metastatic tumor specimens (Kawakami et al., Wright et al., loc. cit.). Consistent with the elevated expression in androgen-independent tumors, PSMA transcription is also known to be downregulated by steroids, and administration of testosterone mediates a dramatic reduction in PSMA protein and mRNA levels (Israeli et al., Cancer Res. 54 (1994), 1807-11; Wright et al., loc. cit.). PSMA is also highly expressed in secondary prostatic tumors and occult metastatic disease. Immunohistochemical analysis has revealed relatively intense and homogeneous expression of PSMA within metastatic lesions localized to lymph nodes, bone, soft tissue, and lungs compared with benign prostatic tissues (Chang et al. (2001), loc. cit.; Murphy et al., Cancer 78 (1996), 809-818; Sweat et al., loc. cit.). Some reports have also indicated limited PSMA expression in extraprostatic tissues, including a subset of renal proximal tubules, some cells of the intestinal brush-border membrane, and rare cells in the colonic crypts (Chang et al. (1999), Horoszewicz et al., Israeli et al. (1994), Lopes et al., Troyer et al., loc. cit.). However, the levels of PSMA in these tissues are generally two to three orders of magnitude less than those observed in the prostate (Sokoloff et al., Prostate 43 (2000), 150-157). PSMA is also expressed in the tumor-associated neovasculature of most solid cancers examined yet is absent in the normal vascular endothelium (Chang et al. (1999), Liu et al., Silver et al., loc. cit.). Although the significance of PSMA expression within the vasculature is unknown, the specificity for tumor-associated endothelium makes PSMA a potential target for the treatment of many forms of malignancy.

SUMMARY

[5] All the half-life extending formats (HLE formats) of bispecific T cell engaging molecules described in the art, which included the hetero Fc (also designated as heterodimeric Fc, hetFc or hFc) format and the fusion of human serum albumin (also designated as HSA or hALB) had individual disadvantages such as unspecific T cell activation, complement activation, instability, or a pharmacokinetic profile which does not meet the desired half-life prolongation of the molecules. It is thus the object of the present invention to provide a half-life extending format of bispecific T cell engaging molecules, which overcomes at least one and, of course, preferably more than one of these individual defects observed for the state of the art molecules. Accordingly, the present invention provides antibody constructs of a specific Fc modality characterized by comprising a first domain binding to PSMA, a second domain binding to an extracellular epitope of the human and the *Macaca* CD3ε chain, and a third domain, which is the specific Fc modality as defined in the claims. Moreover, the invention provides a polynucleotide encoding the antibody construct, a vector comprising this polynucleotide, host cells expressing the construct and a pharmaceutical composition comprising the same as defined in the claims.

DESCRIPTION OF THE FIGURES

[5a] The invention will be described, by way of example only, and with reference to the accompanying figures, in which:

[6] **Figure 1**: FIG. 1a shows a diagram of one embodiment of an antibody construct of the invention. Fig. 1b shows a heterodimeric Fc antibody construct and Fig. 1c shows a X-body construct described in the art. The indicated charged pairs are introduced in order to enforce the heterodimerization. Fig 1d shows the fusion of an antibody construct with a human serum albumin (HSA / hALB).

[7] **Figure 2**: Evaluation of Target-independent T Cell Activation by Target A HLE BiTE® antibody constructs. 2(a) antibody construct of the invention in a 48 h activation assay with human PBMC (3x); HLE BiTE® serial dilutions (start 20 nM; 1:5, 7x+blank); w/o or with FcR blocking [10 mg/mL huIgG (Kiovog, Baxter)]; FACS measurement of CD69 and CD25 [not shown] expression on $CD4^+$, $CD8^+$ T cells. 2(b) Hetero-Fc antibody construct in 48 h activation assay with human PBMC and $CD14^+/CD33^+$ cell depleted PBMC (3x); HLE BiTE® serial dilutions (start 20 nM; 1:5, 7x+blank); FACS measurement of CD69 and CD25 [not shown] expression on $CD4^+$, $CD8^+$ T cells.

[8] **Figure 3**: Evaluation of Target-independent T Cell Activation by Target B HLE BiTE® antibody constructs. 3(a) antibody construct of the invention in a 48 h activation assay with human PBMC (3x); HLE BiTE® serial dilutions (start 20 nM; 1:5, 7x+blank); w/o or with FcR blocking [10 mg/mL huIgG (Kiovog, Baxter)]; FACS measurement of CD69 and CD25 [not shown] expression on $CD4^+$, $CD8^+$ T cells. 3(b) Hetero-Fc antibody construct in a 48 h activation assay with human PBMC and $CD14^+/CD33^+$ cell depleted PBMC (3x); HLE BiTE® serial dilutions (start 20 nM; 1:5, 7x+blank); FACS measurement of CD69 and CD25 [not shown] expression on $CD4^+$, $CD8^+$ T cells. 3(c) X-body construct in a 48 h activation assay with human PBMC and $CD14^+/CD33^+$ cell depleted PBMC (3x); HLE BiTE® serial dilutions (start 20 nM; 1:5, 7x+blank); FACS measurement of CD69 and CD25 [not shown] expression on $CD4^+$, $CD8^+$ T cells. 3(d) – 3(f) Isolated PBMC from three different healthy human donors were cultured with increasing concentrations of HLE bispecific antibody constructs specific for Target B antigens for 48 h. The expression of the activation marker CD69 on CD4+ and CD8+ T cells was determined by flow cytometric analysis using a PE-Cy7 conjugated mab specific for CD69.

[9] **Figure 4**: Complement C1q Binding of BiTE® Fc fusion antibody constructs. BiTE® Fc fusion antibody constructs (BiTE® single chain Fc (triangle), BiTE® hetero Fc (squares), canonical BiTE® (circle)) were coated on a Maxisorp plate (in dilution series), prior to incubation with pooled human serum and incubation with polyclonal anti-human CC1q murine antibody, visualized by goat anti-mouse Fc-AP conjugate.

[10] **Figure 5**: Mean PK profiles of two different PSMA BiTE®-HLE antibody constructs after single dose administration in cynomolgus monkeys. For reasons of comparability, serum concentrations were dose-normalized to 15 µg/kg and indicated in nmol.

[82] In line with this invention either the first, the second or the first and the second domain may comprise a single domain antibody, respectively the variable domain or at least the CDRs of a single domain antibody. Single domain antibodies comprise merely one (monomeric) antibody variable domain which is able to bind selectively to a specific antigen, independently of other V regions or domains. The first single domain antibodies were engineered from heavy chain antibodies found in camelids, and these are called V_HH fragments. Cartilaginous fishes also have heavy chain antibodies (IgNAR) from which single domain antibodies called V_{NAR} fragments can be obtained. An alternative approach is to split the dimeric variable domains from common immunoglobulins *e.g.* from humans or rodents into monomers, hence obtaining VH or VL as a single domain Ab. Although most research into single domain antibodies is currently based on heavy chain variable domains, nanobodies derived from light chains have also been shown to bind specifically to target epitopes. Examples of single domain antibodies are called sdAb, nanobodies or single variable domain antibodies.

[83] A (single domain mAb)$_2$ is hence a monoclonal antibody construct composed of (at least) two single domain monoclonal antibodies, which are individually selected from the group comprising V_H, V_L, V_HH and V_{NAR}. The linker is preferably in the form of a peptide linker. Similarly, an “scFv-single domain mAb” is a monoclonal antibody construct composed of at least one single domain antibody as described above and one scFv molecule as described above. Again, the linker is preferably in the form of a peptide linker.

[84] Whether or not an antibody construct competes for binding with another given antibody construct can be measured in a competition assay such as a competitive ELISA or a cell-based competition assay. Avidin-coupled microparticles (beads) can also be used. Similar to an avidin-coated ELISA plate, when reacted with a biotinylated protein, each of these beads can be used as a substrate on which an assay can be performed. Antigen is coated onto a bead and then precoated with the first antibody. The second antibody is added and any additional binding is determined. Possible means for the read-out includes flow cytometry.

[85] T cells or T lymphocytes are a type of lymphocyte (itself a type of white blood cell) that play a central role in cell-mediated immunity. There are several subsets of T cells, each with a distinct function. T cells can be distinguished from other lymphocytes, such as B cells and NK cells, by the presence of a T cell receptor (TCR) on the cell surface. The TCR is responsible for recognizing antigens bound to major histocompatibility complex (MHC) molecules and is composed of two different protein chains. In 95% of the T cells, the TCR consists of an alpha (α) and beta (β) chain. When the TCR engages with antigenic peptide and MHC (peptide / MHC complex), the T lymphocyte is activated through a series of

acid sequence modifications should result in an antibody construct which still retains the desired biological activity (binding to PSMA and to CD3) of the unmodified parental molecule.

[130] The term “amino acid” or “amino acid residue” typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (GIn or Q); glutamic acid (GIu or E); glycine (GIy or G); histidine (His or H); isoleucine (He or I): leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); pro line (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V), although modified, synthetic, or rare amino acids may be used as desired. Generally, amino acids can be grouped as having a nonpolar side chain (e.g., Ala, Cys, He, Leu, Met, Phe, Pro, Val); a negatively charged side chain (e.g., Asp, GIu); a positively charged sidechain (e.g., Arg, His, Lys); or an uncharged polar side chain (e.g., Asn, Cys, GIn, GIy, His, Met, Phe, Ser, Thr, Trp, and Tyr).

[131] Amino acid modifications include, for example, deletions from, and/or insertions into, and/or substitutions of, residues within the amino acid sequences of the antibody constructs. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the antibody constructs, such as changing the number or position of glycosylation sites.

[132] For example, 1, 2, 3, 4, 5, or 6 amino acids may be inserted, substituted or deleted in each of the CDRs (of course, dependent on their length), while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be inserted, substituted or deleted in each of the FRs. Preferably, amino acid sequence insertions into the antibody construct include amino- and/or carboxyl-terminal fusions ranging in length from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 residues to polypeptides containing a hundred or more residues, as well as intra-sequence insertions of single or multiple amino acid residues. Corresponding modifications may also performed within the third domain of the antibody construct of the invention. An insertional variant of the antibody construct of the invention includes the fusion to the N-terminus or to the C-terminus of the antibody construct of an enzyme or the fusion to a polypeptide.

[133] The sites of greatest interest for substitutional mutagenesis include (but are not limited to) the CDRs of the heavy and/or light chain, in particular the hypervariable regions, but FR alterations in the heavy and/or light chain are also contemplated. The substitutions are preferably conservative substitutions as described herein. Preferably, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids may be substituted in a CDR, while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12,

into the peritoneal cavity of the animals. Mice of vehicle control group 1 do not receive effector cells and are used as an untransplanted control for comparison with vehicle control group 2 (receiving effector cells) to monitor the impact of T cells alone on tumor growth. The antibody treatment starts when the mean tumor volume reaches about 200 mm^3. The mean tumor size of each treatment group on the day of treatment start should not be statistically different from any other group (analysis of variance). Mice are treated with 0.5 mg/kg/day of a PSMAxCD3 bispecific antibody construct by intravenous bolus injection for about 15 to 20 days. Tumors are measured by caliper during the study and progress evaluated by intergroup comparison of tumor volumes (TV). The tumor growth inhibition T/C [%] is determined by calculating TV as T/C% = 100 x (median TV of analyzed group) / (median TV of control group 2).

[159] The skilled person knows how to modify or adapt certain parameters of this study, such as the number of injected tumor cells, the site of injection, the number of transplanted human T cells, the amount of bispecific antibody constructs to be administered, and the timelines, while still arriving at a meaningful and reproducible result. Preferably, the tumor growth inhibition T/C [%] is ≤ 70 or ≤ 60, more preferably ≤ 50 or ≤ 40, even more preferably ≤ 30 or ≤ 20 and most preferably ≤ 10 or ≤ 5 or even ≤ 2.5.

[160] In a preferred embodiment of the antibody construct of the invention the antibody construct is a single chain antibody construct.

[161] Also in a preferred embodiment of the antibody construct of the invention said third domain comprises in an amino to carboxyl order:

hinge-CH2-CH3-linker-hinge-CH2-CH3.

[162] In one embodiment of the invention each of said polypeptide monomers of the third domain has an amino acid sequence that is at least 90% identical to a sequence selected from the group consisting of: SEQ ID NO: 17-24. In a preferred embodiment or the invention each of said polypeptide monomers has an amino acid sequence selected from SEQ ID NO: 17-24.

[163] Also in one embodiment of the invention the CH2 domain of one or preferably each (both) polypeptide monomers of the third domain comprises an intra domain cysteine disulfide bridge. As known in the art the term “cysteine disulfide bridge” refers to a functional group with the general structure *R–**S**–**S**–R*. The linkage is also called an SS-bond or a disulfide bridge and is derived by the coupling of two thiol groups of cysteine residues. It is particularly preferred for the antibody construct of the invention that the cysteines forming the

antibody directed against the CD3-binding part of the construct was used for detection. The serum concentration-time profiles were used to determine PK parameters.

Blood sampling time points are listed for both study designs in Table 5 below.

Table 5 Blood sampling time points during PK studies.

blood sampling time points: HLE antibody construct; [h] after start of infusion	blood sampling time points: canonical antibody construct; [h] after start of infusion
0.085	167.76
0.25	168.96
0.5	172.08
1	175.92
4	180.00
8	192.00
24	
48	
72	
168	
240	
336	

The pharmacokinetics of the two BiTE® antibody constructs are shown exemplarily in Figure 5. Each compound group stands for the same BiTE® antibody construct either fused to a scFc half-life extending moiety or left as canonical molecule. For all proteins serum levels were quantifiable for all time points in all animals after BiTE®-HLE antibody construct administration. The pharmacokinetic parameters were determined using standard non-compartmental analysis (NCA) methods. Using non compartmental analysis, the following PK parameters were estimated: AUC_{inf} (Area under the serum concentration- time curve), Vss (volume of distribution at steady state), CL (systemic clearance) and terminal $t_{1/2}$ (terminal half-life).

The PK parameter for each tested compound are summarized as mean of n=2 in Table–6 below.

Table 6 Pharmacokinetic parameter of two PSMA targeting BiTE® antibody constructs tested in cynomolgus monkeys.

test item	terminal $t_{1/2}$ [h]	AUC_{inf} [normalized to 15 µg/kg] [h*ng/mL]	Cl [mL/h/kg]	Vss [mL/kg]

[283] Additionally, samples derived from heat stress in absence and presence of silicon were assessed for the abundance of subvisible particles by Microfluid Imaging (MFI) using a Flowcam from Fluid Imaging Technologies, Inc. The instrument was equipped with a FC80FV flow cell. A tenfold optical magnification was applied. System suitability was verified with particle free water. An autoimage rate of 20 frames per second was applied. Dark and light thresholds were set to 25 and 20 pixels respectively. Sample volume for a single measurement totals 0.25 mL. Samples were measured in triplicates. Prior to each triplicate the system was flushed of 0.5 mL of the respective sample solutions. At the beginning and between each triplicate a wash with 1.0 mL particle free water was performed. Data evaluation was performed with Visual Spreadsheet software. Samples were measured in triplicates. Results are outlined in Table 25.

Heat stress resulted in subvisible particle formation in preparations containing non HLE and hALB constructs. In contrast, the scFc construct remained stable. Subvisible particle formation was not promoted by the addition of silicon independent on the nature of the BiTE® antibody construct.

Table 25: Assessment of subvisible particles by MFI in Target F-non HLE (canonical), -hALB, and –scFc preparations after heat stress in absence and presence of silicon.

Construct	**Non HLE (canonical)**				**hALB**				**scFc**			
Particle size [µm]	≥ 2	≥ 5	≥ 10	≥ 25	≥ 2	≥ 5	≥ 10	≥ 25	≥ 2	≥ 5	≥ 10	≥ 25
T0	146	35	12	0	281	71	35	0	298	150	33	0
4w 37°C	410	163	23	0	742	225	11	0	110	44	0	0
4w 37°C (25 ppm silicon)	69	35	11	0	272	91	34	0	146	55	11	0

Samples from heat stress were also analyzed by Weak Cation Exchange (WCX) chromatography in order to quantify the percentaged content of charge variants using a UPLC Aquity H class from Waters. A Protein-Pak Hi Res CM 7ìm 4.6 x 100 mm column (Waters, cat No. 186004929) was applied. The column temperature was adjusted to 30°C. The flow rate was set to 0.65 mL/min. The applied gradient was designed as follows (**Table 26**). The temperature of the autosampler was kept at 2-8°C.

Table 26: Gradient applied for WCX chromatography

Time [min:sec]	% A 20 mM sodium phosphate, pH 6.5	% B 20 mM sodium phosphate, 250 mM sodium chloride, pH 6.5
00:00	100	0
04:00	100	0
25:00	50	50
25:01	0	100
29:00	0	100
29:01	100	0
33:00	100	0

[284] A total amount of 3 µg of protein was injected. Detection was based on fluorescence (excitation at 280 nm, emission at 325 nm). Peak integration was performed using Empower® software. Relative areas under the curve of the main peak as well as of acidic and basic charge variants was reported (**Table 27**).

Heat stress resulted in a reduced main peak percentage which had to be attributed to a predominant formation of acidic charge variants. The loss in main peak percentage was least pronounced for the scFc construct (7.5%). Basic charge variants were formed in both constructs with extended half-life upon light exposure. The increase in basic charge variants ranged between 5 and 6% in hALB and scFc constructs.

Table 27: Assessment of charge variants by WCX chromatography in Target F-non HLE (canonical), -hALB, and –scFc preparations after heat and light induced stress.

Construct	Non HLE (canonical)			hALB			scFc		
Fraction	% main	% acidics	% basics	% main	% acidics	% basics	% main	% acidics	% basics
T0	89.9	3.6	6.5	83.3	0.7	16.0	74.5	3.4	22.1
4w 37°C	79.3	11.1	9.5	75.6	9.8	14.6	67.0	11.2	21.8

In addition, sample purity was quantified in heat and light stressed samples using a microfluidic capillary electrophoresis sodium dodecylsulphate (CE-SDS) assay based

In addition, sample purity was quantified in heat and light stressed samples using a microfluidic capillary electrophoresis sodium dodecylsulphate (CE-SDS) assay based on the LabChip GXII system (Perkin Elmer) according to the method described under **Example 14**. An overview on the percentaged purity detected post stress is given by **Table 33** and compared to unstressed samples (T0).

Higher purities were observed for the scFc construct if compared to the non HLE construct irrespective of the stress conditions. Hence, as exemplified hereby, scFc antibody constructs are more stable over a broad array of stress conditions than non-HLE antibody constructs and, thus, safer and better suited for versatile clinical employment with ever changing stress conditions in practice.

Table 33: Overview on percentaged purity in stressed and unstressed (T0) PSMA-non HLE, and -scFc preparations determined via LabChip GXII.

Construct	Non-HLE (canonical)	scFc
T0	89.2	100.0
4w 37°C	85.4	87.3
Light exposure	89.5	93.8

[287] Example 17

Different BiTE® antibody constructs designed for targeting Target B including Target B-Xbody and Target B-scFc were examined. The target protein concentration was 1.0 mg/mL. Formulated BiTE® antibody constructs were filled to 1 mL in type I glass vials which were stoppered with butyl rubber stoppers and crimped with aluminum seals. Filled vials were incubated at -20°C and 37°C for 4 weeks. Additionally, all samples were exposed to 1.2 MLux visible light and 173 W*h/m^2 UVA light. Chamber temperature was adjusted to 25°C. Samples stored at -70°C served as controls (T0). Samples stored at -20 and -37°C were analyzed by SE-UPLC according to the method described under **Example 14**. Results are outlined in **Table 34**.

The scFc construct preserved a higher monomer content when stored for four weeks at -20 and 37°C respectively if compared to the Xbody.

Table 34: Overview on monomer contents in stressed and unstressed (T0) Target B-Xbody and -scFc preparations determined via SE-UPLC.

Construct	Xbody	scFc
T0	100.0	98.8
4w -20°C	97.1	97.9
4w 37°C	94.5	95.7

Additionally, unstressed samples were assessed for the abundance of subvisible particles by Microfluid Imaging (MFI) using the method described under **Example 14**. Results are outlined in **Table 35**. The CD19-scFc preparation exhibited significantly lower amounts of subvisible particles if compared to the CD19-Xbody preparation. This applies to all included size fractions.

Table 35: Assessment of subvisible particles by MFI in unstressed Target B-Xbody and -scFc

Construct	Xbody				scFc			
Particle size [µm]	≥ 2	≥ 5	≥ 10	≥ 25	≥ 2	≥ 5	≥ 10	≥ 25
T0	2648	688	192	32	160	64	43	11

Samples from light stress were also analyzed by Weak Cation Exchange (WCX) chromatography in order to quantify the percentaged content of charge variants using a UPLC Aquity H class from Waters according to the method described under **Example 14**. Relative areas under the curve of the main peak as well as of acidic and basic charge variants was reported (**Table 36**).

Table 36: Assessment of charge variants by WCX chromatography in Target B-Xbody and -scFc preparations after heat and light induced stress.

Construct	Xbody			scFc		
Fraction	% main	% acidics	% basics	% main	% acidics	% basics
T0	51.4	30.3	18.3	83.5	1.3	15.2
Light exposure	45.9	33.2	20.9	82.1	1.2	16.7

The scFc construct showed surprisingly enhanced stability against light exposure if compared to the Xbody indicated by a less pronounced loss in main peak which totaled 1.4%

[290] Example 20: Surface Plasmon Resonance-based determination of binding to human FcRn (FCGRT/B2M)

The constructs D9F, T2G, D3L, T7I and K6C and a human IgG1-kappa antibody MT201 were each tested for their capability of binding against human FcRn in SPR (Biacore) experiments according to standard procedures. In detail, CM5 Sensor Chips (GE Healthcare) were immobilized with around 350 RU of FCGRT/B2M (ACRO Biosystems) by using Na acetate buffer pH 4.5 and a running buffer consisting of 200 mM HEPES, 150 mM NaCl, 3 mM EDTA pH 6.0. The constructs and the human IgG1-kappa control (MT201) were then injected at a concentration of 125 nM diluted in 200 mM HEPES, 150 mM NaCl, 3 mM EDTA, pH 6.0 and 36°C. Association was done for 90 seconds with a 30 µl/min flow rate followed by the dissociation phase for 60 seconds at a 30 µl/min flow rate in 200 mM HEPES, 150 mM NaCl, 3 mM EDTA, pH 6.0 at 36°C. Subsequent regeneration was done for 10 sec with 30 µl/min with 10 mM HEPES, 150 mM NaCl, 3 mM EDTA pH 7.4.

The maximal binding during the injection phase was measured for all constructs as the respective response units (RU), equivalent to the molecular mass increase on the FcRn coated CM5 chip due to bound construct. All constructs were measured in duplicates. Average values of the duplicate determinations are depicted in Figure 8 including standard deviation error bars.

As a result, construct D9F shows significantly higher mass increase on the FcRn coated CM5 chip, as compared to T2G, D3L, T7I and K6C, which indicates stronger binding affinity of D9F to human FcRn. The mass increase on the FcRn-coated CM5 chip for D9F is well comparable to the mass increase of the human IgG1-kappa control antibody MT201, indicating a comparable binding of construct D9F to human FcRn.

The binding against FcRn is mediated through the human IgG1 Fc portion within the constructs. Stronger binding against human FcRn as described in the field is an indicator for longer half-life in vivo due to a higher intracellular rescue of the respective protein and a therefore reduced degradation rate. For this reason, stronger binding of D9F to human FcRn in the range of a human IgG1-kappa antibody (MT201), as compared to the other constructs makes this molecule clearly superior as a basis for therapeutic molecules to allow for longer exposure of the potential drug in the patient, presumably in the range of a full human IgG1antibody, and a lower frequency of drug administration.

Table 38: Sequence Table

The following Table describes the peptides and proteins having SEQ ID NO: 1-487, as well as those having SEQ ID NO: 488-586, corresponding to sequences of WO 2008/119567.

SEQ ID NO:	Designation	Format / Source	Sequence

			ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGGGGSGGGGSGGGGSGGGGSDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGG GGSGGGGSGGGGSGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK
484.	EGFRvIIIccxI2C- Hinge-CH2-linker-CH2-CH3-linker-CH3 (T7I)	bispecific HLE molecule	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLE WVAVIWYDGSDKYYADSVRGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCARDGYDILTGNPRDFDYWGQGTLVTVSSGGGGSGGGGSGGGG SDTVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRP GQPPRLLIYRISRRFSGVPDRFSGSGAGTDFTLEISRVEAEDVGVY YCMQSTHVPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGGGGSGGGGSGGGG SGGGGSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGG GGSGGGGSGGGGSGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK
485.	EGFRvIIIccxI2C-CH2-linker-CH2-CH3-linker-CH3 (K6C)	bispecific HLE molecule	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLE WVAVIWYDGSDKYYADSVRGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCARDGYDILTGNPRDFDYWGQGTLVTVSSGGGGSGGGGSGGGG SDTVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRP GQPPRLLIYRISRRFSGVPDRFSGSGAGTDFTLEISRVEAEDVGVY YCMQSTHVPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGGGGSGGGGSGGGGSGGGGSAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGG GGSGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
486.	IgG3 hinge		ELKTPLGDTTHTCPRCP
487.	IgG1 hinge		EPKSCDKTHTCPPCP
488.	SEQ ID NO: 27 of WO 2008/11956	VL CDR1	GSSTGAVTSGYYPN

	7 CD3ε binder		
489.	SEQ ID NO: 28 of WO 2008/119567 CD3ε binder	VL CDR2	GTKFLAP
490.	SEQ ID NO: 29 of WO 2008/119567 CD3ε binder	VL CDR3	ALWYSNRWV
491.	SEQ ID NO: 117 of WO 2008/119567 CD3ε binder	VL CDR1	RSSTGAVTSGYYPN
492.	SEQ ID NO: 118 of WO 2008/119567 CD3ε binder	VL CDR2	ATDMRPS
493.	SEQ ID NO: 119 of WO 2008/119567 CD3ε binder	VL CDR3	ALWYSNRWV
494.	SEQ ID NO: 153 of WO 2008/119567 CD3ε binder	VL CDR1	GSSTGAVTSGNYPN
495.	SEQ ID NO: 154 of WO 2008/119567 CD3ε binder	VL CDR2	GTKFLAP
496.	SEQ ID NO: 155 of WO 2008/119567 CD3ε binder	VL CDR3	VLWYSNRWV
497.	SEQ ID NO: 12 of WO 2008/119567 CD3ε binder	VH CDR1	IYAMN
498.	SEQ ID NO: 13 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKS

499.	SEQ ID NO: 14 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYVSFFAY
500.	SEQ ID NO: 30 of WO 2008/119567 CD3ε binder	VH CDR1	KYAMN
501.	SEQ ID NO: 31 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKD
502.	SEQ ID NO: 32 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYISYWAY
503.	SEQ ID NO: 48 of WO 2008/119567 CD3ε binder	VH CDR1	SYAMN
504.	SEQ ID NO: 49 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKG
505.	SEQ ID NO: 50 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYLSFWAY
506.	SEQ ID NO: 66 of WO 2008/119567 CD3ε binder	VH CDR1	RYAMN
507.	SEQ ID NO: 67 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKG
508.	SEQ ID NO: 68 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYLSYFAY
509.	SEQ ID NO: 84 of WO	VH CDR1	VYAMN

	2008/119567 CD3ε binder		
510.	SEQ ID NO: 85 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKK
511.	SEQ ID NO: 86 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYLSWWAY
512.	SEQ ID NO: 102 of WO 2008/119567 CD3ε binder	VH CDR1	KYAMN
513.	SEQ ID NO: 103 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKS
514.	SEQ ID NO: 104 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYTSYYAY
515.	SEQ ID NO: 120 of WO 2008/119567 CD3ε binder	VH CDR1	GYAMN
516.	SEQ ID NO: 121 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKE
517.	SEQ ID NO: 122 of WO 2008/119567 CD3ε binder	VH CDR3	HRNFGNSYLSWFAY
518.	SEQ ID NO: 138 of WO 2008/119567 CD3ε binder	VH CDR1	VYAMN
519.	SEQ ID NO: 139 of WO 2008/11956	VH CDR2	RIRSKYNNYATYYADSVKK

	7 CD3ε binder		
520.	SEQ ID NO: 140 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYISWWAY
521.	SEQ ID NO: 156 of WO 2008/119567 CD3ε binder	VH CDR1	SYAMN
522.	SEQ ID NO: 157 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKG
523.	SEQ ID NO: 158 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYVSWWAY
524.	SEQ ID NO: 174 of WO 2008/119567 CD3ε binder	VH CDR1	KYAMN
525.	SEQ ID NO: 175 of WO 2008/119567 CD3ε binder	VH CDR2	RIRSKYNNYATYYADSVKD
526.	SEQ ID NO: 176 of WO 2008/119567 CD3ε binder	VH CDR3	HGNFGNSYISYWAY
527.	SEQ ID NO: 17 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
528.	SEQ ID NO: 21 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
529.	SEQ ID NO: 15 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSS

530.	SEQ ID NO: 19 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSS
531.	SEQ ID NO: 35 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
532.	SEQ ID NO: 39 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
533.	SEQ ID NO: 33 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
534.	SEQ ID NO: 37 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
535.	SEQ ID NO: 53 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
536.	SEQ ID NO: 57 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
537.	SEQ ID NO: 51 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSS
538.	SEQ ID NO: 55 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSS
539.	SEQ ID NO: 71 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL

540.	SEQ ID NO: 75 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
541.	SEQ ID NO: 69 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSS
542.	SEQ ID NO: 73 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSS
543.	SEQ ID NO: 89 of WO 2008/119567 CD3ε binder	VL	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSS
544.	SEQ ID NO: 93 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAP RGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
545.	SEQ ID NO: 87 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSS
546.	SEQ ID NO: 91 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSS
547.	SEQ ID NO: 107 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
548.	SEQ ID NO: 111 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
549.	SEQ ID NO: 105 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSS

550.	SEQ ID NO: 109 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSS
551.	SEQ ID NO: 125 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAP RGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
552.	SEQ ID NO: 129 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAP RGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
553.	SEQ ID NO: 123 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKERFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSS
554.	SEQ ID NO: 127 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKERFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSS
555.	SEQ ID NO: 143 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
556.	SEQ ID NO: 147 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
557.	SEQ ID NO: 141 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSS
558.	SEQ ID NO: 145 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSS
559.	SEQ ID NO: 161 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL

560.	SEQ ID NO: 165 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
561.	SEQ ID NO: 159 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSS
562.	SEQ ID NO: 163 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSS
563.	SEQ ID NO: 179 of WO 2008/119567 CD3ε binder	VL	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
564.	SEQ ID NO: 183 of WO 2008/119567 CD3ε binder	VL	ELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
565.	SEQ ID NO: 177 of WO 2008/119567 CD3ε binder	VH	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
566.	SEQ ID NO: 181 of WO 2008/119567 CD3ε binder	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
567.	SEQ ID NO: 23 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
568.	SEQ ID NO: 25 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
569.	SEQ ID NO: 41 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ

			APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
570.	SEQ ID NO: 43 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
571.	SEQ ID NO: 59 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
572.	SEQ ID NO: 61 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
573.	SEQ ID NO: 77 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
574.	SEQ ID NO: 79 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
575.	SEQ ID NO: 95 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQ APRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
576.	SEQ ID NO: 97 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQ APRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
577.	SEQ ID NO: 113 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
578.	SEQ ID NO: 115 of WO	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTED

	2008/119567 CD3ε binder		TAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
579.	SEQ ID NO: 131 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKERFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQ APRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
580.	SEQ ID NO: 133 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKERFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQ APRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
581.	SEQ ID NO: 149 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVLV
582.	SEQ ID NO: 151 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
583.	SEQ ID NO: 167 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
584.	SEQ ID NO: 169 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
585.	SEQ ID NO: 185 of WO 2008/119567 CD3ε binder	scFv	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
586.	SEQ ID NO: 187 of WO 2008/119567 CD3ε binder	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL

Claims

1. A single chain antibody construct comprising in an amino to carboxyl order:
   - a first domain which binds to PSMA,
   - a second domain which binds to an extracellular epitope of the human and the *Macaca* CD3ε chain; and
   - a third domain which comprises two Fc monomers, each Fc monomer comprising a hinge, a CH2 domain and a CH3 domain, wherein said two Fc monomers are fused to each other via a peptide linker, wherein said third domain comprises in an amino to carboxyl order:

     hinge-CH2-CH3-linker-hinge-CH2-CH3.

2. The antibody construct of claim 1, wherein each of said Fc monomers of the third domain has an amino acid sequence that is at least 90% identical to a sequence selected from the group consisting of SEQ ID NOs: 17-24.

3. The antibody construct of claim 2, wherein each of said Fc monomers of the third domain has an amino acid sequence selected from SEQ ID NOs: 17-24.

4. The antibody construct of claim 3, wherein each of said polypeptide monomers of the third domain comprises the amino acid sequence of SEQ ID NO: 17.

5. The antibody construct of any one of the preceding claims, wherein the CH2 domain comprises an intra domain cysteine disulfide bridge.

6. The antibody construct of any one of the preceding claims, wherein:

   (i) the first domain comprises two antibody variable domains and the second domain comprises two antibody variable domains;

(ii) the first domain comprises one antibody variable domain and the second domain comprises two antibody variable domains;

(iii) the first domain comprises two antibody variable domains and the second domain comprises one antibody variable domain; or

(iv) the first domain comprises one antibody variable domain and the second domain comprises one antibody variable domain.

7. The antibody construct of any one of the preceding claims, wherein the first and second domain are fused to the third domain via a peptide linker.

8. The antibody construct of any one of the preceding claims, wherein the antibody construct comprises in an amino to carboxyl order:

(a) the first domain;

(b) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-3;

(c) the second domain;

(d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 9, 10, 11 and 12;

(e) the first Fc monomer of the third domain;

(f) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 6, 7 and 8; and

(g) the second Fc monomer of the third domain.

9. The antibody construct according to any one of the preceding claims, wherein the first binding domain of the antibody construct comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3, and a VH region comprising CDR-H1, CDR-H2 and CDR-H3 selected from the group consisting of:

(a) CDR-L1 as depicted in SEQ ID NO: 45, CDR-L2 as depicted in SEQ ID NO: 46, CDR-L3 as depicted in SEQ ID NO: 47, CDR-H1 as depicted in SEQ ID NO: 42, CDR-H2 as depicted in SEQ ID NO: 43, and CDR-H3 as depicted in SEQ ID NO: 44;

(b) CDR-L1 as depicted in SEQ ID NO: 63, CDR-L2 as depicted in SEQ ID NO: 64, CDR-L3 as depicted in SEQ ID NO: 65, CDR-H1 as depicted in SEQ ID NO: 60, CDR-H2 as depicted in SEQ ID NO: 61, and CDR-H3 as depicted in SEQ ID NO: 62;

(c) CDR-L1 as depicted in SEQ ID NO: 81, CDR-L2 as depicted in SEQ ID NO: 82, CDR-L3 as depicted in SEQ ID NO: 83, CDR-H1 as depicted in SEQ ID NO: 78, CDR-H2 as depicted in SEQ ID NO: 79, and CDR-H3 as depicted in SEQ ID NO: 80;

(d) CDR-L1 as depicted in SEQ ID NO: 99, CDR-L2 as depicted in SEQ ID NO: 100, CDR-L3 as depicted in SEQ ID NO: 101, CDR-H1 as depicted in SEQ ID NO: 96, CDR-H2 as depicted in SEQ ID NO: 97, and CDR-H3 as depicted in SEQ ID NO: 98;

(e) CDR-L1 as depicted in SEQ ID NO: 117, CDR-L2 as depicted in SEQ ID NO: 118, CDR-L3 as depicted in SEQ ID NO: 119, CDR-H1 as depicted in SEQ ID NO: 114, CDR-H2 as depicted in SEQ ID NO: 115, and CDR-H3 as depicted in SEQ ID NO: 116;

(f) CDR-L1 as depicted in SEQ ID NO: 135, CDR-L2 as depicted in SEQ ID NO: 136, CDR-L3 as depicted in SEQ ID NO: 137, CDR-H1 as depicted in SEQ ID NO: 132, CDR-H2 as depicted in SEQ ID NO: 133, and CDR-H3 as depicted in SEQ ID NO: 134;

(g) CDR-L1 as depicted in SEQ ID NO: 153, CDR-L2 as depicted in SEQ ID NO: 154, CDR-L3 as depicted in SEQ ID NO: 155, CDR-H1 as depicted in SEQ ID NO: 150, CDR-H2 as depicted in SEQ ID NO: 151, and CDR-H3 as depicted in SEQ ID NO: 152;

(h) CDR-L1 as depicted in SEQ ID NO: 171, CDR-L2 as depicted in SEQ ID NO: 172, CDR-L3 as depicted in SEQ ID NO: 173, CDR-H1 as depicted in SEQ ID NO: 168, CDR-H2 as depicted in SEQ ID NO: 169, and CDR-H3 as depicted in SEQ ID NO: 170;

(i) CDR-L1 as depicted in SEQ ID NO: 189, CDR-L2 as depicted in SEQ ID NO: 190, CDR-L3 as depicted in SEQ ID NO: 191, CDR-H1 as depicted in SEQ ID NO: 186, CDR-H2 as depicted in SEQ ID NO: 187, and CDR-H3 as depicted in SEQ ID NO: 188;

(j) CDR-L1 as depicted in SEQ ID NO: 207, CDR-L2 as depicted in SEQ ID NO: 208, CDR-L3 as depicted in SEQ ID NO: 209, CDR-H1 as depicted in SEQ ID NO: 204, CDR-H2 as depicted in SEQ ID NO: 205, and CDR-H3 as depicted in SEQ ID NO: 206;

(k) CDR-L1 as depicted in SEQ ID NO: 225, CDR-L2 as depicted in SEQ ID NO: 226, CDR-L3 as depicted in SEQ ID NO: 227, CDR-H1 as depicted in SEQ ID NO: 222, CDR-H2 as depicted in SEQ ID NO: 223, and CDR-H3 as depicted in SEQ ID NO: 224;

(l) CDR-L1 as depicted in SEQ ID NO: 243, CDR-L2 as depicted in SEQ ID NO: 244, CDR-L3 as depicted in SEQ ID NO: 245, CDR-H1 as depicted in SEQ ID NO: 240, CDR-H2 as depicted in SEQ ID NO: 241, and CDR-H3 as depicted in SEQ ID NO: 242;

(m) CDR-L1 as depicted in SEQ ID NO: 261, CDR-L2 as depicted in SEQ ID NO: 262, CDR-L3 as depicted in SEQ ID NO: 263, CDR-H1 as depicted in SEQ ID NO: 258, CDR-H2 as depicted in SEQ ID NO: 259, and CDR-H3 as depicted in SEQ ID NO: 260;

(n) CDR-L1 as depicted in SEQ ID NO: 279, CDR-L2 as depicted in SEQ ID NO: 280, CDR-L3 as depicted in SEQ ID NO: 281, CDR-H1 as depicted in SEQ ID NO: 276, CDR-H2 as depicted in SEQ ID NO: 277, and CDR-H3 as depicted in SEQ ID NO: 278;

(o) CDR-L1 as depicted in SEQ ID NO: 297, CDR-L2 as depicted in SEQ ID NO: 298, CDR-L3 as depicted in SEQ ID NO: 299, CDR-H1 as depicted in SEQ ID NO: 294, CDR-H2 as depicted in SEQ ID NO: 295, and CDR-H3 as depicted in SEQ ID NO: 296;

(p) CDR-L1 as depicted in SEQ ID NO: 315, CDR-L2 as depicted in SEQ ID NO: 316, CDR-L3 as depicted in SEQ ID NO: 317, CDR-H1 as depicted in SEQ ID NO: 312, CDR-H2 as depicted in SEQ ID NO: 313, and CDR-H3 as depicted in SEQ ID NO: 314;

(q) CDR-L1 as depicted in SEQ ID NO: 330, CDR-L2 as depicted in SEQ ID NO: 331, CDR-L3 as depicted in SEQ ID NO: 332, CDR-H1 as depicted in SEQ ID NO: 327, CDR-H2 as depicted in SEQ ID NO: 328, and CDR-H3 as depicted in SEQ ID NO: 329;

(r) CDR-L1 as depicted in SEQ ID NO: 345, CDR-L2 as depicted in SEQ ID NO: 346, CDR-L3 as depicted in SEQ ID NO: 347, CDR-H1 as depicted in SEQ ID NO: 342, CDR-H2 as depicted in SEQ ID NO: 343, and CDR-H3 as depicted in SEQ ID NO: 344;

(s) CDR-L1 as depicted in SEQ ID NO: 360, CDR-L2 as depicted in SEQ ID NO: 361, CDR-L3 as depicted in SEQ ID NO: 362, CDR-H1 as depicted in SEQ ID NO: 357, CDR-H2 as depicted in SEQ ID NO: 358, and CDR-H3 as depicted in SEQ ID NO: 359;

(t) CDR-L1 as depicted in SEQ ID NO: 375, CDR-L2 as depicted in SEQ ID NO: 376, CDR-L3 as depicted in SEQ ID NO: 377, CDR-H1 as depicted in SEQ ID NO: 372, CDR-H2 as depicted in SEQ ID NO: 373, and CDR-H3 as depicted in SEQ ID NO: 374;

(u) CDR-L1 as depicted in SEQ ID NO: 390, CDR-L2 as depicted in SEQ ID NO: 391, CDR-L3 as depicted in SEQ ID NO: 392, CDR-H1 as depicted in SEQ ID NO: 387, CDR-H2 as depicted in SEQ ID NO: 388, and CDR-H3 as depicted in SEQ ID NO: 389;

(v) CDR-L1 as depicted in SEQ ID NO: 405, CDR-L2 as depicted in SEQ ID NO: 406, CDR-L3 as depicted in SEQ ID NO: 407, CDR-H1 as depicted in SEQ ID NO: 402, CDR-H2 as depicted in SEQ ID NO: 403, and CDR-H3 as depicted in SEQ ID NO: 404;

(w) CDR-L1 as depicted in SEQ ID NO: 420, CDR-L2 as depicted in SEQ ID NO: 421, CDR-L3 as depicted in SEQ ID NO: 422, CDR-H1 as depicted in SEQ ID NO: 417, CDR-H2 as depicted in SEQ ID NO: 418, and CDR-H3 as depicted in SEQ ID NO: 419;

(x) CDR-L1 as depicted in SEQ ID NO: 435, CDR-L2 as depicted in SEQ ID NO: 436, CDR-L3 as depicted in SEQ ID NO: 437, CDR-H1 as depicted in SEQ ID NO: 432, CDR-H2 as depicted in SEQ ID NO: 433, and CDR-H3 as depicted in SEQ ID NO: 434;

(y) CDR-L1 as depicted in SEQ ID NO: 450, CDR-L2 as depicted in SEQ ID NO: 451, CDR-L3 as depicted in SEQ ID NO: 452, CDR-H1 as depicted in SEQ ID NO: 447, CDR-H2 as depicted in SEQ ID NO: 448, and CDR-H3 as depicted in SEQ ID NO: 449; and

(z) CDR-L1 as depicted in SEQ ID NO: 465, CDR-L2 as depicted in SEQ ID NO: 466, CDR-L3 as depicted in SEQ ID NO: 467, CDR-H1 as depicted in SEQ ID NO: 462, CDR-H2 as depicted in SEQ ID NO: 463 and CDR-H3 as depicted in SEQ ID NO: 464.

10. The antibody construct according to any one of the preceding claims, wherein the first binding domain of the antibody construct comprises a VH region and a VL region selected from the group consisting of:

(a) a VH region as depicted in SEQ ID NO: 48 and a VL region as depicted in SEQ ID NO: 49;

(b) a VH region as depicted in SEQ ID NO: 66 and a VL region as depicted in SEQ ID NO: 67;

(c) a VH region as depicted in SEQ ID NO: 72 and a VL region as depicted in SEQ ID NO: 73;

(d) a VH region as depicted in SEQ ID NO: 84 and a VL region as depicted in SEQ ID NO: 85;

(e) a VH region as depicted in SEQ ID NO: 90 and a VL region as depicted in SEQ ID NO: 91;

(f) a VH region as depicted in SEQ ID NO: 102 and a VL region as depicted in SEQ ID NO: 103;

(g) a VH region as depicted in SEQ ID NO: 108 and a VL region as depicted in SEQ ID NO: 109;

(h) a VH region as depicted in SEQ ID NO: 120 and a VL region as depicted in SEQ ID NO: 121;

(i) a VH region as depicted in SEQ ID NO: 126 and a VL region as depicted in SEQ ID NO: 127;

(j) a VH region as depicted in SEQ ID NO: 138 and a VL region as depicted in SEQ ID NO: 139;

(k) a VH region as depicted in SEQ ID NO: 144 and a VL region as depicted in SEQ ID NO: 145;

(l) a VH region as depicted in SEQ ID NO: 156 and a VL region as depicted in SEQ ID NO: 157;

(m) a VH region as depicted in SEQ ID NO: 162 and a VL region as depicted in SEQ ID NO: 163;

(n) a VH region as depicted in SEQ ID NO: 180 and a VL region as depicted in SEQ ID NO: 181;

(o) a VH region as depicted in SEQ ID NO: 192 and a VL region as depicted in SEQ ID NO: 193;

(p) a VH region as depicted in SEQ ID NO: 198 and a VL region as depicted in SEQ ID NO: 199;

(q) a VH region as depicted in SEQ ID NO: 210 and a VL region as depicted in SEQ ID NO: 211;

(r) a VH region as depicted in SEQ ID NO: 216 and a VL region as depicted in SEQ ID NO: 217;

(s) a VH region as depicted in SEQ ID NO: 228 and a VL region as depicted in SEQ ID NO: 229;

(t) a VH region as depicted in SEQ ID NO: 234 and a VL region as depicted in SEQ ID NO: 235;

(u) a VH region as depicted in SEQ ID NO: 246 and a VL region as depicted in SEQ ID NO: 247;

(v) a VH region as depicted in SEQ ID NO: 252 and a VL region as depicted in SEQ ID NO: 253;

(w) a VH region as depicted in SEQ ID NO: 264 and a VL region as depicted in SEQ ID NO: 265;

(x) a VH region as depicted in SEQ ID NO: 270 and a VL region as depicted in SEQ ID NO: 271;

(y) a VH region as depicted in SEQ ID NO: 282 and a VL region as depicted in SEQ ID NO: 283;

(z) a VH region as depicted in SEQ ID NO: 288 and a VL region as depicted in SEQ ID NO: 289;

(aa) a VH region as depicted in SEQ ID NO: 300 and a VL region as depicted in SEQ ID NO: 301;

(ab) a VH region as depicted in SEQ ID NO: 306 and a VL region as depicted in SEQ ID NO: 307;

(ac) a VH region as depicted in SEQ ID NO: 54 and a VL region as depicted in SEQ ID NO: 55;

(ad) a VH region as depicted in SEQ ID NO: 174 and a VL region as depicted in SEQ ID NO: 175;

(ae) a VH region as depicted in SEQ ID NO: 318 and a VL region as depicted in SEQ ID NO: 319;

(af) a VH region as depicted in SEQ ID NO: 333 and a VL region as depicted in SEQ ID NO: 334;

(ag) a VH region as depicted in SEQ ID NO: 348 and a VL region as depicted in SEQ ID NO: 349;

(ah) a VH region as depicted in SEQ ID NO: 363 and a VL region as depicted in SEQ ID NO: 364;

(ai) a VH region as depicted in SEQ ID NO: 378 and a VL region as depicted in SEQ ID NO: 379;

(aj) a VH region as depicted in SEQ ID NO: 393 and a VL region as depicted in SEQ ID NO: 394;

(ak) a VH region as depicted in SEQ ID NO: 408 and a VL region as depicted in SEQ ID NO: 409;

(al) a VH region as depicted in SEQ ID NO: 423 and a VL region as depicted in SEQ ID NO: 424;

(am) a VH region as depicted in SEQ ID NO: 438 and a VL region as depicted in SEQ ID NO: 439;

(an) a VH region as depicted in SEQ ID NO: 453 and a VL region as depicted in SEQ ID NO: 454; and

(ao) a VH region as depicted in SEQ ID NO: 468 and a VL region as depicted in SEQ ID NO: 469.

11. The antibody construct according to any one of the preceding claims, wherein the second domain comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from:

(a) CDR-L1 as depicted in SEQ ID NO: 488, CDR-L2 as depicted in SEQ ID NO: 489 and CDR-L3 as depicted in SEQ ID NO: 490;

(b) CDR-L1 as depicted in SEQ ID NO: 491, CDR-L2 as depicted in SEQ ID NO: 492 and CDR-L3 as depicted in SEQ ID NO: 493; and

(c) CDR-L1 as depicted in SEQ ID NO: 494, CDR-L2 as depicted in SEQ ID NO: 495 and CDR-L3 as depicted in SEQ ID NO: 496; and

comprises a VH region comprising CDR-H 1, CDR-H2 and CDR-H3 selected from:

(a) CDR-H1 as depicted in SEQ ID NO: 497, CDR-H2 as depicted in SEQ ID NO: 498 and CDR-H3 as depicted in SEQ ID NO: 499;

(b) CDR-H1 as depicted in SEQ ID NO: 500, CDR-H2 as depicted in SEQ ID NO: 501 and CDR-H3 as depicted in SEQ ID NO: 502;

(c) CDR-H1 as depicted in SEQ ID NO: 503, CDR-H2 as depicted in SEQ ID NO: 504 and CDR-H3 as depicted in SEQ ID NO: 505;

(d) CDR-H1 as depicted in SEQ ID NO: 506, CDR-H2 as depicted in SEQ ID NO: 507 and CDR-H3 as depicted in SEQ ID NO: 508;

(e) CDR-H1 as depicted in SEQ ID NO: 509, CDR-H2 as depicted in SEQ ID NO: 510 and CDR-H3 as depicted in SEQ ID NO: 511;

(f) CDR-H1 as depicted in SEQ ID NO: 512, CDR-H2 as depicted in SEQ ID NO: 513 and CDR-H3 as depicted in SEQ ID NO: 514;

(g) CDR-H1 as depicted in SEQ ID NO: 515, CDR-H2 as depicted in SEQ ID NO: 516 and CDR-H3 as depicted in SEQ ID NO: 517;

(h) CDR-H1 as depicted in SEQ ID NO: 518, CDR-H2 as depicted in SEQ ID NO: 519 and CDR-H3 as depicted in SEQ ID NO: 520;

(i) CDR-H1 as depicted in SEQ ID NO: 521, CDR-H2 as depicted in SEQ ID NO: 522 and CDR-H3 as depicted in SEQ ID NO: 523; and

(j) CDR-H1 as depicted in SEQ ID NO: 524, CDR-H2 as depicted in SEQ ID NO: 525 and CDR-H3 as depicted in SEQ ID NO: 526.

12. The antibody construct according to any one of the preceding claims, wherein the second domain comprises a VL region and a VH region selected from the group consisting of:

(a) a VL region as depicted in SEQ ID NO: 527 or SEQ ID NO: 528 and a VH region as depicted in SEQ ID NO: 529 or SEQ ID NO: 530;

(b) a VL region as depicted in SEQ ID NO: 531 or SEQ ID NO: 532 and a VH region as depicted in SEQ ID NO: 533 or SEQ ID NO: 534;

(c) a VL region as depicted in SEQ ID NO: 535 or SEQ ID NO: 536 and a VH region as depicted in SEQ ID NO: 537 or SEQ ID NO: 538;

(d) a VL region as depicted in SEQ ID NO: 539 or SEQ ID NO: 540 and a VH region as depicted in SEQ ID NO: 541 or SEQ ID NO: 542;

(e) a VL region as depicted in SEQ ID NO: 543 or SEQ ID NO: 544 and a VH region as depicted in SEQ ID NO: 547 or SEQ ID NO: 546;

(f) a VL region as depicted in SEQ ID NO: 547 or SEQ ID NO: 548 and a VH region as depicted in SEQ ID NO: 549 or 550;

(g) a VL region as depicted in SEQ ID NO: 551 or SEQ ID NO: 552 and a VH region as depicted in SEQ ID NO: 553 or SEQ ID NO: 554;

(h) a VL region as depicted in SEQ ID NO: 555 or SEQ ID NO: 556 and a VH region as depicted in SEQ ID NO: 557 or SEQ ID NO: 558;

(i) a VL region as depicted in SEQ ID NO: 559 or SEQ ID NO: 560 and a VH region as depicted in SEQ ID NO: 561 or SEQ ID NO: 562; and

(j) a VL region as depicted in SEQ ID NO: 563 or SEQ ID NO: 564 and a VH region as depicted in SEQ ID NO: 565 or SEQ ID NO: 566.

13. The antibody construct of any one of the preceding claims, wherein the antibody construct comprises in an amino to carboxyl order:

(a) the first domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 50, 56, 68, 74, 86, 92, 104, 110, 122, 128, 140, 146, 158, 164, 176, 182, 194, 200,

212, 218, 230, 236, 248, 254, 266, 272, 284, 290, 302, 308, 320, 335, 350, 365, 380, 395, 410, 425, 440, 455, and 470;

(b) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-3;

(c) the second domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586 or as depicted in SEQ ID NO: 15;

(d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 9, 10, 11 and 12;

(e) the first Fc monomer of the third domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 17-24;

(f) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 6, 7 and 8; and

(g) the second Fc monomer of the third domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 17-24.

14. The antibody construct of claim 13, having an amino acid sequence selected from the group consisting of SEQ ID NOs: 52, 53, 58, 59, 70, 71, 76, 77, 88, 89, 94, 95, 106, 107, 112, 113, 124, 125, 130, 131, 142, 143, 148, 149, 160, 161, 166, 167, 178, 179, 184, 185, 196, 197, 202, 203, 214, 215, 220, 221, 232, 233, 238, 239, 250, 251, 256, 257, 268, 269, 274, 275, 286, 287, 292, 293, 304, 305, 310, 311, 322, 323, 325, 326, 337, 338, 340, 341, 352, 353, 355, 356, 367, 368, 370, 371, 382, 383, 385, 386, 397, 398, 400, 401, 412, 413, 415, 416, 427, 428, 430, 431, 442, 443, 445, 446, 457, 458, 460, 461, 472, 473, 475 and 476.

15. The antibody construct of claim 14, comprising the amino acid sequence of SEQ ID NO: 220.

16. The antibody construct of claim 14, comprising the amino acid sequence of SEQ ID NO: 304.

17. The antibody construct of claim 14, comprising the amino acid sequence of SEQ ID NO: 382.

18. A polynucleotide encoding an antibody construct as defined in any one of the preceding claims.

19. A vector comprising the polynucleotide as defined in claim 18.

20. A host cell transformed or transfected with the polynucleotide as defined in claim 18 or with the vector as defined in claim 19.

21. A process for the production of the antibody construct of any one of claims 1 to 17, said process comprising culturing the host cell as defined in claim 20 under conditions allowing the expression of the antibody construct as defined in any one of claims 1 to 17 and recovering the produced antibody construct from the culture.

22. A pharmaceutical composition comprising the antibody construct of any one of claims 1 to 17, or produced according to the process of claim 21.

23. The pharmaceutical composition of claim 22, which is stable for at least four weeks at about -20°C.

24. The antibody construct of any one of claims 1 to 17, or produced according to the process of claim 21, for use in the treatment or amelioration of a disease selected from a tumorous disease, cancer or an immunological disorder, wherein said tumorous disease, cancer and immunological disorder correlate with PSMA overexpression.

25. The antibody construct for use according to claim 24, wherein the cancer is prostate cancer.

26. Use of the antibody construct of any one of claims 1 to 17 or produced according to the process of claim 21 in the manufacture of a medicament for the treatment or amelioration of a tumorous disease, cancer, or an immunological disorder, wherein said tumorous disease, cancer, and immunological disorder correlate with PSMA overexpression.

27. The use of claim 26, wherein the cancer is prostate cancer.