralf** [DE/DE]; Fliederstrasse 11, 82061 Neuried (DE). **MAYER, Petra** [DE/DE]; Wertheimerstrasse 82, 81243 München (DE). **SCHALLER, Evelyne** [DE/DE]; Tegernseer Landstrasse 8, 82054 Sauerlach (DE). **RAU, Doris** [DE/DE]; Ter-Meer-Strasse 51, 82008 Unterhaching (DE). **MANGOLD, Susanne** [DE/DE]; Forstenrieder Allee 140a, 81476 München (DE). **KUFER, Peter** [DE/DE]; Am Kapellenacker 13, 85368 Moosburg (DE). **MURR, Alexander** [DE/DE]; Schyrenstrasse 10, 81543 München (DE). **WISSINGER, Monika** [DE/DE]; Am Waldhang 11, 82205 Gilching (DE). **RAUM, Tobias** [DE/DE]; Plenzenauerstrasse 110, 81925 München (DE).

(74) **Agent: VOSSIUS & PARTNER**; Siebertstr. 4, 81675 München (DE).

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(54) **Title:** PHARMACEUTICAL COMPOSITIONS WITH RESISTANCE TO SOLUBLE CEA

(57) **Abstract:** The present invention relates to pharmaceutical compositions for the treatment of an epithelial tumor in a human, said pharmaceutical composition comprising a bispecific single chain antibody which has a first binding domain specifically binding to human CD3, and a second binding domain specifically binding to human CEA, wherein said second binding domain comprises at least a part of the CDR-H3 or the complete CDR-H3 of murine monoclonal antibody A5B7. Furthermore, processes for the production of said pharmaceutical compositions as well as medical/pharmaceutical uses for the specific bispecific single chain antibody molecules bearing specificities for the human CD3 antigen and the human CEA antigen are disclosed.

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Pharmaceutical compositions comprising a bispecific single chain antibody with specificity for human CD3 and human CEA and having resistance to soluble CEA

More than three decades have passed since Gold and Freedman first described the tumor associated carcinoembryonic antigen (CEA) in human colon cancer tissue extracts (Gold and Freedman; J. Exp. Med. 122 (1965); 467-481).

Meanwhile, 28 other genes/pseudogenes relating to the CEA gene family have been discovered. In an attempt to simplify the nomenclature used for the members of the CEA gene family, the family has recently been renamed the “CEA-related cellular adhesion molecules” (CEACAMs) and the nomenclature for its members has been unified (Beauchemin, Exp. Cell Res. 252 (1999), 243-249). For example, according to this nomenclature, human CEA (CD66e) is termed CEACAM5.

The human CEA gene family is clustered on chromosome 19q13.2 (Olsen et al. Genomics 23 (1994); 659-668). Its 29 genes and pseudogenes can be divided into three subgroups, i.e. the CEA subgroup containing seven expressed genes, the pregnancy-specific-glycoprotein (PSG) subgroup containing eleven expressed genes and the third subgroup which contains only pseudogenes (Hammarström, Sem. Cancer Biol. 9 (1999), 67-81; Beauchemin, Exp. Cell Res. 252 (1999), 243-249). The analysis of the amino acid sequences of CEA and the other family members revealed that they belong to the immunoglobulin (Ig) superfamily (Williams and Barclay, Annul. Rev. Immunol. 6 (1988), 381-405). All members of the CEA subgroup are attached to the cell surface membrane: Biliary glycoprotein (CEACAM1; BGP1; TM-CEA; CD66a), CEA gene family member 1 (CEACAM3; CGM1; CD66d) and CEA gene family member 7 (CEACAM4; CGM7) have hydrophobic transmembrane domains, whereas carcinoembryonic antigen (carcinoembryonic antigen-related cell adhesion molecule 5; CEACAM5; CEA; CD66e), non-specific cross-reacting antigen (CEACAM6; NCA; NCA-50/90; CD66c), CEA gene family member 2 (CEACAM7; CGM2) and CEA gene family member 6 (CEACAM8; CGM6; CD66b) are linked to the plasma membrane by glycosylphosphatidylinositol (GPI) lipid moieties. The CEA proteins are highly glycosylated with a molecular weight of up to approximately 300 kDa, depending on the number of Ig domains.

As regards the biological activity of the CEA proteins, in vitro studies with tumor cell lines suggested that several CEA subfamilies including biliary glycoprotein, CEA and non-specific cross-reacting antigen can act as homophilic and heterotypic cell adhesion molecules when expressed on the tumor cell surface (Oikawa et al., Biochem. Biophys. Res. Commun. 186 (1992), 881-887; Zhou et al., Cancer Res. 53 (1993), 3817-3822). More recently, a possible role of CEA and non-specific cross-reacting antigen in the innate immune defense protecting colon from microbial attack has been discussed (Hammarström and Baranov, Trends Microbiol. 9 (2001), p. 119-125). In particular, it has been proposed that these proteins bind and trap microorganisms preventing them from reaching and invading the epithelial cells of the microvilli.

It was hypothesized that CEA is an oncofetal antigen which is expressed during fetal life, absent in the healthy adult and re-expressed in cancer. However, CEA is also expressed in normal adult tissue. For instance, biliary glycoprotein, CEA, non-specific cross-reacting antigen and CEA gene family member 2 are expressed in normal human colon, particularly in the mature columnar epithelial cells facing the gut lumen and in the highly differentiated cells at the crypt mouth (Frängsmyr et al., Cancer Res. 55 (1995), 2963-2967; Frängsmyr et al., Tumor Biol. 20 (1999), 277-292). More specifically, these proteins are localized to the brush-border glycocalyx of the mature colonocytes lining the free luminal surface. Biliary glycoprotein, CEA and non-specific cross-reacting antigen are also expressed in a number of tumors of epithelial origin (Hammarström, Sem. Cancer Biol. 9 (1999), 67-81; Shively and Beatty CRC Crit. Rev. Oncol. Hematol. 2 (1985), 355-399).

Already in the late 1970s and early 1980s, CEA became a favored target antigen for radioimmunolocalization of colorectal and other epithelial tumors. This is due to the fact that CEA is overexpressed in 95% of gastrointestinal and pancreatic cancers, as well as in most small-cell and non-small-cell lung carcinomas. It is also expressed in breast carcinoma and squamous cell carcinoma of the head and neck (Primus et al., Cancer 42 (1978), 1540-1545). In fact, CEA is one of the most extensively used clinical tumor markers. It is used as a serum tumor marker for colorectal and some other cancers due to its stability, its fairly restricted expression in normal adult tissue and its high expression in tumors of epithelial origin. The bulk of CEA in a healthy individual is produced in colon. There it is released from the apical surface of mature columnar cells into the gut lumen and disappears with the feces. Thus, only very low levels are normally seen in the blood from healthy individuals. For instance, CEA levels in the blood of healthy individuals is less than 2μg/l. In contrast, CEA levels in serum from patients with colorectal and other carcinomas are increased, ranging up to more than 2000 μg/l (Thomson et al., PNAS 64 (1969), 161-167). In particular, progressive, malignant, or late stage epithelial tumors are frequently accompanied by high serum concentrations of soluble CEA (Fletcher; Ann. Intern. Med. 104 (1986), 66-73). It is known that components from the plasma membrane, including CEA, are continually exfoliated from the surface as plasma membrane-derived vesicles (Taylor and Black, J. Natl. Cancer Inst. 74 (1985), 859-866; Sack et al., J Clin Invest. 82 (1988), 586-93) which through draining lymph and blood vessels can end up in the blood. As the tumor size increases, more CEA will accumulate in the blood. The main use of serum CEA determinations as a tumor marker is in the post-surgical surveillance of colon cancer. Increased CEA levels was the first indicator of recurrent disease in 81% (Minton et al., Cancer 55 (1985), 1284-1290) and 89% (Wanebo et al., Surg. Gynecol. Obstet. 169 (1989), 479-487) of patients, respectively. Serum CEA levels can also be used as a prognostic indicator (Mulcahy and Benson, Curr. Oncol. Rep. 1 (1999), 168-172).

Due to its over-expression in many epithelial cancers CEA is not only used as a tumor marker but also as a target for anti-tumor therapy. For example, gastrointestinal cancers account for a large proportion of human epithelial tumors, with an estimated 21.700 new cases of gastric cancer and 135.400 new cases of colorectal cancer in the United States in the year 2001 (Greenlee; CA Cancer J Clin 51 (2001), 15-36). Colorectal cancer is the third most common malignancy and the third leading cause of death from cancer in both males and females (Ries; Cancer 88 (2000), 2398-2424). In an attempt to find new therapeutics against these tumors, anti-CEA monoclonal antibodies have been explored as possible therapeutics for CEA-positive cancers (Murakami et al., Immunol. Invest. 25 (1996), 23-35).

One example for an approach in which patients with low tumor load (corresponding to low serum CEA levels) have been successfully treated is a study performed by Behr et al. In this approach, a ^{131}I-labeled variant of labetuzumab (labetuzumab is a humanized form of anti-CEA monoclonal antibody MN-14; Behr et al., Cancer, 94: 1373-1381, (2002), 1559-64) has been analysed in a phase II trial in which 30 CRC patients with small volume metastatic disease chemorefractory to 5-fluorouracil and folinic acid or in an adjuvant setting after liver metastasis have been enrolled. A single injection of ^{131}I-labeled labetuzumab was given. Of 19 assessable patients, 3 had partial remissions and eight showed minor responses up to 15 months in duration. In the adjuvant setting, 7 of 9 patients were disease free for up to 3 years, whereas the relapse rate in the control group was 67% in the same time period. The serum CEA levels of the patients ranged from 3.9 – 45 ng/ml (Behr et al., Cancer, 94: 1373-1381, 2002). In another study characterized by patients with low CEA serum levels (<5ng/ml), CEA radio-immunotherapy with ^{131}I-labetuzumab (loc. cit.) has been shown to improve survival post salvage resection of colorectal cancer metastases in the liver. 23 patients received a dose of 40–60 mCi/m^2 ^{131}I-labetuzumab. Five-year survival was 51.3% for treated and 7.4% for control groups, respectively (Liersch et al., JCO, 2005, ASCO Proc, Vol 23, No 16S: 3627).

Yet, therapeutic approaches dealing with high serum CEA concentrations frequently resulted in low or no anti-tumor responses. For example, in a clinical study performed to evaluate a humanized anti-CEA monoclonal antibody in clinic, a CDR-grafted version of MN-14 (hMN-14; Sharkey, Cancer Res. 55 (23 Suppl) (1995) 5935s-5945s.) has been labeled with ^{131}I. 19 patients with advanced CEA-producing tumors received ^{131}I labeled hMN-14. The biodistribution, tumor targeting, and pharmacokinetic behavior of the hMN-14 was similar to that seen with the murine MN-14. However, patients with elevated CEA (> 200 ng/ml) in plasma had more than 30% of the labeled antibody complexed within 1 h after injection. In some of these patients, increased complication resulted in enhanced metabolism of the antibody with more rapid clearance from the blood than that seen in patients with lower plasma CEA (Sharkey, loc. cit.). In another phase I trial carried out by Yu et al., an ^{131}I-labeled high-affinity murine monoclonal antibody (mAb) against CEA, COL-1 (Muraro, Cancer Res. 45 (1985), 5769-80), has been investigated in patients with gastrointestinal malignancies. In particular, the influence of serum CEA and tumor bulk on pharmacokinetics has been analysed. To this end, 18 patients with advanced gastrointestinal malignancies received 20 mg of COL-1 labeled with ^{131}I, with doses from 10 mCi/m^2 to 75 mCi/m^2. Serum CEA level ranged from 6 to 2739 ng/mL (mean +/- SD, 500 +/- 639). 82% of all tumor-involved organs were positive and 58% of all lesions. However, it has been again observed that elevated serum CEA (> 500 ng/mL) and tumor bulk directly correlated with clearance of serum radioactivity. The authors concluded that patients with highly elevated circulating CEA levels and/or increased tumor bulk clear ^{131}I-labeled COL-1 more rapidly from the circulation (Yu et al., J. Cli. Oncol. 14 (1996), 1798-1809). Similar results have been obtained in a study by Hajjar et al. with iodine-131--labeled humanized MN-14 anti-CEA monoclonal antibody in patients with metastatic gastrointestinal and colorectal cancer. In this phase I trial, 21 patients either after prior external beam radiation or after standard chemotherapy have been treated with antibody. 7 of 21 patients had human anti-human antibodies (HAHAs), but no adverse effects. No antitumor response was observed. Again it has been found that elevated plasma CEA levels increase the clearance of the antibody from the blood and whole body (Hajjar et al., Clin Colorectal Cancer, 2 (2002), 31-42) which at least in part may provide for an explanation of the lacking anti-tumor response observed in this study. The phenomenon of rapid clearance of therapeutic antibody from blood and body may be explained by increased formation of immune complexes which have to be rapidly removed from the body in order to prevent organ damage. No therapeutic effect could be observed in the tumor patients enrolled in these studies, most probably due to the rapid clearance of the monoclonal antibodies.

In order to circumvent problems caused by immune complex formation and rapid clearance of therapeutic monoclonal antibodies which are most likely mediated by the Fc part of the antibodies recognized by Fc receptors of immune cells, antibody derivatives (e.g. scFv constructs) or fragments (e.g. Fab and Fab$_2$ fragments) without Fc part have been produced and analysed in clinic. Most of these studies are directed to tumor imaging and detection/localization (see e.g. Chester et al., Cancer Chemother Pharmacol, 46 (2000) Suppl: S8-12; Mayer et al., Clin Cancer Res, *6:* (2000) 1711-1719; Begent et al., Nat Med, 2 (1996): 979-984). Only a few studies investigated the therapeutic efficacy of such antibody derivatives/fragments in clinic. For example, in a clinical approach by Francis et al. (Francis, Br. J. Cancer 87(6) (2002), 600-607) anti-tumor activity of a scFv-carboxypeptidase construct has been investigated. In this phase I trial, the antibody directed enzyme prodrug therapy (ADEPT) has been used in patients with advanced colorectal carcinoma or other CEA producing tumours. To this end, A5CP, consisting of a F(ab)$_2$ fragment of a mouse monoclonal antibody to CEA (A5B7) linked to the bacterial enzyme carboxypeptidase (CPG2) as the antibody-enzyme targeting agent and ZD2767P, a bis-iodo phenol mustard prodrug have been utilized. As a result, no clinical or radiological responses have been seen in the study. Pre-treatment serum CEA levels ranged up to 1000 ng/ml. These high CEA concentrations in serum of the treated tumor patients may be at least in part responsible for the lacking anti-tumor response observed in this study.

In view of the problems set forth above, the provision of means and methods for efficient therapeutics for progressive, malignant, or late stage epithelial tumors is highly desirable.

Accordingly, one aspect of the invention relates to a pharmaceutical composition, said pharmaceutical composition comprising a bispecific single chain antibody which has

(a) a first binding domain specifically binding to human CD3, and

(b) a second binding domain specifically binding to human CEA,

wherein said second binding domain comprises at least the amino acid sequence "$DX_1X_2X_3X_4FYFDY$" (SEQ ID NO. 65), wherein "X_1", "X_2", "X_3" or "X_4" represents any amino acid residue, and the amino acid residue "D" corresponds to Kabat position 95 of CDR-H3 of murine monoclonal antibody A5B7 and the amino acid residues "FYFDY" correspond to Kabat positions 100, 100a, 100b, 101, and 102, respectively, of CDR-H3 of murine monoclonal antibody A5B7. In one embodiment, "X_1" represents "R" (Arginine), "F" (Phenylalanine), "M" (Methionine), "E" (Glutamic acid), or "T" (Threonine); "X_2" represents "G" (Glycine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), or "S" (Serine); "X_3" represents "L" (Leucine), "F" (Phenylalanine), "M" (Methionine), "E" (Glutamic acid), or "T" (Threonine); and "X_4" represents "R" (Arginine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), or "S" (Serine).

In an embodiment of the pharmaceutical composition of the invention, said second binding domain specific for human CEA of the bispecific single chain antibody defined herein comprises at least the amino acid sequence "DRGLRFYFDY" (SEQ ID NO. 66) corresponding to Kabat positions 95 – 102 of the CDR-H3 of murine monoclonal antibody A5B7.

The present invention provides means and methods particularly suited for the treatment of epithelial tumor patients with high soluble CEA concentrations in their plasma. Such high soluble CEA concentrations are found in the serum/plasma of epithelial tumor patients with progressive tumors, recurrent, metastatic, late stage tumors and for patients with high tumor load/burden. It has been found that bispecific single chain antibodies with a CEA binding domain comprising the amino acid sequence "DRGLRFYFDY" (SEQ ID NO. 66) not only bind to CEA-positive target cells, but also to soluble CEA; see Example 3 and Figure 2 of the present invention; and EP B1 491031. The indicated amino acid sequence "DRGLRFYFDY" corresponds to Kabat positions 95 – 102 (SEQ ID NO. 66) of the CDR-H3 of murine monoclonal antibody A5B7 (Harwood, Br J Cancer. 54 (1986), 75-82). Surprisingly, although binding to soluble CEA, said bispecific single chain antibodies kill CEA-bearing tumor cells, even in the presence of high concentrations of soluble CEA (up to 1µg/ml soluble CEA has been tested). Put in other words, said bispecific constructs are not inhibited by soluble CEA in their cytotoxic activity against CEA-positive tumor cells.

As shown in the following Examples 5 and 8 (in combination with Figures 5, 6, 8, 10, 19, 20, 22 and 27), bispecific single chain antibodies with a CEA binding domain comprising the amino acid sequence "DRGLRFYFDY" mediated cytotoxicity to CEA-positive tumor cells, in the presence of even high concentrations of soluble CEA. For instance, Figure 10 shows a cytotoxicity assay of CEA-reactive bispecific single chain constructs redirected to Kato III cells (CEA-positive human gastric carcinoma cell line) in the presence of increasing amounts of soluble CEA antigen. Stimulated human CD8 positive cytotoxic T cells (CTLs) were used as effector cells. CEAI VHVLxSEQ ID NO.77 VHVL-mediated cytotoxicity is resistant to soluble CEA. In contrast, CEAII VHVLxSEQ ID NO.77 VHVL-mediated cytotoxic activity is inhibited by increasing amounts of soluble CEA. CEAI is a variable region derived from murine mAb A5B7, whereas CEAII VHVL is derived from mAb T84.66.

Importantly, it has been found that the amino acid sequence "DRGLRFYFDY" is sufficient to mediate resistance to soluble CEA when used in a human CEA-binding domain (i.e. a human binding domain specifically binding to human CEA) of anti-CEAxanti-CD3 bispecific single chain antibodies; see e.g. Figures 19, 20, 22 and 27.

In the following, bispecific single chain antibodies as defined herein are therefore referred to as being resistant to soluble CEA antigen. The term "resistance to soluble CEA antigen", "resistant to soluble CEA" or related terms as used herein refers to the fact that the cytotoxicity against CEA-positive target or tumor cells mediated by said bispecific single chain antibodies is not affected by increasing concentrations of soluble CEA. In particular, the cytotoxic activity is not inhibited by even high concentrations of soluble CEA (up to 1μg/ml has been tested). As set forth above, CEA levels in the blood of healthy individuals is less than 2ng/ml. High soluble CEA concentrations in the serum/plasma of tumor patients are characteristic for progressive, recurrent, metastatic, or late stage tumors and for patients with high tumor load. Thus, the present invention provides means and methods particularly suited for the treatment of epithelial tumor patients with such high soluble CEA concentrations in their plasma. The term "high soluble CEA concentrations" as used herein denotes a soluble serum/plasma-CEA concentration higher than 10, 20, 50, 70, 80, 90 or 100 ng/ml. This serum/plasma-CEA concentration may be determined, inter alia, by ELISA. Preferably, said soluble serum/plasma-CEA concentration is higher than 100 ng/ml, as determined e.g. by ELISA.

The generation of said bispecific single chain antibodies with resistance to soluble CEA antigen was no trivial task, as evident from the following Examples. For instance, bispecific single chain antibodies with a CEA binding domain derived from a monoclonal antibody (mAb) known to bind membrane-bound CEA but not soluble CEA, i.e. mAb PR1A3 (Durbin, Proc Natl Acad Sci U S A. 91 (1994), 4313-7), could not be produced: When used in the bispecific single chain antibody format, no expression/secretion of the anti-CD3xanti-CEA bispecific single chain construct could be achieved. When a humanized version of PR1A3 (Durbin, loc. cit.) has been utilized for the generation, the bispecific single chain antibody construct was expressed and secreted from the host cell. However, no binding of the anti-CEA binding domain to membrane-bound CEA could be obtained.

When bispecific single chain antibodies derived from the well-described monoclonal antibodies T84.66 (Neumaier, M. et al., Cancer Res 50 (1990), 2128-34) or MFE-23 (Boehm, M. K. Biochem J 2 (2000), 519-28) have been generated, these bispecific antibodies were highly sensitive to soluble CEA antigen, ie. their cytotoxic activity against CEA-positive target or tumor cells has been blocked in the presence of soluble CEA antigen. Since said constructs have been found to bind to soluble CEA, it was concluded that soluble CEA antigen prevents the antibody from binding to membrane-bound CEA, thereby blocking antibody-mediated cytotoxic activity. For example, Figure 7 shows a cytotoxicity assay of a CEA-reactive bispecific single chain construct redirected to CHO cells transfected with CEA in the presence of soluble human CEA. Stimulated human CD8 positive cytotoxic T cells (CTLs) were used as effector cells. Cytotoxic activity of CEAII VHVLxSEQ ID NO.77 VHVL is clearly inhibited by increasing amounts of soluble CEA. CEAII VHVL is derived from mAb T84.66; SEQ ID NO.77 is an anti-CD3 VH-VL domain.

Resistance to soluble CEA antigen could be found only for bispecific single chain antibodies, the CEA binding domain of which comprised the amino acid sequence "DRGLRFYFDY" of the CDR-H3 of murine monoclonal antibody A5B7 (Harwood, Br J Cancer. 54 (1986), 75-82). As for MFE-23- and T84.66-derived bispecific single chain constructs, A5B7-derived bispecific single chain antibodies bind to soluble CEA. In light of the results obtained for MFE-23- and T84.66-derived bispecific single chain constructs, it could not be expected that soluble CEA does not influence cytotoxic activity in A5B7-derived single chain bispecific antibody constructs.

As set forth above, many therapeutic approaches directed against CEA-bearing epithelial tumors in human are seriously hampered by the presence of high levels of soluble CEA antigen in the plasma of patients cancer. For example, increased immune-complex formation and clearance of therapeutic anti-CEA monoclonal antibodies in the presence of high CEA concentrations in plasma has been observed in several clinical studies. In addition, soluble CEA antigen - frequently present in high concentrations in the serum of cancer patients with progressive tumors, recurrent cancer, metastasic tumors, high tumor load/burden, or late-stage tumors - blocks the therapeutics directed against CEA-positive tumor cells, thus preventing tumor cell recognition and destruction. Therefore, the actual amount of the therapeutic which reaches the tumor is reduced, resulting in a decreased, low or even no anti-tumor activity. This limitation so far restricts e.g. antibody-based approaches to those patients with very low amounts of soluble CEA antigen unlikely to prevent therapeutic-tumor cell interaction.

In the present invention, it has been found that it is possible to generate bispecific single chain antibody-therapeutics with specificity for human CD3 and human CEA, wherein the cytotoxic activity directed against tumor cells is resistant to even high concentrations of soluble CEA antigen (up to 1μg/ml soluble CEA have been tested). This finding is entirely unexpected in view of the fact that the bispecific single chain antibodies of the invention binds to soluble CEA antigen (see Example 3 and Figure

2 of the present invention; see also EP B1 491031). Nevertheless, the bispecific single chain antibodies as defined herein are entirely resistant to the presence of even high levels of soluble CEA in its cytotoxic activity towards tumor cells. Thus, the present invention provides means and methods particularly suited for the treatment of tumor patients with high soluble CEA concentrations in their plasma, as observed e.g. during tumor progression, for recurrent cancer, for metastasis, for patients with high tumor load/burden, or late-stage tumors.

In accordance with this invention, the term "pharmaceutical composition" relates to a composition for administration to a human patient. Preferably, the pharmaceutical composition comprises suitable formulations of carriers, stabilizers and/or excipients. In a preferred embodiment, the pharmaceutical composition comprises a composition for parenteral, transdermal, intraluminal, intraarterial, intrathecal and/or intranasal administration or by direct injection into tissue. It is in particular envisaged that said composition is administered to a patient via infusion or injection. Administration of the suitable compositions may be effected by different ways, e.g., by intravenous, intraperitoneal, subcutaneous, intramuscular, topical or intradermal administration. The composition of the present invention may further comprise a pharmaceutically acceptable carrier. Examples of suitable pharmaceutical carriers are well known in the art and include phosphate buffered saline solutions, water, various types of wetting agents, sterile solutions, liposomes, etc.. Compositions comprising such carriers can be formulated by well known conventional methods. These compositions can be administered to the subject at a suitable dose which can be determined e.g. by dose escalating studies by administration of increasing doses of the bispecific single chain antibody exhibiting resistance to soluble serum CEA antigen described herein. As set forth above, the bispecific single chain antibody described herein with resistance to soluble serum CEA antigen can be advantageously used in the treatment of cancer patients with high CEA serum concentrations, such as progressive tumors, recurrent cancer, metastatic tumors, high tumor load/burden, or late stage tumors. These compositions can also be administered in combination with other proteinaceous and non-proteinaceous drugs, e.g. in the form of a co-therapy. These drugs may be administered simultaneously with the composition comprising the bispecific single chain antibody as defined herein or separately before or after administration of said bispecific antibody in timely defined intervals and doses. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical arts, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, and suspensions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, aqueous solutions, or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, or lactated Ringer's. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, inert gases and the like. In addition, the composition of the present invention might comprise proteinaceous carriers, like, e.g., serum albumin or immunoglobulin, preferably of human origin. It is envisaged that the co-therapy comprise, in addition to the bispecific single chain antibody as defined herein, further biologically active agents, depending on the intended use of the composition. Such agents might be drugs acting on the gastro-intestinal system, drugs acting as antineoplastic agents, chemotherapeutics, cytostatica, drugs preventing hyperurikemia, drugs inhibiting immunoreactions (e.g. corticosteroids), drugs modulating the inflammatory response, drugs acting on the circulatory system and/or agents such as cytokines known in the art.

Preferably, the bispecific single chain antibody as defined herein is formulated in a buffer, a stabilizer and a surfactant. The buffer may be a phosphate, citrate, succinate or acetate buffer. The stabilizer may be (an) amino acid(s) and/or a sugar. The surfactants may be detergents, PEGs, or the like. More preferably, the bispecific single chain antibody as defined herein is formulated in citrate, lysine, trehalose and Tween^{TM} 80. As a diluent for the pharmaceutical composition of the invention, isotonic saline and Tween^{TM} 80 is preferred.

As used herein, a “bispecific single chain antibody” denotes a single polypeptide chain comprising two binding domains. Each “binding domain” as used herein comprises one variable region from an antibody heavy chain (“VH region”), wherein the VH region of the first binding domain specifically binds to said first molecule, i.e. the human CD3 molecule, and the VH region of the second binding domain specifically binds to human CEA, as defined in more detail below. The two binding domains are optionally linked to one another by a short polypeptide spacer generally comprising on the order of 5 amino acids. Each binding domain may additionally comprise one variable region from an antibody light chain ("VL region"), the VH region and VL region within each of the first and second binding domains being linked to one another via a polypeptide linker, for example of the type disclosed and claimed in EP B1 623679, but in any case long enough to allow the VH region and VL region of the first binding domain and the VH region and VL region of the second binding domain to pair with one another such that, together, they are able to specifically bind to the respective first and second molecules. The arrangement of the V regions of the first or second binding domain may be VH-VL or VL-VH. Preferably, the arrangement of the first binding domain specifically binding to human CD3 is VH-VL, as shown in the following Examples. It is envisaged that the first binding domain may be located N-terminally or C-terminally to the second binding domain. Thus, the arrangement of the binding domains of the bispecific single chain antibodies defined herein may be VH_{CEA}-VL_{CEA}-VH_{CD3}-VL_{CD3}, VL_{CEA}-VH_{CEA}-VH_{CD3}-VL_{CD3}, VH_{CD3}-VL_{CD3}-VH_{CEA}-VL_{CEA} or VH_{CD3}-VL_{CD3}-VL_{CEA}-VH_{CEA}. Preferably, said first binding domain specific for CD3 is located C-terminally to the second binding domain. More preferably, the binding domains of the bispecific single chain antibodies defined herein are arranged in the order VH_{CEA}-VL_{CEA}-VH_{CD3}-VL_{CD3} or VL_{CEA}-VH_{CEA}-VH_{CD3}-VL_{CD3}. Even more preferred, the arrangement is VL_{CEA}-VH_{CEA}-VH_{CD3}-VL_{CD3}. Most preferred is the bispecific single chain antibody construct A240 VL-B9 VHxSEQ ID NO. 77 VHVL as defined in SEQ ID NO. 34. It is envisaged that said first and/or second binding domains of the bispecific single chain antibodies defined herein may be of non-human origin (i.e. derived from non-human sequences). For example, said first and/or second binding domains may be derived from murine monoclonal antibodies. However, bispecific single chain antibodies derived from murine antibodies may be recognised as foreign, when being administered to human patients. Thus, said first and/or second binding domains of the bispecific single chain antibodies defined herein are preferably of human origin (i.e. derived from human sequences). Such human binding domains specifically binding to CEA or CD3 may be identified e.g. by phage display-based techniques. It is also envisaged that e.g.

the VH region of the first (or second) binding domain is a human VH region, whereas the corresponding VL region of the first (or second) binding domain may be of non-human origin. Such binding domains may be also referred to as chimeric binding domains. Or one of said binding domains is of non-human origin, whereas the other is of human origin, resulting in a chimeric bispecific single chain antibody. Said first and/or second binding domains may be further modified in order to reduce the immunogenicity of the bispecific single chain antibody described herein, when being administered to human patients. For example, at least one of said first or second binding domains of the bispecific single chain antibodies defined herein may be humanized, CDR-grafted, chimeric and/or deimmunized or human, as set forth in more detail below. It is also envisaged that the polypeptide linker linking the VH and VL region within the first and/or second binding domain is deimmunized. Preferably, the polypeptide linker linking the VH and VL region within the deimmunized first binding domain (specific for CD3) is a deimmunized polypeptide linker having the sequence "GEGTSTGS$(G_2S)_2$GGAD" (SEQ ID NO. 141). It is furthermore envisaged, that one or both of said binding domains of the bispecific single chain antibodies defined herein carry so-called "tags" which may be used e.g. for protein expression, purification, detection or enrichment, such as Flag-tags, c-myc-tags, GST-tags or His-tags. For example, for the Flag-tag the most widely used hydrophilic octapeptide now is DYKDDDDK (Chubet and Brizzard, Biotechniques 20 (1996):136-141) though recent studies suggest that a shorter peptide, DYKD, can be recognized with almost the same affinity by the M1 monoclonal antibody (Knappik A, Pluckthun A; Biotechniques 17 (1994):754-761). Flag-tags, c-myc-tags, GST-tags, His-tags or the like may be positioned either at the N-terminus or the C-terminus of the bispecific single chain antibodies such as, for instance, tag-VH_{CEA}-VL_{CEA}-VH_{CD3}-VL_{CD3} or VL_{CEA}-VH_{CEA}-VH_{CD3}-VL_{CD3}–tag. The sources for and properties of such tags for expression, detection or purification purposes are well described in the art; see e.g. Lichty, Protein Expr Purif. 41 (2005), 98-105.

As used herein, the term "single-chain Fv" or "scFv" refers to antibody fragments comprising the VH and VL domains of an antibody, wherein these domains are present in a single polypeptide chain. Variable domains can be arranged in the order VH-VL or VL-VH. Generally, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the scFv to form the desired structure for antigen binding. For a review of scFv see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds. Springer-Verlag, New York, pp. 269-315 (1994). In a specific embodiment, the invention relates to anti-CEA scFvs derived from the bispecific single chain antibodies defined herein.

According to the present invention, the term "binding domain" or "variable region" used in the context with Ig-derived antigen-interaction comprises fragments and derivatives of polypeptides which at least comprise one CDR derived from an antibody, antibody fragment or derivative thereof. It is envisaged by the invention, that the second binding domain specifically binding to human CEA of the bispecific single chain antibody defined herein comprises at least one CDR, preferably a CDR-H3, more preferably a part of the CDR-H3 of murine monoclonal antibody A5B7 with the amino acid sequence "FYFDY" (SEQ ID NO. 112) corresponding to Kabat positions 100, 100a, 100b, 101, and 102, respectively, of CDR-H3 of murine monoclonal antibody A5B7; even more preferred with the amino acid sequence "$DX_1X_2X_3X_4FYFDY$" (SEQ ID NO. 65), wherein "X_1", "X_2", "X_3" or "X_4" represents any amino acid residue, and the amino acid residue "D" corresponds to Kabat position 95 of CDR-H3 of murine monoclonal antibody A5B7 and the amino acid residues "FYFDY" correspond to Kabat positions 100, 100a, 100b, 101, and 102, respectively, of CDR-H3 of murine monoclonal antibody A5B7. It is envisaged that "X_1", "X_2", "X_3" or "X_4" corresponding to Kabat positions 96 ("X_1"), 97 ("X_2"), 98 ("X_3") and 99 ("X_4"), respectively, of CDR-H3 of murine monoclonal antibody A5B7, represent amino acid residue "R" (Arginine), "G" (Glycine), "L" (Leucine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), "S" (Serine), "W" (Tryptophan), "F" (Phenylalanine) or "T" (Threonine). Herein, it is excluded from the scope of the invention that "X_1", "X_2", "X_3" and "X_4" represent the same amino acid, e.g. that "X_1", "X_2", "X_3" and "X_4" are all "F" (Phenylalanine). Preferably, "X_1" represents "R" (Arginine), "F" (Phenylalanine), "M" (Methionine), "E" (Glutamic acid), or "T" (Threonine); "X_2" represents "G" (Glycine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), or "S" (Serine); "X_3" represents "L" (Leucine), "F" (Phenylalanine), "M" (Methionine), "E" (Glutamic acid), or "T" (Threonine); and "X_4" represents "R" (Arginine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), or "S" (Serine). Or most preferred the second binding domain specifically binding to human CEA of the bispecific single chain antibody defined herein comprises the complete CDR-H3 of A5B7 with the amino acid sequence "DRGLRFYFDY" (SEQ ID NO. 66) corresponding to Kabat positions 95 – 102 of the CDR-H3 of A5B7. As shown in the following Examples, the cytotoxic activity against tumor cells of the bispecific single chain antibody defined herein comprising said mAb A5B7-derived CDR-H3 "DRGLRFYFDY" (SEQ ID NO. 66) amino acid sequence in the second binding domain interacting with CEA are resistant to soluble CEA antigen, thereby allowing the treatment of tumor patients with high serum CEA concentrations in their plasma. Determination of CDRs is known to the person skilled in the art; see e.g. http://www.bioinf.org.uk/abs/#cdrid. Numbering of amino acid sequences in antibodies can be carried out e.g. according to the Kabat numbering scheme described in the art; see e.g. Kabat, E. A., T. T. Wu, H. M. Perry, K. S. Gottesman, and C. Foeller. 1991. Sequences of Proteins of Immunological Interest, 5th ed. Bethesda, Md.: National Center for Biotechnology Information, National Library of Medicine.

Most preferably and as documented in the appended examples, the "bispecific single chain antibody" to be employed in the pharmaceutical composition of the invention is a bispecific single chain Fv (scFv) with a deimmunized anti-CD3 binding domain (WO 2005/040220) and a human anti-CEA binding domain comprising at least the amino acid sequence "DRGLRFYFDY" corresponding to Kabat positions 95 – 102 (SEQ ID NO. 66) of the CDR-H3 of murine monoclonal antibody A5B7. Bispecific single chain molecules are known in the art and are described e.g. in WO 99/54440 or Mack, PNAS, (1995), 92, 7021-7025.

The term "single-chain" as used in accordance with the present invention means that said first and second domain of the bispecific single chain construct are covalently linked, preferably in the form of a co-linear amino acid sequence encodable by a single nucleic acid molecule.

As used herein, "human" refers to the species *Homo sapiens*. A "human" molecule, e.g. human CEA or human CD3 (CD3 epsilon), is therefore the variant of that molecule as it is naturally expressed in *Homo sapiens*.

The term "epithelial tumor" as used herein denotes a tumor of epithelial origin which is CEA positive (Cancer Medicine; 6th ed.; Kufe, Donald W.; Pollock, Raphael E.;

Weichselbaum, Ralph R.; Bast, Robert C., Jr.; Gansler, Ted S.; Holland, James F.; Frei III, Emil, editors. Hamilton (Canada): BC Decker Inc. 2003; http://www.dkfz.de; http://www.krebsinformationsdienst.de/Krebsarten/index.html). The epithelial tumor to be treated may be a gastrointestinal adenocarcinoma, a breast adenocarcinoma or a lung adenocarcinoma. Said gastrointestinal adenocarcinoma is preferably a colorectal, pancreatic, an oesophageal or a gastric adenocarcinoma. As set forth herein, the pharmaceutical composition of the invention is particularly advantageous for the treatment of patients with progressive tumors, metastasis, recurrent cancer, late stage epithelial tumors, high epithelial tumor load/tumor burden, or tumor patients with a CEA serum concentration higher than 100 ng/ml (as determined e.g. by ELISA), characterized by high levels of soluble CEA antigen in the plasma of the tumor patients. It is also within the scope of the invention that said pharmaceutical composition be used after surgical removal of the primary tumor. For example, disseminated residual tumor cells derived from a CEA producing epithelial tumor also shed CEA into their microenvironments. Thus, in the surrounding of these tumor cells the level of soluble CEA is also high. Accordingly, resistance to soluble CEA of cytotoxic activity of pharmaceutical compositions of the invention is advantageous also for the treatment of minimal residual disease. It is envisaged that said pharmaceutical compositions may be administered in a period in which serum CEA levels decrease (due to the removal of the CEA source, i.e. the primary tumor) in order to kill remaining tumor cells. The pharmaceutical compositions may also be useful after the removal of the primary tumor, in the case that serum CEA levels increase due to the formation of secondary tumors or metastasis. The CEA serum concentration can be determined e.g. by CEA ELISA assays (see e.g. IBL CEA EIA, IBL Hamburg, Germany). As set forth above, in many antibody-based therapeutic approaches, said serum CEA inhibits binding of the antibody to membrane-bound CEA on the tumor cells and blocks the activity of antibody, thereby worsening the success of the anti-tumor therapy.

As used herein, the term “specifically binds” or related expressions such as “specifically binding” or “specific reactivity with/to” etc. refer to the ability of the first and/or second binding domains of the bispecific single chain antibody as defined herein to discriminate between the respective first and/or second molecule to such an extent that, from a pool of a plurality of different molecules as potential binding partners, only said respective first and/or second molecule is/are bound, or is/are significantly bound. Such binding measurements can be routinely performed e.g. on a Biacore^{TM} apparatus, by ELISA, FACS analysis or the like. More specifically, the first binding domain of the bispecific single chain antibody as defined herein binds to human CD3, preferably human CD3 epsilon. The second binding domain of the bispecific single chain antibodies as defined herein binds to a epithelial tumor antigen, i.e. human CEA (carcinoembryonic antigen, carcinoembryonic antigen-related cell adhesion molecule 5; CEACAM5; CD66e), as set forth below. The term "specifically binding" means in accordance with this invention that the bispecific single chain antibody molecule is capable of specifically interacting with and/or binding to at least two, three, four, five, six, seven, eight or even more amino acids of each of the human target molecule as defined herein. Said term relates to the specificity of the antibody molecule, i.e. to its ability to discriminate between the specific regions of the human target molecule as defined herein. The specific interaction of the antigen-interaction-site with its specific antigen may result in an initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc. Further, said binding may be exemplified by the specificity of a "key-lock-principle". Thus, specific motifs in the amino acid sequence of the antigen-interaction-site and the antigen bind to each other as a result of their primary, secondary or tertiary structure as well as the result of secondary modifications of said structure. The specific interaction of the antigen-interaction-site with its specific antigen may result as well in a binding of said site to the antigen.

The "specific binding" of an antibody is characterized primarily by two parameters: a qualitative parameter (the binding epitope, or *where* the antibody binds) and a quantitative parameter (the binding affinity, or *how strongly* it binds where it does). Which epitope is bound by an antibody can advantageously be determined by e.g. known FACS methodology, peptide-spot epitope mapping, mass spectroscopy or peptide ELISA. The strength of antibody binding to a particular epitope may be advantageously be determined by e.g. known Biacore^{TM} and/or ELISA methodologies. A combination of such techniques allows the calculation of a signal:noise ratio as a representative measure of binding specificity. In such a signal:noise ratio, the signal represents the strength of antibody binding to the epitope of interest, whereas the noise represents the strength of antibody binding to other, non-related epitopes differing from the epitope of interest. Preferably, a signal:noise ratio for an epitope of interest which is about 50-fold higher than for other epitopes different from the epitope of interest may be taken as an indication that the antibody evaluated binds the epitope of interest in a specific manner, i.e. is a “specific binder”.

The term "specific binding” or “specific interaction" as used in accordance with the present invention means that the bispecific single chain construct does not or essentially does not cross-react with polypeptides of similar structures. Cross-reactivity of a panel of bispecific single chain construct under investigation may be tested, for example, by assessing binding of said panel of bispecific single chain construct under conventional conditions (see, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1988 and Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1999) to the polypeptide of interest as well as to a number of more or less (structurally and/or functionally) closely related polypeptides. For example, it is within the scope of the invention that the first binding domain of the bispecific single chain antibody of the invention binds to human CEA (carcinoembryonic antigen; CEACAM5; CEA; CD66e) i.e. both to soluble CEA antigen and to membrane-bound CEA, whereas bispecific antibodies binding to other CEA family members, such as biliary glycoprotein (CEACAM1; BGP1; TM-CEA; CD66a), are excluded from said scope.

Examples for the specific interaction of an antigen-interaction-site with a specific antigen comprise the specificity of a ligand for its receptor. Said definition particularly comprises the interaction of ligands which induce a signal upon binding to its specific receptor. Examples for corresponding ligands comprise cytokines which interact/bind with/to its specific cytokine-receptors. Also particularly comprised by said definition is the binding of an antigen-interaction-site to antigens like antigens of the selectin family, integrins and of the family of growth factors like EGF. Another example for said interaction, which is also particularly comprised by said definition, is the interaction of an antigenic determinant (epitope) with the antigenic binding site of an antibody.

The term “binding to/interacting with” may also relate to a conformational epitope, a structural epitope or a discontinuous epitope consisting of two regions of the human target molecules or parts thereof. In context of this invention, a conformational epitope is defined by two or more discrete amino acid sequences separated in the primary sequence which come together on the surface of the molecule when the

polypeptide folds to the native protein (Sela, (1969) Science 166, 1365 and Laver, (1990) Cell 61, 553-6).
The term “discontinuous epitope” means in context of the invention non-linear epitopes that are assembled from residues from distant portions of the polypeptide chain. These residues come together on the surface of the molecule when the polypeptide chain folds into a three-dimensional structure to constitute a conformational/structural epitope.

“CD3” as used herein denotes an antigen that is expressed on T-cells as part of the multimolecular T-cell receptor complex and that consists of at least five different chains, CD3-gamma, -delta, -epsilon, -zeta, and –eta. Clustering of CD3 on T-cells, e.g., by immobilized anti-CD3-antibodies, leads to T-cell activation similar to the engagement of the T-cell receptor but independent from its clone typical specificity. Actually, most anti-CD3-antibodies recognize the CD3 epsilon-chain. The amino acid sequence of human CD3 epsilon is depicted in GenBank accession number NM_000733 and comprises SEQ ID NO. 111.

“CEA” denotes the carcinoembryonic antigen (carcinoembryonic antigen-related cell adhesion molecule 5; CEACAM5; CEA; CD66e), an antigen expressed in a large number of tumors of epithelial origin (Hammarström, Sem. Cancer Biol. 9 (1999), 67-81; Shively and Beatty CRC Crit. Rev. Oncol. Hematol. 2 (1985), 355-399). The amino acid sequence of human CEA is depicted in GenBank accession number NM_004363 and comprises SEQ ID NO. 76.

In the present invention, it has been surprisingly found that it is possible to generate antibody-based therapeutics with specificity for human CD3 and human CEA, wherein the cytotoxic activity directed against tumor cells is resistant to even high concentrations of soluble CEA antigen. This finding is entirely unexpected in view of the fact that the bispecific single chain antibodies of the invention bind to soluble CEA antigen. For example, when bispecific single chain antibody constructs derived from monoclonal antibodies T84.66 or MFE-23 have been generated, these antibodies were highly sensitive to soluble CEA antigen, i.e. their cytotoxic activity has been blocked in the presence of soluble CEA antigen. The inhibition of the cytotoxic activity of said constructs by soluble CEA could also not be overcome by increased amounts of antibody. These constructs have also been found to be capable of binding to soluble CEA. In view of this, it was concluded that soluble CEA antigen prevents the antibody from exerting its cytotoxic activity. In contrast, the bispecific single chain antibodies as defined herein are entirely resistant to the presence of even high levels of soluble CEA in their cytotoxic activity towards tumor cells. Moreover, due to their high cytotoxic activity, said bispecific constructs as defined herein elicit their biological activity at even low concentrations. Hence, low amounts of pharmaceutical compositions comprising the bispecific single chain antibodies as defined herein are sufficient to achieve a therapeutic effect in epithelial tumor patients characterized by high soluble CEA concentrations in their serum/plasma. High soluble CEA concentrations in the serum/plasma of epithelial tumor patients are characteristic for progressive, recurrent, metastatic, or late stage tumors and for patients with high tumor load. Even more surprising, it has been found that the amino acid sequence "DRGLRFYFDY" (SEQ ID NO. 66) corresponding to Kabat positions 95 – 102 of the CDR-H3 of murine monoclonal antibody A5B7 is sufficient to mediate resistance to soluble CEA antigen when used in a human CEA-binding domain (i.e. human binding domains specifically binding to human CEA) of anti-CEAxanti-CD3 bispecific single chain antibodies. Due to their human origin, said constructs are low or non-immunogenic when being administered to human tumor patients. In summary, the pharmaceutical compositions comprising the bispecific single chain antibodies as defined herein are particularly useful for the treatment of epithelial tumor patients with high soluble CEA concentrations in their plasma, as observed e.g. during tumor progression, for recurrent cancer, for metastasis, for patients with high tumor load/burden, or late-stage tumors.

In another preferred embodiment of the pharmaceutical composition of the invention, said first binding domain specific for CD3 of the bispecific single chain antibodies defined herein is located C-terminally to the second binding domain.

Within the scope of the invention and all embodiments thereof, the order of arrangement of the first and second binding domains on the single polypeptide chain, i.e. within the bispecific single chain antibody defined herein, is relevant. It is envisaged that the arrangement of the binding domains of the bispecific single chain antibodies defined herein may be VH_{CEA}-VL_{CEA}-VH_{CD3}-VL_{CD3}, VL_{CEA}-VH_{CEA}-VH_{CD3}-

VL_{CD3}, VH_{CD3}-VL_{CD3}-VH_{CEA}-VL_{CEA} or VH_{CD3}-VL_{CD3}-VL_{CEA}-VH_{CEA}. As shown in the following examples, the advantages as described hereinabove are particularly realizable when the first binding domain (specifically binding to CD3) is located C-terminally to the second binding domain, i.e. closer to the C-terminus of the bispecific single chain antibody than the second binding domain. It is preferred that the first binding domain specifically binding to human CD3 is arranged in the VH-VL orientation.For example, the binding domains of the bispecific single chain antibodies defined herein may be arranged in the order VH_{CEA}-VL_{CEA}-VH_{CD3}-VL_{CD3} or VL_{CEA}-VH_{CEA}-VH_{CD3}-VL_{CD3}. As used herein, "N-terminally to" or "C-terminally to" and grammatical variants thereof denote relative location within the primary amino acid sequence rather than placement at the absolute N- or C-terminus of the bispecific single chain antibody. Hence, as a non-limiting example, a first binding domain which is "located C-terminally to the second binding domain" simply denotes that the first binding domain is located to the carboxyl side of the second binding domain within the bispecific single chain antibody, and does not exclude the possibility that an additional sequence, for example a tag as set forth above, or another proteinaceous or non-proteinaceous compound such as a radioisotope, is located at the ultimate C-terminus of the bispecific single chain antibody.

Preferably, said binding domains of the bispecific single chain antibodies defined herein are arranged in the order VH_{CEA}-VL_{CEA}-VH_{CD3}-VL_{CD3} or VL_{CEA}-VH_{CEA}-VH_{CD3}-VL_{CD3}. Even more preferred, the arrangement is VL_{CEA}-VH_{CEA}-VH_{CD3}-VL_{CD3}. Most preferred is the bispecific single chain antibody construct A240 VL-B9 VHxSEQ ID NO. 77 VHVL as defined in SEQ ID NO. 34.

It is preferred that the second binding domain specifically binding to human CEA of the bispecific single chain antibody defined herein comprises at least one CDR, preferably a CDR-H3, more preferably a part of the CDR-H3 of murine monoclonal antibody A5B7 with the amino acid sequence "FYFDY" (SEQ ID NO. 112) corresponding to Kabat positions 100, 100a, 100b, 101, and 102, respectively, of CDR-H3 of murine monoclonal antibody A5B7; even more preferred with the amino acid sequence "$DX_1X_2X_3X_4FYFDY$" (SEQ ID NO. 65), wherein "X_1", "X_2", "X_3" or "X_4" represents any amino acid residue, and the amino acid residue "D" corresponds to

Kabat position 95 of CDR-H3 of murine monoclonal antibody A5B7 and the amino acid residues "FYFDY" correspond to Kabat positions 100, 100a, 100b, 101, and 102, respectively, of CDR-H3 of murine monoclonal antibody A5B7. Herein, "X_1", "X_2", "X_3" and "X_4" correspond to Kabat positions 96 ("X_1"), 97 ("X_2"), 98 ("X_3") and 99 ("X_4"), respectively, of CDR-H3 of murine monoclonal antibody A5B7. It is envisaged that "X_1", "X_2", "X_3" or "X_4" represent amino acid residue "R" (Arginine), "G" (Glycine), "L" (Leucine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), "S" (Serine), "W" (Tryptophan), "F" (Phenylalanine) or "T" (Threonine). Herein, it is excluded from the scope of the claims of the invention that "X_1", "X_2", "X_3" and "X_4" represent the same amino acid, e.g. that "X_1", "X_2", "X_3" and "X_4" are all "F" (Phenylalanine). Preferably, "X_1" represents "R" (Arginine), "F" (Phenylalanine), "M" (Methionine), "E" (Glutamic acid), or "T" (Threonine); "X_2" represents "G" (Glycine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), or "S" (Serine); "X_3" represents "L" (Leucine), "F" (Phenylalanine), "M" (Methionine), "E" (Glutamic acid), or "T" (Threonine); and "X_4" represents "R" (Arginine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), or "S" (Serine). Even more preferred, the second binding domain specific for human CEA comprises at least the amino acid sequence "RFYFDY" (SEQ ID NO. 113), "LRFYFDY" (SEQ ID NO. 114), "GLRFYFDY" (SEQ ID NO. 115), or "RGLRFYFDY" (SEQ ID NO. 116) of CDR-H3 of monoclonal antibody A5B7. Most preferred is the complete CDR-H3 of A5B7 with the amino acid sequence "DRGLRFYFDY" (SEQ ID NO. 66) corresponding to Kabat positions 95 ("D", Aspartic acid), 96 ("R"; Arginine), 97 ("G"; Glycine), 98 ("L"; Leucine), 99 ("R"; Arginine), 100 ("F"; Phenylalanine), 100a ("Y"; Tyrosine), 100b ("F"; Phenylalanine), 101 ("D"; Aspartic acid), and 102 ("Y"; Tyrosine), respectively. Numbering according to the Kabat system is set forth e.g. in Kabat, E. A., T. T. Wu, H. M. Perry, K. S. Gottesman, and C. Foeller. 1991. Sequences of Proteins of Immunological Interest, 5th ed. Bethesda, Md.: National Center for Biotechnology Information, National Library of Medicine.

As shown in the following Examples, the cytotoxic activity against tumor cells of the bispecific single chain antibody defined herein comprising said mAb A5B7-derived CDR-H3 "DRGLRFYFDY" (SEQ ID NO. 66) amino acid sequence in the second binding domain interacting with CEA are resistant to soluble CEA antigen, thereby allowing the treatment of tumor patients with high serum CEA concentrations in their plasma.

It may be desirable to further modify this A5B7-derived "DRGLRFYFDY" CDR-H3 amino acid sequence e.g. in order to improve affinity for the CEA target antigen (on the epithelial tumor cells) and/or to optimize "fine specificity" of the bispecific single chain antibody as defined herein. To this end, in the amino acid sequence "D$X_1X_2X_3X_4$FYFDY" (SEQ ID NO. 65)", various amino acid residues may be tested at positions "X_1", "X_2", "X_3" and/or "X_4" (corresponding to Kabat positions 96 ("X_1"), 97 ("X_2"), 98 ("X_3") and 99 ("X_4"), respectively, of CDR-H3 of murine monoclonal antibody A5B7) in order to identify a modified CDR-H3 with improved affinity and/or fine specificity. For instance, "X_1", "X_2", "X_3" or "X_4" may represent amino acid residue "R" (Arginine), "G" (Glycine), "L" (Leucine), "Y" (Tyrosine), "A" (Alanine), "D" (Aspartic acid), "S" (Serine), "W" (Tryptophan), "F" (Phenylalanine) or "T" (Threonine). Herein, one, two, three or all four of the indicated "X" positions may be exchanged in comparison to the original "RGLR" amino acid sequence at Kabat positions 96 to 99 in the CDR-H3 "DRGLRFYFDY" (SEQ ID NO. 66) amino acid sequence. However, it is excluded from the scope of the claims of the invention that "X_1", "X_2", "X_3" and "X_4" represent the same amino acid, e.g. that "X_1", "X_2", "X_3" and "X_4" are all "F" (Phenylalanine). The above-mentioned modification of the A5B7-derived "DRGLRFYFDY" CDR-H3 amino acid sequence can be achieved by methods known in the art, such as PCR using randomized primers, which allows the generation of bispecific single chain antibodies with such modified CDR-H3 regions in the CEA-binding domain. Affinity or fine specificity of these modified bispecific single chain antibodies can be tested by methods described in the art, e.g. by ELISA, Biacore or FACS analysis. The resistance to soluble CEA antigen of a bispecific single chain antibody with such a modified CDR-H3 can be tested in cytotoxicity assays in the presence of increasing amounts of soluble CEA, as described in the following Examples.

More preferably, said second binding domain specific for human CEA of the bispecific single chain antibodies defined herein comprises SEQ ID NO. 65 or 66 and/or a CDR-H1 having the amino acid sequence "SYWMH" (SEQ ID NO. 68) and/or a CDR-H2 having the amino acid sequence "FIRNKANGGTTEYAASVKG" (SEQ ID NO. 67) or "FILNKANGGTTEYAASVKG" (SEQ ID NO. 145). Thus, said second binding domain specific for human CEA of the bispecific single chain antibodies defined herein may comprise one, two or three CDR-H regions as defined above. Alternatively, said second binding domain specific for human CEA of the bispecific single chain antibodies defined herein comprises SEQ ID NO. 65 or 66 and/or a CDR-H1 having the amino acid sequence "TYAMH" (SEQ ID NO. 70) and/or a CDR-H2 having the amino acid sequence "LISNDGSNKYYADSVKG" (SEQ ID NO. 69). Thus, alternatively, said second binding domain specific for human CEA of the bispecific single chain antibodies defined herein may comprise one, two or three CDR-H regions as defined above. Even more preferred, said second binding domain specific for human CEA of the bispecific single chain antibodies defined herein in addition to the one, two or three CDR-H regions as depicted above comprises a CDR-L1 having the amino acid sequence "TLRRGINVGAYSIY" (SEQ ID NO. 73) and/or a CDR-L2 having the amino acid sequence "YKSDSDKQQGS" (SEQ ID NO. 72) and/or a CDR-L3 having the amino acid sequence "MIWHSGASAV" (SEQ ID NO. 71).

The amino acid sequence of the VH region of the second binding domain specific for human CEA of the bispecific single chain antibodies defined herein is preferably SEQ ID NO. 60 comprising "DRGLRFYFDY" (SEQ ID NO. 66) corresponding to Kabat positions 95 – 102 of the CDR-H3 of murine monoclonal antibody A5B7 and a CDR-H1 having the amino acid sequence "SYWMH" (SEQ ID NO. 68) and a CDR-H2 having the amino acid sequence "FIRNKANGGTTEYAASVKG" (SEQ ID NO. 67).

The amino acid sequence of the VH region of the second binding domain specific for human CEA of the bispecific single chain antibodies defined herein is preferably SEQ ID NO. 146 comprising "DRGLRFYFDY" (SEQ ID NO. 66) corresponding to Kabat positions 95 – 102 of the CDR-H3 of murine monoclonal antibody A5B7 and a CDR-H1 having the amino acid sequence "SYWMH" (SEQ ID NO. 68) and a CDR-H2 having the amino acid sequence "FILNKANGGTTEYAASVKG" (SEQ ID NO. 145).

The amino acid sequence of the VH region of the second binding domain specific for human CEA of the bispecific single chain antibodies defined herein is preferably SEQ ID NO. 58 or SEQ ID NO. 62 comprising "DRGLRFYFDY" (SEQ ID NO. 66) corresponding to Kabat positions 95 – 102 of the CDR-H3 of murine monoclonal antibody A5B7 and a CDR-H1 having the amino acid sequence "TYAMH" (SEQ ID

NO. 70) and a CDR-H2 having the amino acid sequence “LISNDGSNKYYADSVKG” (SEQ ID NO. 69).

The VL region of the second binding domain specific for human CEA of the bispecific single chain antibodies defined herein is preferably SEQ ID NO. 64 comprising CDR-L1 having the amino acid sequence “TLRRGINVGAYSIY” (SEQ ID NO. 73) and a CDR-L2 having the amino acid sequence “YKSDSDKQQGS” (SEQ ID NO. 72) and a CDR-L3 having the amino acid sequence “MIWHSGASAV” (SEQ ID NO. 71).

As set forth above, the order or arrangement of the variable regions of the second binding domain specifically binding to CEA may be VH-VL or VL-VH. Both arrangements are within the scope of the invention. For a second binding domain comprising the VH of SEQ ID NO. 60 and the VL of SEQ ID NO. 64, the VH-VL arrangement is shown in SEQ ID NO. 52, whereas the VL-VH arrangement is depicted in SEQ ID NO. 122. For a second binding domain comprising the VH of SEQ ID NO. 146 and the VL of SEQ ID NO. 64, the VH-VL arrangement is shown in SEQ ID NO. 147.

For a secondbinding domain comprising the VH of SEQ ID NO. 58 and the VL of SEQ ID NO. 64, the VH-VL arrangement is shown in SEQ ID NO 50, whereas the VL-VH arrangement is shown in SEQ ID NO. 120. For a secondbinding domain comprising the VH of SEQ ID NO. 62 and the VL of SEQ ID NO. 64, the VH-VL arrangement is shown in SEQ ID NO. 54, whereas the VL-VH arrangement is depicted in SEQ ID NO. 124. For a secondbinding domain comprising the VH of SEQ ID NO. 56 and the VL of SEQ ID NO. 64, the VH-VL arrangement is shown in SEQ ID NO. 48, whereas the VL-VH arrangement is depicted in SEQ ID NO. 118.

Even more preferred, the V regions of the second binding domain specific for CEA of the bispecific single chain antibodies defined herein are selected from the group consisting of:

(a) the VH region consists of the amino acid sequence shown in SEQ ID NO. 60 and the VL region consists of the amino acid sequence shown in SEQ ID NO. 64;

(b) the VH region consists of the amino acid sequence shown in SEQ ID NO. 146 and the VL region consists of the amino acid sequence shown in SEQ ID NO. 64;

(c) the VH region consists of the amino acid sequence shown in SEQ ID NO. 58 and the VL region consists of the amino acid sequence shown in SEQ ID NO. 64;
(d) the VH region consists of the amino acid sequence shown in SEQ ID NO. 62 and the VL region consists of the amino acid sequence shown in SEQ ID NO. 64; and
(e) the VH region consists of the amino acid sequence shown in SEQ ID NO. 56 and the VL region consists of the amino acid sequence shown in SEQ ID NO. 64.

Most preferred, said bispecific single chain antibody comprises an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence as depicted in any of SEQ ID NOs. 6, 8, 16, 18, 24, 26, 32, 34, 40, 42, 126, 130, 134 or 143;

(b) an amino acid sequence encoded by a nucleic acid sequence as shown in SEQ ID NOs. 5, 7, 15, 17, 23, 25, 31, 33, 39, 41, 125, 129, 133 or 142;

(c) an amino acid sequence encoded by a nucleic acid sequence hybridising under stringent conditions to the complementary nucleic acid sequence of (b);

(d) an amino acid sequence encoded by a nucleic acid sequence which is degenerate as a result of the genetic code to a nucleotide sequence of (b); and

(e) an amino acid sequence at least 85 % identical, more preferred at least 90 % identical, most preferred at least 95 % identical to the amino acid sequence of (a) or (b).

In another preferred embodiment of the pharmaceutical composition of the invention, said epithelial tumor to be treated is a gastrointestinal adenocarcinoma, a breast adenocarcinoma or a lung adenocarcinoma. Said gastrointestinal adenocarcinoma is preferably a colorectal, pancreatic, an oesophageal or a gastric adenocarcinoma.

More preferably, said pharmaceutical composition of the invention is for the treatment of progressive tumors, late stage tumors, tumor patients with high tumor load/burden, metastatic tumors, or tumor patients with a CEA serum concentration higher than 100 ng/ml. Said CEA serum concentration may be determined e.g. by ELISA.

In a further preferred embodiment of the pharmaceutical composition of the invention, at least one of said first or second binding domains of the bispecific single chain antibodies defined herein is chimeric, humanized, CDR-grafted, and/or deimmunized or human.

The term "chimeric" as used herein has been defined above. The term “human” binding domain, e.g. a human binding domain specifically binding to human CEA as used herein is to be understood as meaning that the bispecific single chain antibody as defined herein comprises (an) amino acid sequence(s) contained in the human germline antibody repertoire or antibody repertoire having at least the amino acid sequence “FYFDY” corresponding to Kabat positions 100, 100a, 100b, 101, and 102 (SEQ ID NO. 112) of the CDR-H3 of murine monoclonal antibody A5B7 or a A5B7-derived CDR-H3 as defined above. A bispecific single chain antibody as defined herein may also be regarded as human if it consists of (a) sequence(s) that deviate(s) from its (their) closest human germline sequence(s) by no more than would be expected due to the imprint of somatic hypermutation. Additionally, the antibodies of many non-human mammals, for example rodents such as mice and rats, comprise VH CDR amino acid sequences which one may expect to exist in the expressed human antibody repertoire as well. Any such sequence(s) of human or non-human origin which may be expected to exist in the expressed human repertoire would also be considered “human” for the purposes of the present invention.

As used herein, the term “humanized”, “humanization” or “human-like” are used interchangeably to refer to a bispecific single chain antibody comprising in at least one of its binding domains at least one complementarity determining region (“CDR”) from a non-human antibody or fragment thereof. Humanization approaches are described for example in WO 91/09968 and US 6,407,213. As non-limiting examples, the term encompasses the case in which a variable region of at least one binding domain comprises a single CDR region, for example the third CDR region of the VH, from another non-human animal, for example a rodent, as well as the case in which a or both variable region/s comprise at each of their respective first, second and third CDRs the CDRs from said non-human animal. In the event that all CDRs of a binding domain of the bispecific single chain antibody have been replaced by their corresponding equivalents from, for example, a rodent, one typically speaks of

"CDR-grafting", and this term is to be understood as being encompassed by the term "humanized" or grammatically related variants thereof as used herein. The term "humanized" or grammatically related variants thereof also encompasses cases in which, in addition to replacement of one or more CDR regions within a VH and/or VL of the first and/or second binding domain further mutation/s (e.g. substitutions) of at least one single amino acid residue/s within the framework ("FR") regions between the CDRs has/have been effected such that the amino acids at that/those positions correspond/s to the amino acid/s at that/those position/s in the animal from which the CDR regions used for replacement is/are derived. As is known in the art, such individual mutations are often made in the framework regions following CDR-grafting in order to restore the original binding affinity of the non-human antibody used as a CDR-donor for its target molecule. The term "humanized" may further encompass (an) amino acid substitution(s) in the CDR regions from a non-human animal to the amino acid(s) of a corresponding CDR region from a human antibody, in addition to the amino acid substitutions in the framework regions as described above.

As used herein, the term "deimmunized" or "deimmunization" denotes modification of the first and/or second binding domain vis-à-vis an original wild type construct by rendering said wild type construct non-immunogenic or less immunogenic in humans. Deimmunization approaches are shown e.g. in WO 00/34317, WO 98/52976, WO 02/079415 or WO 92/10755. The term "deimmunized" also relates to constructs, which show reduced propensity to generate T cell epitopes. In accordance with this invention, the term "reduced propensity to generate T cell epitopes" relates to the removal of T-cell epitopes leading to specific T-cell activation. Furthermore, "reduced propensity to generate T cell epitopes" means substitution of amino acids contributing to the formation of T cell epitopes, i.e. substitution of amino acids, which are essential for formation of a T cell epitope. In other words, "reduced propensity to generate T cell epitopes" relates to reduced immunogenicity or reduced capacity to induce antigen independent T cell proliferation. The term "T cell epitope" relates to short peptide sequences which can be released during the degradation of peptides, polypeptides or proteins within cells and subsequently be presented by molecules of the major histocompatibility complex (MHC) in order to trigger the activation of T cells; see inter alia WO 02/066514. For peptides presented by MHC class II such activation of T cells can then give rise to an antibody response by direct stimulation of T cells to produce said antibodies. “Reduced propensity to generate T-cell epitopes” and/or “deimmunization” may be measured by techniques known in the art. Preferably, de-immunization of proteins may be tested in vitro by T cell proliferation assay. In this assay PBMCs from donors representing > 80 % of HLA-DR alleles in the world are screened for proliferation in response to either wild type or de-immunized peptides. Ideally cell proliferation is only detected upon loading of the antigen-presenting cells with wild type peptides. Alternatively, one may test deimmunization by expressing HLA-DR tetramers representing all haplotypes. These tetramers may be tested for peptide binding or loaded with peptides substitute for antigen-presenting cells in proliferation assays. In order to test whether deimmunized peptides are presented on HLA-DR haplotypes, binding of e.g. fluorescence-labeled peptides on PBMCs can be measured. Furthermore, deimmunization can be proven by determining whether antibodies against the deimmunized molecules have been formed after administration in patients. Preferably, antibody derived molecules are deimmunized in the framework regions and most of the CDR regions are not modified in order to generate reduced propensity to induce T cell epitope so that the binding affinity of the CDR regions is not affected. Even elimination of one T cell epitope results in reduced immunogenicity.

In summary, the above approaches help to reduce the immunogenicity of the therapeutic bispecific single chain antibodies as defined herein when being administered to epithelial tumor patients. For example, the first binding domain specifically binding to CD3 as shown in SEQ ID NO. 77 is deimmunized; see also WO2005/040220. Preferably, the arrangement of the V regions in this CD3-binding domain is VH-VL.

In another aspect, the invention relates to a bispecific single chain antibody comprising an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence as depicted in any of SEQ ID NOs. 6, 8, 16, 18, 24, 26, 32, 34, 40, 42, 126, 130, 134 or 143;

(b) an amino acid sequence encoded by a nucleic acid sequence as shown in SEQ ID NOs. 5, 7, 15, 17, 23, 25, 31, 33, 39, 41, 125, 129, 133 or 142;

(c) an amino acid sequence encoded by a nucleic acid sequence hybridising under stringent conditions to the complementary nucleic acid sequence of (b);

(d) an amino acid sequence encoded by a nucleic acid sequence which is degenerate as a result of the genetic code to a nucleotide sequence of (b); and

(e) an amino acid sequence at least 85 % identical, more preferred at least 90 % identical, most preferred at least 95 % identical to the amino acid sequence of (a) or (b).

In one embodiment, the invention relates to a composition comprising a bispecific single chain antibodies as defined above. Preferably, said bispecific single chain antibodies as defined above are used as pharmaceutical compositions for the treatment of an epithelial tumor or epithelial tumors in a human. Said epithelial tumor(s) is (are) CEA-positive. The cytotoxic activity against CEA-positive epithelial tumor cells of these pharmaceutical compositions is resistant to even high concentrations of soluble CEA antigen in the plasma of tumor patients. Moreover, said bispecific single chain antibodies as defined above or anti-CEA scFvs derived thereof may be used as diagnostic compositions for the detection of an epithelial tumor or epithelial tumors in a human as set forth in more detail below.

The term "hybridizing under stringent conditions" as used herein refers to nucleic acid sequences capable of hybridizing, under stringent hybridization conditions, to sequences depicted in SEQ ID NOs. 5, 7, 15, 17, 23, 25, 31, 33, 39, 41, 125, 129, 133 or 142, or the complement thereof, and which encode a bispecific single chain antibody having cytotoxic activity against CEA-positive tumor cells. "Stringent hybridization conditions" refers to an overnight incubation at 42 °C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65° C.

Whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide or amino acid sequence defined herein can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence defined herein) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245(1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's.

The invention also provides for a pharmaceutical composition comprising a nucleic acid sequence encoding a bispecific single chain antibody as defined herein. Said nucleic acid can be utilized e.g. for gene therapy approaches in order to treat an epithelial tumor in a human, as set forth in more detail below.

The invention further relates to a pharmaceutical composition comprising a vector which comprises a nucleic acid sequence as defined above. Preferably, said vector further comprises a regulatory sequence which is operably linked to said nucleic acid sequence defined above. More preferably, said vector is an expression vector.
Furthermore, the vector of the present invention may also be a gene transfer or gene targeting vector. Gene therapy, which is based on introducing therapeutic genes or nucleic acids into cells by ex-vivo or in-vivo techniques is one of the most important applications of gene transfer. Suitable vectors, methods or gene-delivering systems for in-vitro or in-vivo gene therapy are described in the literature and are known to the person skilled in the art; see, e.g., Giordano, Nature Medicine 2 (1996), 534-539; Schaper, Circ. Res. 79 (1996), 911-919; Anderson, Science 256 (1992), 808-813, Isner, Lancet 348 (1996), 370-374; Muhlhauser, Circ. Res. 77 (1995), 1077-1086; Onodua, Blood 91 (1998), 30-36; Verzeletti, Hum. Gene Ther. 9 (1998), 2243-2251; Verma, Nature 389 (1997), 239-242; Anderson, Nature 392 (Supp. 1998), 25-30; Wang, Gene Therapy 4 (1997), 393-400; Wang, Nature Medicine 2 (1996), 714-716; WO 94/29469; WO 97/00957; US 5,580,859; US 5,589,466; US 4,394,448 or Schaper, Current Opinion in Biotechnology 7 (1996), 635-640, and references cited therein. The nucleic acid molecules and vectors as defined herein may be designed for direct introduction or for introduction via liposomes, viral vectors (e.g. adenoviral, retroviral), electroporation, or other delivery systems into the cell. Additionally, a baculoviral system can be used as eukaryotic expression system for the nucleic acid molecules as defined herein. The introduction and gene therapeutic approach should, preferably, lead to the expression of a functional bispecific single chain

antibody construct as defined herein, whereby said expressed bispecific single chain antibody construct is particularly useful in the treatment, amelioration and/or prevention of an epithelial tumor in a human.

In a further aspect, the invention relates to a pharmaceutical composition comprising a host transformed or transfected with a vector or a nucleic acid as defined above.

A further aspect of the invention relates to a pharmaceutical composition as defined hereinabove, further comprising a proteinaceous compound capable of providing an activation signal for immune effector cells.

Preferably, the pharmaceutical composition further comprises suitable formulations of carriers, stabilizers and/or excipients.

In another aspect, the invention relates to a process for the production of a pharmaceutical composition as defined above, said process comprising culturing a host as defined above under conditions allowing the expression of the bispecific single chain antibody as defined hereinabove and recovering the produced bispecific single chain antibody from the culture.

A further aspect of the invention relates to a use of a bispecific single chain antibody as defined hereinabove or as produced by the process as defined hereinabove, a nucleic acid molecule as defined hereinabove, a vector as defined hereinabove or a host as defined hereinabove for the preparation of a pharmaceutical composition for the prevention, treatment or amelioration of an epithelial tumor in a human. Another aspect of the invention relates to a method for the prevention, treatment or amelioration of an epithelial tumor in a human, said method comprising the step of administration of an effective amount of a pharmaceutical composition of the invention or as produced according by the process set forth above. The person skilled in the art, in particular the attending physician can evaluate the successful treatment of the patient in need of administration of the bispecific molecule/bispecific single chain antibody of the invention. Accordingly, the administration scheme as well as the dosage and the administration time may be assessed by said person skilled in the art: A corresponding "amelioration" and/or "treatment" to be assessed is defined below.

As used herein, an "effective amount" or "therapeutically effective amount" of a pharmaceutical composition of the invention in the context of epithelial tumors refers to that amount of the therapeutic agent sufficient to destroy, modify, control or remove primary, regional or metastatic tumor tissue. A therapeutically effective amount may refer to the amount of therapeutic agent sufficient to delay or minimize the spread of the epithelial tumor(s). A therapeutically effective amount may also refer to the amount of the therapeutic agent or pharmaceutical agent that provides a therapeutic benefit in the treatment or management of the epithelial tumor(s). Further, a therapeutically effective amount with respect to a therapeutic agent or pharmaceutical agent of the invention means that amount of therapeutic agent or pharmaceutical agent alone, or in combination with other therapies, that provides a therapeutic benefit in the treatment or management of an epithelial tumor. Used in connection with an amount of the bispecific single chain antibody defined herein, the term can encompass an amount that improves overall therapy, reduces or avoids unwanted effects, or enhances the therapeutic efficacy of or synergies (as defined herein) with another therapeutic agent. Preferably, a therapeutically effective amount of a therapeutic improves overall therapy, reduces or avoids unwanted effects, or enhances the therapeutic efficacy of or synergies with another therapeutic agent in the treatment of (an) epithelial tumor(s). For example, a bispecific single chain antibody as defined herein may cause a shrinkage of the diameter of an epithelial tumor of 20% if administered to a patient as a mono-therapy. In contrast, a second therapeutic e.g. an anti-cancer agent as defined below, may cause a tumor shrinkage of 10%. However, if both the bispecific single chain antibody as defined herein and said second therapeutic are administered in combination in form of a co-therapy, a tumor shrinkage of 50% may be observed. Such an effect is understood as a synergestic effect as used herein.

As referred to herein, the term "therapy" refers to any administration scheme, method and/or agent that can be used in the prevention, treatment or amelioration of an epithelial tumor. The term "prevention, treatment or amelioration of an epithelial tumor" is set forth in more detail below. The terms "therapies" and "therapy" may refer to a biological therapy, supportive therapy, chemotherapy, radiation therapy and/or other therapies useful in treatment, prevention, or amelioration of an epithelial tumor, or one or more symptoms thereof.

As used herein, the terms “treat”, “treatment” and “treating” in the context of administering a therapy or therapies to a patient refer to the reduction or amelioration of the progression, severity, and/or duration of an epithelial tumor. Said epithelial tumor(s) may be associated with aberrant expression e.g., overexpression or activity of CEA, and/or the amelioration of one or more symptoms thereof resulting from the administration of one or more therapies (including the administration of one or more pharmaceutical or therapeutic agents).

The most preferred mode of administration is an intravenous administration over a given time/time period. While the bispecific single chain antibody as defined herein may be administered per alone, preferred is administration in a pharmaceutically acceptable carrier. Examples of suitable pharmaceutical carriers are well known in the art and include phosphate buffered saline solutions, water, liposomes, various types of wetting agents, sterile solutions, etc. Compositions comprising such carriers can be formulated by well known conventional methods. These pharmaceutical compositions can be administered to the subject at a suitable dose. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical arts, dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, and suspensions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, aqueous solutions, or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishes, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, and inert gases and the like. In addition, the composition might comprise proteinaceous carriers, like, e.g., serum albumine or immunoglobuline, preferably of human origin. It is envisaged that the co-therapy might comprise, in addition to the proteinaceous bispecific single chain antibody further biologically active agents, depending on the intended use of the pharmaceutical composition. Such agents might be agents acting on the gastro-intestinal system, agents acting as cytostatica, agents preventing hyperurikemia, agents inhibiting immune reactions (e.g. corticosteroids, FK506), drugs acting on the circulatory system and/or agents such as T-cell co-stimulatory molecules or cytokines known in the art. Preferably, the bispecific single chain antibody as defined herein is formulated in a buffer, a stabilizer and a surfactant. The buffer may be a phosphate, citrate, succinate or acetate buffer. The stabilizer may be (an) amino acid(s) and/or a sugar. The surfactants may be detergents, PEGs, or the like. More preferably, the bispecific single chain antibody as defined herein is formulated in citrate, lysine, trehalose and Tween 80. As a diluent for said pharmaceutical composition, isotonic saline and Tween 80 is preferred.

The term “amelioration” as used herein refers to an improvement or a moderation in the severity of a disease, i.e. an epithelial tumor. For example, such an amelioration may be the achievement of a stable disease - or even more preferred - a shrinkage of the epithelial tumor(s), i.e. a minimal, partial response or complete response, due to the administration of the pharmaceutical compositions of the invention. “Stable disease” refers to a disease state in which no or no significant tumor progression/growth can be observed or detected by clinical and/or histological diagnostic methods. For example, a shrinkage of the tumor greater than 50% shrinkage of the sum of cross-sectional areas of index lesions may be considered as a “partial response”. A “complete response” denotes a state in which no lesion(s) can be detected any more after treatment. A response with a tumor shrinkage between stable disease and partial response may be considered as a minimal response. For instance, a 20%, 25% or 30% shrinkage of the sum of cross-sectional areas of index lesions may be referred to as a minimal response.

The term “amelioration” as used herein encompasses also a reduction of the number of epithelial tumors. It furthermore denotes the prevention/slowdown of tumor progression. Moreover, an improvement of the overall survival of treated tumor patients in comparison to non-treated tumor patients may be considered as an “amelioration” as used herein. This applies mutatis mutandis to an improvement of the progression-free survival or the relapse-free survival of treated tumor patients as compared to non-treated tumor patients. In addition, the term “amelioration” can also refer to a reduction of the intensity of the symptoms of an epithelial tumor, resulting e.g. in an improvement of the quality of life of the treated tumor patients.

The term “prevention of an epithelial tumor” as used herein is to be understood as follows: After surgical removal of the primary epithelial tumor(s) from a human patient and/or after chemotherapeutic or radiological treatment of the primary epithelial tumor(s), it may be the case that not all tumor cells could be eliminated from the body. However, these remaining tumor cells may give rise to recurrent cancer, i.e. local recurrence and/or metastases in the patient. Metastasis is a frequent complication of cancer, yet the process through which cancer cells disseminate from the primary tumor(s) to form distant colonies is poorly understood. Metastatic cancers are almost without exception uncurable raising the necessity for new therapeutic modalities. The pharmaceutical composition of the invention can be used to kill these disseminated tumor cells in order to prevent the formation of secondary tumors (originating from the tumor cells remaining in the body after primary therapy). In this way, the pharmaceutical composition helps to prevent the formation of local recurrence and/or metastases in tumor patients.

The success of the anti-tumor therapy may be monitored by established standard methods for the respective disease entities, e.g. by computer-aided tomography, X-ray, nuclear magnetic resonance tomography (e.g. for National Cancer Institute-criteria based response assessment [Cheson (1999), J. Clin. Oncol.; 17(4):1244]), positron-emission tomography scanning, endoscopy, Fluorescence Activated Cell Sorting, aspiration of bone marrow, pleural or peritoneal fluid, tissue /histologies, and various epithelial tumor specific clinical chemistry parameters (e.g. soluble CEA concentration in serum) and other established standard methods may be used. In addition, assays determining T cell activation may be used; see e.g. WO99/054440. Statistics for the determination of overall survival, progression-free survival or relapse-free survival of treated tumor patients in comparison to non-treated tumor patients may also be used.

Preferably, said epithelial tumor is a gastrointestinal adenocarcinoma, a breast adenocarcinoma or a lung adenocarcinoma. Said gastrointestinal adenocarcinoma is more preferably a colorectal, pancreatic, an oesophageal or a gastric adenocarcinoma.

Even more prefererred, said pharmaceutical composition of the invention is for the treatment of progressive tumors, late stage tumors, tumor patients with high tumor load/burden, metastatic tumors, or tumor patients with a CEA serum concentration higher than 100 ng/ml (as determined e.g. by ELISA).

In another preferred embodiment of the uses or methods of the invention, said pharmaceutical composition as defined hereinabove is suitable to be administered in combination with an additional drug, i.e. as part of a co-therapy.

In certain embodiments, the bispecific single chain antibody or pharmaceutical composition as defined herein is administered in combination with one or more other therapies. In certain embodiments, the bispecific single chain antibody or pharmaceutical composition as defined herein is administered to a patient concurrently with one or more other therapies. Preferably, such therapies are useful for the treatment of epithelial tumors. The term “concurrently” is not limited to the administration of pharmaceutical compositions or therapeutic agents at exactly the same time, but rather it is meant that the bispecific single chain antibody or pharmaceutical composition as defined herein and the other agent(s) are administered to a patient in a sequence and within a time interval such that the bispecific single chain antibody or pharmaceutical composition as defined herein can act together with the other agent to provide an increased benefit than if they were administered otherwise. For example, each therapeutic agent may be administered at the same time or sequentially in any order at different points in time; however, if not administered at the same time, they should be administered sufficiently close in time so as to provide the desired therapeutic effect.
Each therapeutic agent can be administered separately, in any appropriate form and by any suitable route. In other embodiments, the bispecific single chain antibody or pharmaceutical composition as defined herein are administered before, concurrently or after surgery. Preferably the surgery completely removes localized epithelial tumors or reduces the size of large epithelial tumors. Surgery can also be done as a preventive measure or to relieve pain.

The dosage amounts and frequencies of administration provided herein are encompassed by the term “therapeutically effective” as defined above. The dosage and frequency further will typically vary according to factors specific for each patient depending on the specific therapeutic or prophylactic agents administered, the severity and type of epithelial tumor, the route of administration, as well as age, body weight, response, and the past medical history of the patient. Suitable regimens can be selected by one skilled in the art by considering such factors and by following, for example, dosages reported in the literature and recommended in the Physicians' Desk Reference (59th ed., 2005).

In some embodiments, therapy by administration of the bispecific single chain antibody or pharmaceutical composition as defined herein is combined with the administration of one or more therapies such as chemotherapies, radiation therapies, hormonal therapies, and/or biological therapies/immunotherapies. Therapeutic agents include, but are not limited to, proteinaceous molecules, including, but not limited to, peptides, polypeptides, proteins, including post-translationally modified proteins, antibodies etc.; or small molecules (less than 1000 daltons), inorganic or organic compounds; or nucleic acid molecules including double-stranded or single-stranded DNA, or double-stranded or single-stranded RNA, as well as triple helix nucleic acid molecules. Therapeutic agents can be derived from any known organism (including, but not limited to, animals, plants, bacteria, fungi, and protista, or viruses) or from a library of synthetic molecules.

In a specific embodiment, the methods and uses of the invention encompass administration of the bispecific single chain antibody or pharmaceutical composition as defined herein in combination with the administration of one or more therapeutic agents that are inhibitors of kinases such as Gefitinib (Iressa), Erlotinib (Tarceva), anti-EGFR-antibodies (e.g. Cetuximab; Erbitux), or anti-Her2/neu-antibodies (e.g. Trastuzumab; Herceptin) described in the art; see e.g., Hardie and Hanks (1995) The Protein Kinase Facts Book, I and II, Academic Press, San Diego, California.

In another specific embodiment, the methods and uses of the invention encompass administration of the bispecific single chain antibody or pharmaceutical composition as defined herein in combination with the administration of one or more therapeutic agents that are angiogenesis inhibitors such as anti-VEGF-antibodies (e.g. Bevacizumab; Avastin), small molecular compounds (e.g. Vatalanib or Sorafenib) or COX-inhibitors described in the art.

In another specific embodiment, the methods and uses of the invention encompass administration of the bispecific single chain antibody or pharmaceutical composition as defined herein in combination with the administration of one or more therapeutic agents that are anti-cancer agents such as 5-Fluorouracil, Leucovorin, Capecitabine, Oxaliplatin, Irinotecan, Gemcitabine, Doxorubicin, Epirubicin, Etoposide, Cisplatin, Carboplatin, Taxanes (e.g. Docetaxel, Paclitaxel) described in the art.

Preferably, a co-therapy of a patient with an epithelial tumor using a bispecific single chain antibody or pharmaceutical composition as defined herein in combination with (a) further therapeutic agent(s) results in an synergistic effect. As used herein, the term "synergistic" refers to a combination of therapies (e.g., a combination of a bispecific single chain antibody as defined herein and (a) further therapeutic agent(s) as set forth above) which is more effective than the additive effects of any two or more single therapies (e.g., one or more therapeutic agents). For example, a bispecific single chain antibody as defined herein may cause a shrinkage of the diameter of an epithelial tumor of 20% if administered to a patient as a mono-therapy. In contrast, a second therapeutic e.g. an anti-cancer agent as defined below, may cause a tumor shrinkage of 10%. However, if both the bispecific single chain antibody as defined herein and said second therapeutic are administered in combination in form of a co-therapy, a tumor shrinkage of 50% may be observed.

A synergistic effect of a combination of therapies (e.g., a combination of a bispecific single chain antibody as defined herein and (a) further therapeutic agent(s) as set forth above) permits the use of lower dosages of one or more of therapies (e.g., one or more therapeutic agents) and/or less frequent administration of said therapies to a patient with a disease, e.g. an epithelial tumor. The ability to utilize lower dosages of therapies (e.g., therapeutic agents) and/or to administer said therapies less frequently reduces the toxicity associated with the administration of said therapies to a subject without reducing the efficacy of said therapies in the prevention or treatment of a disease, e.g. an epithelial tumor. In addition, a synergistic effect can result in improved efficacy of therapies (e.g., therapeutic agents) in the prevention, management, treatment and/or amelioration of an epithelial tumor (which may be associated with aberrant expression (e.g., overexpression) or activity of CEA). Finally, synergistic effect of a combination of therapies (*e.g.*, therapeutic agents) may avoid or reduce adverse or unwanted side effects associated with the use of any single therapy.

In said co-therapy, an active agent may be optionally included in the same pharmaceutical composition as the bispecific single chain antibody defined herein, or may be included in a separate pharmaceutical composition. In this latter case, said separate pharmaceutical composition is suitable for administration prior to, simultaneously as or following administration of said pharmaceutical composition comprising the bispecific single chain antibody as defined herein. The additional drug or pharmaceutical composition may be a non-proteinaceous compound or a proteinaceous compound. In the case that the additional drug is a proteinaceous compound, it is advantageous that the proteinaceous compound be capable of providing an activation signal for immune effector cells.

Preferably, said proteinaceous compound or non-proteinaceous compound may be administered simultaneously or non-simultaneously with a bispecific single chain antibody as defined hereinabove, a nucleic acid molecule as defined hereinabove, a vector as defined as defined hereinabove, or a host as defined as defined hereinabove. Preferably, said subject to be treated is a human.

In a further embodiment, a single chain bispecific antibody or anti-CEA scFvs as defined herein may be conjugated to a diagnostic or detectable agent. Such diagnosis and detection can be accomplished by coupling the antibody or scFv to detectable substances for example to various enzymes, such as horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; prosthetic groups, such as streptavidin/biotin and avidin/biotin; fluorescent materials, such as, umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; luminescent materials, such as, luminol; bioluminescent materials, such as, luciferase, luciferin, and aequorin; radioactive materials and isotopes, such as cobalt (57Co), indium (115In, 113In, 112In, 111In), iodine (131I, 125I, 123I, 121I), or yttrium (90Y), positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions.

Techniques for conjugating moieties to antibodies are well known. Moieties can be conjugated to antibodies by any method known in the art, including, but not limited to aldehyde/Schiff linkage, sulphydryl linkage, acid-labile linkage, cis-aconityl linkage, hydrazone linkage, enzymatically degradable linkage; see generally Garnett, 2002, Adv. Drug Deliv. Rev. 53:171-216. Additional techniques for conjugating moieties to antibodies are well known, see, *e.g.*, Arnon et al., Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy. In Monoclonal Antibodies And Cancer Therapy, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985). Methods for fusing or conjugating antibodies to polypeptide moieties are known in the art; see, e.g.; Ashkenazi et al., 1991, PNAS 88: 10535-10539. The fusion of an antibody to a moiety does not necessarily need to be direct, but may occur through linker sequences. Such linker molecules are commonly known in the art and described in Denardo et al., 1998, Clin Cancer Res. 4:2483-90; Peterson et al., 1999, Bioconjug. Chem. 10:553.

In a further aspect, the invention relates to a kit comprising a bispecific single chain antibody as defined hereinabove, a nucleic acid molecule as defined hereinabove, a vector as defined hereinabove, or a host as defined hereinabove.

These and other embodiments are disclosed and encompassed by the description and Examples of the present invention. Recombinant techniques and methods in immunology are described e.g. in Sambrook et al. Molecular Cloning: A Laboratory Manual; Cold Spring Harbor Laboratory Press, 3rd edition 2001; Lefkovits; Immunology Methods Manual; The Comprehensive Sourcebook of Techniques; Academic Press, 1997; Golemis; Protein-Protein Interactions: A Molecular Cloning Manual; Cold Spring Laboratory Press, 2002. Further literature concerning any one of the antibodies, methods, uses and compounds to be employed in accordance with the present invention may be retrieved from public libraries and databases, using for example electronic devices. For example, the public database "Medline", available on the Internet, may be utilized, for example under http://www.ncbi.nlm. nih.qov/PubMed/medline.html. Further databases and addresses, such as http:

//www.ncbi.nim.nih.qov/,http://www.infobioaen.fr/,http://www.fmi.ch/bioloqv/research tools.html, http://www.tiqr.orQ/. are known to the person skilled in the art and can also be obtained using, e. g., http://www.lvcos.com. For tumor-related topics see e.g. http://www.nih.gov or http://www.dkfz.de.

The Figures show:

Figure 1: FACS binding analysis of various human CEA-reactive bispecific single chain constructs to CHO cells transfected with human CEA and CD3 positive HPB-All cells, respectively. As a positive control for binding to CEA, monoclonal antibody Col-1 has been used. For control of binding to human CD3, a CD19xCD3 bispecific single chain construct as described in WO 99/054440 was used. In this positive control, the thick line represents cells incubated with 10 µg/ml purified CD19xCD3 bispecific single chain antibody that was subsequently incubated with the anti-His antibody and the detection antibody. The thin histogram line reflects the negative control: cells incubated with the anti-His antibody and the detection antibody. Binding activity for human (membrane-bound) CEA and human CD3 were detectable for CEAI VHVLxSEQ ID NO.77 VHVL, CEAI VLVHxSEQ ID NO.77 VHVL, CEAII VHVLxSEQ ID NO.77 VHVL, CEAIII VLVHxSEQ ID NO.77 VHVL and CEAIII VHVLxSEQ ID NO.77 VHVL. In the respective histograms corresponding to the bispecific single chain antibodies as described in the invention, the thin line

represents the negative control, the bright thick line represents cells incubated with culture supernatant, whereas the dark thick (most right) line represents cells incubated with 10 µg/ml purified bispecific single chain antibody.

Figure 2: Binding signals of bispecific single chain anti-CEA/anti-CD3 antibodies CEAI VHVLxSEQ ID NO. 77 VHVL, CEAII VHVLxSEQ ID NO. 77 VHVL and CEAIII VHVLxSEQ ID NO. 77 VHVL and anti-CEA antibody Col-1 to soluble CEA detected by direct ELISA. CEAI VHVLxSEQ ID NO. 77 VHVL (anti-CEA binding domain derived from mAb A5B7), CEAII VHVLxSEQ ID NO.77 VHVL (anti-CEA binding domain derived from mAb T84.66), and CEAIII VHVLxSEQ ID NO.77 VHVL (anti-CEA binding domain derived from mAb MFE-23) bispecific single chain antibodies and the mouse monoclonal antibody Col-1 specifically bound to immobilized soluble human CEA. No binding signal was observed in the absence of the soluble CEA antigen (PBS control).

Figure 3: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse CHO cells transfected with CEA, in the absence of soluble CEA. Stimulated human CD8 positive CTLs were used as effector cells. To demonstrate the specificity of the redirected lysis, a non-CEA reactive bispecific single chain construct was included as negative control. Cytotoxic activity against human CEA-transfected target cells (CHO-CEA$^+$ cells) for various domain arrangements, i.e. for SEQ ID NO.77 VHVLxCEAI VHVL and SEQ ID NO.77 VHVLxCEAI VLVH (both constructs with anti-CD3 binding domain N-terminally), as well as for CEAI VLVHxSEQ ID NO.77 VHVL and CEAI VHVLxSEQ ID NO.77 VHVL (anti-CD3 binding domain C-terminally) could be shown. Non-transfected CHO cells (lacking human CEA) were used as a negative control.

Figure 4: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse CHO cells transfected with CEA, in the absence of soluble CEA. To demonstrate the specificity of the redirected lysis, non-transfected CHO cells were included as negative control. Stimulated human CD8 positive CTLs were used as effector cells. CEA I-HL (CEAI VHVLxSEQ ID NO.77 VHVL), CEA III-LH (CEAIII VLVHxSEQ ID NO.77 VHVL), CEA III-HL (CEAIII VHVLxSEQ ID NO.77 VHVL), and CEA II HL (CEAII VHVLxSEQ ID NO.77 VHVL) showed cytotoxic activity against

human CEA-transfected CHO cells. Non-transfected CHO cells (lacking human CEA) were used as a negative control for CEA I-LH (CEAI VLVHxSEQ ID NO.77 VHVL), CEA III-HL (CEAIII VHVLxSEQ ID NO.77 VHVL) and CEA II HL (CEAII VHVLxSEQ ID NO.77 VHVL). CEAI denotes a variable region derived from murine mAb A5B7, CEAII is a variable region derived from murine mAb T84.66 and CEAIII refers to a variable region from murine mAb MFE-23.

Figure 5: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse CHO cells transfected with CEA in the presence of soluble human CEA. Stimulated human CD8 positive CTLs were used as effector cells. The cytotoxic activity mediated by CEAI VLVHxSEQ ID NO.77 VHVL and CEAI VHVLxSEQ ID NO.77 VHVL is not inhibited by increasing amounts of soluble human CEA, up to 1µg/ml. CEAI is a variable region derived from murine mAb A5B7.

Figure 6: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse CHO cells transfected with CEA in the presence of soluble human CEA. Stimulated human CD8 positive CTLs were used as effector cells. The cytotoxic activity mediated by SEQ ID NO.77 VHVLxCEAI VHVL and SEQ ID NO.77 VHVLxCEAI VLVH is not inhibited by increasing amounts of soluble human CEA, up to 1µg/ml. CEAI is a variable region derived from murine mAb A5B7.

Figure 7: The indicated CEA-reactive bispecific single chain construct redirected T cells to lyse CHO cells transfected with CEA in the presence of soluble human CEA. Stimulated human CD8 positive CTLs were used as effector cells. Cytotoxic activity of CEAII VHVLxSEQ ID NO.77 VHVL is inhibited by increasing amounts of soluble CEA. CEAII VHVL is derived from mAb T84.66.

Figure 8: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse CHO cells transfected with CEA in the presence of soluble human CEA. Stimulated human CD8 positive CTLs were used as effector cells. Whereas CEAI VHVLxSEQ ID NO.77 VHVL-mediated cytotoxicity is resistant to inhibition by soluble CEA antigen, CEAIII VHVLxSEQ ID NO.77 VHVL-mediated cytotoxic activity is inhibited by even low amounts of soluble CEA. CEAIII VHVL is derived from mAb MFE-23, whereas CEAI is a variable region derived from murine mAb A5B7.

Figure 9: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse Kato III cells in the presence of increasing amounts of soluble CEA antigen. Native human PBMCs were used as effector cells. CEAII VHVLxSEQ ID NO. 77-mediated cytotoxic activity is not resistant to soluble CEA. CEAII VHVL is derived from mAb T84.66.

Figure 10: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse Kato III cells in the presence of increasing amounts of soluble CEA antigen. Stimulated human CD8 positive CTLs were used as effector cells. CEAI VHVLxSEQ ID NO.77 VHVL-mediated cytotoxicity is resistant to soluble CEA. In contrast, CEAII VHVLxSEQ ID NO.77 VHVL-mediated cytotoxic activity is inhibited by increasing amounts of soluble CEA. CEAII VHVL is derived from mAb T84.66, whereas CEAI is a variable region derived from murine mAb A5B7.

Figure 11: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse CHO cells transfected with CEA in the presence of increasing amounts of soluble CEA antigen. Stimulated human CD8 positive CTLs were used as effector cells. CEAII VHVLxSEQ ID NO.77 VHVL-mediated cytotoxic activity is inhibited by increasing amounts of soluble CEA. CEAII VHVL is derived from mAb T84.66.

Figure 12: Flow cytometric analysis of periplasmic preparations containing Flag-tagged scFv protein fragments from selected clones. Periplasmic preparations of soluble scFv protein fragments were added to 100,000 to 200,000 CEA-transfected CHO cells. For detection a monoclonal anti-Flag antibody was used followed by a PE-labeled polyclonal anti-mouse antibody. ScFvs binding to cells was measured by an increase in fluorescence intensity as compared to cells that were incubated with PBS alone. Fluorescence intensity is blotted on the X-axis, the number of events is blotted on the Y-axis. The negative control (PBS and detection reagents) is shown as filled curve, the respective scFvs are shown as grey lines. Shifting to the right indicates positive binding to the cells. All of the scFvs, i.e. A-121, A-183, A-240, A-313, A-290, A-315, A4-35, A4-52 and MP2-A5, bind to membrane-bound CEA on CHO cells. Each of the scFv consists of the murine A5B7 VH region and a human VL region, as described in Example 6.

Figure 13: Flow cytometric analysis of periplasmic preparations containing Flag-tagged scFv protein fragments from selected. Periplasmic preparations of soluble scFv protein fragments were added to 100,000 to 200,000 CEA-transfected CHO cells. Detection was performed by a monoclonal anti-Flag antibody followed by a PE-labeled polyclonal anti-mouse antibody. ScFvs binding to cells was measured by an increase in fluorescence intensity as compared to cells that were incubated with PBS alone. Fluorescence intensity is blotted on the X-axis, the number of events is blotted on the Y-axis. The negative control (PBS and detection reagents) is shown as filled curve, the respective scFvs are shown as grey lines. Shifting to the right indicates positive binding to the cells. The fully human scFv constructs MP510_3-A5.3, MP510_3-B9.1, and MP510_3-D8.1 bind to membrane-bound CEA on CHO cells. Each of these scFvs consists of a human VH region and the human VL region A240, as described in Example 7. 240 Vlambda.3 is a scFv consisting of the murine A5B7 VH region and the human VL A-240 region. This construct shows also CEA-binding activity.

Figure 14: FACS binding analysis of various human CEA-reactive bispecific single chain constructs to Kato III cells and HPB-All cells, respectively. The thick line represents cells incubated with cell culture supernatant of transfected CHO cells incubated with the anti-His antibody and the detection antibody. The thin histogram line reflects the negative control: cells incubated with the anti-His antibody and the detection antibody. The human bispecific single chain antibody constructs A5 VH-A240 VLxSEQ ID NO.77 VHVL, B9 VH-A240 VLxSEQ ID NO.77 VHVL, and D8 VH-A240 VLxSEQ ID NO.77 VHVL bind to human CEA on Kato cells and to human CD3 on HPB-All cells. CEAI VH-A240 VLxSEQ ID NO.77 VHVL with the VH region of the CEA binding domain derived from mAb A5B7 shows the same binding activity.

Figure 15: Cytotoxicity assay of the indicated CEA-reactive bispecific single chain constructs redirected to CHO cells transfected with CEA, in the absence of soluble CEA. Stimulated human CD8 positive CTLs were used as effector cells. Cytotoxic activity could be detected for A5 VH-A240 VLxSEQ ID NO.77 VHVL, B9 VH-A240 VLx SEQ ID NO.77 VHVL, D8 VH-A240 VLxSEQ ID NO.77 VHVL and CEAI VH-A240 VLx SEQ ID NO.77 VHVL. CEAI VH is a VH region derived from mAb A5B7.

Figure 16: Cytotoxicity assay of the indicated CEA-reactive bispecific single chain constructs redirected to CHO cells transfected with CEA, in the absence of soluble CEA. Stimulated human CD8 positive CTLs were used as effector cells. This Figure demonstrates cytotoxic activity for A240 VL-A5 VHxSEQ ID NO.77 VHVL, A240 VL-B9 VHxSEQ ID NO.77 VHVL, A240 VL-D8 VHx SEQ ID NO.77 VHVL, and A240 VL-CEAI VHx SEQ ID NO.77 VHVL.

Figure 17: Cytotoxicity assay of the indicated CEA-reactive bispecific single chain constructs redirected to CHO cells transfected with CEA, in the absence of soluble CEA. Stimulated human CD8 positive CTLs were used as effector cells. Cytotoxicity against CEA+ target cells is shown for SEQ ID NO.77 VHVLxA5 VH-A240 VL, SEQ ID NO.77 VHVLxB9 VH-A240 VL, SEQ ID NO.77 VHVLxD8 VH-A240 VL, SEQ ID NO.77 VHVLxCEAI VH-A240 VL and SEQ ID NO.77 VHVLxCEAI VLVH.

Figure 18: Cytotoxicity assay of the indicated CEA-reactive bispecific single chain constructs redirected to CHO cells transfected with CEA, in the absence of soluble CEA. Stimulated human CD8 positive CTLs were used as effector cells. Cytotoxic activity is shown for SEQ ID NO.77 VHVLxA240 VL-A5 VH, SEQ ID NO.77 VHVLxA240 VL-B9 VH, SEQ ID NO.77 VHVLxA240 VL-D8 VH, and SEQ ID NO.77 VHVLx A240VL-CEAI VH and SEQ ID NO.77 VHVLxCEAI VLVH.

Figure 19: Cytotoxicity assay of the indicated CEA-reactive bispecific single chain constructs redirected to CHO cells transfected with CEA in the presence of increasing amounts of soluble CEA antigen. Stimulated human CD8 positive CTLs were used as effector cells. The Figure demonstrates the resistance of cytotoxic activity of human bispecific single chain antibody constructs to soluble CEA antigen, as exemplified for A5 VH-A240 VLx SEQ ID NO.77 VHVL and B9 VH-A240 VLx SEQ ID NO.77 VHVL.

Figure 20: Cytotoxicity assay of the indicated CEA-reactive bispecific single chain constructs redirected to CHO cells transfected with CEA in the presence of increasing amounts of soluble CEA antigen. Stimulated human CD8 positive CTLs were used as effector cells. Human bispecific single chain antibody constructs D8

VH-A240 VLxSEQ ID NO.77 VHVL and CEAI VH-A240 VLx SEQ ID NO.77 VHVL also show resistance to soluble CEA antigen.

Figure 21: The indicated CEA-reactive bispecific single chain constructs redirected T cells to lyse CHO cells transfected with CEA, in the absence of soluble CEA. To demonstrate the specificity of the redirected lysis, non-transfected CHO cells were included as negative control. Stimulated human CD8 positive CTLs were used as effector cells. A240 VL–B9 VHxSEQ ID NO.77 VHVL, SEQ ID NO.77 VHVLxA240 VL–B9 VH, SEQ ID NO.77 VHVLxB9 VH–A240 VL, B9 VH–A240 VLxSEQ ID NO.77 VHVL, and SEQ ID NO.77 VHVLxCEA I VHVL revealed cytotoxic activity against human CEA-transfected CHO cells.**Figure 22:** The indicated CEA-reactive bispecific single chain construct redirected T cells to lyse CHO-CEA+ cells in the presence of increasing amounts of soluble CEA antigen. Stimulated human CD8+ T cells were used as effector cells. A240 VL–B9 VHx SEQ ID NO.77 VHVL-mediated cytotoxic activity is resistant to soluble CEA.

Figure 23: High resolution cation exchange chromatogram of the bispecific single chain construct A240 VL–B9 VHxSEQ ID NO.77 VHVL, the blue line (upper curve) shows the overall charge isoforms of the protein. One single peak was detected showing high homogeneity of the construct.

Figure 24: Protein stability assay based on the assessment of cytotoxicity after incubation in human plasma for 24h. The CEA-reactive bispecific single chain construct redirected to CHO cells transfected with CEA, in the absence of soluble CEA. Stimulated human CD8 positive CTLs were used as effector cells. The Figure demonstrates the plasma stability of the bispecific single chain construct A240 VL–B9 VHxSEQ ID NO.77 VHVL in human plasma. Cytotoxic activity of the construct is not influenced by plasma proteins under physiological conditions.

Figure 25: High resolution cation exchange chromatogram of the bispecific single chain construct SEQ ID NO.77 VHVLxE12 VH-A240 VL, the blue line (upper curve) shows the overall charge isoforms of the protein. The Figure demonstrates the homogeneity of the bispecific single chain construct SEQ ID NO.77 VHVLxE12 VH-A240 VL.

Figure 26: Protein stability assay based on the assessment of cytotoxicity after incubation in human plasma for 24 h. The CEA-reactive bispecific single chain

construct redirected to CHO cells transfected with CEA, in the absence of soluble CEA. Stimulated human CD8 positive CTLs were used as effector cells. This Figure demonstrates the plasma stability of the bispecific single chain construct SEQ ID NO.77 VHVLxE12 VH-A240 VL in human plasma. Cytotoxic activity of the construct is not influenced by plasma proteins under physiological conditions.

Figure 27: The indicated CEA-reactive bispecific single chain construct redirected T cells to lyse CHO-CEA+ cells in the presence of increasing amounts of soluble CEA antigen. Stimulated human CD8+ T cells were used as effector cells. The bispecific single chain construct SEQ ID NO.77 VHVLxE12 VH-A240 VL mediated cytotoxic activity that is resistant to soluble CEA.

The following Examples illustrate the invention:

EXAMPLE 1: Generation of CHO cells transfected with human CEA (carcinoembryonic antigen-related cell adhesion molecule 5; CEACAM5)

CEA-positive Kato III cells (human gastric carcinoma cell line; ATCC HTB-103) were used to obtain the total RNA that was isolated according to the instructions of the kit manual (Qiagen, RNeasy Mini Kit). The obtained RNA was used for cDNA synthesis by random-primed reverse transcription. For cloning of the full length sequence of the CEA antigen, the following oligonucleotides were used: 5′ CEACAM5 EcoRI GAATTCGCCACCATGGAGTCTCCCTCGGCCCC (SEQ ID NO. 74) and 3′ CEACAM5 Sal I GTCGACCTATATCAGAGCAACCCC (SEQ ID NO. 75). A PCR (denaturation at 93 °C for 5 min, annealing at 58°C for 1 min, elongation at 72°C for 1 min for the first cycle; denaturation at 93°C for 1 min, annealing at 58°C for 1 min, elongation at 72°C for 1 min for 30 cycles; terminal extension at 72°C for 5 min) was used to amplify the coding sequence. The PCR product was subsequently digested with EcoRI and SalI, ligated into the appropriately digested expression vector pEF-DHFR, and transformed into E.coli. The isolated plasmid DNA was sequenced and compared with the established nucleotide sequence of CEACAM5 (NM_004363 at the National Center for biotechnology information, http://www.ncbi.nlm.nih.gov/) The aforementioned procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (1989; 2001). The clone with the verified nucleotide sequence was transfected into DHFR deficient CHO cells for eukaryotic expression of the construct. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described in Kaufmann (Kaufmann R.J., Methods Enzymol. 185 (1990), 537-566). Gene amplification of the construct was induced by increasing concentrations of MTX to a final concentration of up to 20 nM MTX. The transfected cells were then tested for expression of CEA antigen using an FACS assay. For that purpose, $2.5x10^5$ transfected cells were incubated with 5 µg/ml of the murine monoclonal antibody COL-1 (No. MS-613-P1ABX, Neomakers; Fremont, CA, USA). The binding of the antibody was detected with a R-Phycoerythrin-conjugated affinity purified F(ab')2 fragment, goat anti-mouse IgG, Fc-gamma fragment specific antibody, diluted 1:100 in 50 µl PBS with 2% FCS (obtained from Dianova, Hamburg, Germany). Cells were analyzed by flow cytometry on a FACS-Calibur (Becton Dickinson, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002). As a result, the transfectants demonstrated a clearly positive staining for the human CEA antigen.

EXAMPLE 2: Generation of CEAxCD3 bispecific single chain antibodies

Generally, bispecific single chain antibody molecules, each comprising a domain with binding specificity for the human CEA antigen as well as a deimmunized domain with binding specificity for the human CD3 antigen depicted in SEQ ID NO.77 were designed as set out in Table 1. The arrangement of the V regions in this CD3 binding domain is always VH-VL. This de-immunised anti-CD3 binding domain used in the bispecific single chain antibodies as defined herein has been described previously, e.g. in WO2005/040220.

1. Formats of bispecific single chain antibody molecules comprising anti-CEA and anti-CD3 specificities (Table 1)

SEQ ID NO. (amino acid sequence)	Formats of protein constructs (N terminus→ C terminus)
2	SEQ ID NO.77 VHVL x CEA I VLVH
4	SEQ ID NO.77 VHVL x CEA I VHVL
6	CEA I VLVH x SEQ ID NO.77 VHVL
8	CEA I VHVL x SEQ ID NO.77 VHVL
10	CEA II VHVL x SEQ ID NO.77 VHVL
12	CEA III VLVH x SEQ ID NO.77 VHVL
14	CEA III VHVL x SEQ ID NO.77 VHVL
16	CEA I VH-A240VL x SEQ ID NO.77 VHVL
18	A240VL - CEA I VH x SEQ ID NO.77 VHVL
20	SEQ ID NO.77 VHVL x CEA I VH – A240 VL
22	SEQ ID NO.77 VHVL x A240 VL - CEA I VH
24	A5 VH – A240 VL x SEQ ID NO.77 VHVL
26	A240 VL – A5 VH x SEQ ID NO.77 VHVL
28	SEQ ID NO.77 VHVL x A240 VL – A5 VH
30	SEQ ID NO.77 VHVL x A5 VH – A240 VL
32	B9 VH – A240 VL x SEQ ID NO.77 VHVL
34	A240 VL – B9 VH x SEQ ID NO.77 VHVL
36	SEQ ID NO.77 VHVL x B9 VH – A240 VL
38	SEQ ID NO.77 VHVL x A240 VL – B9 VH
40	D8 VH – A240 VL x SEQ ID NO.77 VHVL
42	A240 VL - D8 VH x SEQ ID NO.77 VHVL
44	SEQ ID NO.77 VHVL x D8 VH – A240 VL
46	SEQ ID NO.77 VHVL x A240 VL - D8 VH
126	A5 VH-A240 VL# x SEQ ID NO.77 VHVL
128	SEQ ID NO.77 VHVLxA5 VH-A240VL#
130	B9 VH-A240 VL# x SEQ ID NO.77 VHVL
132	SEQ ID NO.77 VHVLxB9 VH-A240VL#
134	D8 VH-A240 VL# x SEQ ID NO.77 VHVL
136	SEQ ID NO.77 VHVLxD8 VH-A240VL#

143	SEQ ID NO.77 VHVLxE12 VH-A240VL

The aforementioned constructs containing the variable light-chain (VL) and variable heavy-chain (VH) regions specific for the human CEA antigen derived from monoclonal antibodies, hybridomas or obtained by phage display guided selection (PDGS) were obtained by gene synthesis and subsequent cloning into an expression vector comprising the CD3-specific VH and VL combinations. The generation of said bispecific single chain constructs can also be carried out according to recombinant techniques described e.g. in Sambrook (loc.cit.). A detailed instruction therefor is provided for e.g. in WO 99/054440.

The anti-CD3 binding domain corresponds to a de-immunized domain with binding specificity for the human CD3 antigen. The arrangement of the V regions of the deimmunized anti-CD3 binding domain in the bispecific single chain constructs described herein is always VH-VL. The corresponding amino acid sequence of said VH-VL domain is depicted in SEQ ID NO. 77. CEAI, CEAII and CEAIII specific for the human carcinoembryonic antigen contain the variable light-chain (VL) and variable heavy-chain (VH) regions derived from mAbs A5B7 (Chester, K. A. et al., Int J Cancer 57 (1994), 67-72), T84.66 (Neumaier, M. et al., Cancer Res 50 (1990), 2128-34) and MFE-23 (Boehm, M. K. Biochem J 2 (2000), 519-28), respectively. A5, B9, D8, and E12 are human VH regions specific for human CEA, whereas A240 is a human VL region with the same specificity. The generation of the human A5, B9, D8, E12 and A240 V regions is described in detail in Examples 6 and 7. The corresponding nucleotide and amino acid sequences of all bispecific single chain antibodies described herein are shown in the sequence listing.

In the following the generation of the CEA I VLVH x SEQ ID NO.77 VHVL (SEQ ID NO.6) construct is described in more detail. The generation of the other constructs mentioned above can be performed accordingly with the necessary implementation of modifications to the methods being well in the scope of the person skilled in the art.

To generate bispecific single chain antibody molecules comprising the aforementioned CEAI specificity and the deimmunized anti-CD3 (SEQ ID NO.77) specificity firstly the variable regions of CEAI obtained by gene synthesis according to standard protocols had to be modified by PCR to obtain the corresponding single chain Fv antibody fragment. To this end a two-step fusion PCR was used to amplify the sequence coding for the variable regions. A set of appropriate primers was designed to perform the PCR-based cloning steps, finally resulting in a single chain antibody connecting the two variable domains with a 15 amino acid linker ([Gly$_4$Ser]$_3$) in the order VL-Linker-VH.

In short the following primer combinations were used:

PCR step	Used primers		PCR step	Used primers	Resulting scFv
1	5'CEAI LH + 3'CEAI VL Linker	->	Fusion PCR	5'CEAI LH + 3'CEAI LH	CEAI LH
2	5'CEAI VH Linker + 3'CEAI LH	->			

The nucleotide sequences of the oligonucleotide primers are given below:

5'CEAI LH: 5' AGGTGTACACTCCGACATTGAGCTCACCCAG 3' (SEQ ID NO. 137)

3'CEAI VL Linker: 5' GGAGCCGCCGCCGCCAGAACCACCACCACC TTTGATCTCGAGCTTGG 3' (SEQ ID NO. 138)

5'CEAI VH Linker: 5' GGCGGCGGCGGCTCCGGTGGTGGTGGTTCT CAGGTCCAACTGCAGGAG 3' (SEQ ID NO. 139)

3'CEAI LH: 5' AATCCGGAGGAGACGGTGACCG 3' (SEQ ID NO. 140)

To generate the single chain antibody, two PCRs with the respective primer combinations described above as PCR step 1 and 2 were performed. During this PCR overlapping complementary sequences were introduced into the PCR-products (stemming from the respective linker primers) that combined to form the coding sequence of the 15 amino acid linker during the subsequent fusion PCR. Subsequently the amplified VH and VL domains were joined in this fusion PCR in which only the outer primers and both PCR-products were required. The resulting scFv antibody is flanked at the 5′end with the restriction enzyme recognition site for BsrGI and at the 3′end with the restriction enzyme recognition site for BspEI. Addition of the BsrGI site was performed as to allow for the in frame fusion with the coding sequence of a murine immunoglobulin leader peptide as described in WO2005/040220. The BspEI site was created as to allow for the in frame fusion with the sequence coding for the CD3 specific single chain antibody to generate the bispecific single chain antibody. To accomplish the fusion of the single chain Fv antibodies and to allow for eukaryotic expression the coding sequence of the CEA specific single chain Fv antibody was cloned via BsrGI and BspEI into the pEFDHFR expression vector (pEFDHFR was described in Mack et al. Proc. Natl. Acad. Sci. USA 92 (1995) 7021-7025) containing the deimmunized anti-CD3 single chain Fv antibody as described in WO2005/040220; in the present invention referred to as SEQ ID NO.77. Single clones of the construct were isolated and sequenced with primers complementary to flanking regions in the expression vector according to standard protocols (Sambrock, Molecular Cloning; A Laboratory Manual, 2nd edition, Cold Spring Harbour laboratory Press, Cold Spring Harbour, New York (1989)). For further experiments a clone of the construct with a verified nucleotide sequence was selected.

2. Expression and purification of the CEAxCD3 bispecific single chain antibodies

The bispecific single chain antibodies were expressed in chinese hamster ovary (CHO) cells. Eukaryotic protein expression in DHFR deficient CHO cells was performed as described in Kaufmann (loc. cit.). Gene amplification of the constructs were induced by increasing concentrations of MTX to a final concentration of up to 20 nM MTX. After two passages of stationary culture the cells were grown in roller bottles with CHO modified DMEM medium (HiQ®, HiClone) for 7 days before harvest. The cells were removed by centrifugation and the supernatant containing the expressed protein was stored at –20°C.

Äkta® FPLC System (Pharmacia) and Unicorn® Software were used for chromatography. All chemicals were of research grade and purchased from Sigma (Deisenhofen) or Merck (Darmstadt). Immobilized metal affinity chromatography ("IMAC") was performed using a Fractogel® column (Merck) which was loaded with $ZnCl_2$ according to the protocol provided by the manufacturer. The column was equilibrated with buffer A2 (20 mM sodium phosphate buffer pH 7.5, 0.4 M NaCl) and the cell culture supernatant (500 ml) was applied to the column (10 ml) at a flow rate of 3 ml/min. The column was washed with buffer A2 to remove unbound sample. Bound protein was eluted using a 2 step gradient of buffer B2 (20 mM sodium phosphate buffer pH 7.5, 0.4 M NaCl, 0.5 M Imidazol) according to the following:

Step 1: 20% buffer B2 in 6 column volumes;

Step 2: 100% buffer B2 in 6 column volumes.

Eluted protein fractions from step 2 were pooled for further purification.

Gel filtration chromatography was performed on a Sephadex™ S200 HiPrep column (Pharmacia) equilibrated with PBS (Gibco). Eluted protein samples (flow rate 1 ml/min) were subjected to standard SDS-PAGE and Western Blot for detection. Prior to purification, the column was calibrated for molecular weight determination (molecular weight marker kit, Sigma MW GF-200). Protein concentrations were determined using protein assay dye (MicroBCA, Pierce) and IgG (Biorad) as standard protein.

The CEAxCD3 bispecific single chain antibodies were isolated in a two step purification process of IMAC and gel filtration. The main product had a molecular weight of ca. 52 kDa under native conditions as determined by gel filtration in PBS. This molecular weight corresponds to the bispecific single chain antibody. All constructs were purified according to this method.

Purified bispecific single chain antibody protein was analyzed in SDS PAGE under reducing conditions performed with pre-cast 4-12% Bis Tris gels (Invitrogen). Sample preparation and application were performed according to the protocol provided by the manufacturer. The molecular weight was determined with MultiMark protein standard (Invitrogen). The gel was stained with colloidal Coomassie (Invitrogen protocol). The purity of the isolated protein was >95% as determined by SDS-PAGE.

Western Blot was performed using an Optitran® BA-S83 membrane and the Invitrogen Blot Module according to the protocol provided by the manufacturer. The antibodies used were directed against the His Tag (Penta His, Qiagen) and Goat-anti-mouse Ig labeled with alkaline phosphatase (AP) (Sigma), and BCIP/NBT (Sigma) as substrate. The bispecific single chain antibody could be specifically detected by Western Blot. A single band was detected at 52 kD corresponding to the purified bispecific single chain antibody molecule.

3. Flow cytometric binding analysis of the CEAxCD3 bispecific single chain antibodies

In order to test the functionality of the constructs with regard to binding capability to membrane-bound human CEA and human CD3, FACS analysis was performed. For this purpose, human CEA-transfected CHO cells and CD3 positive human T cell leukemia cell line HPB-All (DSMZ, Braunschweig, ACC483) were used. 200,000 CEA positive CHO cells or 200,000 HPB-All cells were incubated for 30 min on ice with 50 µl of the pure cell supernatant of CHO cell cultures each expressing bispecific antibodies with different arrangements of VH and VL regions of CEA and CD3 (as described above). The cells were washed twice in PBS and binding of the construct was detected with an unlabeled murine Penta His antibody (diluted 1:20 in 50 µl PBS with 2% FCS; Qiagen), which specifically binds to cell-bound construct via the construct's C-terminal histidine tag. A washing step followed to remove unbound murine Penta His antibody. Bound anti-His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in 50 µl PBS with 2% FCS. As a positive control for binding to human CEA, monoclonal antibody Col-1 (see Example 3) has been used. For control of binding to human CD3, a CD19xCD3 bispecific single chain construct as described in WO 99/054440 has been utilized. As a negative control fresh culture medium was used in place of culture supernatant.

Cells were analyzed by flow cytometry (FACS-Calibur; Becton Dickinson, Heidelberg). FACS staining and measuring of the fluorescence intensity were performed as described in Current Protocols in Immunology (Coligan, Kruisbeek, Margulies, Shevach and Strober, Wiley-Interscience, 2002).

As shown in Figure 1, several domain arrangements of the bispecific single chain antibodies, i.e. CEAI VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 8), CEAI VLVHxSEQ ID NO.77 VHVL (SEQ ID NO. 6), CEAII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 10), CEAIII VLVHxSEQ ID NO.77 VHVL (SEQ ID NO. 12) and CEAIII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 14), bound to human membrane-bound CEA and human CD3. As a negative control, culture medium and 1. and 2. detection antibodies have been used.

EXAMPLE 3: Binding of CEAxCD3 bispecific single chain antibodies to soluble human CEA

In order to determine the specificity against soluble human CEA, various CEAxCD3 bispecific single chain antibodies were tested in ELISA.

To this end, soluble human CEA antigen was first biotinylated. Biotinylation was accomplished in PBS containing 5% DMSO (Sigma) with a fifteen-fold molar excess of EZ-Link Sulfo NHS-LC-LC-Biotin (Pierce) for 1 hour at room temperature in a sample mixer (Dynal). For the separation of free Biotin and biotinylated CEA antigen, the assay was excessively dialyzed against PBS according to standard protocols.

The retained bioactivity of the biotin-labeled CEA was confirmed in ELISA binding experiments.

The direct ELISA to determine the specificity of CEAxCD3 bispecific single chain antibody against soluble human CEA was carried out according to standard procedures. Briefly, 50 µl/well PBS or soluble biotinylated human CEA (Abcam; 5 µg/ml in 1xPBS) were immobilized on a 96-well streptavidin-coated ELISA plate (Nunc) by incubating at 4°C for about 16 hours. After washing with 200 µl water per well 200 µl of blocking solution (PBS/3 % BSA) was added. After blocking for 1 h at room temperature the blocking solution was removed. All subsequent washing (200 µl/well of 1xPBS/0.05% (v/v) Tween™ 20) and incubation steps were performed at room temperature. After washing once, the CEAI VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 8; anti-CEA part derived from mAb A5B7), CEAII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 10; anti-CEA part derived from mAb T84.66), and CEAIII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 14; anti-CEA part derived from mAb MFE-23) bispecific single chain antibodies, and mouse monoclonal antibody CEA/CD66 Ab-3 (Col-1; Dunn) were incubated in different concentrations (0.5 µg/ml and 5 µg/ml in 1xPBS; 50 µl/well) for 1 hour. 1xPBS (50 µl/well) was added as a control for unspecific binding. 3 washing steps were followed by adding 50 µl/well Penta-His IgG (Qiagen; 2 µg/ml in 1xPBS) for detection of the His-tagged bispecific single chain antibodies. Subsequently, the wells were washed 3 times and incubated with 50 µl of a horseradish peroxidase-labelled goat anti-mouse Fc gamma-specific antibody (Jackson ImmuneResearch; 1:1000 in 1xPBS) for 1 hour. After washing 3 times the ELISA was developed by adding ABTS substrate solution (Roche) and the absorbance was measured at a wavelength of 405 nm.

Figure 2 shows the absorbance of the different bispecific single chain antibodies detected in the ELISA. The CEAI VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 8; anti-CEA part derived from mAb A5B7), CEAII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 10; anti-CEA part derived from mAb T84.66), and CEAIII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 14; anti-CEA part derived from mAb MFE-23) bispecific single chain antibodies and the mouse monoclonal antibody Col-1 specifically bound to soluble human CEA. No binding signal was observed in the absence of the CEA antigen (PBS control). In summary, the anti-CEA binding domains derived from mAbs A5B7, T84.66 and MFE-23 bind to both soluble and membrane-bound CEA.

EXAMPLE 4: Bioactivity of CEAxCD3 bispecific single chain antibodies

Bioactivity of the generated CEAxCD3 bispecific single chain antibodies was analyzed by in vitro chromium release cytotoxicity assays using the human gastric carcinoma cell line Kato III or the human CEA-transfected CHO cells as target cells and stimulated human CD8 positive T cells or native PBMC as effector cells, respectively.

The generation of the stimulated CD8+ T cells was performed as follows:

A petri dish (145 mm diameter, greiner bio-one) was precoated with an anti-CD3 antibody (OKT3 Janssen-Cilag GmbH, Orthoclone 1mg/ml; final concentration 1µg/ml) and an anti-CD28 antibody (BD, 1mg/ml; final concentration 1µg/ml) for 1 hour at 37°C. After the incubation period, the unbound protein was removed by one washing step with PBS. The fresh PBMC´s were isolated from peripheral blood (30 – 50 ml) by Ficoll™ gradient centrifugation according to standard protocols. 3 – 5 x 10^7 PBMCs were added to the precoated petri dish in 150 ml of RPMI 1640 / 10% FCS / IL-2 20 U/ml (Proleukin, Chiron) and stimulated for 2 days. At the third day the cells were collected, washed once with RPMI 1640 and transfered to a large T-flask. IL-2 was added to a final concentration of 20 U/ml and cultivated again for one day. The CD8+ CTLs were isolated with help of the CD8 negative isolation kit (Dynal Biotech) by following the instructions of the manual. The native PBMC's were used directly after the Ficoll™ gradient centrifugation without the stimulation procedure. Target cells were washed twice with PBS and labeled with 11.1 MBq ^{51}Cr in a final volume of 100µl RPMI with 50% FCS for 45 minutes at 37°C. Subsequently, the labeled target cells were washed 3 times with 5 ml RPMI and then used in the cytotoxicity assay. The assay was performed in a 96 round bottom plate in a total volume of 250µl supplemented RPMI (as above) with an E:T ratio of 10:1 corresponding to 5000 target cells and 50000 effector cells per well. For the evaluation of the constructs a starting concentration of 1µg/ml of the bispecific single chain molecules in the assay volume and 12 threefold dilutions thereof were applied. The assay time was 18 hours and cytotoxicity was measured as relative values of released chromium in the supernatant related to the difference of maximum lysis (addition of Triton™-X) and spontaneous lysis (without effector cells). All measurements were done in triplicates. Measurement of chromium activity in the supernatants was performed with a Wizard 3 gammacounter (Perkin Elmer Life

Sciences GmbH, Köln, Germany). Analysis of the experimental data was performed with Prism 4 for Windows (version 4.02, GraphPad Software Inc., San Diego, California, USA). Sigmoidal dose response curves typically had R^2 values >0.90 as determined by the software. EC_{50} values calculated by the analysis program were used for comparison of bioactivity.

Figure 3 shows cytotoxic activity against human CEA-transfected target cells (CHO-CEA^+ cells) for various domain arrangements, i.e. for SEQ ID NO.77 VHVLxCEAI VHVL (SEQ ID NO. 4) and SEQ ID NO.77 VHVLxCEAI VLVH (SEQ ID NO. 2) (both constructs with anti-CD3 part N-terminally), as well as for CEAI VLVHxSEQ ID NO.77 VHVL (SEQ ID NO. 6) and CEAI VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 8) (anti-CD3 C-terminally). Non-transfected CHO cells (lacking human CEA) were used as a negative control.

In Figure 4, CEAI VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 8), CEAIII VLVHxSEQ ID NO.77 VHVL (SEQ ID NO. 12), CEAIII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 14), and CEAII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 10) exhibited cytotoxic activity against human CEA-transfected CHO cells. Non-transfected CHO cells (lacking human CEA) were used as a negative control. As set forth above, CEAI denotes a variable region derived from murine mAb A5B7, CEAII is a variable region derived from murine mAb T84.66 and CEAIII refers to a variable region from murine mAb MFE-23.

In summary, all tested constructs showed cytotoxic activity against (human) CEA expressing Kato III and human CEA-transfected CHO cells, in the absence of soluble human CEA.

EXAMPLE 5: Bioactivity of CEAxCD3 bispecific single chain antibodies specific in the presence of soluble CEA antigen

The competition assays are performed as described in Example 4, with the following exception: The bioactivity of the CEAxCD3 bispecific single chain antibodies is tested in the presence of various concentrations of soluble human CEA antigen. The soluble human CEA antigen (AbCAM Ltd. Cambridge UK) used was isolated from a metastatic colonic carcinoma from the liver of a single patient. Experimentally, the competition assay was carried out by pre-incubation of a given amount of the bispecific single chain antibody with increasing amounts of soluble human CEA antigen (either 0 µg/ml; 0.1 µg/ml; 1 µg/ml, or 0 µg/ml; 0.004 µg/ml; 0.02 µg/m; 0.1

μg/ml; 0.5 μg/ml; 1 μg/ml) for 30 minutes at 37°C prior to the addition of the cells. The remainder of the assay was carried out as described in Example 4. The results of these competition experiments are shown in Figures 5 to 11.

Cytotoxic activity of bispecific single chain antibodies CEAII VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 10; see Figures 7 and 9 to 11) with the anti-CEA part derived from mAb T84.66, and CEAIII VLVHxSEQ ID NO.77 VHVL (SEQ ID NO. 12; see Figure 8) with the anti-CEA region derived from mAb MFE-23, against human CEA-positive target cells was drastically inhibited by increasing amounts of soluble human CEA antigen. As set forth above, said constructs bind to both membrane-bound and soluble human CEA antigen; see e.g. Examples 2 and 3 and Figures 1 and 2. Thus, most probably, soluble human CEA prevents the anti-CEA part of said bispecific single chain antibodies from binding to membrane-bound human CEA on the target cells, for instance CHO-CEA+ or Kato III tumor cells, thereby inhibiting the cytotoxic activity mediated by said antibody constructs.

In contrast, it has been surprisingly found that bispecific single chain antibodies with an anti-CEA part derived from mAb A5B7 are resistant to soluble human CEA: For instance, the cytotoxic activity mediated by CEAI VLVHxSEQ ID NO.77 VHVL (SEQ ID NO. 6; see Figure 5), CEAI VHVLxSEQ ID NO.77 VHVL (SEQ ID NO. 8; see Figures 5, 8 and 10), SEQ ID NO.77 VHVLxCEAI VHVL (SEQ ID NO. 4; see Figure 6) and SEQ ID NO.77 VHVLxCEAI VLVH (SEQ ID NO. 2; see Figure 6) is not inhibited by increasing amounts of soluble human CEA, not even by high concentrations (1μg/ml). This could not be expected in view of the fact that the anti-CEA part of said bispecific single chain antibodies binds to soluble human CEA (Figure 2). Rather, inhibition of cytotoxic activity against CEA-positive target cells by increasing amounts of soluble human CEA could have been expected, as it was the case for T84.66- and MFE-23-derived constructs; see above.

Thus, the present invention provides for pharmaceutical compositions with cytotoxic anti-tumor activity in the presence of even high levels of soluble CEA antigen. Therefore, these pharmaceutical compositions are particularly suitable for the treatment of tumor patients with high soluble CEA antigen concentrations in their plasma, such as patients with progressive epithelial tumors, metastatic epithelial tumors, high tumor load/burden, late stage epithelial tumors or tumor patients with a CEA serum concentration higher than 100 ng/ml, as determined by ELISA.

EXAMPLE 6: Selection of human VL regions

In order to provide for pharmaceutical compositions with reduced immunogenicity when being administered to cancer patients, human bispecific single chain antibodies with resistance to soluble CEA antigen have been generated. In a first step, human VL regions with resistance to soluble CEA have been isolated. Thus, the aim of this experiment is the selection of human VL regions which can pair with the maternal, murine VH of monoclonal antibody (mAb) A5B7.

1. Biotinylation of soluble human CEA antigen

For phage library selection, soluble CEA antigen was biotinylated. Biotinylation was accomplished in PBS containing 5% DMSO (Sigma) with a fifteenfold molar excess of EZ-Link Sulfo NHS-LC-LC-Biotin (Pierce) for 1 hour at room temperature in a sample mixer (Dynal). For the separation of free Biotin and biotinylated CEA antigen, the assay was excessively dialized against PBS according to standard protocols.
The retained bioactivity of the biotin-labeled CEA was confirmed in ELISA binding experiments.

2. Isolation of RNA from human B-cells

100 mL blood were taken from five healthy human donors. Peripheral blood mononuclear cells (PBMCs) were isolated by a ficoll-gradient according to standard methods. Total RNA was isolated from the isolated cells using the RNeasy® Midi Kit (QIAGEN) following the manufacturer's instructions. cDNA was synthesized according to standard methods (Sambrook, Cold Spring Harbor Laboratory Press 1989, 2001).

3. PCR-Amplification of variable light chain regions (VL-regions)

For the isolation of light chain V-region DNA, RT-PCR was carried out using V-kappa- (5'-huVK1-SacI-2001 (5'-GAGCCGCACG AGCCCGAGCT CCAGATGACC CAGTCTCC-3') (SEQ ID NO. 78), 5'-huVK2/4-SacI-2001 (5'-GAGCCGCACG AGCCCGAGCT CGTGATGACY CAGTCTCC-3') (SEQ ID NO. 79), 5'-huVK3-SacI-2001 (5'-GAGCCGCACG AGCCCGAGCT CGTGWTGACR CAGTCTCC-3') (SEQ ID NO. 80), 5'-huVK5-SacI-2001 (5'-GAGCCGCACG AGCCCGAGCT CACACTCACG CAGTCTCC-3') (SEQ ID NO. 81), 5'-huVK6-SacI-2001 (5'-GAGCCGCACG AGCCCGAGCT CGTGCTGACT CAGTCTCC-3') (SEQ ID NO. 82), 3'-hu-Vk-J1-

SpeI-BsiWI (5’-GACGACACTA GTTGCAGCCA CCGTACGTTT GATTTCCACC TTGGTCC-3’) (SEQ ID NO. 83), 3’-hu-Vk-J2/4-SpeI-BsiWI (5’-GACGACACTA GTTGCAGCCA CCGTACGTTT GATCTCCASC TTGGTCC-3’) (SEQ ID NO. 84), 3’-hu-Vk-J3-SpeI-BsiWI (5’-GACGACACTA GTTGCAGCCA CCGTACGTTT GATATCCACT TTGGTCC-3’) (SEQ ID NO. 85), 3’-hu-Vk-J5-SpeI-BsiWI (5’-GACGACACTA GTTGCAGCCA CCGTACGTTT AATCTCCAGT CGTGTCC-3’) (SEQ ID NO. 86)) and V lambda (5′-huVL1a-SacI-2001 (GAG CCG CAC GAG CCC GAG CTC GTG TTG ACG CAG CCG CCC TC) (SEQ ID NO. 87), 5′-huVL1b-SacI-2001 (GAG CCG CAC GAG CCC GAG CTC GTG CTG ACT CAG CCA CCC TC) (SEQ ID NO. 88), 5′-huVL2-SacI-2001 (GAG CCG CAG GAG CCC GAG CTC GCC CTG ACT CAG CCT SCC TCC GT) (SEQ ID NO. 89), 5′-huVL4-SacI-2001 (ACC TGC GAG CTC GTG CTG ACT CAR YCM YCC TCT GC) (SEQ ID NO. 90), 5′-huVL5-SacI-2001 (ACC TGC GAG CTC GTG CTG ACT CAG CCR SCT TCC) (SEQ ID NO. 91), 5′-huVL6-SacI-2001 (ACC TGC GAG CTC ATG CTG ACT CAG CCC CAC TC) (SEQ ID NO. 92), 5′-huVL3/9-SacI-2001 (GAG CCG CAC GAG CCC GAG CTC GWG CTG ACT CAG CCA CCY TC) (SEQ ID NO. 93), 5′-huVL7/8-SacI-2001 (GAG CCG CAC GAG CCC GAG CTC GTG GTG ACY CAG GAG CCM TC) (SEQ ID NO. 94), 3′-hu-Vlam-BlnI-SpeI-2001 (CGT GGG ACT AGT CTT GGG CTG ACC TAG GAC GGT) (SEQ ID NO. 95), 3′-hu-Vlam2-BlnI-SpeI-2002: CGT GGG ACT AGT CTT GGG CTG ACC GAG GAC GGT) (SEQ ID NO. 96) primer sets.

RNA from human B-cells was transcribed into cDNA (as described above) and used as template DNA in PCR reactions. Per PCR reaction, one 5’-primer was combined with one 3’-primer. The number of different PCR reactions was determined by the number of possible combinations of 5’- and 3’-primers. The following PCR-program was used for amplification: Denaturation at 94°C for 15 seconds, primer annealing at 52°C for 50 seconds and primer extension at 72°C for 90 seconds were performed over 40 cycles, followed by final extension at 72°C for 10 minutes. Light chain DNA V-fragments were then isolated according to standard protocols.

4. Library construction – cloning of the human VL pool

A phage display library was generally constructed based on standard procedures, as for example disclosed in “Phage Display: A Laboratory Manual”; Ed. Barbas, Burton, Scott & Silverman; Cold Spring Harbor Laboratory Press, 2001.

The primers chosen for PCR amplification gave rise to 5'-SacI and 3'-SpeI recognition sites for the light chain V-fragments. Four ligation reactions were set up, each consisting of 400 ng of light chain fragments (SacI-SpeI digested, 2 x kappa and 2 x lambda) and 1400 ng of the phagemid pComb3H5BHis (SacI-SpeI digested; large fragment; this vector is described in the thesis dissertation of Dr. Ralf Lutterbüse. The four resulting antibody V-light chain pools were then each transformed into 300 µL of electrocompetent Escherichia coli XL1 Blue by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 mF, 200 Ohm, Biorad gene-pulser) resulting in library sizes of

kappa1:	2×10^8
kappa2:	6×10^7
lambda1:	9×10^7
lambda2:	6×10^7

independent clones.

Kappa (light chain) DNA-fragments from the different PCR amplifications were weighted for each ligation as follows: Each 5'-primer defines a specific group. Within these groups the 3'-primers define the subgroups. The kappa subgroups were weighted 1:2:1:1 corresponding to the primers 3'-hu-Vk-J1-SpeI-BsiWI : 3'-hu-Vk-J2/4-SpeI-BsiWI : 3'-hu-Vk-J3-SpeI-BsiWI : 3'-hu-Vk-J5-SpeI-BsiWI. The groups were weighted according to their germline distribution 1:1:1:0.2:0.2 corresponding to the primers 5'-huVK1-Sac-2001 : 5'-huVK3-Sac-2001 : 5'-huVK2/4-Sac-2001 : 5'-huVK5-Sac-2001 : 5'-huVK6-Sac-2001.

Lambda (light chain) DNA-fragments from the different PCR amplifications were weighted for each ligation as follows: Each 5'-primer defines a specific group. Within these groups the 3'-primers define the subgroups. The lambda subgroups were weighted 3:1 corresponding to the primers 3′-hu-Vlam-BlnI-SpeI-2001: 3′-hu-Vlam2-BlnI-SpeI-2002.

The groups were weighted according to their germline distribution 1:1:2:2:2:3 corresponding to the primers 5′-huVL1a-SacI-2001: 5′-huVL1b-SacI-2001 : 5′-huVL2-SacI-2001: 5′-huVL4-SacI-2001 + 5′-huVL5-SacI-2001 : 5′-huVL6-SacI-2001 + 5′-huVL7/8-SacI-2001 : 5′-huVL3/9-SacI-2001.

After electroporation each reaction was incubated in SOC broth (Fluka) for phenotype expression. The two kappa cultures were combined as well as the two lambda cultures .The resulting kappa culture and the resulting lambda culture were then each incubated in 500 mL of SB selection medium containing 50 μg/mL carbenicillin and 2 % w/v glucose overnight. The next day, cells were harvested by centrifugation and plasmid preparation was carried out using a commercially available plasmid preparation kit (Qiagen).

5. Construction of the antibody library - human VL – maternal VH

PCR was performed to amplify the maternal VH of mAb A5B7 from a vector containing said maternal VH. For amplification a PCR protocol according to standard procedures was followed using the 5'-primer 5'-AVH-XhoI (5'-GTC ACA CTC GAG TCA GGA GGA GGC TTG GTA C-3') (SEQ ID NO. 97) and the 3'-primer 3'-AVH-BstEII (5'-GTC ACA GGT GAC CGT GGT CCC TTG GCC CCA G-3' (SEQ ID NO. 98). After purification of the approximately 350 bp amplification product from an analytical agarose gel, the DNA fragment was cut with the restriction enzymes BstEII and XhoI. The phagemid pComb3H5BHis (this vector is described in the thesis dissertation of Dr. Ralf Lutterbüse) was digested accordingly and the large fragment was ligated with the above mentioned fragment. After transformation into E. coli XL1 blue, a single clone was cultivated in 100 mL SB medium (containing 50 μg/mL carbenicilline) and the plasmid was prepared according to standard protocols. The successful cloning was confirmed by sequencing the insert (Sequiserve, Munich).

This vector pComb3H5BHis/maternalVH of mAb A5B7 was restricted with the restriction enzymes SacI and SpeI. The large vector fragment was isolated. Plasmid-DNA containing the Vkappa- and the Vlambda library was restricted with the restriction enzymes SacI and SpeI. The small Vkappa - and the respective Vlambda fragment (each approximately 350 bp) were isolated according to standard protocols.

1200 ng of the vector fragment were ligated with a mix of each 200 ng of both the Vkappa and the Vlambda fragments. The ligation reaction was transformed into 300 μL of electrocompetent E. coli XL1 Blue by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 mF, 200 Ohm) resulting in a total scFv library size of 1.2 x 10^8 independent clones.

After phenotype expression and slow adaptation to carbenicillin, the antibody library was transferred into SB-Carbenicillin (50 μg/mL) selection medium. The antibody library was then infected with an infectious dose of 1 x 10^{12} particles of helper phage VCSM13 resulting in the production and secretion of filamentous M13 phage, wherein each phage particle contained single stranded pComb3H5BHis-DNA encoding a half-human scFv-fragment and displayed the corresponding scFv-protein as a translational fusion to phage coat protein III.

6. Phage display selection of a human VL

The phage particles carrying the scFv-repertoire were harvested from the culture supernatant by PEG8000/NaCl precipitation and centrifugation. Then approximately 1 x 10^{11} to 1 x 10^{12} scFv phage particles were resuspended in 0.5 mL of TBS/1% BSA and incubated with biotinylated soluble CEA, that was immobilized in Streptavidine coated wells of an ELISA plate (Nunc) for 1 h. A 10 µg antigen/ml PBS solution (50 µl) was incubated for over night at 4°C in the streptavidine coated wells, washed once with water, followed by blocking for 1 hour at 37°C with 200 µl of 3% BSA in TBS, that was removed after incubation.

scFv phage that did not specifically bind to the target antigen were eliminated by washing steps with TBS/0,05 % Tween. This washing procedure was repeated up to 10 times in further rounds.

After washing, binding entities were eluted by using HCl-glycine, pH 2.2. Following neutralization with 2 M Tris, pH 12, the eluate was used for infection of a fresh uninfected E. coli XL1 Blue culture.

To elute remaining high binding entities 50 µL of a fresh E. coli XL1 blue culture (OD600 ≥ 0.5) were added to the wells and incubated for 15 minutes. Both cultures were then mixed and cells successfully transduced with a phagemid copy, encoding a human scFv-fragment, were again selected for carbenicillin resistance and subsequently infected with VCMS13 helper phage to start the second round of antibody display and in vitro selection.

Plasmid DNA corresponding to 4 rounds of panning was isolated from E. coli cultures. For the production of soluble scFv-protein, VH-VL-DNA fragments were excised from the plasmids (XhoI-SpeI), and cloned via the same restriction sites in the plasmid pComb3H5BFlag/His, in which the expression construct (e.g. scFv) includes a Flag-tag (TGDYKDDDDK) (SEQ ID NO. 99) between the scFv and the His6-tag and the additional phage proteins are deleted.

After ligation each pool (different rounds of panning) of plasmid DNA was transformed into 100 µL heat shock competent E. coli TG1 and plated onto carbenicillin LB-agar. Single colonies were picked and inoculated into 120 µL of LB carb (50µg/mL) 1% glucose in 96-well plates (Greiner). The wells were sealed with a semipermeable membrane (Greiner) and the plates were incubated overnight at 37°C in a shaking incubator (master plate). Then 10 µL of the master plate cultures were transferred into a second 96 well plate (working plate) containing 90 µL LB carb (50µg/mL) 0.1% glucose per well. After incubation for 4 h in a 37°C shaking incubator, scFv production was induced by adding 20 µL LB carb 6 mM IPTG to each well. After another incubation step overnight at 30°C with shaking, cells were lysed in a 1h incubation at room temperature with 40 µL lysis buffer (400 mM boric acid, 320 mM NaCl, 4 mM EDTA pH 8, 2.5 mg/mL lysozyme). Residual cells and cell debris were separated by centrifugation for 12 minutes at 1,900 x g (Hettich).

The supernatants containing scFv molecules were then tested for binding in flow cytometric binding assays. CHO cells transfected with human CEA were used as CEA-positive cell line. Cell binding assays were carried out by initially incubating between 100,000 and 200,000 cells with periplasmic preparation containing human scFv or relevant controls. After incubation the cells were washed in PBS/1 % FCS (fetal calf serum) and further incubated with 5-10 µg/ml of anti-FLAG M2 antibody (Sigma). After the cells had again been washed, they were incubated with polyclonal, PE-labeled anti-mouse antibodies (Dianova) and subsequently analyzed by flow cytometry. Approximately 600 clones were tested for binding signals on CEA-positive CHO cells. 27 positive clones were obtained. After sequencing of the respective scFv DNA, a total of 9 different sequences were obtained.

Figure 12 depicts binding of the nine different half-human scFv (i.e. murine A5B7 VH-human VL) constructs to various cell lines as measured by flow cytometric analysis. The Figure contains multiple diagrams, one for each construct tested. In any given diagram, the black distribution shows fluorescence intensity for cells incubated only with PBS alone in the absence of any construct but with all appropriate detection agents as used for detection of scFvs. In this way, any fluorescence shift observed can be definitely attributed to scFv construct rather than detection agents or buffer. Shifts in fluorescence which are indicative of construct binding to the respective cell line are depicted by a gray line in each diagram. Generally, a shift of higher magnitude away from, i.e. further to the (black) control indicates stronger binding, whereas a shift of lower magnitude away from, i.e. closer to the (black) control indicates weaker binding.

It can be seen from Figure 12 that the constructs A-121, A-183, A-240, A-313, A-290, A-315, A4-35, A4-52, MP2-A5 show clearly discernable shifts in fluorescence intensity as compared to the respective control, indicative of binding of the scFvs to membrane-bound CEA on the CHO target cells. In the following, the human VL region of scFv A-240 (SEQ ID NO. 48) has been selected and used for the isolation of a human VH region. Said human VL region is depicted in SEQ ID NOs. 63 (nucleotide sequence) and 64 (amino acid sequence).

EXAMPLE 7: Construction of the antibody libraries and phage display selection of human VH regions resistant to soluble CEA antigen

The aim of the following experiments is the selection of a set of human VH regions resistant to soluble CEA antigen that pair with the human VL region of scFv A-240, selected as described in Example 6. Said human VL region is depicted in SEQ ID NOs. 63 (nucleotide sequence) and 64 (amino acid sequence).

1. Isolation of RNA from peripheric blood mononuclear cells (PBMCs)

100 mL blood were taken from five healthy human donors. Peripheral blood mononuclear cells (PBMCs) were isolated by a ficoll-gradient according to standard methods. Total RNA was isolated from PBMCs using the RNeasy® Midi Kit (QIAGEN) following the manufacturer's instructions. cDNA was synthesized according to standard methods (Sambrook, Cold Spring Harbor Laboratory Press 1989, 2001).

2. PCR-Amplification of variable heavy chain regions (VH-regions)

The VH library was constructed and named Lib 134-VH. This VH-library consists of the human repertoire of FR1-CDR1-FR2-CDR2-FR3 from the PCR amplified VH-regions of the above described PBMC pool, linked operatively to the VH CDR3 of the maternal antibody followed by a human FR4 germline sequence.

For the isolation of human template VH-regions, RT-PCR was carried out using a 5'-VH-specific primer set (5'-huVH1,3,5-XhoI-2001 (5'-AGG TGC AGC TGC TCG AGT CTG G-3') (SEQ ID NO. 100), 5'-huVH4-XhoI-2001 (5'-CAG GTG CAG CTG CTC GAG TCG GG-3') (SEQ ID NO. 101), 5'-huVH4B-XhoI-2001 (5'-CAG GTG CAG CTA CTC GAG TGG GG-3') (SEQ ID NO. 102)) and a set of two 3'-VH-specific primers (3'-hu-VH-BstEII-2001 (5'-CTG AGG AGA CGG TGA CC-3') (SEQ ID NO. 103), 3'-

hu-VH-J3-BstEII-2001 (5'-CTG AAG AGA CGG TGA CC-3') (SEQ ID NO. 104)). Per PCR reaction, one 5'-primer was combined with one 3'-primer; the number of different PCR reactions was determined by the number of possible combinations of 5'- and 3'-primers. The PBMC cDNA of five donors was used as a source of VH-genes. The following PCR-program was used for amplification: Denaturation at 94°C for 15 seconds, primer annealing at 52°C for 50 seconds and primer extension at 72°C for 60 seconds was performed over 40 cycles, followed by final extension at 72°C for 10 minutes. The amplification products with a size of approximately 350 bp were isolated according to standard methods.

For the isolation of Lib 134-VH-regions, RT-PCR was carried out in two steps. First, the human heavy chain VH-segments (FR1-CDR1-FR2-CDR2-FR3) were PCR-amplified from the isolated template VH fragments using the same 5'-VH-specific primer set as described above (5'-huVH1,3,5-XhoI-2001, 5'-huVH4-XhoI-2001, 5'-huVH4B-XhoI-2001; SEQ ID NOs. 100-102) and a 3'-specific primer set (<u>3'-A134-VH1A</u> (5'-GTA GTC AAA GTA GAA CCG TAG CCC CCT ATC TCT YGC ACA GTA ATA CAC GGC -3') (SEQ ID NO. 105) , <u>3'-A134-VH1B</u> (5'-GTA GTC AAA GTA GAA CCG TAG CCC CCT ATC TCT YGC ACA GTA ATA CAY RGC -3') (SEQ ID NO. 106), <u>3'-A134-VH3A</u> (5'-GTA GTC AAA GTA GAA CCG TAG CCC CCT ATC TCT **T**GY ACA GTA ATA CAC RGC -3') (SEQ ID NO. 107), wherein the indicated "**T**" may also be replaced by "A", "C" or "G", <u>3'-A134-VH3B</u> (5'-GTA GTC AAA GTA GAA CCG TAG CCC CCT ATC TCT **T**GC ACA GTA ATA CAA RGC -3') (SEQ ID NO. 108), wherein the indicated "**T**" may also be replaced by "A", "C" or "G", <u>3'-A134-VH4</u> (5'-GTA GTC AAA GTA GAA CCG TAG CCC CCT ATC TCT SGC ACA GTA ATA CAC RGC -3') (SEQ ID NO. 109)) for the human VH subfamilies 1, 3 and 4 matching in the very terminal region of FR3.

The following primer combinations were used:

a) 5'-huVH1,3,5-XhoI-2001 x <u>3'-A134-VH1A</u>
b) 5'-huVH1,3,5-XhoI-2001 x <u>3'-A134-VH1B</u>
c) 5'-huVH1,3,5-XhoI-2001 x <u>3'-A134-VH3A</u>
d) 5'-huVH1,3,5-XhoI-2001 x <u>3'-A134-VH3B</u>
e) 5'-huVH4-XhoI-2001 x <u>3'-A134-VH4</u>
f) 5'-huVH4B-XhoI-2001 x <u>3'-A134-VH4</u>

Per PCR reaction, one 5'-primer was combined with the 3'-primer; the number of different PCR reactions was determined by the number of possible combinations of 5'- and the 3'-primer. The following PCR-program was used for amplification: Denaturation at 94°C for 15 seconds, primer annealing at 52°C for 50 seconds and primer extension at 72°C for 90 seconds was performed over 40 cycles, followed by final extension at 72°C for 10 minutes. Through this PCR step and the respective 3'-primer sequence, the human VH segments are prolonged for a part of the maternal VH CDR3, which then in turn is the priming site for the second step PCR 3'-primer. These VH-(FR1-CDR1-FR2-CDR2-FR3) DNA-fragments were then used as templates in a second PCR reaction using again the respective 5'VH-specific primer and a universal 3' primer matching to the universal 3'-terminus of the amplified DNA-fragments (3' A134-JH6-BstEII, 5'- CGA GAC GGT GAC CGT GGT CCC TTG GCC CCA GTA GTC AAA GTA GAA CCG TAG CC -3') (SEQ ID NO. 110).

The following PCR-program was used for amplification:

Denaturation at 94°C for 15 seconds, primer annealing at 52°C for 50 seconds and primer extension at 72°C for 60 seconds were performed over 40 cycles, followed by final extension at 72°C for 10 minutes. The DNA V-fragments were isolated according to standard protocols.

3. Library construction – cloning of the human VH pool

In a second round of the foregoing method, the human VL of scFv A-240 identified in the first, previous selection (see Example 6) was chosen, and subsequently combined with the library of human VH fragments with the aim of generating a human scFv. A phage display library was generally constructed based on standard procedures, as for example disclosed in "Phage Display: A Laboratory Manual"; Ed. Barbas, Burton, Scott & Silverman; Cold Spring Harbor Laboratory Press, 2001.

Heavy chain DNA-fragments from the different PCR amplifications were weighted for each ligation as follows:

a:b:c:d:e:f = 3:1:3:1:1:1, wherein a-f have the following meanings:

a) 5'-huVH1,3,5-XhoI-2001 x 3'-A134-VH1A
b) 5'-huVH1,3,5-XhoI-2001 x 3'-A134-VH1B
c) 5'-huVH1,3,5-XhoI-2001 x 3'-A134-VH3A
d) 5'-huVH1,3,5-XhoI-2001 x 3'-A134-VH3B
e) 5'-huVH4-XhoI-2001 x 3'-A134-VH4

f) 5'-huVH4B-XhoI-2001 x 3'-A134-VH4

One ligation reaction was set up consisting of 400 ng of human Lib 134-VH fragment pool (XhoI-BstEII digested) and 1200 ng of the plasmid pComb3H5BHis/A-240 VL (the DNA encoding the VL region of scFv A-240 was cloned via the restriction sites SacI and SpeI into pComb3H5BHis according to standard procedures). The resulting antibody human VH pool was then transformed into 300 µL of electrocompetent Escherichia coli XL1 Blue by electroporation (2.5 kV, 0.2 cm gap cuvette, 25 mF, 200 Ohm, Biorad gene-pulser) resulting in a library size of 0.8 x 10^8 independent clones in total.

After electroporation the assay was incubated in SOC broth (Fluka) for phenotype expression. The cultures were then each incubated in 500 mL of SB selection medium containing 50 µg/mL carbenicillin and 2 % v/v glucose overnight. The next day, cells of the cultures were harvested by centrifugation and plasmid preparation was carried out using a commercially available plasmid preparation kit (Qiagen) to preserve the DNA library.

1.5 µg of this plasmid pool encoding the respective scFv pool were then electroporated into E. coli XL1blue (2.5 kV, 0.2 cm gap cuvette, 25 mF, 200 Ohm, Biorad gene-pulser) resulting in a library size of 2.4 x 10^9 independent clones in total. After phenotype expression and slow adaption to carbenicillin the antibody library was transferred into SB-Carbenicillin (50 µg/mL) selection medium. The antibody library was then infected with an infectious dose of 1 x 10^{12} particles of helper phage VCSM13 resulting in the production and secretion of filamentous M13 phage, wherein each phage particle contained single stranded pComb3H5BHis-DNA encoding a human scFv-fragment and displayed the corresponding scFv-protein as a translational fusion to phage coat protein III.

4. Phage display selection of a human VH

The phage particles carrying the human scFv-repertoire were harvested from the culture supernatant by PEG8000/NaCl precipitation and centrifugation. Then approximately 1 x 10^{11} to 1 x 10^{12} scFv phage particles were resuspended in 0.5 mL of TBS/1% BSA and incubated with biotinylated soluble CEA, that was immobilized in Streptavidine coated wells of an ELISA plate (Nunc) for 1 h. A 10 µg antigen/ml PBS solution (50 µl) was incubated for over night at 4°C in the streptavidine coated wells, washed once with water, followed by blocking for 1 hour at 37°C with 200 µl of 3% BSA in TBS, that was removed after incubation.

scFv phage that did not specifically bind to the target antigen were eliminated by washing steps with TBS/0,05 % Tween. This washing procedure was repeated up to 10 times in further rounds.

After washing, binding entities were eluted by using HCl-glycine, pH 2.2. Following neutralization with 2 M Tris, pH 12, the eluate was used for infection of a fresh uninfected E. coli XL1 Blue culture.

To elute remaining high binding entities 50 µL of a fresh E. coli XL1 blue culture (OD600 ≥ 0.5) were added to the wells and incubated for 15 minutes. Both cultures were then mixed and cells successfully transduced with a phagemid copy, encoding a human scFv-fragment, were again selected for carbenicillin resistance and subsequently infected with VCMS13 helper phage to start the second round of antibody display and in vitro selection.

Plasmid DNA corresponding to 4 rounds of panning was isolated from E. coli cultures. For the production of soluble scFv-protein, VH-VL-DNA fragments were excised from the plasmids (XhoI-SpeI), and cloned via the same restriction sites in the plasmid pComb3H5BFlag/His, in which the expression construct (e.g. scFv) includes a Flag-tag (TGDYKDDDDK; SEQ ID NO. 99) between the scFv and the His6-tag and the additional phage proteins are deleted.

After ligation each pool (different rounds of panning) of plasmid DNA was transformed into 100 µL heat shock competent E.coli TG1 and plated onto carbenicillin LB-agar. Single colonies were picked and inoculated into 120 µL of LB carb (50µg/mL) 1% glucose in 96-well plates (Greiner). The wells were sealed with a semipermeable membrane (Greiner) and the plates were incubated overnight at 37°C in a shaking incubator (master plate). Then 10 µL of the master plate cultures were transferred into a second 96 well plate (working plate) containing 90 µL LB carb (50µg/mL) 0.1% glucose per well. After incubation for 4 h in a 37°C shaking incubator, scFv production was induced by adding 20 µL LB carb 6 mM IPTG to each well. After another incubation step overnight at 30°C with shaking, cells were lysed in a 1h incubation at room temperature with 40 µL lysis buffer (400 mM boric acid, 320 mM NaCl, 4 mM EDTA pH 8, 2.5 mg/mL lysozyme). Residual cells and cell debris were separated by centrifugation for 12 minutes at 1,900 x g (Hettich).

The supernatants containing scFv molecules were then tested for binding in flow cytometric binding assays.

CHO cells transfected with human CEA were used as CEA-positive cell line. Cell binding assays were carried out by initially incubating between 100,000 and 200,000 cells with periplasmic preparation containing human scFv or relevant controls. After incubation the cells were washed in PBS/1 % FCS (fetal calf serum) and further incubated with 5-10 µg/ml of anti-FLAG M2 antibody. After the cells had again been washed, they were incubated with polyclonal, PE-labeled anti-mouse antibodies (Dianova) and subsequently analyzed by flow cytometry. 46 clones were tested for binding signals on CEA-positive CHO cells. All of them showed positive signals. After sequencing of the respective scFv DNA a total of 9 different sequences were obtained, eight of which displayed a high degree of homology. The human constructs MP510_3-A5.3 (MP510-A5; SEQ ID NO. 50), MP510_3-B9.1 (MP511-B9; SEQ ID NO. 52), MP510_3-D8.1 (MP511-D8; SEQ ID NO. 54) have been selected for further characterization. The corresponding amino acid sequences are shown inthe sequence listing.

Periplasmic extracts of said human constructs MP510-A5, MP511-B9, MP511-D8 as well as the half human construct A-240 Vlambda.3 (murine VH A5B7/human VL A240; SEQ ID NO. 48) were further analyzed in flow cytometric experiments with CEA-positive and –negative cell lines. It can be seen from Figure 13, that the human constructs MP510-A5 (SEQ ID NO. 50), MP511-B9 (SEQ ID NO. 52), MP511-D8 (SEQ ID NO. 54) show clearly discernable shifts in fluorescence intensity as compared to the respective half-human control A-240 Vlambda.3 (murine VH A5B7/human VL A240; SEQ ID NO. 48). Thus, the human scFv constructs show stronger binding activity to membrane-bound human CEA than the half human construct A-240 Vlambda.3. In addition, all of the human constructs showed distinct binding to CEA-positive human KATO III cells (human gastric cancer cell line), whereas none of them showed binding to CEA-negative, untransfected CHO cells as well as to CEA-negative human NALM 6 cells (human B cell line) (data not shown).

EXAMPLE 8: Generation and cytotoxic activity of human CEAxCD3 bispecific single chain antibodies

1. Arrangements

In the next step, various domain arrangements of human bispecific single chain antibody molecules have been generated. These molecules comprise the human anti-CEA binding domain (the generation of which has been described in Example 7, supra) and the de-immunized binding domain with specificity for the human CD3 antigen shown in SEQ ID NO.77 VHVL were designed as set out in Table 1; see also Example 2, supra. All bispecific single chain antibody constructs with the human anti-CEA binding domains described herein (apparently) bind to soluble human CEA antigen since they have been isolated after four rounds of phage display selection on soluble CEA antigen immobilized on ELISA plates.

In particular, the following arrangements have been generated:

(a) human anti-CEA part located N-terminally:
(i) VH-VL orientation of anti-CEA:
A5 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 24),
A5 VH-A240 VL# x SEQ ID NO.77 VHVL (SEQ ID NO. 126),
B9 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 32),
B9 VH-A240 VL# x SEQ ID NO.77 VHVL (SEQ ID NO. 130),
D8 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 40)
D8 VH-A240 VL# x SEQ ID NO.77 VHVL (SEQ ID NO. 134), and
CEAI VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 16).
(ii) VL-VH orientation of anti-CEA:
A240 VL-A5 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 26),
A240 VL-B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34),
A240 VL-D8 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 42),
and A240 VL-CEAI VHxSEQ ID NO.77 VHVL (SEQ ID NO. 18).

(b) human anti-CEA part located C-terminally:
(i) VH-VL orientation of anti-CEA:
SEQ ID NO.77 VHVLxA5 VH-A240VL (SEQ ID NO. 30),
SEQ ID NO.77 VHVLxA5 VH-A240VL# (SEQ ID NO. 128),
SEQ ID NO.77 VHVLxB9 VH-A240VL (SEQ ID NO. 36),
SEQ ID NO.77 VHVLxE12 VH-A240VL (SEQ ID NO. 143),

SEQ ID NO.77 VHVLxB9 VH-A240VL# (SEQ ID NO. 132),SEQ ID NO.77 VHVLxD8 VH-A240VL (SEQ ID NO. 44),
SEQ ID NO.77 VHVLxD8 VH-A240VL# (SEQ ID NO. 136),
and SEQ ID NO.77 VHVLxCEAI VH-A240VL (SEQ ID NO. 20).
(ii) VL-VH orientation of anti-CEA:
SEQ ID NO.77 VHVLxA240VL-A5 VH (SEQ ID NO. 28),
SEQ ID NO.77 VHVLxA240VL-B9VH (SEQ ID NO. 38),
SEQ ID NO.77 VHVLxA240VL-D8VH (SEQ ID NO. 46), and
SEQ ID NO.77 VHVLx A240VL-CEAI VH (SEQ ID NO. 22).

CEAI VH (SEQ ID NO. 56) denotes a VH region derived from murine mAb A5B7, whereas CEAI VHVL or CEAI VLVH refer to a VH-VL domain and a VL-VH domain, respectively, derived from mAb A5B7. A240 corresponds to a human VL region (see SEQ ID NO. 64 and Example 7). Accordingly, e.g. CEAI VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO.16) corresponds to a bispecific construct with a half-human CEA-binding domain having a murine VH region from mAb7 and a human VL region A240. For the cloning of the human antibody library, the nucleotide sequences encoding the original N-termini of the A240 VL region had to be converted to restriction sites. In A5 VH-A240 VL# x SEQ ID NO.77 VHVL (SEQ ID NO. 126), SEQ ID NO.77 VHVLxA5 VH-A240VL# (SEQ ID NO. 128), B9 VH-A240 VL# x SEQ ID NO.77 VHVL (SEQ ID NO. 130), SEQ ID NO.77 VHVLxB9 VH-A240VL# (SEQ ID NO. 132), D8 VH-A240 VL# x SEQ ID NO.77 VHVL (SEQ ID NO. 134), and SEQ ID NO.77 VHVLxD8 VH-A240VL# (SEQ ID NO. 136), the original N-termini have been reintroduced.
The bispecific single chain antibody construct SEQ ID NO.77 VHVLxE12 VH-A240VL (SEQ ID NO. 143) differs from the SEQ ID NO.77 VHVLxB9 VH-A240VL (SEQ ID NO. 36) construct in only one amino acid residue: The CDR-H2 sequence in the E12 VH reads "FI**L**NKANGGTTEYAASVKG" (SEQ ID NO. 145), whereas in the B9 VH it reads "FI**R**NKANGGTTEYAASVKG" (SEQ ID NO. 67). The human E12 VH region has been isolated as set forth in Example 7.

2. Expression, purification and flow cytometry analysis

Expression, purification and flow cytometry analysis of these human CEAxCD3 bispecific single chain antibodies has been carried out by methods described in Example 2, supra.

3. Binding activity

As exemplified in Figure 14, human bispecific single chain antibody constructs A5 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 24), B9 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 32), D8 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 40) and CEAI VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 16) bind to CEA-positive human Kato III cells and to CD3-positive HPB- ALL cells.

4. Cytotoxic activity in the absence of soluble CEA antigen

Cytotoxic activity against CHO-CEA+ target cells has been demonstrated for the following domain arrangements of the human bispecific single chain antibodies:

For constructs with the anti-CEA part located N-terminally and a VH-VL orientation of the anti-CEA part, Figure 15 shows cytotoxic activity for A5 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 24), B9 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 32), D8 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 40) and CEAI VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 16). Figure 16 demonstrates cytotoxic activity for the VL-VH orientation of the anti-CEA domain (located N-terminally) for A240 VL-A5 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 26), A240 VL-B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34), A240 VL-D8 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 42), and A240 VL-CEAI VHxSEQ ID NO.77 VHVL (SEQ ID NO. 18).

For constructs with the anti-CEA part located C-terminally and a VH-VL orientation of the anti-CEA part, Figure 17 exhibits cytotoxicity against CEA+ target cells for SEQ ID NO.77 VHVLxA5 VH-A240VL (SEQ ID NO. 30), SEQ ID NO.77 VHVLxB9 VH-A240VL (SEQ ID NO. 36), SEQ ID NO.77 VHVLxD8 VH-A240VL (SEQ ID NO. 44), and SEQ ID NO.77 VHVLxCEAI VH-A240VL (SEQ ID NO. 20). SEQ ID NO.77 VHVLxCEAI LH was used as a positive control. Figure 18 shows cytotoxic activity of constructs with VL-VH orientation of the anti-CEA domain (located C-terminally) for SEQ ID NO.77 VHVLxA240VL-A5 VH (SEQ ID NO. 28), SEQ ID NO.77 VHVLxA240VL-B9VH (SEQ ID NO. 38), SEQ ID NO.77 VHVLxA240VL-D8VH (SEQ ID NO. 46), and SEQ ID NO.77 VHVLx A240VL-CEAIVH (SEQ ID NO. 22). SEQ ID NO.77 VHVLxCEAI LH (SEQ ID NO. 2) was used as a positive control.

Figure 21 shows cytotoxic activity of bispecific single chain antibody constructs comprising the human B9 VH region and the human A240 VL region in different arrangements: A240 VL–B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34), SEQ ID NO.77 VHVLxA240 VL–B9 VH (SEQ ID NO. 38), SEQ ID NO.77 VHVLxB9 VH–A240 VL (SEQ ID NO. 36), and B9 VH–A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 32) revealed cytotoxic activity against human CEA-transfected CHO cells.

5. Resistance of human CEAxCD3 bispecific single chain antibodies to soluble CEA antigen

Competition assays in the presence of soluble human CEA antigen for the human bispecific single chain antibodies have been performed as set out in Example 5, supra. Figures 19 and 20 demonstrate the resistance to soluble CEA antigen of cytotoxic activity also for human constructs, as exemplified for constructs A5 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 24), B9 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 32), D8 VH-A240 VLxSEQ ID NO.77 VHVL (SEQ ID NO. 40) and CEAI VH-A240 VLxSEQ ID NO.77 VHVL(SEQ ID NO. 16); for resistance to soluble CEA of murine-derived bispecific single chain antibodies see Example 5. Moreover, Figure 22 shows that CEA-reactive bispecific single chain construct A240 VL–B9 VHx SEQ ID NO.77 VHVL (SEQ ID NO. 34) redirected T cells to lyse CHO-CEA+ cells in the presence of increasing amounts of soluble CEA antigen. This experiment demonstrates that also A240 VL–B9 VHxSEQ ID NO.77 VHVL-mediated cytotoxic activity is resistant to soluble CEA. Finally, as can be derived from Figure 27, bispecific single chain construct SEQ ID NO.77 VHVLxE12 VH-A240 VL (SEQ ID NO. 143) -mediated cytotoxic activity is resistant to soluble CEA.

Thus, the present invention provides for pharmaceutical compositions with cytotoxic anti-tumor activity in the presence of even high levels of soluble CEA antigen. As set forth above, high serum CEA concentrations in patients with epithelial tumors reduce the success of anti-CEA antibody-based therapeutics. Therefore, the pharmaceutical compositions of the invention are particularly suitable for the treatment of patients with progressive epithelial tumors (e.g. secondary, metastatic tumors after surgical removal of the primary tumor(s)), malignant epithelial tumors, high (epithelial) tumor load and late stage epithelial tumors characterized by high soluble CEA antigen concentrations in the serum/plasma of said patients. Further, pharmaceutical compositions of the invention are also expected to be administered at low dosages. In addition, said pharmaceutical compositions are unlikely to be immunogenic when administered to the patients due to the human origin of the anti-CEA part and the de-immunised anti-CD3 part of the bispecific single chain antibodies in the pharmaceutical compositions of the invention. Moreover, the pharmaceutical compositions of the invention are expected to provide for high tumor penetration due to the low molecular weight and small size of the bispecific single chain constructs. Additionally, for the tumor treatment low amounts of bispecific single chain antibodies will be used because of the high cytotoxic activity of said molecules. Because low amounts are expected to be administered to the patients, the adverse effects for the patients are also expected to be reduced. Finally, bispecific single chain antibodies without resistance to soluble CEA would be highly sensitive to even low concentrations of soluble CEA antigen in the plasma of tumor patients since they would be administered in low concentrations, as set forth above. This problem is also circumvented by the pharmaceutical compositions of the invention.

EXAMPLE 9: Protein homogeneity assessment of purified monomer of A240 VL – B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34) by High Resolution Cation Exchange Chromatography

To further characterize the homogeneity of the purified A240 VL – B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34) construct, the isolated monomer fraction was subjected to a High Resolution Cation Exchange Chromatography. The chromatography was performed on a MiniS column (Mini S PE 4.6/50 CatX 0.8 ml; GE Healthcare 17-5005-01), equilibrated with 20mM MES buffer pH 5.5. The sample was diluted 1:3 with the same buffer before loading to the column. Bound protein was eluted with a gradient of equilibration buffer containing 1M NaCl: 0-30% in 60 column volumes. Remaining protein was eluted in 3 column volumes of 1M NaCl. The resulting chromatogram is shown in Figure 23 and exhibits a homogenous protein fraction with a single main peak.

EXAMPLE 10: Plasma stability of A240 VL–B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34)

The plasma stability of the A240 VL – B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34) construct was tested under different incubation conditions followed by a standard 51-chromium release based cytotoxicity assay as described in Example 4.

A human plasma pool with the blood of five healthy donors was generated by collecting blood in EDTA-coated syringes. The cellular components were removed by centrifugation and the upper plasma phase was collected and subsequently pooled. The A240 VL – B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34) construct was either incubated at 37°C or 4°C in the presence or absence of plasma. As controls, the construct was diluted immediately prior to the cytotoxicity assay in plasma or RPMI 1640 medium, respectively. CHO-CEA+ served as target cells; stimulated CD8+ T cells were used as effector cells. The effector:target (E:T) ratio was 10:1. The assay duration was 18 hours.

As shown in Figure 24, the CEA-reactive bispecific single chain construct A240 VL – B9 VHxSEQ ID NO.77 VHVL (SEQ ID NO. 34) proved to be very stable; no loss of cytotoxic activity could be detected after incubation in human plasma for 24 hours at 37°C.

EXAMPLE 11: Protein homogeneity assessment of purified monomer of SEQ ID NO.77 VHVLxE12 VH-A240 VL (SEQ ID NO. 143) by High Resolution Cation Exchange Chromatography

The experiment was conducted in analogy with Example 9, except that SEQ ID NO.77 VHVLxE12 VH-A240 VL (SEQ ID NO. 143) was analyzed. The resulting chromatogram is shown in Figure 25 and exhibits a homogenous protein fraction with a single main peak.

EXAMPLE 12: Plasma stability of SEQ ID NO.77 VHVLxE12 VH-A240 VL (SEQ ID NO. 143)

The experiment was conducted in analogy with Example 10, except that SEQ ID NO.77 VHVL x E12 VH-A240 VL (SEQ ID NO. 143) was analyzed. As displayed in Figure 26, the CEA-reactive bispecific single chain construct SEQ ID NO.77 VHVL x E12 VH-A240 VL (SEQ ID NO. 143) proved to be very stable; no loss of cytotoxic activity could be detected after incubation in human plasma for 24 hours at 37°C.

CLAIMS:

1. A bispecific single chain antibody comprising:
   (a) a first binding domain specifically binding to human CD3; and
   (b) a second binding domain specifically binding to human CEA, said second binding domain comprising:
      (i) a CDR-H1 having the amino acid sequence "SYWMH" (SEQ ID NO: 68), a CDR-H2 having the amino acid sequence "FIRNKANGGTTEYAASVKG" (SEQ ID NO: 67), a CDR-L1 having the amino acid sequence "TLRRGINVGAYSIY" (SEQ ID NO: 73), a CDR-L2 having the amino acid sequence "YKSDSDKQQGS" (SEQ ID NO: 72) and a CDR-L3 having the amino acid sequence "MIWHSGASAV" (SEQ ID NO: 71);
      (ii) a CDR-H1 having the amino acid sequence "SYWMH" (SEQ ID NO: 68), a CDR-H2 having the amino acid sequence "FILNKANGGTTEYAASVKG" (SEQ ID NO: 145), a CDR-L1 having the amino acid sequence "TLRRGINVGAYSIY" (SEQ ID NO: 73), a CDR-L2 having the amino acid sequence "YKSDSDKQQGS" (SEQ ID NO: 72) and a CDR-L3 having the amino acid sequence "MIWHSGASAV" (SEQ ID NO: 71); or
      (iii) a CDR-H1 having the amino acid sequence "TYAMH" (SEQ ID NO: 70), a CDR-H2 having the amino acid sequence "LISNDGSNKYYADSVKG" (SEQ ID NO: 69), a CDR-L1 having the amino acid sequence "TLRRGINVGAYSIY" (SEQ ID NO: 73), a CDR-L2 having the amino acid sequence "YKSDSDKQQGS" (SEQ ID NO: 72) and a CDR-L3 having the amino acid sequence "MIWHSGASAV" (SEQ ID NO: 71); and

wherein said second binding domain specific for human CEA comprises at least the amino acid sequence "DRGLRFYFDY" as set forth in SEQ ID NO: 66 corresponding to Kabat positions 95-102 of the CDR-H3 of murine monoclonal antibody A5B7.

2. The antibody of claim 1, wherein said first binding domain specific for CD3 is located C-terminally.

3. The antibody of claim 1 or 2, wherein said binding domains are arranged in the order VH_{CEA}-VL_{CEA}-VH_{CD3}-VL_{CD3} or VL_{CEA}-VH_{CEA}-VH_{CD3}-VL_{CD3}.

4. The antibody of any one of claims 1 to 3, wherein the amino acid sequence of the VH region of the second binding domain specific for human CEA is SEQ ID NO: 60 or 146.

5. The antibody of any one of claims 1 to 3, wherein the amino acid sequence of the VH region of the second binding domain specific for human CEA is SEQ ID NO: 58 or SEQ ID NO: 62.

6. The antibody of any one of claims 1 to 3, wherein the amino acid sequence of the VL region of the second binding domain specific for human CEA is SEQ ID NO: 64.

7. The antibody of any one of claims 1 to 6, wherein the V regions of the second binding domain specific for CEA comprise at least:
   (a) the VH region consisting of the amino acid sequence shown in SEQ ID NO: 60 and the VL region consisting of the amino acid sequence shown in SEQ ID NO: 64;
   (b) the VH region consisting of the amino acid sequence shown in SEQ ID NO: 146 and the VL region consisting of the amino acid sequence shown in SEQ ID NO: 64;
   (c) the VH region consisting of the amino acid sequence shown in SEQ ID NO: 58 and the VL region consisting of the amino acid sequence shown in SEQ ID NO: 64;
   (d) the VH region consisting of the amino acid sequence shown in SEQ ID NO: 62 and the VL region consisting of the amino acid sequence shown in SEQ ID NO: 64; or
   (e) the VH region consisting of the amino acid sequence shown in SEQ ID NO: 56 and the VL region consisting of the amino acid sequence shown in SEQ ID NO: 64.

8. The antibody of any one of claims 1 to 7, wherein said bispecific single chain antibody comprises at least one of:

(a) an amino acid sequence as depicted in SEQ ID NO: 6, 8, 16, 18, 24, 26, 32, 34, 40, 42, 126, 130, 134 or 143;
(b) an amino acid sequence encoded by a nucleic acid sequence as shown in SEQ ID NO: 5, 7, 15, 17, 23, 25, 31, 33, 39, 41, 125, 129, 133 or 142; or
(c) an amino acid sequence encoded by a nucleic acid sequence which is degenerate as a result of the genetic code to a nucleotide sequence of (b).

9. The antibody of any one of claims 1 to 8, wherein at least one of said first and second binding domains is chimeric, human or humanized, CDR-grafted, deimmunized, or any combination thereof.

10. A nucleic acid molecule encoding a bispecific single chain antibody as defined in any one of claims 1 to 9.

11. A vector comprising a nucleic acid sequence as defined in claim 10.

12. The vector of claim 11, wherein said vector further comprises a regulatory sequence which is operably linked to said nucleic acid molecule.

13. The vector of claim 11 or 12, wherein said vector is an expression vector.

14. A host cell transformed or transfected with a nucleic acid molecule as defined in claim 10, or a vector as defined in any one of claims 11 to 13.

15. A pharmaceutical composition comprising the nucleic acid molecule of claim 10, the vector of any one of claims 11 to 13, or the host cell of claim 14; and a suitable carrier, stabilizer and/or excipient.

16. The pharmaceutical composition of claim 15, further comprising a proteinaceous compound providing an activation signal for immune effector cells.

17. A process for the production of the bispecific single chain antibody of any one of claims 1 to 9, said process comprising culturing a host cell as defined in claim 14 under conditions allowing expression of the bispecific single chain antibody and recovering the produced bispecific single chain antibody from the culture.

18. The process of claim 17, further comprising mixing the recovered bispecific single chain antibody with a suitable carrier, stabilizer and/or excipient to produce a pharmaceutical composition comprising the recovered bispecific single chain antibody.

19. A process for the production of a pharmaceutical composition comprising the bispecific single chain antibody of any one of claims 1 to 9, said process comprising culturing a host cell as defined in claim 14 under conditions allowing the expression of the antibody, recovering the produced antibody from the culture, and formulating the antibody with a suitable pharmaceutical carrier to produce the pharmaceutical composition.

20. A process for the production of a pharmaceutical composition comprising the bispecific single chain antibody of any one of claims 1 to 9, said process comprising formulating the antibody with a suitable pharmaceutical carrier to produce the pharmaceutical composition.

21. A pharmaceutical composition comprising a bispecific single chain antibody as defined in any one of claims 1 to 9 and a carrier, for the prevention, treatment or amelioration of an epithelial tumor.

22. The pharmaceutical composition of claim 21, wherein said epithelial tumor is a gastrointestinal adenocarcinoma, a breast adenocarcinoma or a lung adenocarcinoma.

23. The pharmaceutical composition of claim 22, wherein said gastrointestinal adenocarcinoma is a colorectal, pancreatic, an oesophageal or a gastric adenocarcinoma.

24. The pharmaceutical composition of any one of claims 21 to 23 for the treatment of progressive tumors, late stage tumors, tumor patients with high tumor load/burden, metastatic tumors, or tumor patients with a CEA serum concentration higher than 100 ng/ml.

25. The pharmaceutical composition of any one of claims 21 to 24 for administration in combination with an additional drug.

26. The pharmaceutical composition of claim 25, wherein said additional drug is a non-proteinaceous compound.

27. The pharmaceutical composition of claim 25, wherein said additional drug is a proteinaceous compound.

28. The pharmaceutical composition of claim 27, wherein said proteinaceous compound is for providing an activation signal for immune effector cells.

29. The pharmaceutical composition of claim 26 or 27, wherein said proteinaceous compound or non-proteinaceous compound is for administration simultaneously or non-simultaneously with the bispecific single chain antibody.

30. Use of the bispecific single chain antibody of any one of claims 1 to 9 for the prevention, treatment or amelioration of an epithelial tumor in a human.

31. Use of the bispecific single chain antibody of any one of claims 1 to 9 for the preparation of a pharmaceutical composition for the prevention, treatment or amelioration of an epithelial tumor in a human.

32. The use of claim 30 or 31, wherein said epithelial tumor is a gastrointestinal adenocarcinoma, a breast adenocarcinoma or a lung adenocarcinoma.

33. The use of claim 32, wherein said gastrointestinal adenocarcinoma is a colorectal, pancreatic, an oesophageal or a gastric adenocarcinoma.

34. The use of any one of claims 30 to 33, for the treatment of progressive tumors, late stage tumors, tumor patients with high tumor load/burden, metastatic tumors, or tumor patients with a CEA serum concentration higher than 100 ng/ml.

35. The use of any one of claims 30 to 34, for administration in combination with an additional drug.

36. The use of claim 35, wherein said additional drug is a non-proteinaceous compound.

37. The use of claim 35, wherein said additional drug is a proteinaceous compound.

38. The use of claim 37, wherein said proteinaceous compound is for providing an activation signal for immune effector cells.

39. The use of claim 36 or 37, wherein said proteinaceous compound or non-proteinaceous compound is for administration simultaneously or non-simultaneously with the bispecific chain antibody.

40. A kit comprising:

(a) a bispecific single chain antibody as defined in any one of claims 1 to 9;
(b) a nucleic acid molecule as defined in claim 10;
(c) a vector as defined in any one of claims 11 to 13; or
(d) a host cell as defined in claim 14;

and a suitable container.

41. The pharmaceutical composition of any one of claims 21 to 29, wherein said prevention, treatment or amelioration of said epithelial tumor comprises a determination of CEA serum concentration by ELISA.

42. The use of any one of claims 30 to 39, wherein said prevention, treatment or amelioration of said epithelial tumor comprises a determination of CEA serum concentration by ELISA.

FIGURE 1

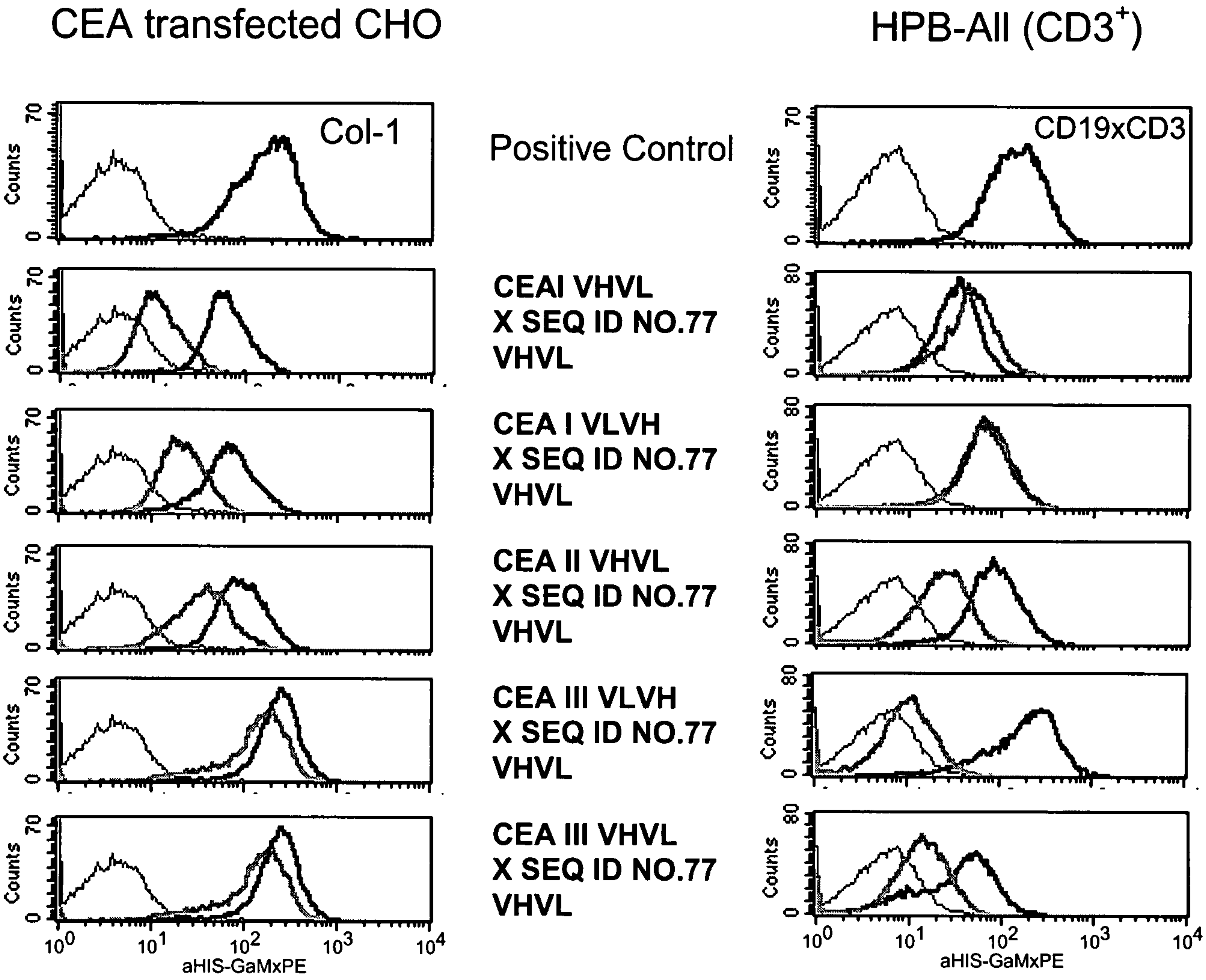

CEA transfected CHO
HPB-All (CD3+)
Col-1
Positive Control
CD19xCD3
CEAI VHVL
X SEQ ID NO.77
VHVL
CEA I VLVH
X SEQ ID NO.77
VHVL
CEA II VHVL
X SEQ ID NO.77
VHVL
CEA III VLVH
X SEQ ID NO.77
VHVL
CEA III VHVL
X SEQ ID NO.77
VHVL
Counts
0
70
80
10^0
10^1
10^2
10^3
10^4
aHIS-GaMxPE

FIGURE 2

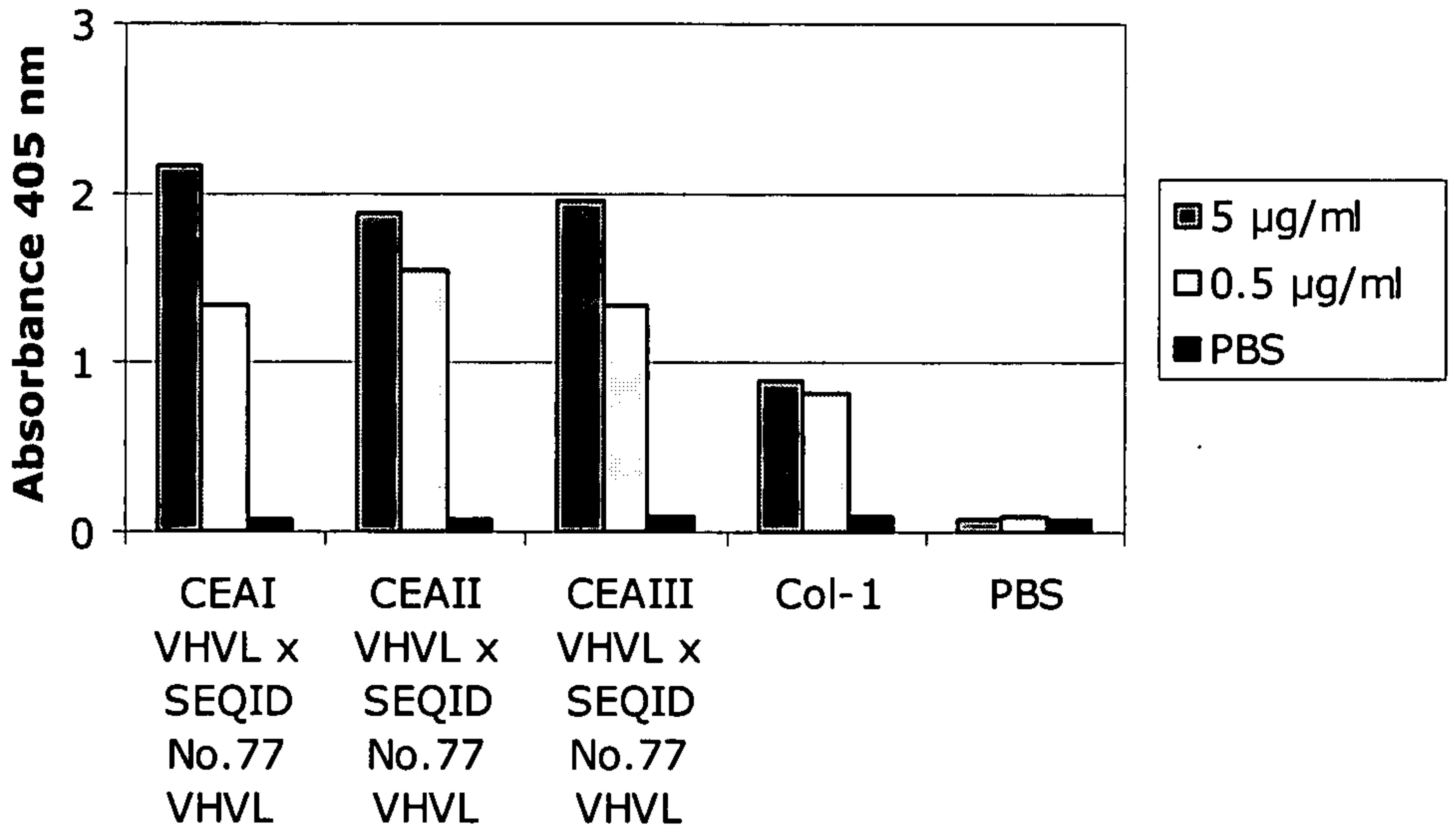
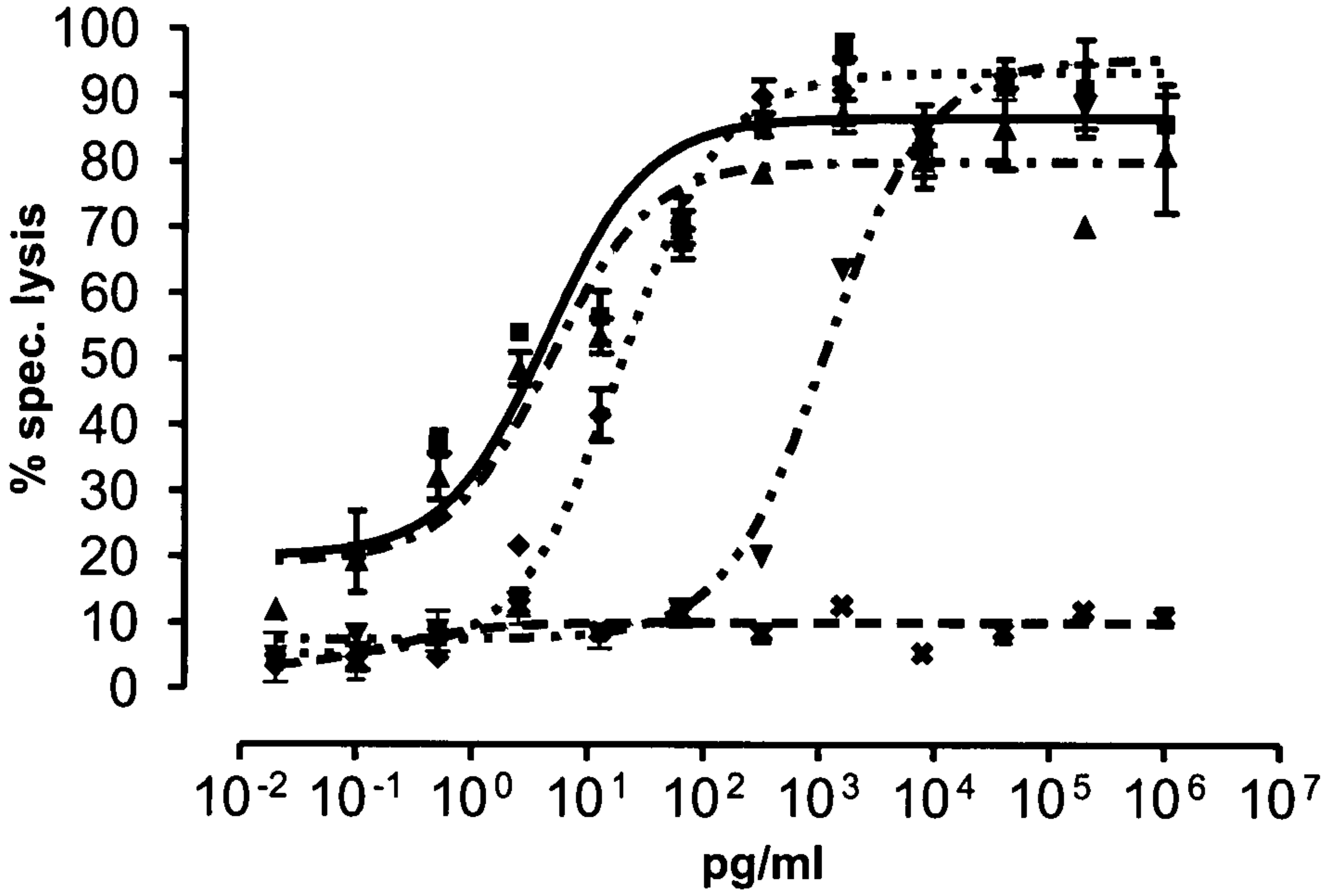
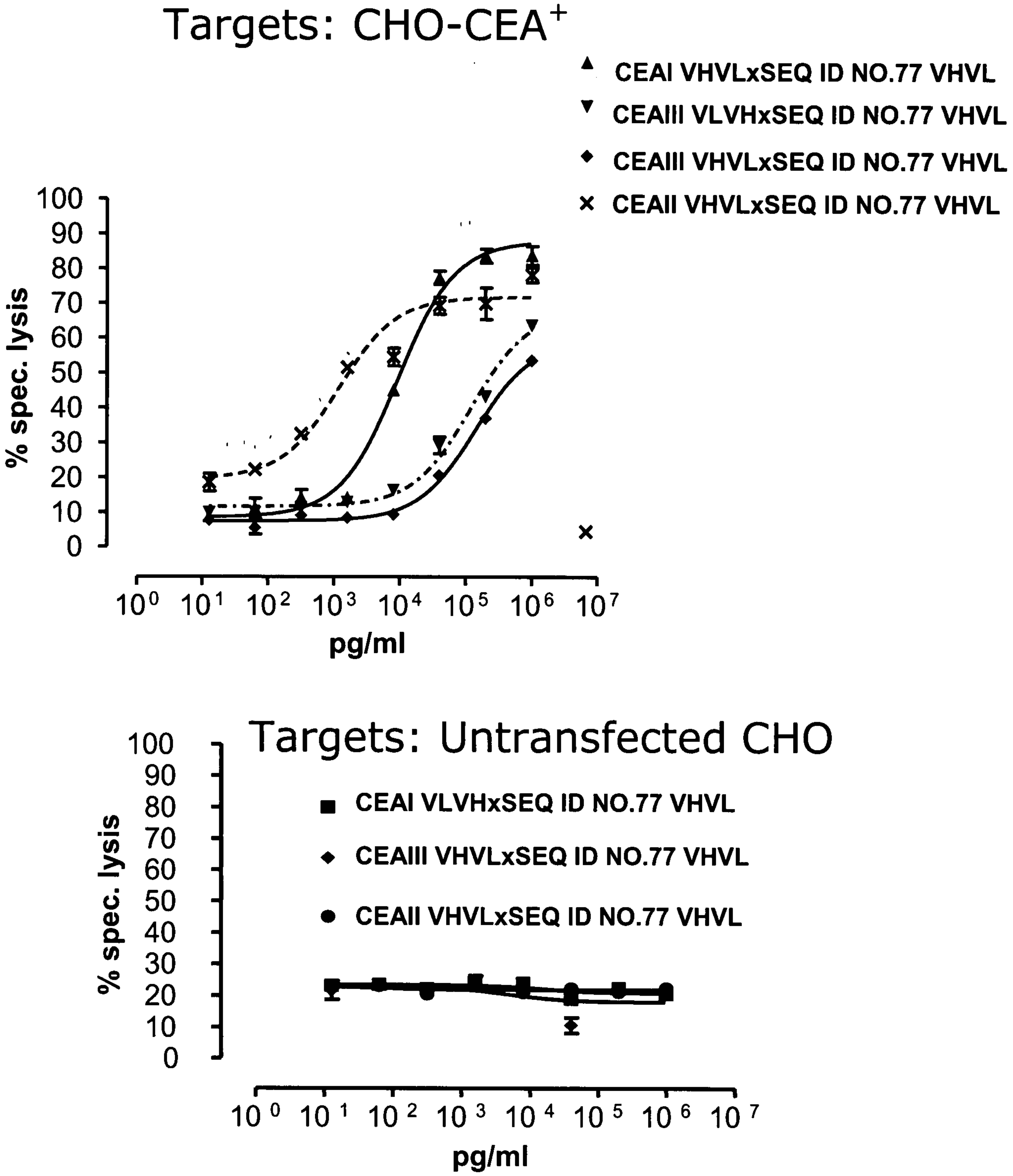

Absorbance 405 nm
3
2
1
0
5 µg/ml
0.5 µg/ml
PBS
CEAI VHVL x SEQID No.77 VHVL
CEAII VHVL x SEQID No.77 VHVL
CEAIII VHVL x SEQID No.77 VHVL
Col-1
PBS

FIGURE 3



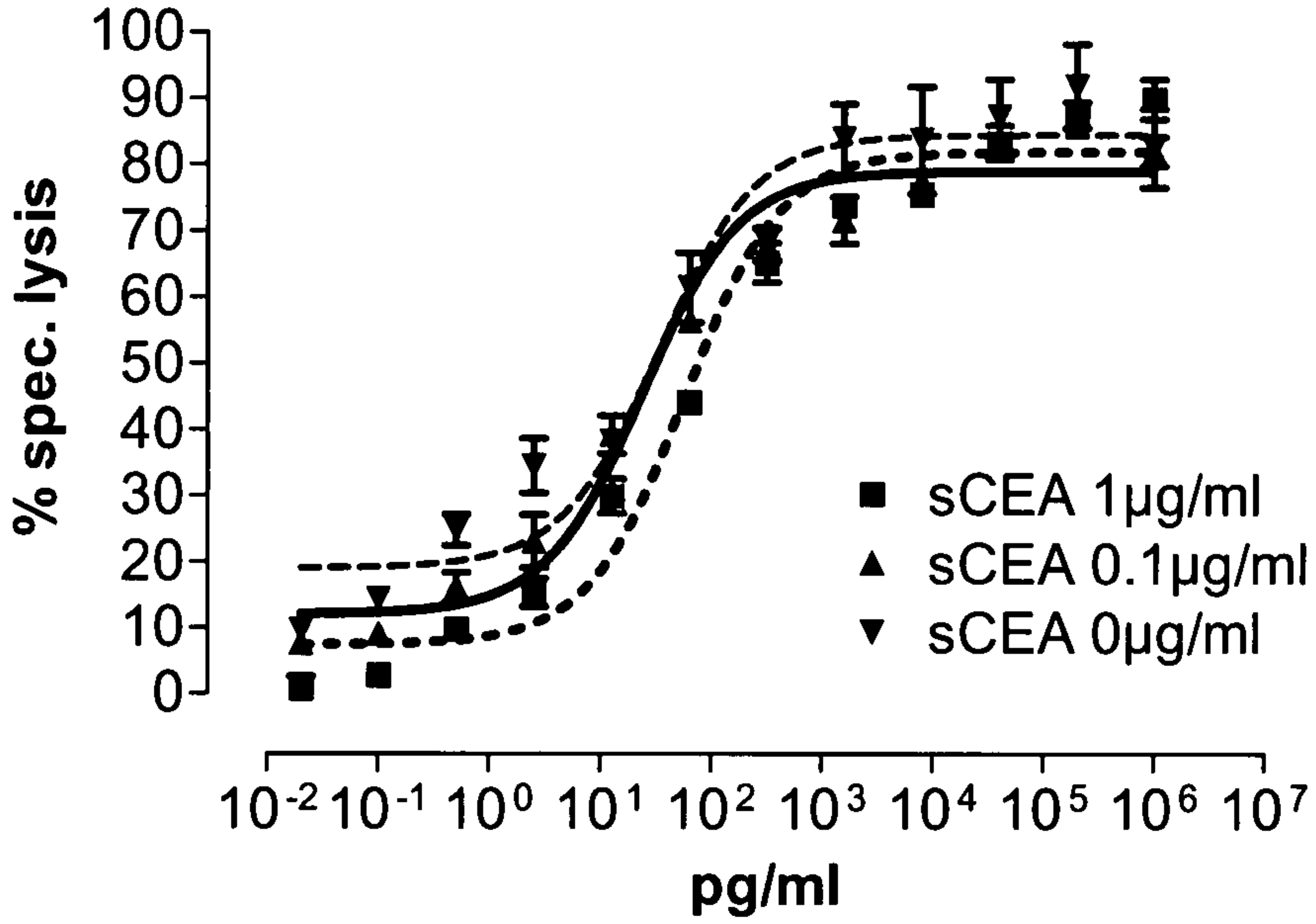
		EC 50 [ng/ml]
■	SEQ ID NO. 77 VHVL x CEAI VHVL	0.0045
▲	SEQ ID NO. 77 VHVL x CEAI VLVH	0.0035
◆	CEAI VLVH x SEQ ID NO. 77 VHVL	0.0196
▼	CEAI VHVL x SEQ ID NO. 77 VHVL	1.2
✖	Negative control	n.a.

FIGURE 4

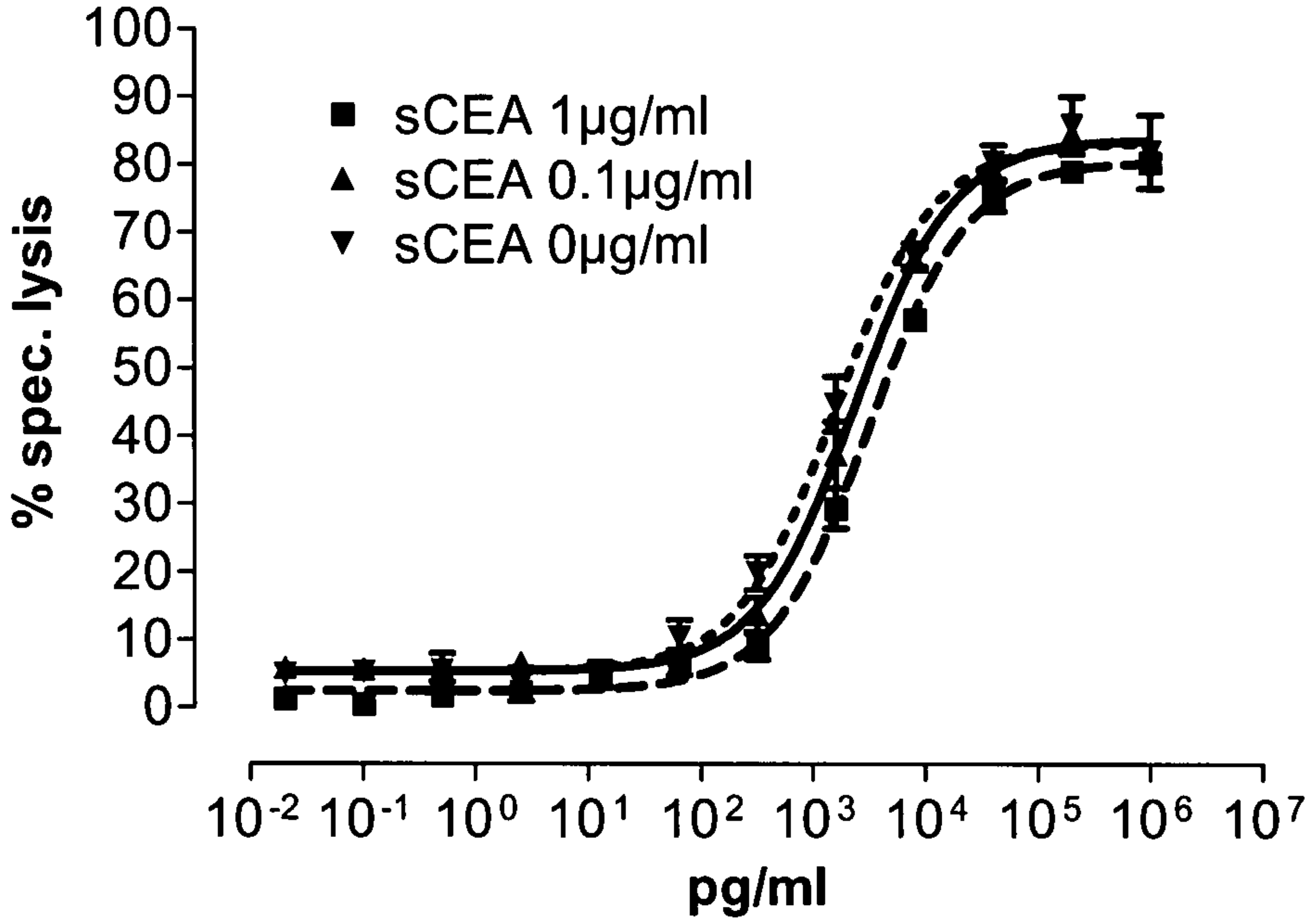


EC50 [ng/ml]	**I -HL**	**II -HL**	**III -LH**	**III -HL**
CHO-CEA$^+$	9.3	1.2	119	139

FIGURE 5



CEA I VLVH x SEQ ID NO.77 VHVL

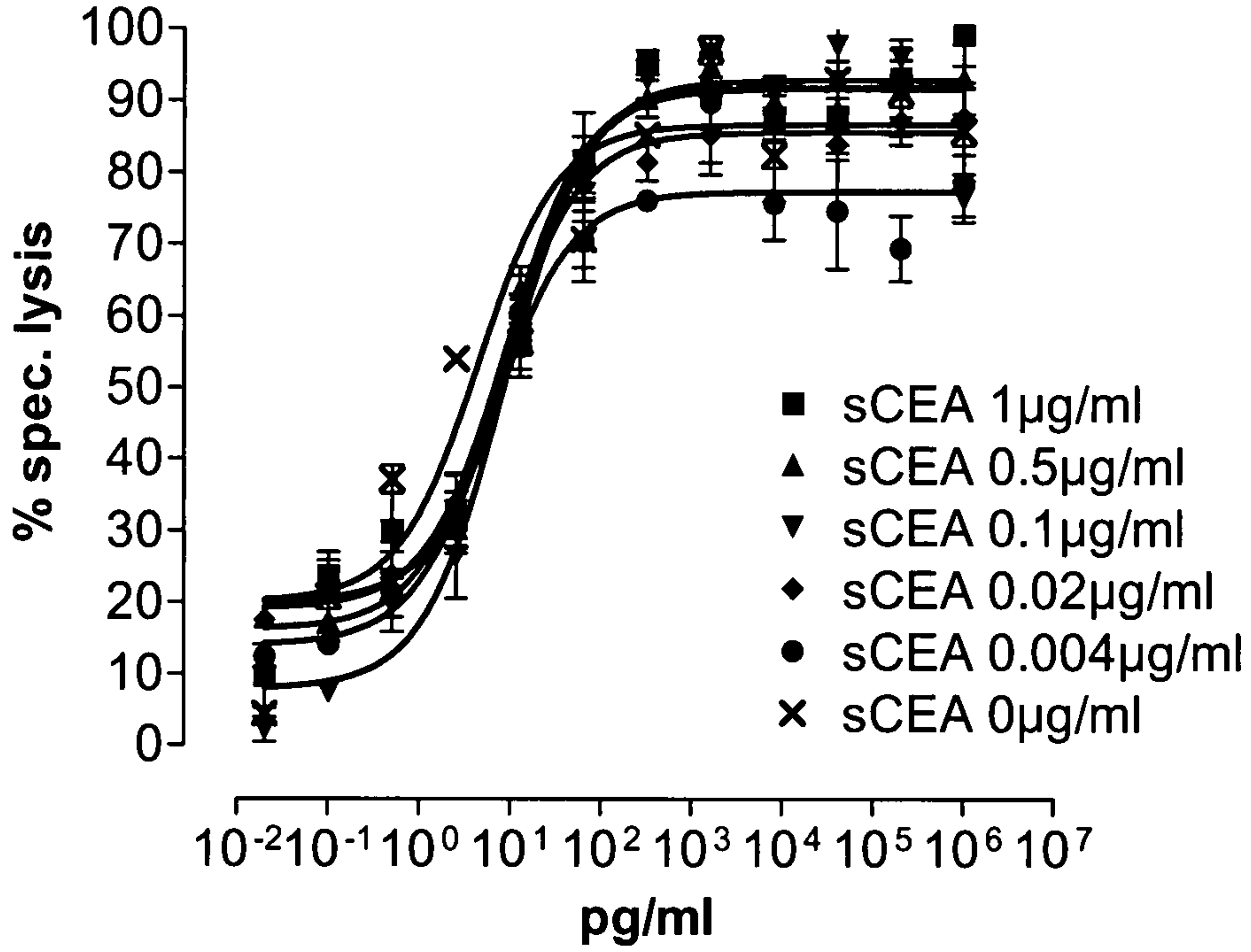


CEA I VHVL x SEQ ID NO.77 VHVL

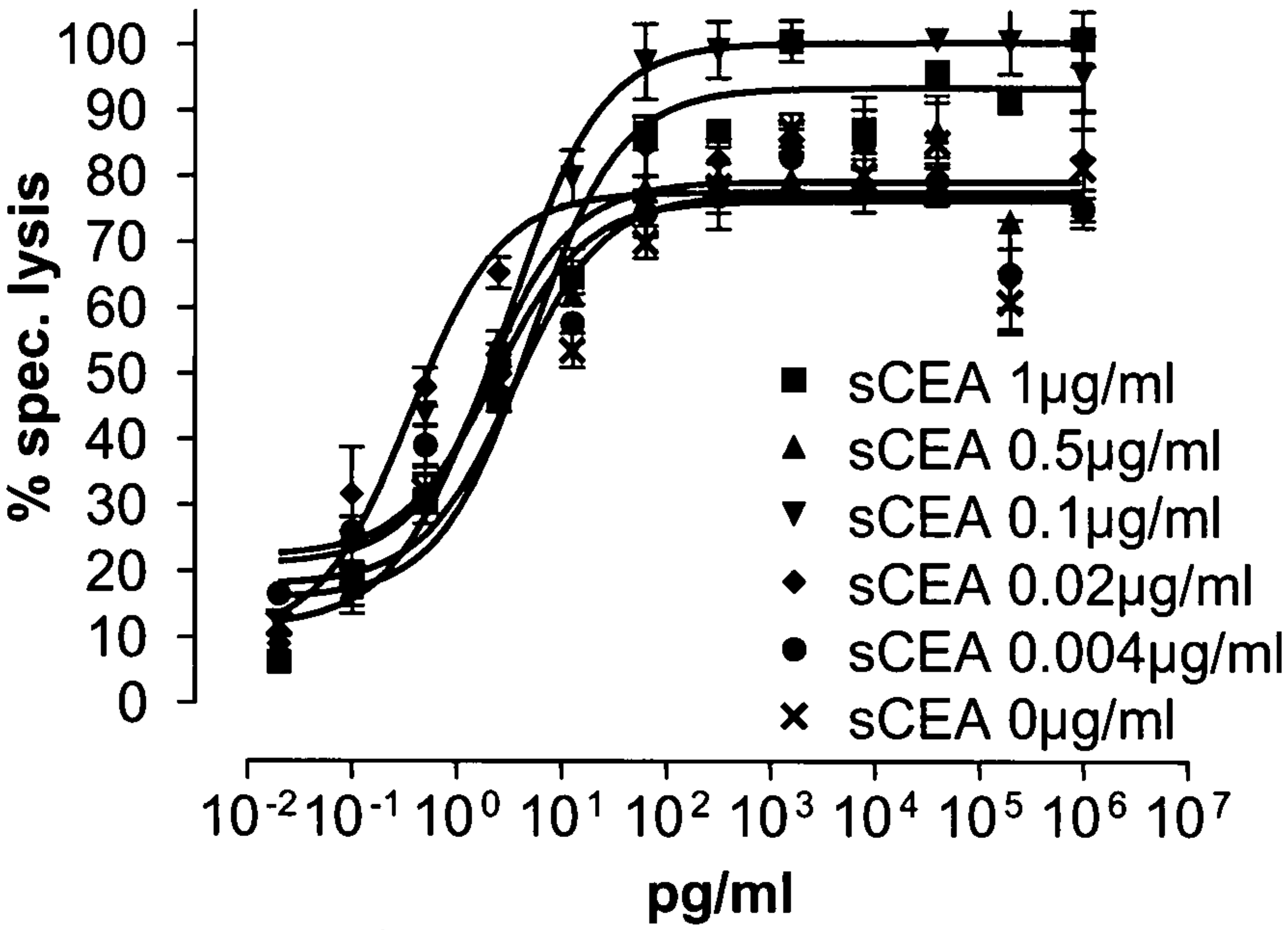
Sol. CEA [µg/ml]	**0**	**0.1**	**1**
CEA I VHVL x SEQ ID NO.77 VHVL EC50 [ng/ml]	1.6	2.4	3.2
CEA I VLVH x SEQ ID NO.77 VHVL EC50 [ng/ml]	0.034	0.024	0.058

FIGURE 6

SEQ ID NO.77 VHVLxCEAI VHVL

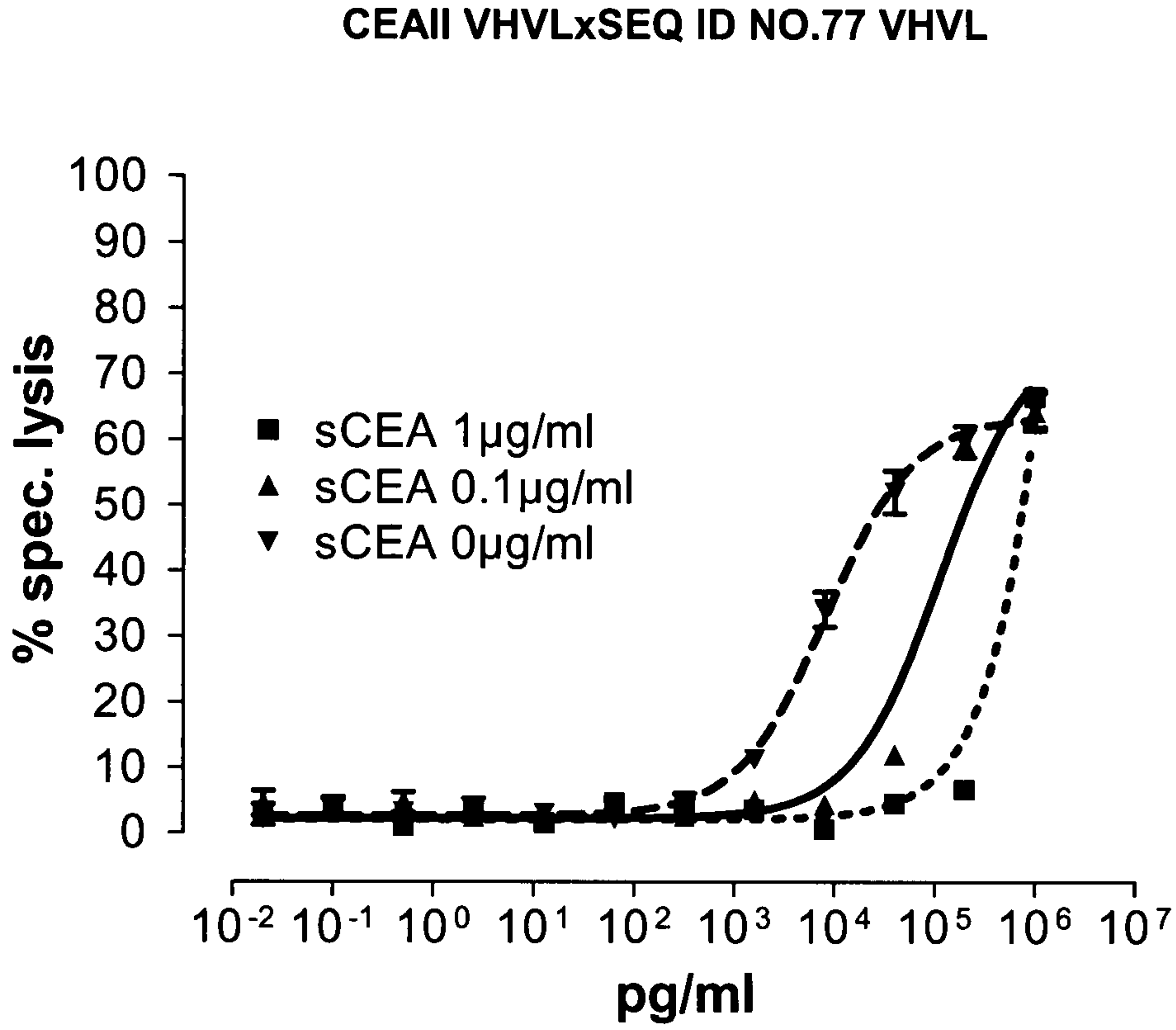


SEQ ID NO.77 VHVLxCEAI VLVH



Sol. CEA [µg/ml]	**0**	**0.004**	**0.02**	**0.1**	**0.5**	**1**
SEQ ID NO.77 VHVLx CEA-I LH EC_{50} [pg/ml]	3.5	2.3	0.4	3.5	1.6	5.1
SEQ ID NO.77 VHVL x CEA-I HL EC_{50} [pg/ml]	4.5	6.2	7.4	8.4	9.1	11.6

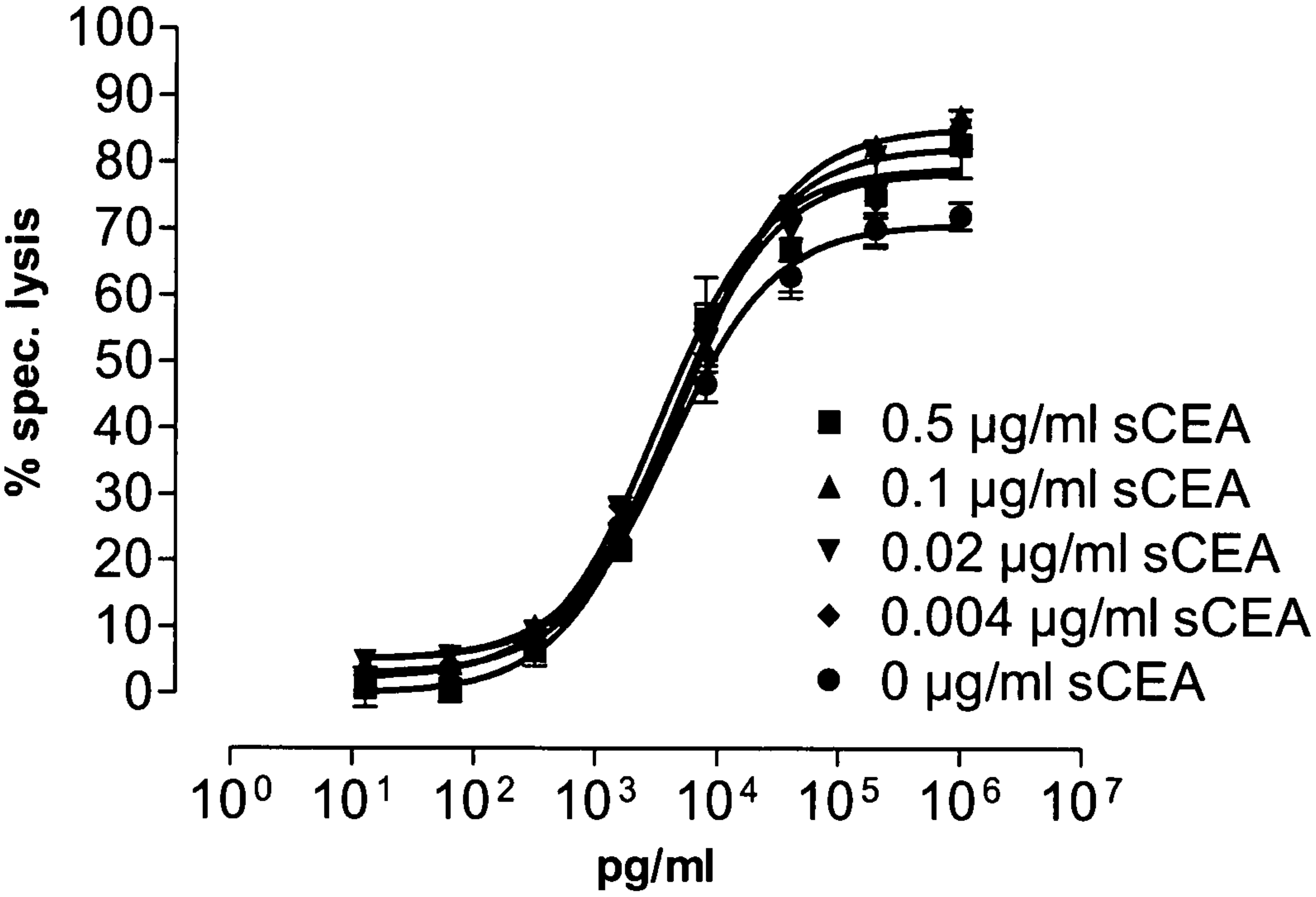
FIGURE 7



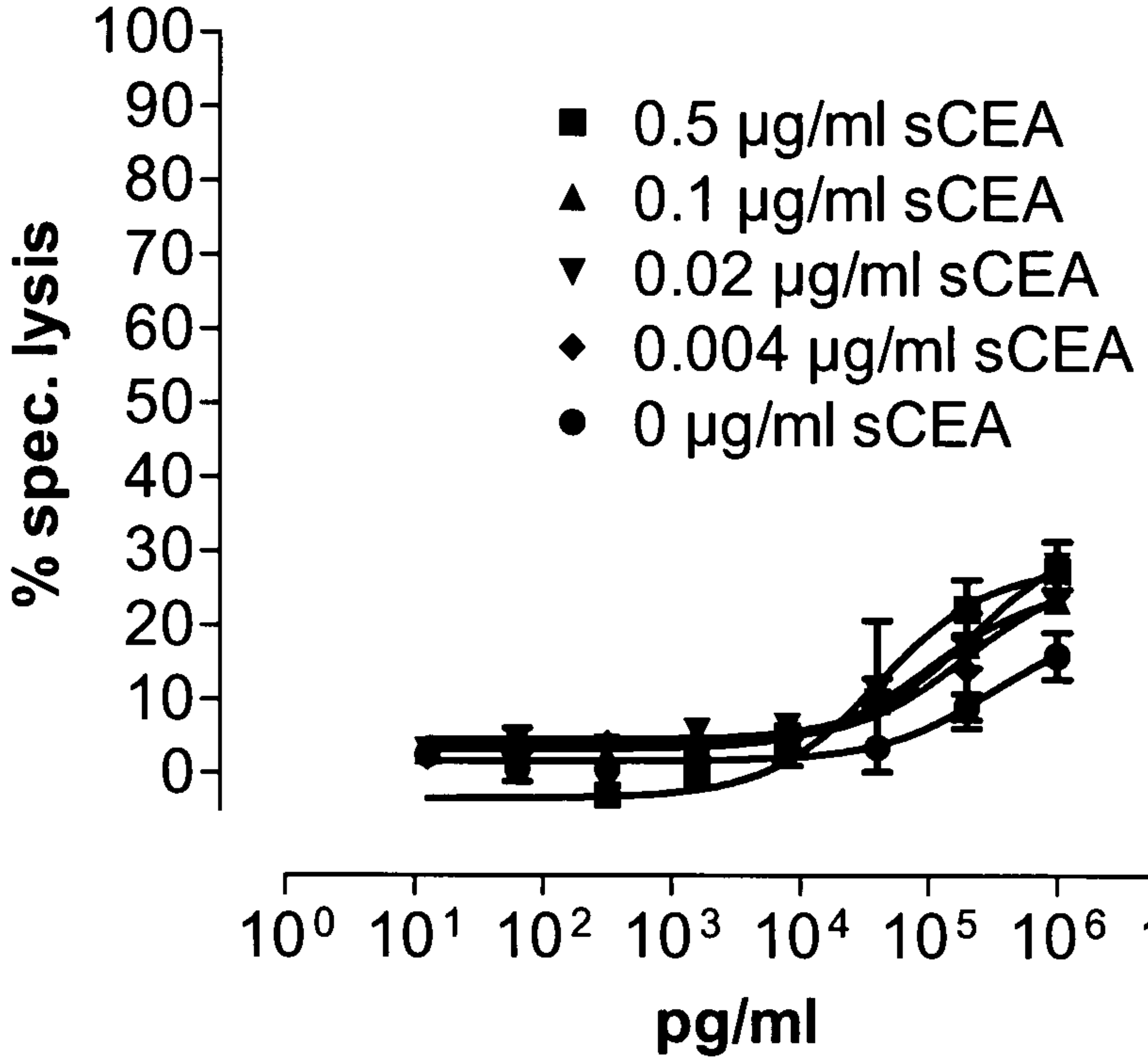
Sol. CEA [µg/ml]	0	0.1	1
CEAII VHVLxSEQ ID NO.77 VHVL EC50 [ng/ml]	8.2	114.6	3980

FIGURE 8

CEAI VHVLxSEQ ID NO.77 VHVL

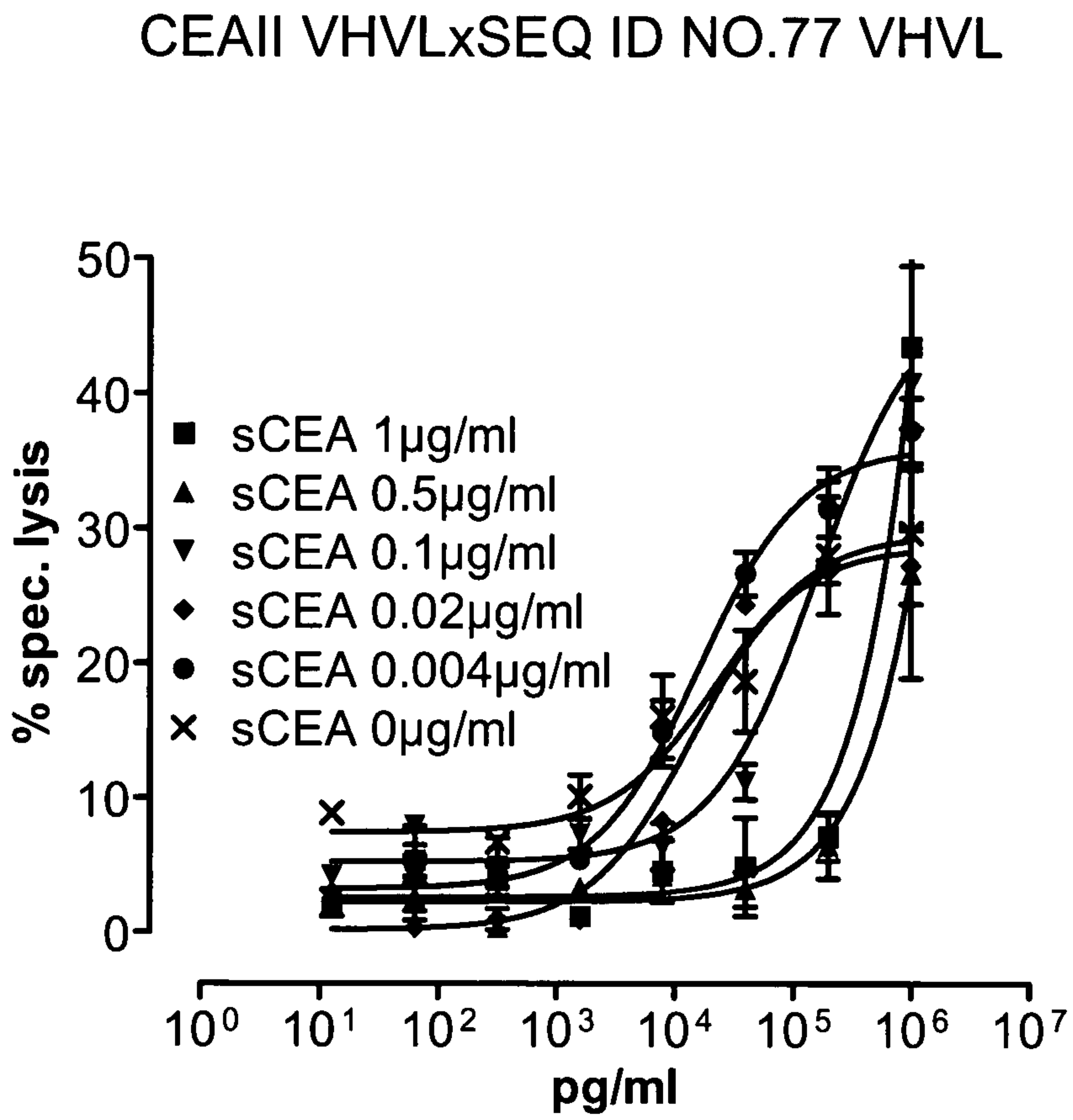


CEAIII VHVLxSEQ ID NO.77 VHVL



Sol. CEA [µg/ml]	**0**	**0.004**	**0.02**	**0.1**	**0.5**
CEAIVHVLxSEQ ID NO.77VHVL EC50 [ng/ml]	3.9	3.3	4.7	5.5	3.8
CEAIIIVHVLxSEQ ID NO.77VHVL EC50 [ng/ml]	n.d.	n.d.	n.d.	n.d	n.d.

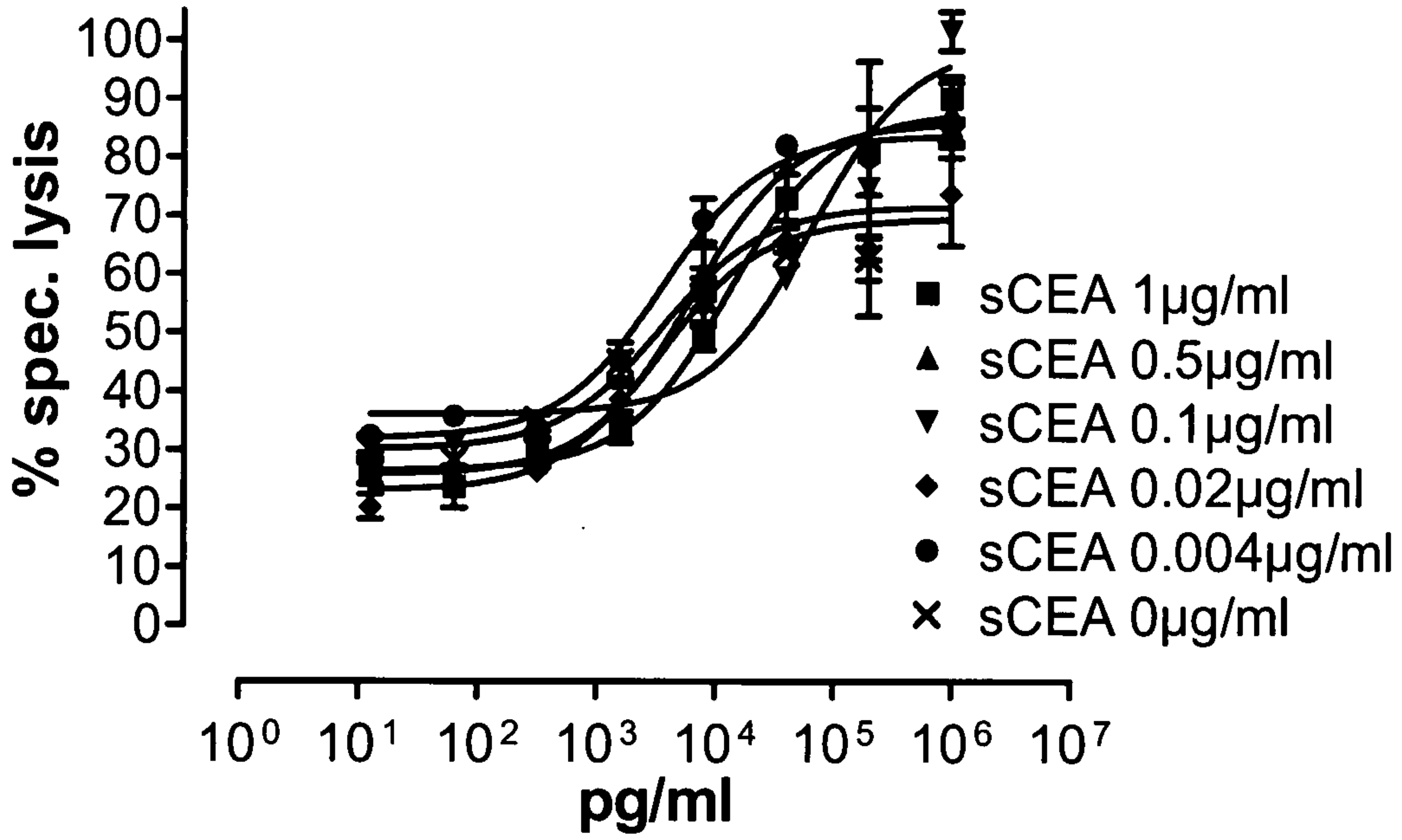
FIGURE 9



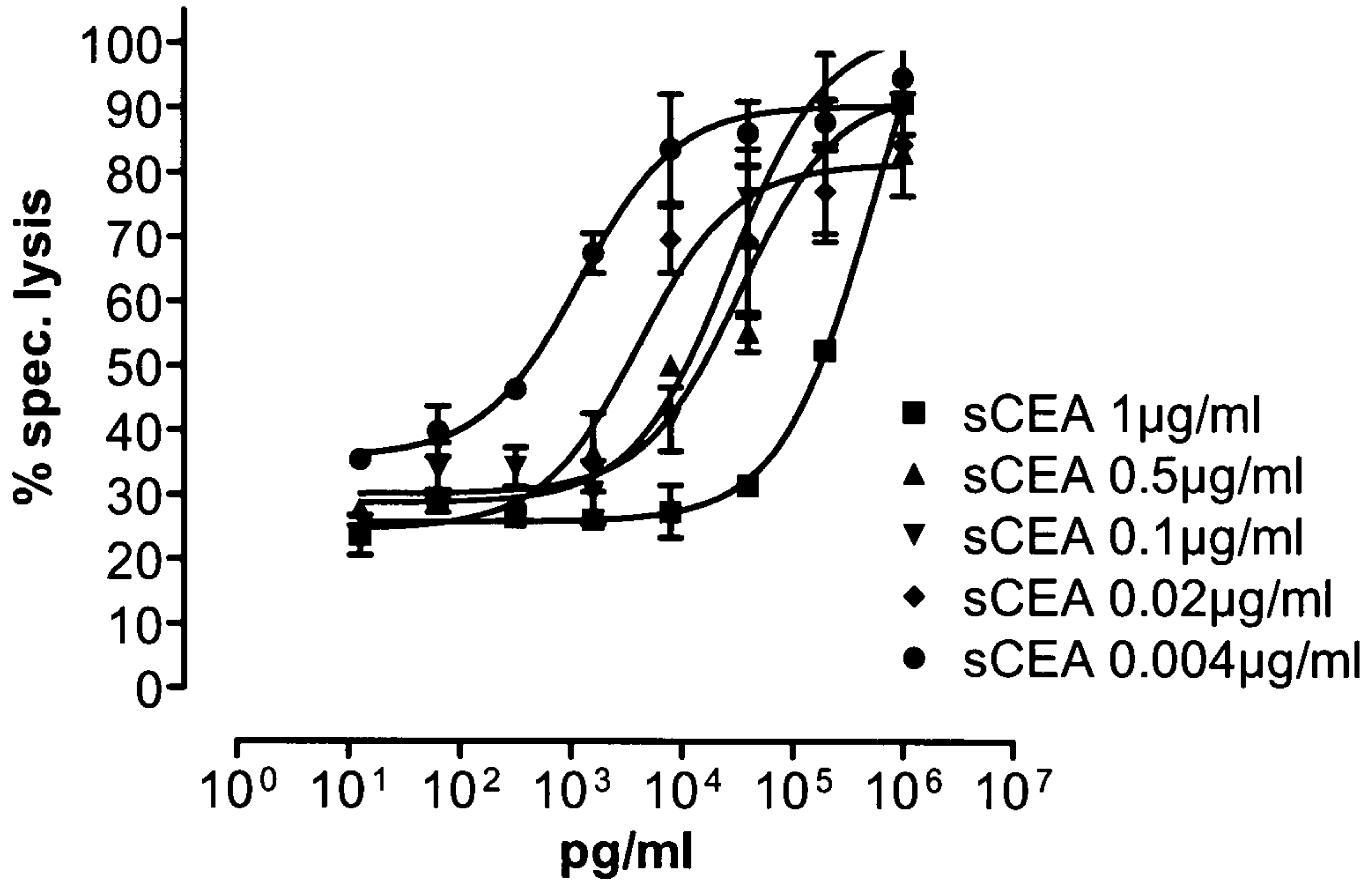
Sol. CEA [µg/ml]	0	0.02	0.1	0.5	1.0
CEAIIVHVLxSEQ ID NO.77VHVL EC50 [ng/ml]	23	14	159	1415	5057

FIGURE 10

CEAI VHVL x SEQ ID NO.77 VHVL

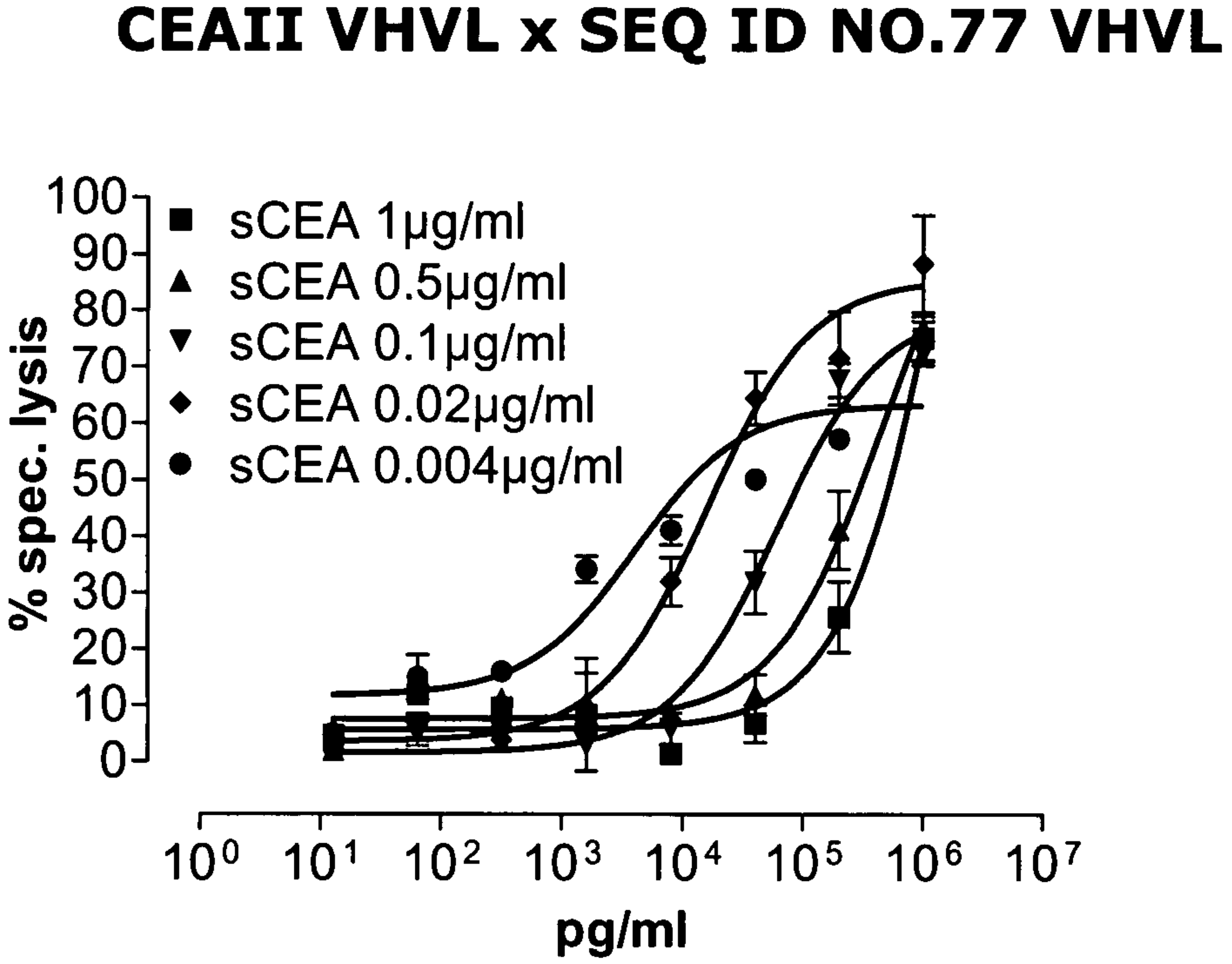


CEAII VHVL x SEQ ID NO.77 VHVL



Sol. CEA [µg/ml]	0	0.004	0.1	0.5	1.0
CEAIVHVLxSEQ ID NO.77VHVL EC50 [ng/ml]	3.6	3.6	65.4	6.3	5.1
CEAIIVHVLxSEQ ID NO.77VHVL EC50 [ng/ml]	--	1.2	36.5	77.9	578

FIGURE 11



Sol. CEA [µg/ml]	**0.004**	**0.02**	**0.1**	**0.5**	**1.0**
CEAIIVHVLxSEQ ID NO.77 VHVL EC50 [ng/ml]	4.0	16	60	432	1983

FIGURE 12

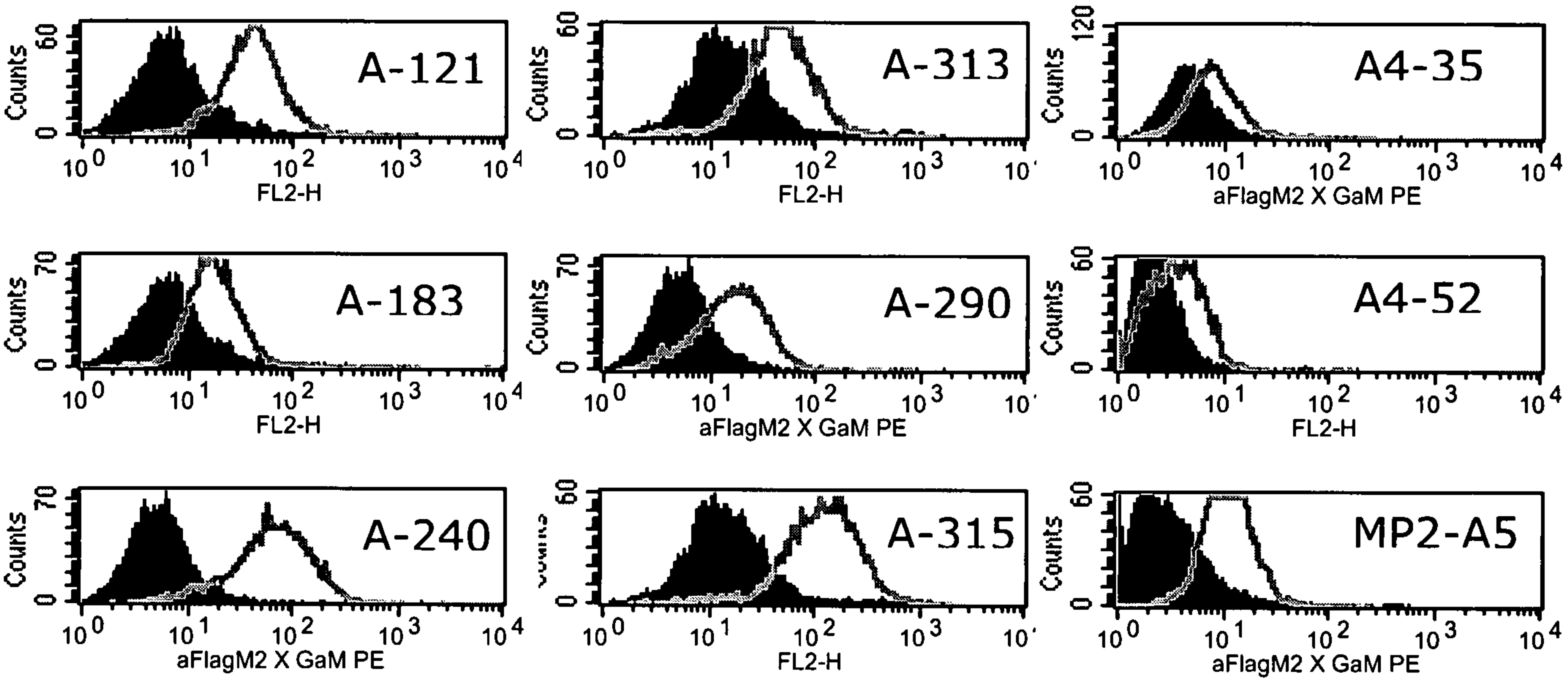

A-121
A-313
A4-35
A-183
A-290
A4-52
A-240
A-315
MP2-A5
Counts
0
60
70
120
10^0
10^1
10^2
10^3
10^4
FL2-H
aFlagM2 X GaM PE

FIGURE 13

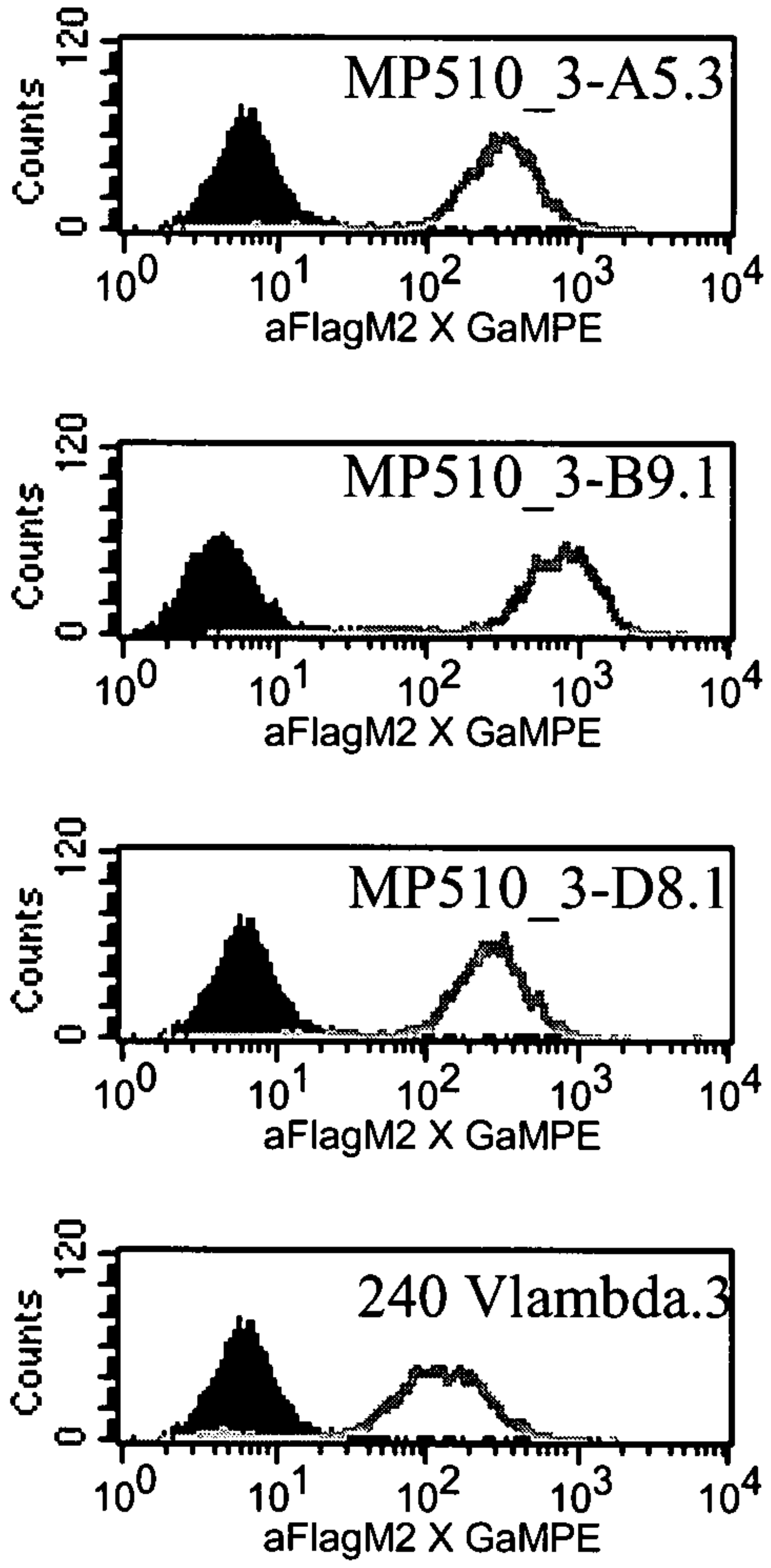
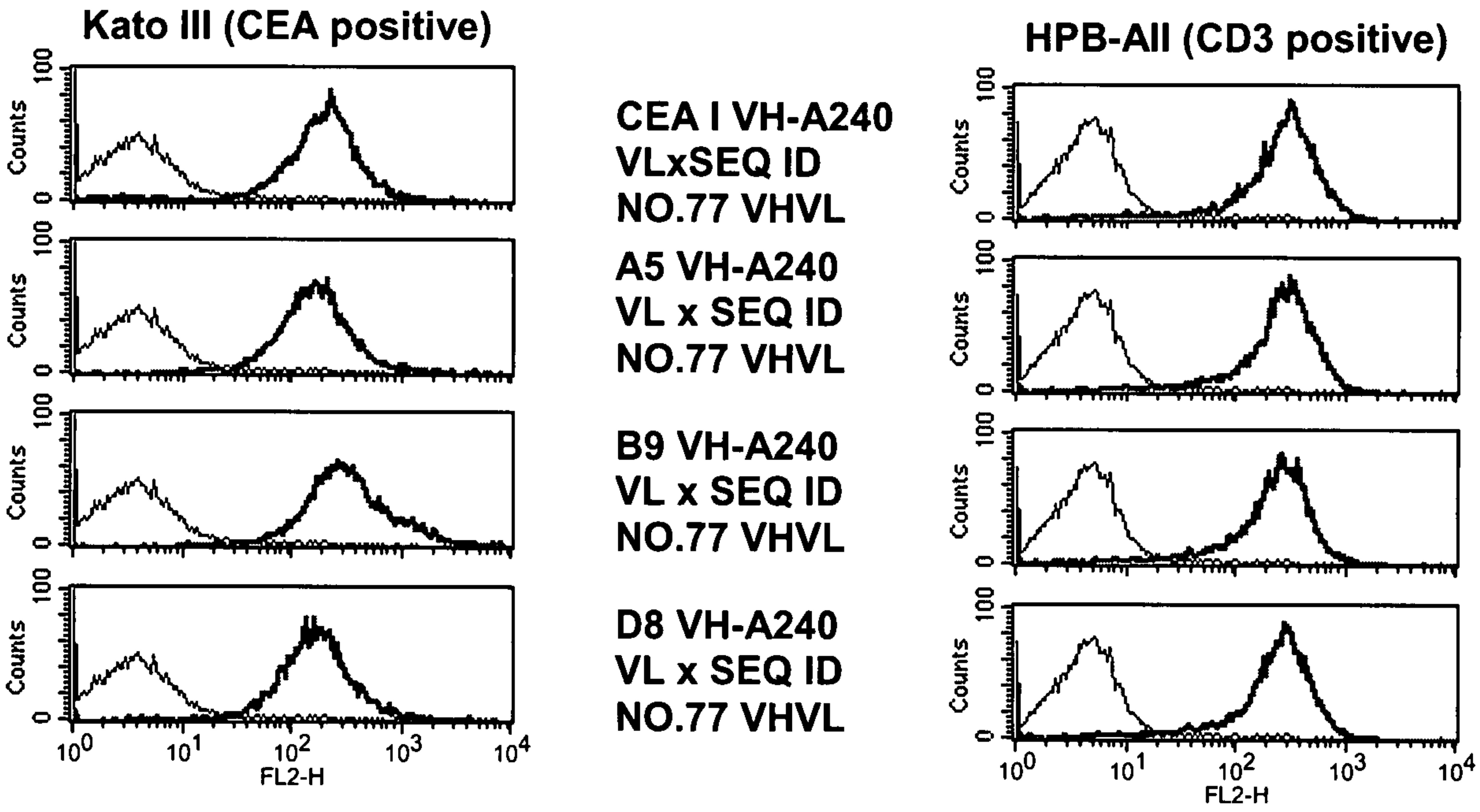

MP510_3-A5.3
MP510_3-B9.1
MP510_3-D8.1
240 Vlambda.3
Counts
0
120
10^0
10^1
10^2
10^3
10^4
aFlagM2 X GaMPE

FIGURE 14



Kato III (CEA positive)

HPB-All (CD3 positive)

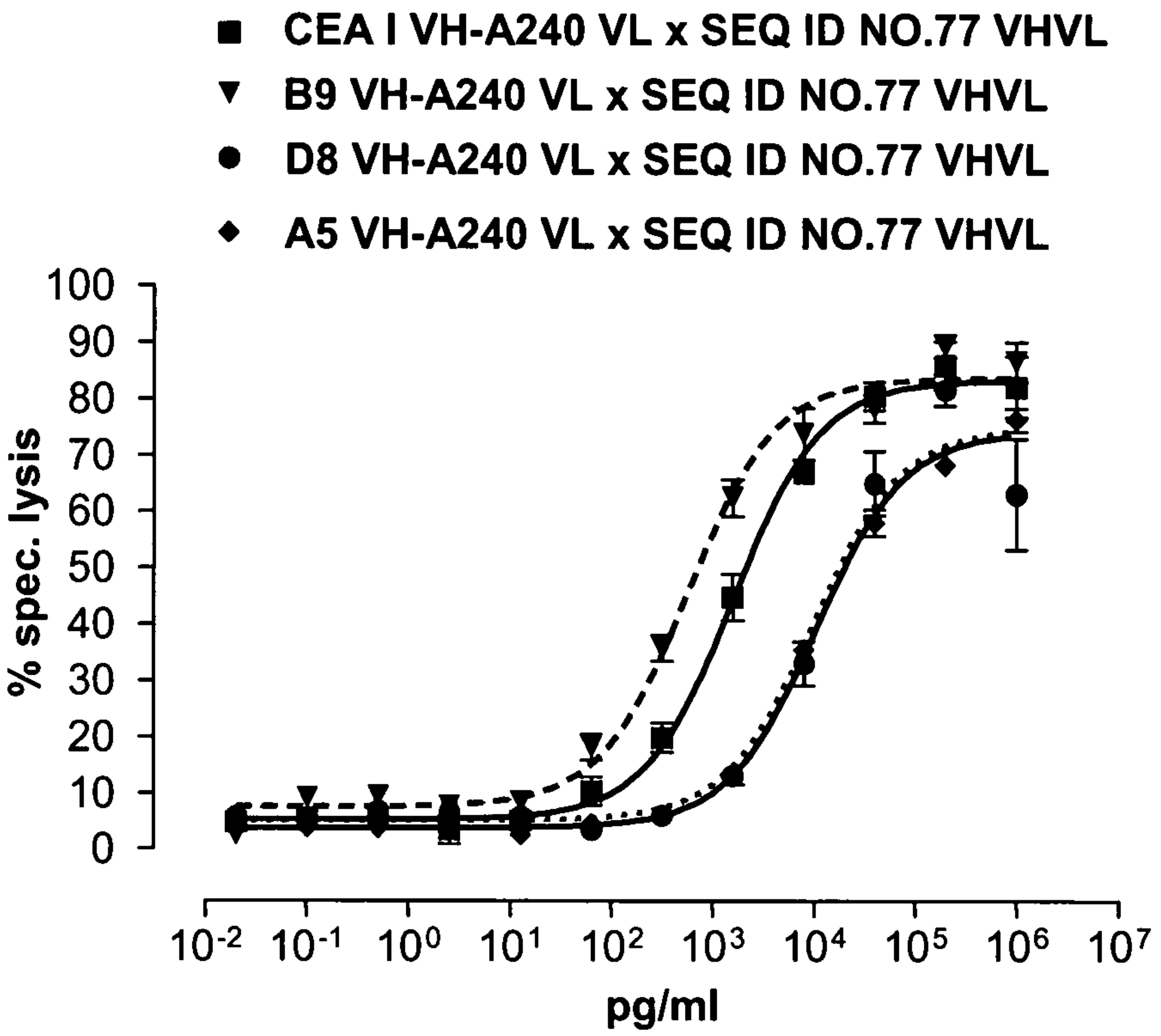
CEA I VH-A240 VLxSEQ ID NO.77 VHVL

A5 VH-A240 VL x SEQ ID NO.77 VHVL

B9 VH-A240 VL x SEQ ID NO.77 VHVL

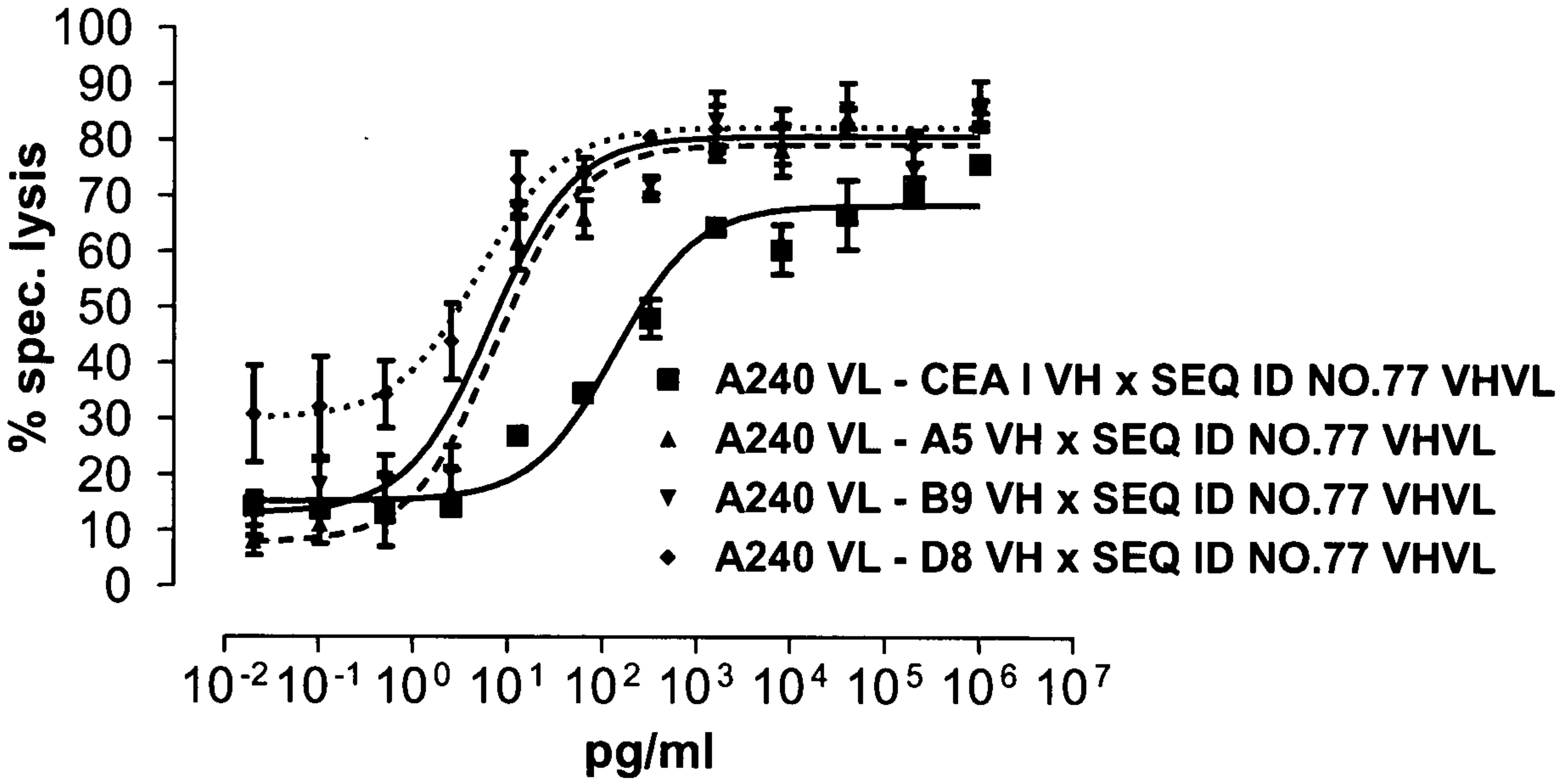
D8 VH-A240 VL x SEQ ID NO.77 VHVL

FIGURE 15



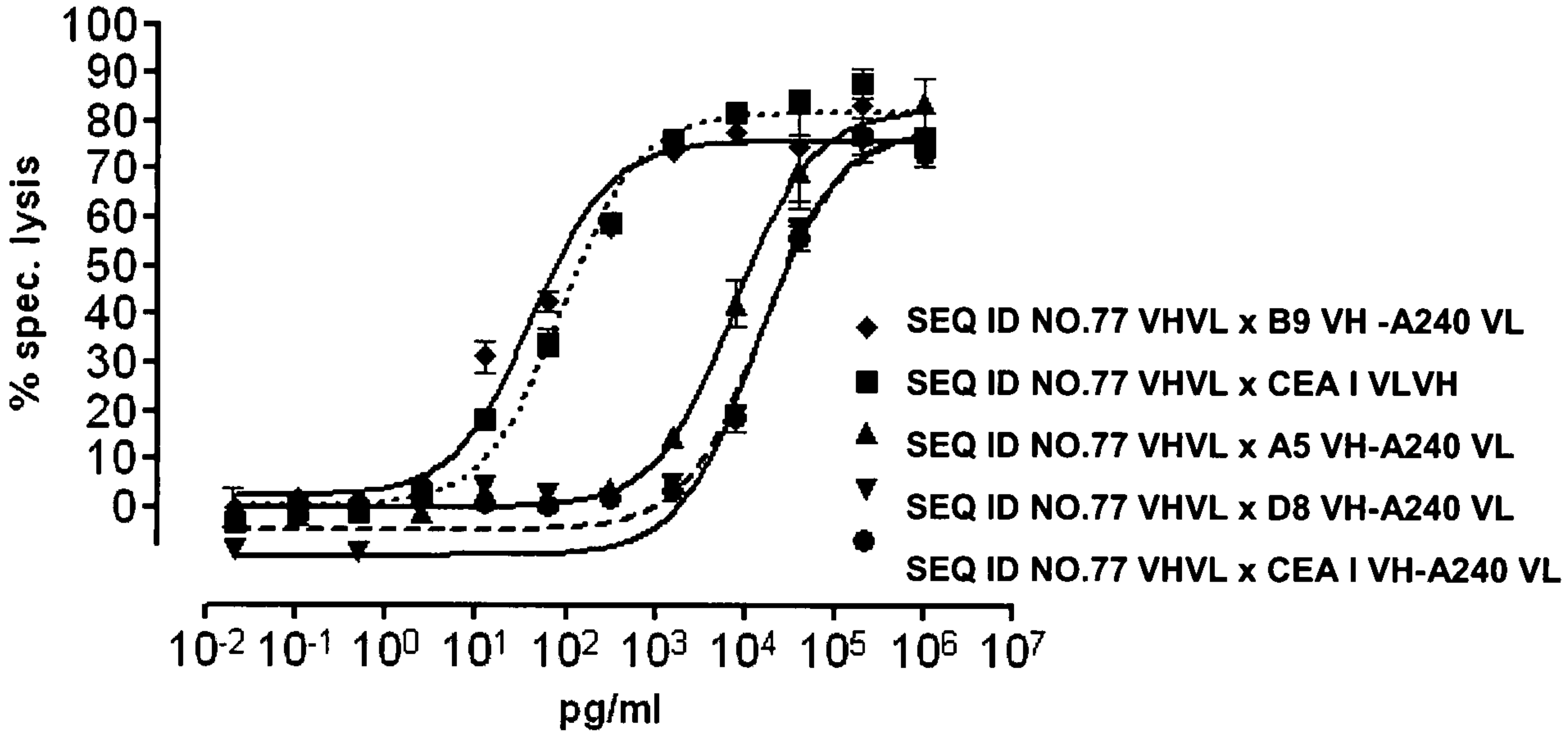
	EC 50 [ng/ml]
B9 VH - A240 VL x SEQ ID NO.77 VHVL	0.58
CEA I VH - A240 VL x SEQ ID NO.77 VHVL	1.61
D8 VH - A240 VL x SEQ ID NO.77 VHVL	10.0
A5 VH - A240 VL x SEQ ID NO.77 VHVL	10.5

FIGURE 16



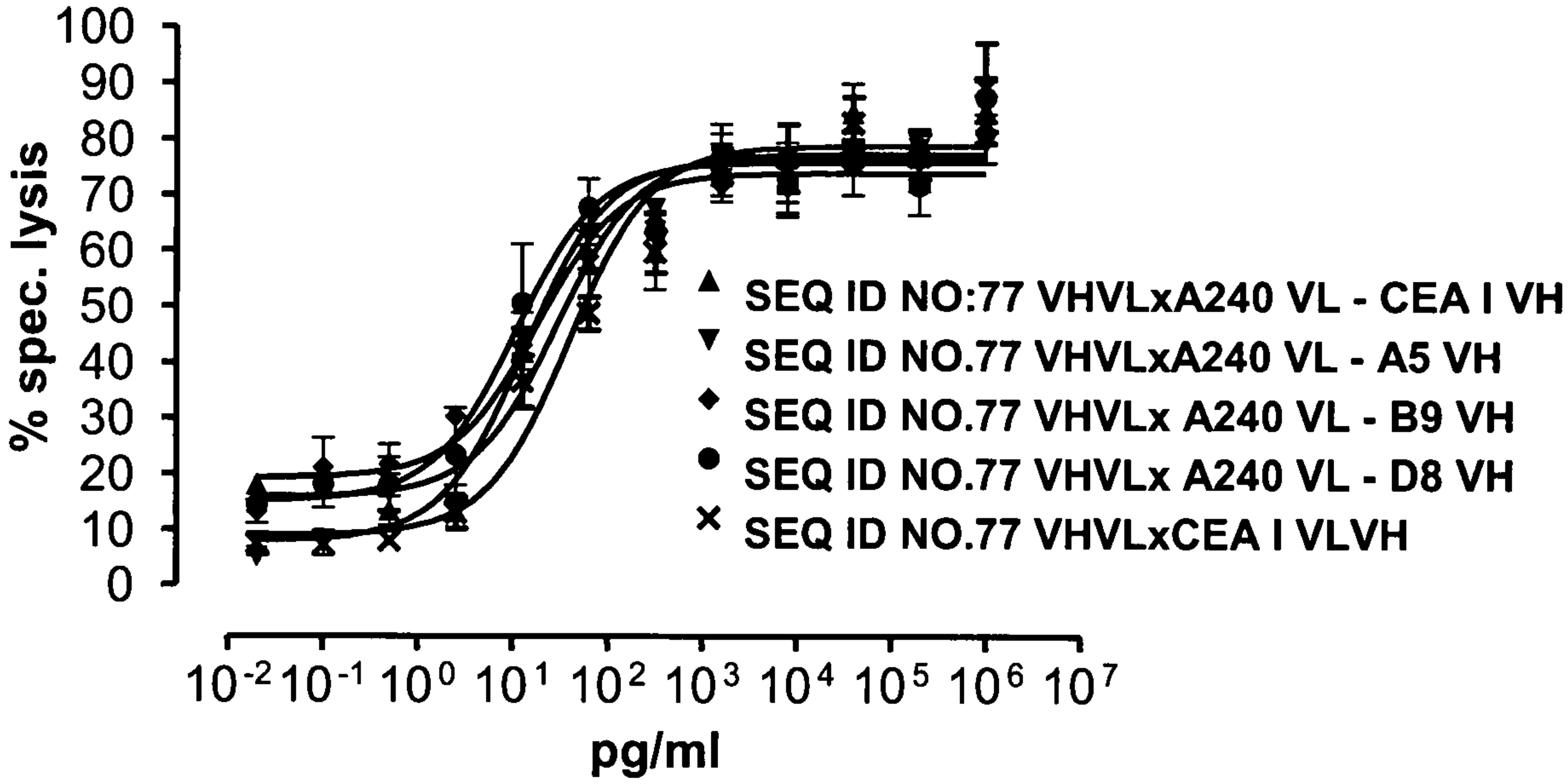
	EC 50 [pg/ml]
A240 VL-D8 VHxSEQ ID NO.77 VHVL	**5.1**
A240 VL-A5 VHxSEQ ID NO.77 VHVL	**7.7**
A240 VL-B9 VHxSEQ ID NO.77 VHVL	**6.7**
A240 VL-CEAI VHxSEQ ID NO.77 VHVL	**135.9**

FIGURE 17



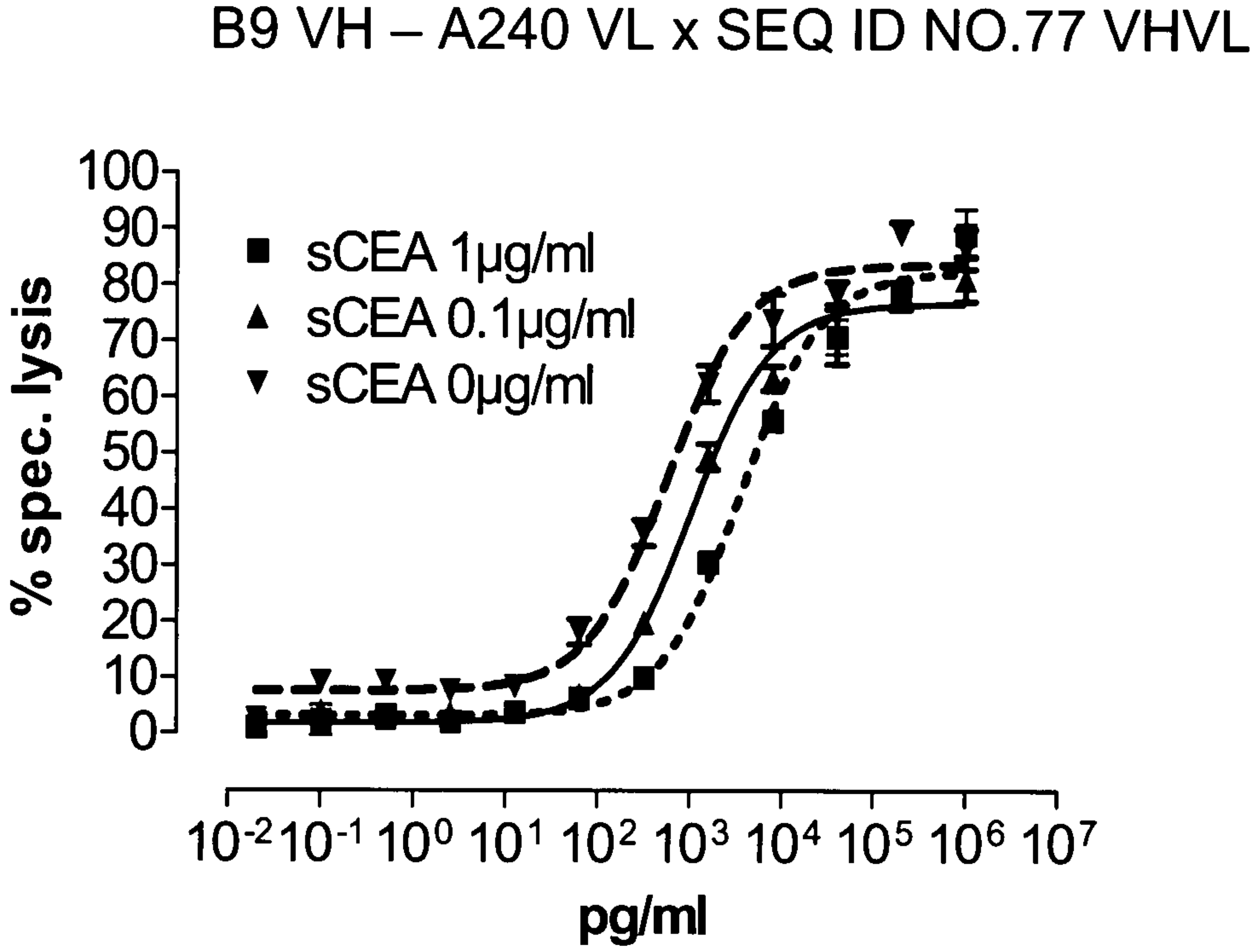
	EC 50 [ng/ml]
SEQ ID NO.77 VHVL x B9 VH -A240 VL	0.042
SEQ ID NO.77 VHVL x CEA I VLVH	0.092
SEQ ID NO.77 VHVL x A5 VH-A240 VL	7.5
SEQ ID NO.77 VHVL x D8 VH-A240 VL	13.8
SEQ ID NO.77 VHVL x CEA I VH-A240 VL	15.6

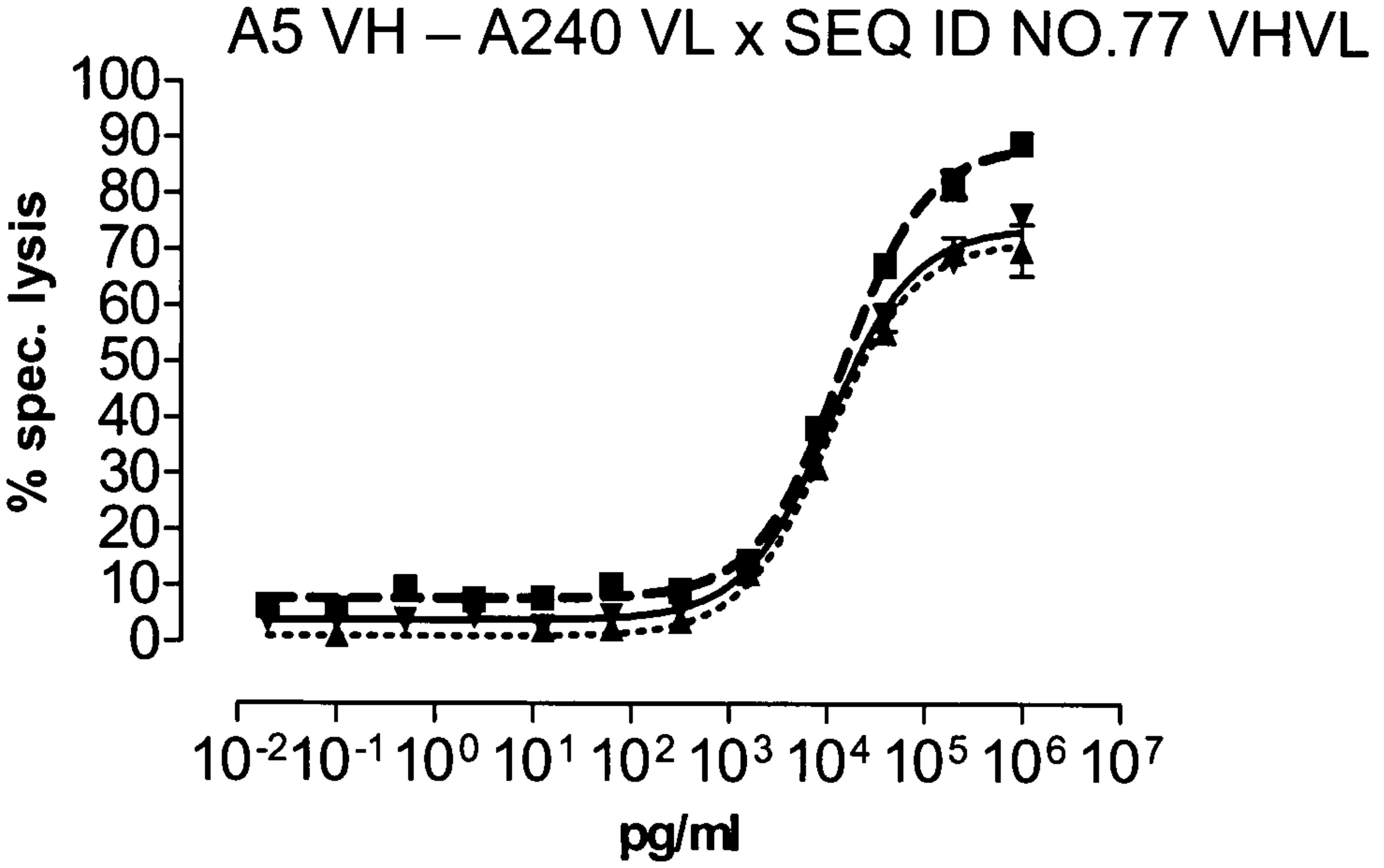
FIGURE 18



	EC 50 [pg/ml]
SEQ ID NO:77 VHVL x A240 VL - D8 VH	11.0
SEQ ID NO:77 VHVL x A240 VL - A5 VH	13.5
SEQ ID NO:77 VHVL x A240 VL - B9 VH	18.4
SEQ ID NO:77 VHVL x A240 VL - CEA I VH	29.8
SEQ ID NO:77 VHVL x CEA I VLVH	40.0

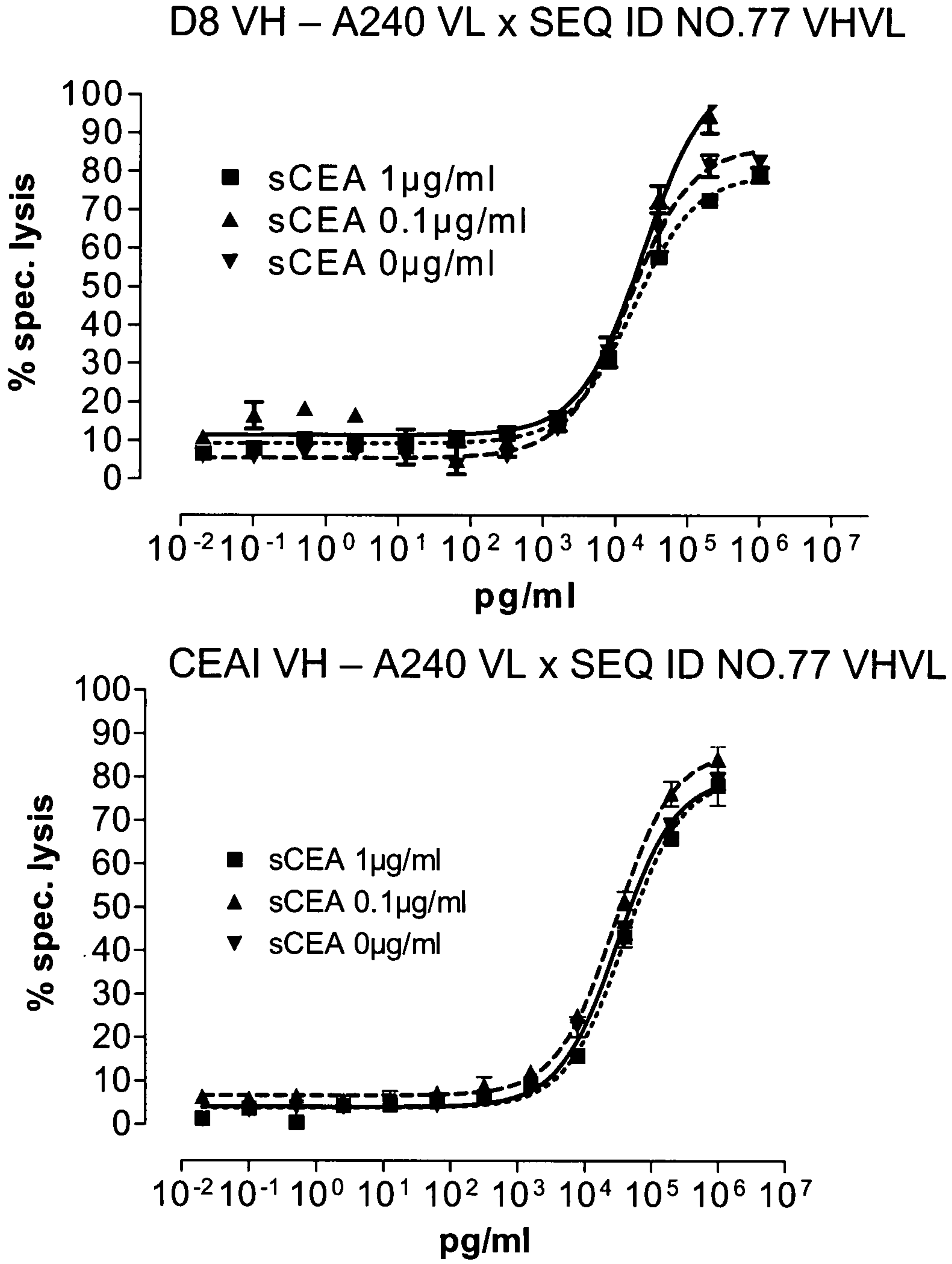
FIGURE 19





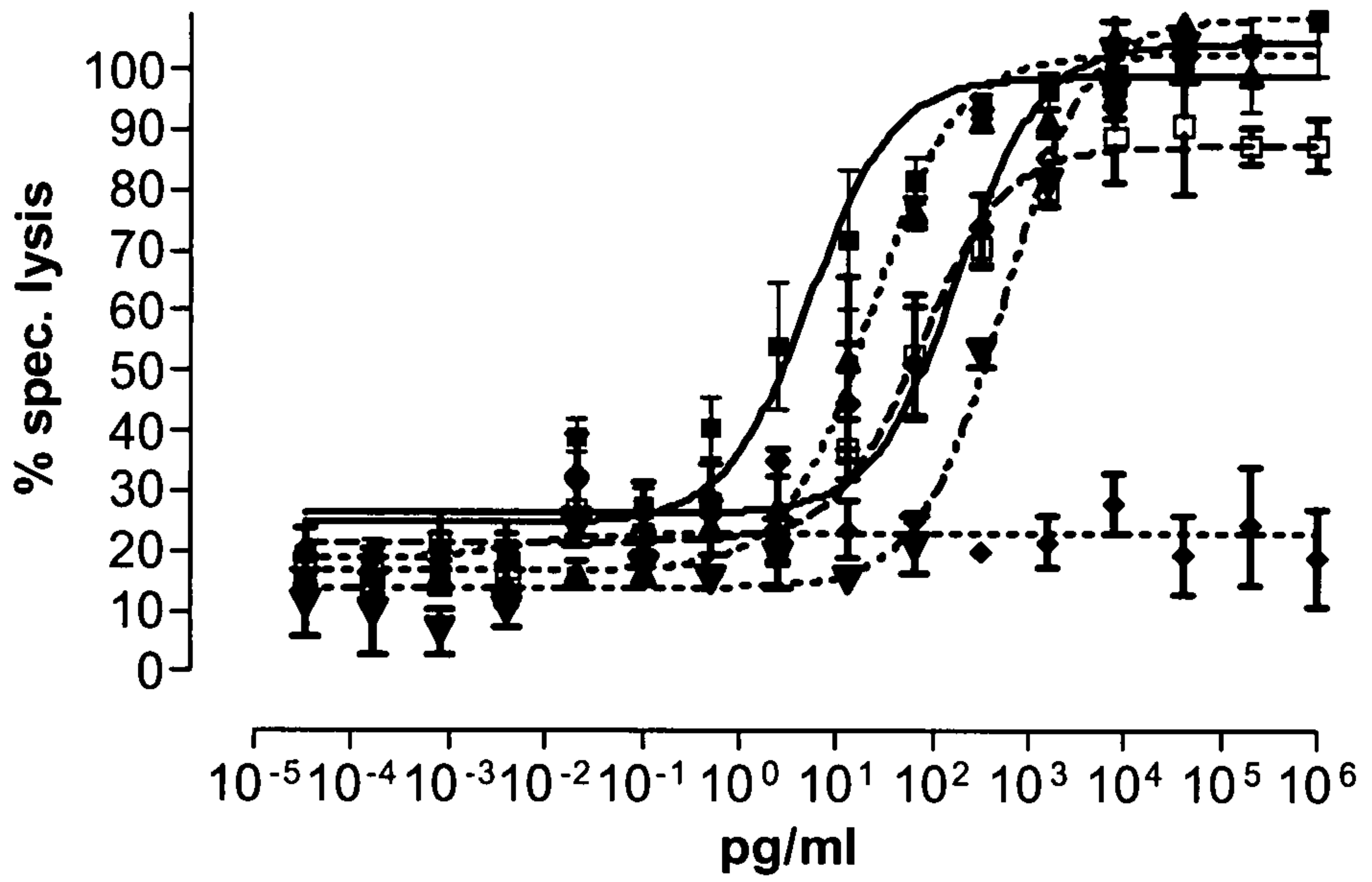
Sol. CEA [µg/ml]	0	0.1	1
B9 VH – A240 VL x SEQ ID NO.77 VHVL EC50 [ng/ml]	0.58	1.04	3.65
A5 VH – A240 VL x SEQ ID NO.77 VHVL EC50 [ng/ml]	10.5	10.4	14.0

FIGURE 20



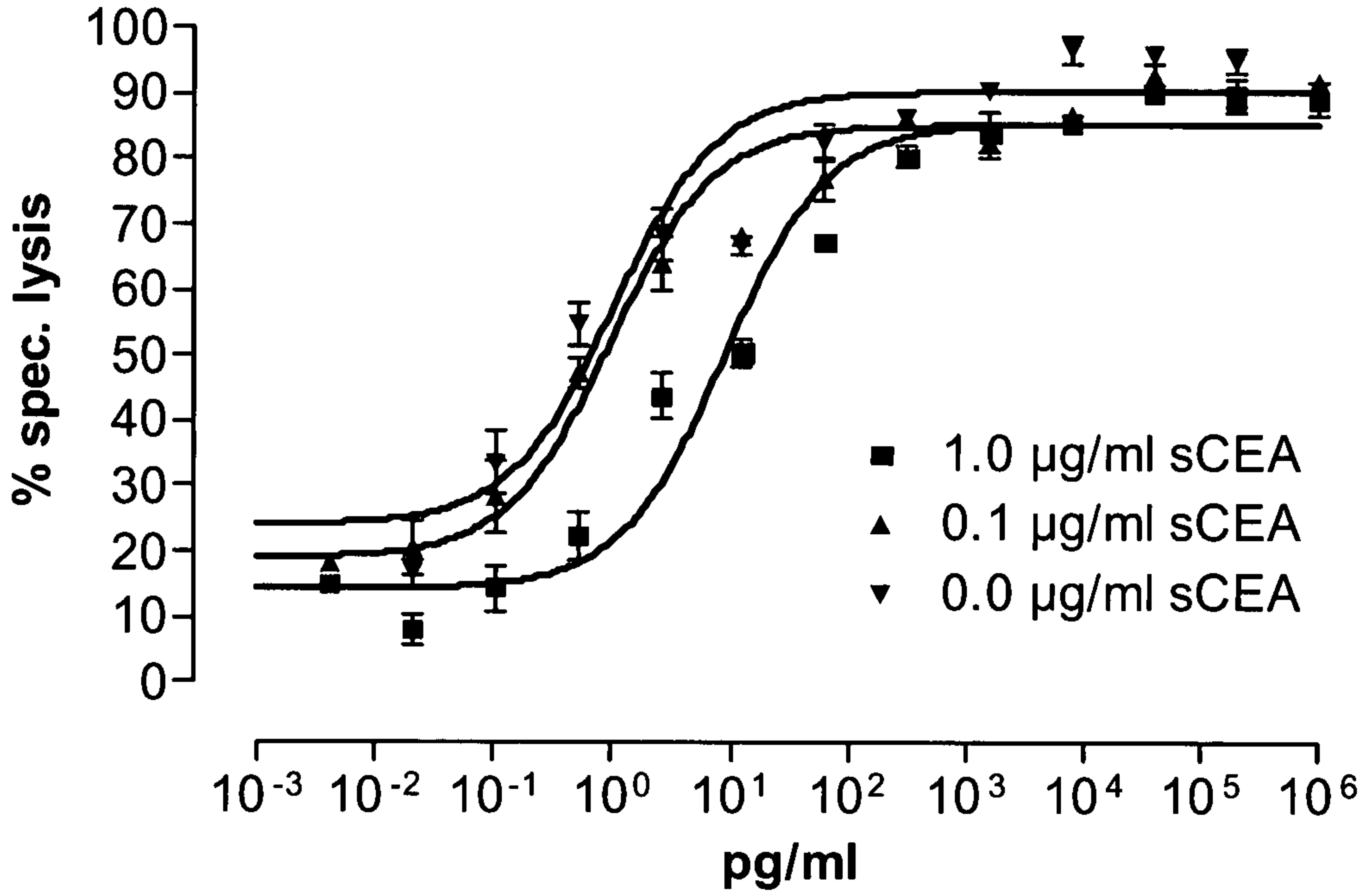
Sol. CEA [µg/ml]	**0**	**0.1**	**1**
D8 VH – A240 VL x SEQ ID NO.77 VHVL EC50 [ng/ml]	15.1	24.1	17.5
CEAI VH- A240 VL x SEQ ID NO.77 VHVL EC50 [ng/ml]	31.6	28.8	39.0

FIGURE 21



	EC 50 [pg/ml]
——■ A240(VL)-B9(VH) x SEQ ID NO.77 VHVL	5.3
····▲ SEQ ID NO.77 VHVL x A240(VL)-B9(VH)	22.9
- - -□ SEQ ID NO.77 VHVL x B9(VH) A240(VL)	74.2
——◇ B9(VH) A240(VL) x SEQ ID NO.77 VHVL	178.2
- - -▼ SEQ ID NO.77 VHVL x CEA I	538.6
·····◆ Negative Control	n.a.

FIGURE 22



Sol. CEA [µg/ml]	**0**	**0.1**	**1**
A240 VL – B9 VH x SEQ ID NO.77 VHVL EC50 [pg/ml]	1.0	1.0	8.9

FIGURE 23

High Resolution Cation Exchange Chromatography

of A240 VL–B9 VH x SEQ ID NO.77 VHVL

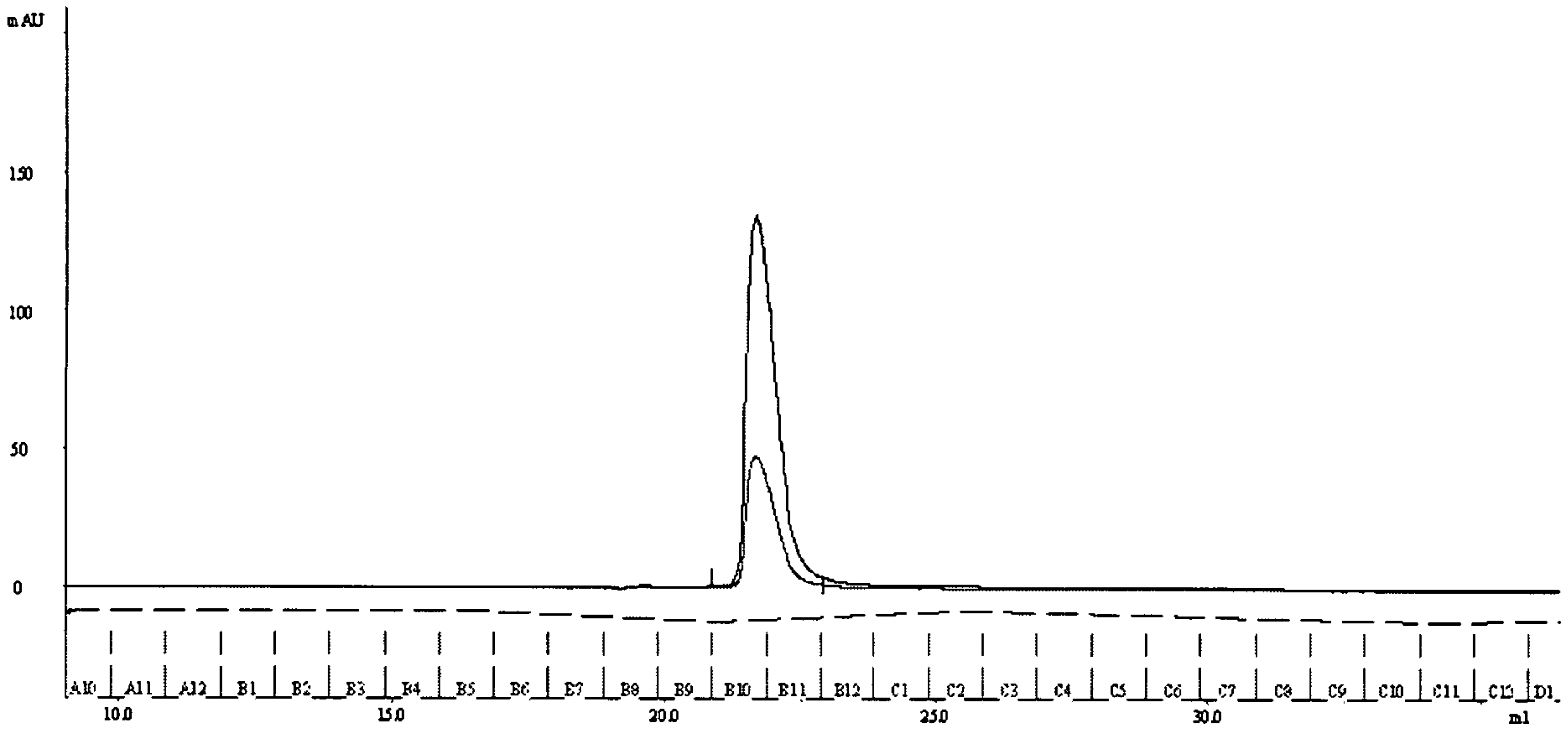
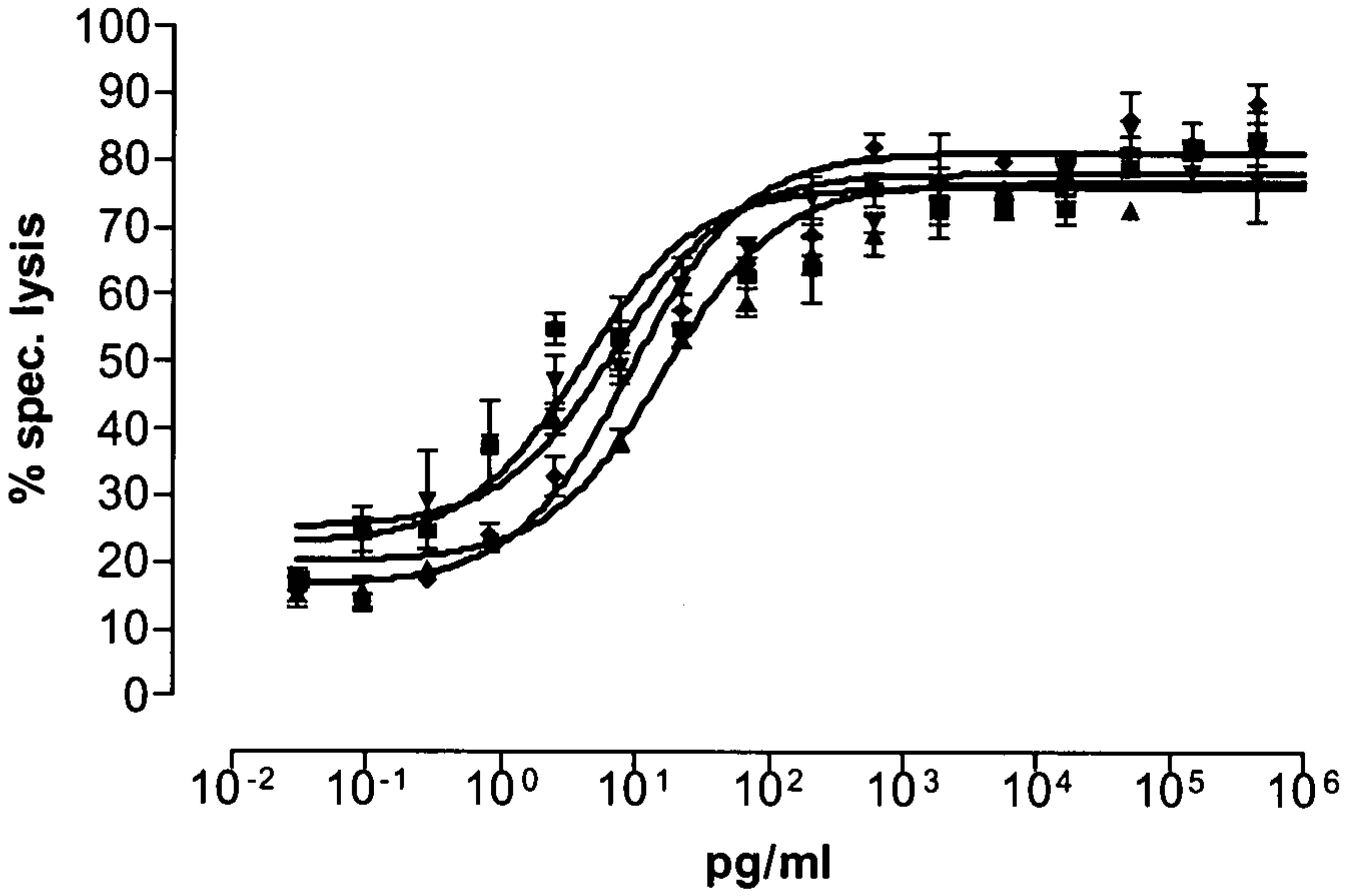


FIGURE 24

Protein stability testing of A240 VL–B9 VHxSEQ ID NO.77 VHVL in human plasma



	EC 50 [pg/ml]
■ Incubation for 24 h in plasma at 37 °C	**4.0**
▲ Incubation for 24 h in plasma at 4 °C	**16.5**
● Protein dilution immediately before the assay in RPMI	**7.1**
♦ Protein dilution immediately before the assay in plasma	**9.4**

FIGURE 25

High Resolution Cation Exchange Chromatography

of SEQ ID NO.77 VHVLxE12 VH–A240 VL

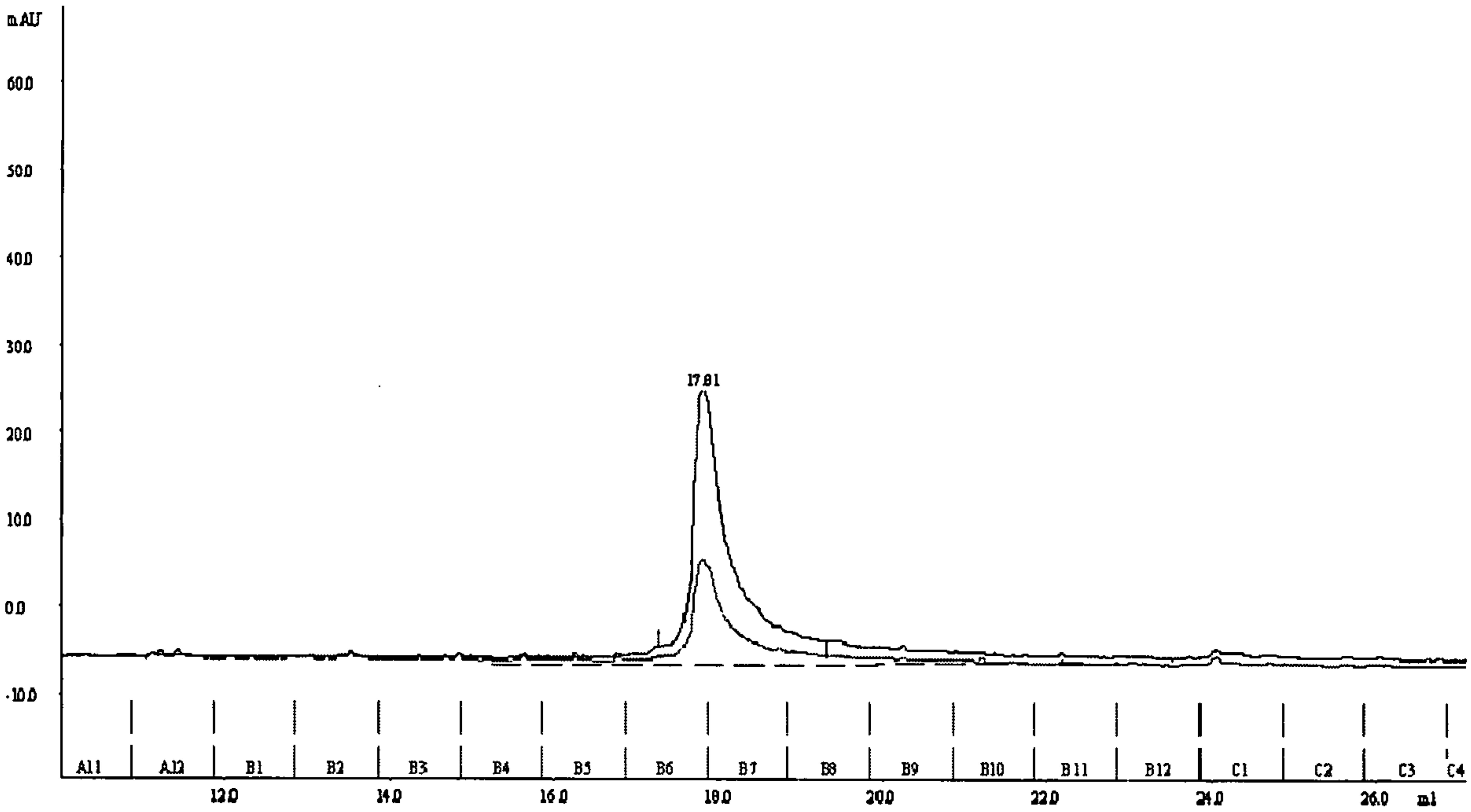
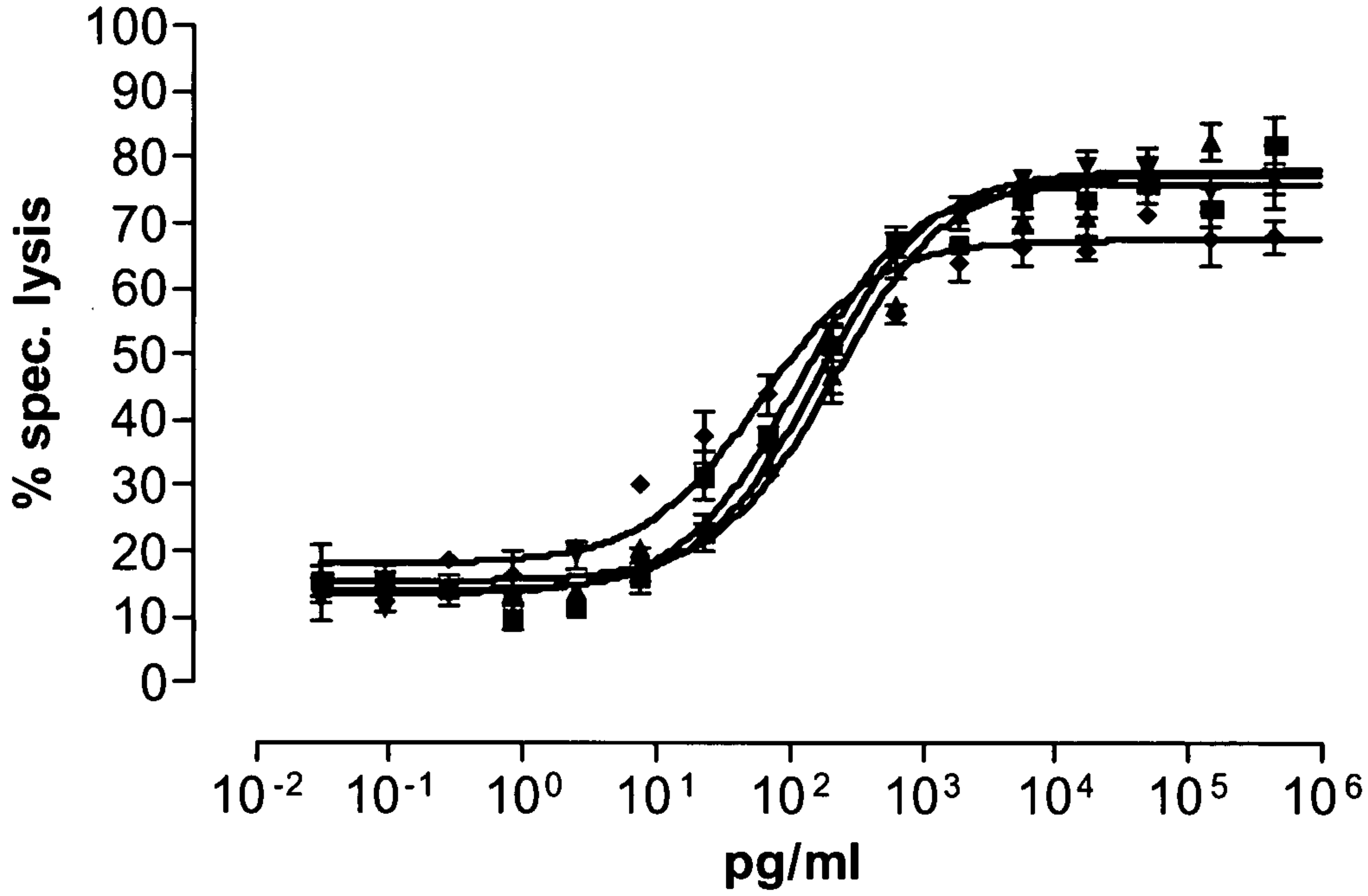


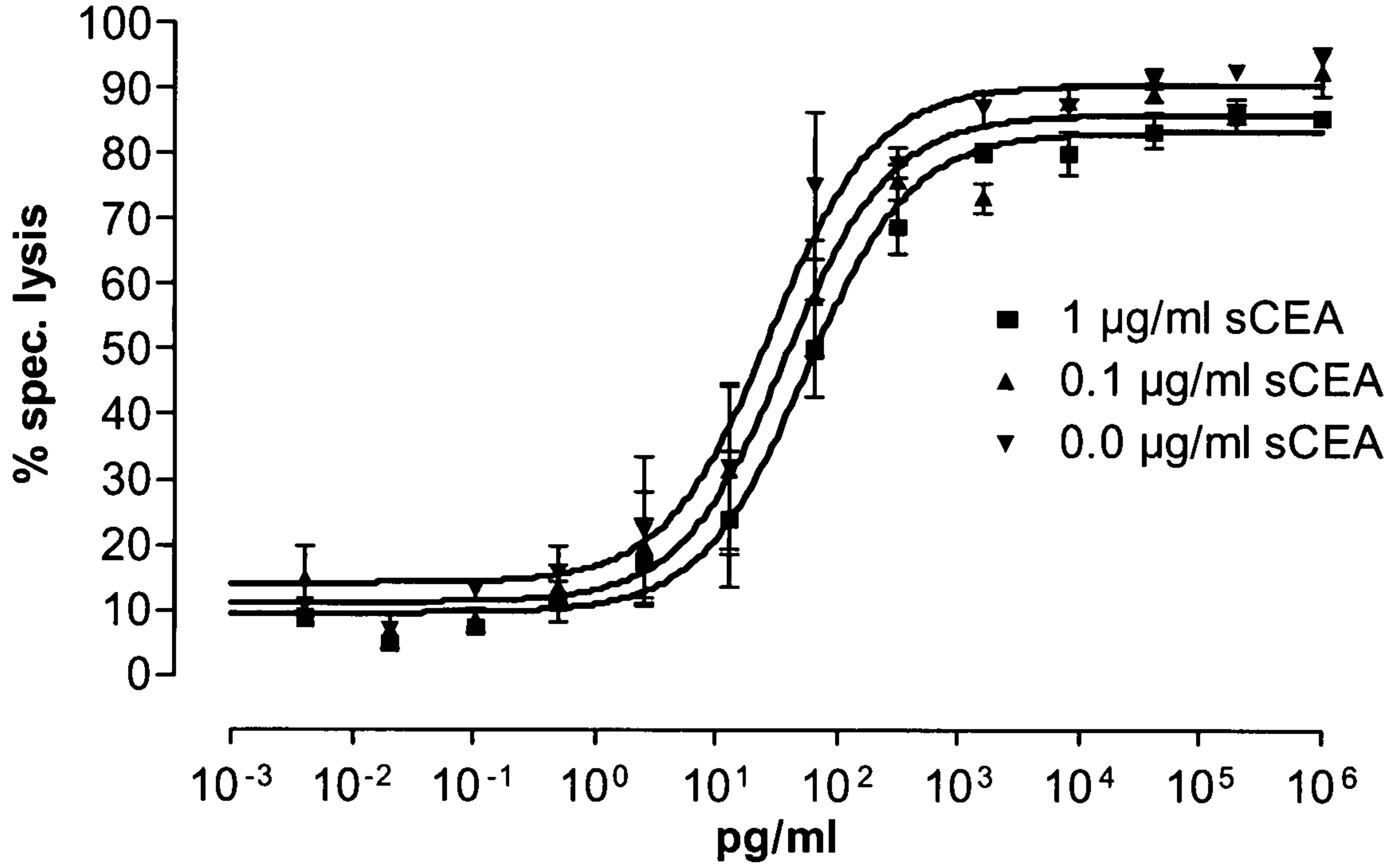
FIGURE 26

Protein stability testing of SEQ ID NO.77 VHVLxE12 VH–A240 VL in human plasma



	EC 50 [pg/ml]
■ Incubation for 24 h in plasma at 37 °C	**111.4**
▲ Incubation for 24 h in plasma at 4 °C	**214.0**
● Protein dilution immediately before the assay in RPMI	**159.5**
♦ Protein dilution immediately before the assay in plasma	**59.1**

FIGURE 27



Sol. CEA [µg/ml]	**0**	**0.1**	**1**
SEQ ID NO.77 VHVL x E12 VH - A240 VL EC50 [pg/ml]	28.2	37.6	55.3