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(54) Benævnelse: **HER3-ANTIGEN-BINDENDE MOLEKYLER**

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DESCRIPTION

Field of the Invention

[0001] The present invention relates to the fields of molecular biology, more specifically antibody technology. The present invention also relates to methods of medical treatment and prophylaxis.

Background to the Invention

[0002] Increased HER3 expression is linked to poor prognosis in multiple solid tumors, including breast, gastric, head & neck, pancreatic, ovarian, and lung cancers. HER3-mediated signalling has adverse consequences for tumour progression; HER3 upregulation is associated with resistance to anti-HER2 and anti-EGFR therapy, and solid tumors refractory to anti-PD-1 therapy have been shown to have higher HER3 expression compared to responders to anti-PD-1 therapy.

[0003] HER3-binding antibodies are described e.g. in Zhang et al., Acta Biochimica et Biophysica Sinica (2016) 48(1): 39-48. The anti-HER3 antibody LJM-716 binds to an epitope on subdomains II and IV of the HER3 extracellular domain, locking HER3 in the inactive conformation (Garner et al., Cancer Res (2013) 73: 6024-6035). MM-121 (also known as seribantumab) has been shown to inhibit HER3-mediated signalling by blocking binding of heregulin (HRG) to HER3 (Schoeberl et al., Sci. Signal. (2009) 2(77): ra31). Patritumab (also known as U-1287 and AMG-888) also blocks binding of heregulins to HER3 (see e.g. Shimizu et al. Cancer Chemother Pharmacol. (2017) 79(3):489-495. RG7116 (also known as lumretuzumab and RO-5479599) recognises an epitope in subdomain I of the HER3 extracellular domain (see e.g. Mirschberger et al. Cancer Research (2013) 73(16) 5183-5194). KTN3379 binds to HER3 through interaction with amino acid residues in subdomain III (corresponding to the following positions of SEQ ID NO:1: Gly476, Pro477, Arg481, Gly452, Arg475, Ser450, Gly420, Ala451, Gly419, Arg421, Thr394, Leu423, Arg426, Gly427, Lys356, Leu358, Leu358, Lys356, Ala330, Lys329 and Gly337), and Met310, Glu311 and Pro328 of subdomain II (see Lee et al., Proc Natl Acad Sci USA. 2015 Oct 27; 112(43):13225). AV-203 (also known as CAN-017) has been shown to block binding of NRG1 to HER3 and to promote HER3 degradation (see Meetze et al., Eur J Cancer 2012; 48:126). REGN1400 also inhibits binding of ligand to HER3 (see Zhang et al., Mol Cancer Ther (2014) 13:1345-1355). RG7597 (duligotuzumab) is a dual action Fab (DAF) capable of binding to both HER3 and EGFR, and binds to subdomain III of HER3 (see Schaefer et al., Cancer Cell (2011) 20(4):472-486). MM-111 and MM-141 are bispecific antibodies having HER3-binding arms which inhibit HRG ligand binding to HER3 (see McDonagh et al. Mol Cancer Ther (2012) 11:582-593 and Fitzgerald et al., Mol Cancer Ther (2014) 13:410-425). WO 2013/084148 A2 discloses anti-HER3 antibodies including clones MOR12616 and MOR12925, which are disclosed to bind to position L268 within the dimerisation loop of domain II. US 8735551 B2 discloses anti-HER3 antibody clones including MOR09823 and MOR09825 which are disclosed to bind to HER3 through positions in domains II and IV; contact points with domain II are within the dimerisation loop and downstream thereof. Malm et al., mAbs (2016) 8(7): 1195-1209, Gaborit et al., Hum Vacc Immunother (2015) 12(3): 576-592 and Zhang et al., Act Biochim Biophys Sin (2016): 48(1) 39-48 are review articles which discuss several anti-HER3 antibodies. WO 2011/144749 A1 discloses HER3-specific nanobodies.

Summary of the Invention

[0004] The present invention is defined in the claims.

[0005] In a first aspect the present disclosure provides an antigen-binding molecule, optionally isolated, which is capable of binding to HER3 in extracellular region subdomain II.

[0006] In some aspects of the disclosure the antigen-binding molecule inhibits interaction between HER3 and an interaction partner for HER3.

[0007] In some aspects of the disclosure the antigen-binding molecule is capable of binding to a polypeptide comprising or consisting of the amino acid sequence of SEQ ID NO:16.

[0008] In some aspects of the disclosure the antigen-binding molecule is capable of binding to a polypeptide comprising the amino acid sequence of SEQ ID NO:229.

[0009] In some aspects of the disclosure the antigen-binding molecule is capable of binding to a polypeptide comprising the amino acid sequences of SEQ ID NO:230 and 231.

[0010] In some aspects of the disclosure the antigen-binding molecule is capable of binding to a polypeptide comprising the amino acid sequence of SEQ ID NO:230.

[0011] In some aspects of the disclosure the antigen-binding molecule is capable of binding to a polypeptide comprising the amino acid sequence of SEQ ID NO:231.

[0012] In some aspects of the disclosure the antigen-binding molecule is capable of binding to a polypeptide comprising the amino acid sequence of SEQ ID NO:23.

[0013] In some aspects of the disclosure the antigen-binding molecule is capable of binding to a polypeptide comprising the amino acid sequence of SEQ ID NO:21.

[0014] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:43

   HC-CDR2 having the amino acid sequence of SEQ ID NO:46

   HC-CDR3 having the amino acid sequence of SEQ ID NO:51; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:91

   LC-CDR2 having the amino acid sequence of SEQ ID NO:94

   LC-CDR3 having the amino acid sequence of SEQ ID NO:99.

[0015] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:44

   HC-CDR3 having the amino acid sequence of SEQ ID NO:47; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:88

   LC-CDR2 having the amino acid sequence of SEQ ID NO:92

   LC-CDR3 having the amino acid sequence of SEQ ID NO:95.

[0016] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:44

   HC-CDR3 having the amino acid sequence of SEQ ID NO:47; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:89

   LC-CDR2 having the amino acid sequence of SEQ ID NO:92

   LC-CDR3 having the amino acid sequence of SEQ ID NO:95.

[0017] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:44

   HC-CDR3 having the amino acid sequence of SEQ ID NO:47; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:90

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:96.

[0018] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:44

   HC-CDR3 having the amino acid sequence of SEQ ID NO:47; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:88

   LC-CDR2 having the amino acid sequence of SEQ ID NO:92

   LC-CDR3 having the amino acid sequence of SEQ ID NO:98.

[0019] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:47; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:88

   LC-CDR2 having the amino acid sequence of SEQ ID NO:93

   LC-CDR3 having the amino acid sequence of SEQ ID NO:95.

[0020] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:49; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:93

LC-CDR3 having the amino acid sequence of SEQ ID NO:95.

[0021] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

HC-CDR1 having the amino acid sequence of SEQ ID NO:41

HC-CDR2 having the amino acid sequence of SEQ ID NO:45

HC-CDR3 having the amino acid sequence of SEQ ID NO:50; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:93

LC-CDR3 having the amino acid sequence of SEQ ID NO:95.

[0022] The invention provides an isolated antigen-binding molecule, which is capable of binding to HER3, wherein the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

HC-CDR1 having the amino acid sequence of SEQ ID NO:41

HC-CDR2 having the amino acid sequence of SEQ ID NO:45

HC-CDR3 having the amino acid sequence of SEQ ID NO:48; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:95.

[0023] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

HC-CDR1 having the amino acid sequence of SEQ ID NO:41

HC-CDR2 having the amino acid sequence of SEQ ID NO:45

HC-CDR3 having the amino acid sequence of SEQ ID NO:48; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:97.

[0024] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

HC-CDR1 having the amino acid sequence of SEQ ID NO:42

HC-CDR2 having the amino acid sequence of SEQ ID NO:45

HC-CDR3 having the amino acid sequence of SEQ ID NO:48; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:95.

[0025] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

HC-CDR1 having the amino acid sequence of SEQ ID NO:158

HC-CDR2 having the amino acid sequence of SEQ ID NO:159

HC-CDR3 having the amino acid sequence of SEQ ID NO:160; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:165

LC-CDR2 having the amino acid sequence of SEQ ID NO:166

LC-CDR3 having the amino acid sequence of SEQ ID NO:167.

[0026] In some aspects the antigen-binding molecule is capable of binding to a polypeptide comprising the amino acid sequence of SEQ ID NO:22.

[0027] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:128

   HC-CDR2 having the amino acid sequence of SEQ ID NO:129

   HC-CDR3 having the amino acid sequence of SEQ ID NO:130; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:136

   LC-CDR2 having the amino acid sequence of SEQ ID NO:137

   LC-CDR3 having the amino acid sequence of SEQ ID NO:138.

[0028] In some aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:144

   HC-CDR2 having the amino acid sequence of SEQ ID NO:145

   HC-CDR3 having the amino acid sequence of SEQ ID NO:146; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:151

   LC-CDR2 having the amino acid sequence of SEQ ID NO:152

   LC-CDR3 having the amino acid sequence of SEQ ID NO:153.

[0029] In particular aspects of the disclosure the antigen-binding molecule comprises:

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:48; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:95;

or

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:48; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:88

   LC-CDR2 having the amino acid sequence of SEQ ID NO:92

   LC-CDR3 having the amino acid sequence of SEQ ID NO:97;

or

1. (i) a heavy chain variable (VH) region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:42

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:48; and

2. (ii) a light chain variable (VL) region incorporating the following CDRs:

   LC-CDR1 having the amino acid sequence of SEQ ID NO:88

   LC-CDR2 having the amino acid sequence of SEQ ID NO:92

   LC-CDR3 having the amino acid sequence of SEQ ID NO:95.

[0030] In some aspects the antigen-binding molecule comprises:

1. (i) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:24; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:74;
   or
2. (ii) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:25; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:75;

or

3. (iii) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:26; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:76;
   or
4. (iv) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:27; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:77;
   or
5. (v) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:28; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:78;
   or
6. (vi) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:29; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:78;
   or
7. (vii) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:30; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:78;
   or
8. (viii) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:31; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:79;
   or
9. (ix) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:32; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:79;
   or
10. (x) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:33; and
    a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:80;
    or
11. (xi) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:34; and
    a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:81;
    or
12. (xii) a VH region comprising an amino acid sequence having at least 70% sequence identity to

the amino acid sequence of SEQ ID NO:35; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:82;
or

13. (xiii) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:36; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:83;
or
14. (xiv) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:37; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:84;
or
15. (xv) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:38; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:85;
or
16. (xvi) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:39; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:86;
or
17. (xvii) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:40; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:87;
or
18. (xviii) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:127; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:135;
or
19. (xix) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:143; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:150;
or
20. (xx) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:157; and
a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:164.

[0031] In particular embodiments the antigen-binding molecule comprises:

1. (i) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:36; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:83;

[0032] In some aspects described herein:

1. (i) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:37; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:84;
   or
2. (ii) a VH region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:38; and
   a VL region comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO:85.

[0033] In some aspects the antigen-binding molecule is capable of binding to human HER3 and one or more of mouse HER3, rat HER3 and cynomolgous macaque HER3.

[0034] Also provided is an antigen-binding molecule, optionally isolated, comprising (i) an antigen-binding molecule according to the present disclosure, and (ii) an antigen-binding molecule capable of binding to an antigen other than HER3.

[0035] In some aspects the antigen-binding molecule is capable of binding to cells expressing HER3 at the cell surface.

[0036] In some aspects the antigen-binding molecule is capable of inhibiting HER3-mediated signalling.

[0037] In some aspects the antigen-binding molecule comprises an Fc region, the Fc region comprising a polypeptide having: (i) C at the position corresponding to position 242, and C at the position corresponding to position 334, and (ii) one or more of: A at the position corresponding to position 236, D at the position corresponding to position 239, E at the position corresponding to position 332, L at the position corresponding to position 330, K at the position corresponding to position 345, and G at the position corresponding to position 430. In some aspects the Fc region comprises a polypeptide having C at the position corresponding to position 242, C at the position corresponding to position 334, A at the position corresponding to position 236, D at the position corresponding to position 239, E at the position corresponding to position 332, and L at the position corresponding to position 330.

[0038] Also provided is a chimeric antigen receptor (CAR) comprising an antigen-binding molecule according to the present disclosure.

[0039] Also provided is a nucleic acid, or a plurality of nucleic acids, optionally isolated, encoding an antigen-binding molecule or a CAR according to the present disclosure.

[0040] Also provided is an expression vector, or a plurality of expression vectors, comprising a nucleic acid or a plurality of nucleic acids according to the present disclosure.

[0041] Also provided is a cell comprising an antigen-binding molecule, a CAR, a nucleic acid or a plurality of nucleic acids, or an expression vector or a plurality of expression vectors according to the present disclosure.

[0042] Also provided is a method comprising culturing a cell comprising a nucleic acid or a plurality of nucleic acids or an expression vector or a plurality of expression vectors according to the present disclosure, under conditions suitable for expression of the antigen-binding molecule or CAR from the nucleic acid(s) or expression vector(s).

[0043] Also provided is a composition comprising an antigen-binding molecule, a CAR, a nucleic acid or a plurality of nucleic acids, an expression vector or a plurality of expression vectors, or a cell according to the present disclosure.

[0044] Also provided is an antigen-binding molecule, a CAR, a nucleic acid or a plurality of nucleic acids, an expression vector or a plurality of expression vectors, a cell, or a composition according to the present disclosure for use in a method of medical treatment or prophylaxis.

[0045] Also provided is an antigen-binding molecule, a CAR, a nucleic acid or a plurality of nucleic acids, an expression vector or a plurality of expression vectors, a cell, or a composition according to the present disclosure for use in a method of treatment or prevention of a cancer.

[0046] Also provided is the use of an antigen-binding molecule, a CAR, a nucleic acid or a plurality of nucleic acids, an expression vector or a plurality of expression vectors, a cell, or a composition according to the present disclosure in the manufacture of a medicament for use in a method of treatment or prevention of a cancer.

[0047] Also provided is a method of treating or preventing a cancer, comprising administering to a subject a therapeutically or prophylactically effective amount of an antigen-binding molecule, a CAR, a nucleic acid or a plurality of nucleic acids, an expression vector or a plurality of expression vectors, a cell, or a composition according to the present disclosure.

[0048] In some aspects in accordance with various aspects of the present disclosure, the method additionally comprises administration of an inhibitor of signalling mediated by an EGFR family member, optionally wherein the inhibitor of signalling mediated by an EGFR family member is an inhibitor of signalling mediated by HER2 and/or EGFR.

[0049] In some aspects the cancer is selected from: a cancer comprising cells expressing an EGFR family member, a cancer comprising cells expressing HER3, a solid tumor, breast cancer, breast carcinoma, ductal carcinoma, gastric cancer, gastric carcinoma, gastric adenocarcinoma, colorectal cancer, colorectal carcinoma, colorectal adenocarcinoma, head and neck cancer, squamous cell carcinoma of the head and neck (SCCHN), lung cancer, lung adenocarcinoma, squamous cell lung

carcinoma, ovarian cancer, ovarian carcinoma, ovarian serous adenocarcinoma, kidney cancer, renal cell carcinoma, renal clear cell carcinoma, renal cell adenocarcinoma, renal papillary cell carcinoma, pancreatic cancer, pancreatic adenocarcinoma, pancreatic ductal adenocarcinoma, cervical cancer, cervical squamous cell carcinoma, skin cancer, melanoma, esophageal cancer, esophageal adenocarcinoma, liver cancer, hepatocellular carcinoma, cholangiocarcinoma, uterine cancer, uterine corpus endometrial carcinoma, thyroid cancer, thyroid carcinoma, pheochromocytoma, paraganglioma, bladder cancer, bladder urothelial carcinoma, prostate cancer, prostate adenocarcinoma, sarcoma and thymoma.

[0050] Also provided is a method of inhibiting HER3-mediated signalling, comprising contacting HER3-expressing cells with an antigen-binding molecule according to the present disclosure.

[0051] Also provided is a method of reducing the number or activity of HER3-expressing cells, the method comprising contacting HER3-expressing cells with an antigen-binding molecule according to the present disclosure.

[0052] Also provided is an *in vitro* complex, optionally isolated, comprising an antigen-binding molecule according to the present disclosure bound to HER3.

[0053] Also provided is a method comprising contacting a sample containing, or suspected to contain, HER3 with an antigen-binding molecule according to the present disclosure, and detecting the formation of a complex of the antigen-binding molecule with HER3.

[0054] Also provided is a method of selecting or stratifying a subject for treatment with a HER3-targeted agent, the method comprising contacting, *in vitro,* a sample from the subject with an antigen-binding molecule according to the present disclosure and detecting the formation of a complex of the antigen-binding molecule with HER3.

[0055] Also provided is the use of an antigen-binding molecule according to the present disclosure as an *in vitro* or *in vivo* diagnostic or prognostic agent.

[0056] Also provided is the use of an antigen-binding molecule according to the present disclosure in a method for detecting, localizing or imaging a cancer, optionally wherein the cancer is selected from: a cancer comprising cells expressing an EGFR family member, a cancer comprising cells expressing HER3, a solid tumor, breast cancer, breast carcinoma, ductal carcinoma, gastric cancer, gastric carcinoma, gastric adenocarcinoma, colorectal cancer, colorectal carcinoma, colorectal adenocarcinoma, head and neck cancer, squamous cell carcinoma of the head and neck (SCCHN), lung cancer, lung adenocarcinoma, squamous cell lung carcinoma, ovarian cancer, ovarian carcinoma, ovarian serous adenocarcinoma, kidney cancer, renal cell carcinoma, renal clear cell carcinoma, renal cell adenocarcinoma, renal papillary cell carcinoma, pancreatic cancer, pancreatic adenocarcinoma, pancreatic ductal adenocarcinoma, cervical cancer, cervical squamous cell carcinoma, skin cancer, melanoma, esophageal cancer, esophageal adenocarcinoma, liver cancer, hepatocellular carcinoma, cholangiocarcinoma, uterine cancer, uterine corpus endometrial carcinoma, thyroid cancer, thyroid carcinoma, pheochromocytoma, paraganglioma, bladder cancer, bladder urothelial carcinoma, prostate cancer, prostate adenocarcinoma, sarcoma and thymoma.

Description

[0057] The present disclosure relates to novel HER3-binding molecules having improved properties as compared to known anti-HER3 antibodies.

[0058] The inventors undertook the targeted generation of antigen-binding molecules which bind to particular regions of interest in the extracellular region of HER3. The HER3-binding molecules of the present disclosure are provided with combinations of desirable biophysical and/or functional properties as compared to antigen-binding molecules disclosed in the prior art.

[0059] In aspects of the present disclosure the antigen binding molecules are capable of binding to the subdomain II of the extracellular region of HER3 (SEQ ID NO:16), and inhibit association of the bound HER3 molecule with interaction partners.

[0060] In particular, HER3-binding antigen-binding molecules described herein are demonstrated to bind to an epitope of HER3 providing for potent inhibition of association of HER3 with interaction partners, strong inhibition of downstream signalling and exceptional anti-cancer activity against a wide range of cancers.

HER3

[0061] HER3 (also known e.g. as ERBB3 LCCS2, MDA-BF-1) is the protein identified by UniProt P21860. Alternative splicing of mRNA encoded by the human *ERBB3* gene yields five different isoforms: isoform 1 (UniProt: P21860-1, v1; SEQ ID NO:1); isoform 2 (UniProt: P21860-2; SEQ ID NO:2), which comprises a different sequence to SEQ ID NO:1 from position 141, and which lacks amino acid sequence corresponding to positions 183 to 1342 of SEQ ID NO:1; isoform 3 (UniProt: P21860-3; SEQ ID NO:3), which comprises the substitution C331F relative to SEQ ID NO:1, and which lacks the amino acid sequence corresponding to positions 332 to 1342 of SEQ ID NO:1; isoform 4 (UniProt: P21860-4; SEQ ID NO:4), which lacks the amino acid sequence corresponding to positions 1 to 59 of SEQ ID NO:1; and isoform 5 (UniProt: P21860-5; SEQ ID NO:5), which lacks the amino acid sequence corresponding to positions 1 to 643 of SEQ ID NO:1.

[0062] The N-terminal 19 amino acids of SEQ ID NOs:1 to 3 constitute a signal peptide, and so the mature form of HER3 isoforms 1, 2 and 3 (i.e. after processing to remove the signal peptide) have the amino acid sequences shown in SEQ ID NOs:6, 7 and 8, respectively.

[0063] The structure and function of HER3 is described e.g. in Cho and Leahy Science (2002) 297 (5585):1330-1333, Singer et al., Journal of Biological Chemistry (2001) 276, 44266-44274, Roskoski et al., Pharmacol. Res. (2014) 79: 34-74, Bazley and Gullick Endocrine-Related Cancer (2005) S17-S27 and Mujoo et al., Oncotarget (2014) 5(21):10222-10236. HER3 is a single-pass transmembrane ErbB receptor tyrosine kinase having an N-terminal extracellular region (SEQ ID NO:9) comprising two leucine-rich subdomains (domains I and III, shown in SEQ ID NOs:15 and 17, respectively) and two cysteine-rich subdomains (domains II and IV, shown in SEQ ID NOs:16 and 18, respectively). Domain II comprises a β hairpin dimerisation loop (SEQ ID NO:19) which is involved in intermolecular interaction with other HER receptor molecules. The extracellular region is linked via a transmembrane region (SEQ ID NO:10) to a cytoplasmic region (SEQ ID NO:11). The cytoplasmic region comprises a

juxtamembrane segment (SEQ ID NO:12), a protein kinase domain (SEQ ID NO:13), and a C-terminal segment (SEQ ID NO:14).

[0064] Signalling through HER3 involves receptor homodimerisation (i.e. with other HER3 receptors) or heterodimerisation (with other HER receptors, e.g. HER2) and consequent autophosphorylation by the protein kinase domain of tyrosines of the cytoplasmic region. The phosphorylated tyrosine residues recruit adaptor/effector proteins (e.g. Grb2 and phospholipase Cγ (PLCγ), containing src homology domain 2 (SH2) or phosphotyrosine binding (PTB) domains.

[0065] Signalling through HER3 can be activated in a ligand-dependent or ligand-independent manner. In the absence of ligand, HER3 receptor molecules are normally expressed at the cell surface as monomers with a conformation which prevents receptor dimerisation in which the dimerisation loop of subdomain II makes intramolecular contact with a pocket on subdomain IV. Binding of a HER3 ligand such as a neuregulin (NRG), e.g. NRG1 (also known as heregulin, HRG) or NRG2 to subdomains I and III of the extracellular region causes a conformational change which results in the exposure of the dimerisation loop of subdomain II, facilitating receptor dimerisation and signalling. Some cancer-associated mutations in HER3 may disrupt interaction of subdomains II and IV required for the formation of the inactive 'closed' conformation and thereby cause constitutive presentation of the dimerisation loop and activation of HER3-mediated signalling in the absence of ligand binding (see e.g. in Jaiswal et al., Cancer Cell (2013) 23(5): 603-617).

[0066] In this specification "HER3" refers to HER3 from any species and includes HER3 isoforms, fragments, variants (including mutants) or homologues from any species.

[0067] As used herein, a "fragment", "variant" or "homologue" of a protein may optionally be characterised as having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of the reference protein (e.g. a reference isoform). In some aspects fragments, variants, isoforms and homologues of a reference protein may be characterised by ability to perform a function performed by the reference protein.

[0068] A "fragment" generally refers to a fraction of the reference protein. A "variant" generally refers to a protein having an amino acid sequence comprising one or more amino acid substitutions, insertions, deletions or other modifications relative to the amino acid sequence of the reference protein, but retaining a considerable degree of sequence identity (e.g. at least 60%) to the amino acid sequence of the reference protein. An "isoform" generally refers to a variant of the reference protein expressed by the same species as the species of the reference protein (e.g. HER3 isoforms 1 to 5 are all isoforms of one another). A "homologue" generally refers to a variant of the reference protein produced by a different species as compared to the species of the reference protein. For example, human HER3 isoform 1 (P21860-1, v1; SEQ ID NO:1) and Rhesus macaque HER3 (UniProt: F7HEH3-1, v2; SEQ ID NO:20) are homologues of one another. Homologues include orthologues.

[0069] A "fragment" of a reference protein may be of any length (by number of amino acids), although may optionally be at least 20% of the length of the reference protein (that is, the protein from which the fragment is derived) and may have a maximum length of one of 50%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the length of the reference protein.

[0070] A fragment of HER3 may have a minimum length of one of 10, 20, 30, 40, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1100, 1200 amino acids, and may have a maximum length of one of 20, 30, 40, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1100, 1200, or 1300 amino acids.

[0071] In some aspects, the HER3 is HER3 from a mammal (e.g. a primate (rhesus, cynomolgous, non-human primate or human) and/or a rodent (e.g. rat or murine) HER3). Isoforms, fragments, variants or homologues of HER3 may optionally be characterised as having at least 70%, preferably one of 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of an immature or mature HER3 isoform from a given species, e.g. human.

[0072] Isoforms, fragments, variants or homologues may optionally be functional isoforms, fragments, variants or homologues, e.g. having a functional property/activity of the reference HER3 (e.g. human HER3 isoform 1), as determined by analysis by a suitable assay for the functional property/activity. For example, an isoform, fragment, variant or homologue of HER3 may display association with one or more of: HER2, NRG1 (type I, II, III, IV, V or VI) or NRG2 (α or β).

[0073] In some aspects, the HER3 comprises, or consists of, an amino acid sequence having at least 70%, preferably one of 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to one of SEQ ID NOs:1 to 8.

[0074] In some aspects, a fragment of HER3 comprises, or consists of, an amino acid sequence having at least 70%, preferably one of 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to one of SEQ ID NOs:9 to 19, e.g. one of 9, 16 or 19.

Regions of particular interest on the target molecule

[0075] The antigen-binding molecules of the present disclosure were specifically designed to target regions of HER3 of particular interest. In a two-step approach, HER3 regions to be targeted were selected following analysis for predicted antigenicity, function and safety. Antibodies specific for the target regions of HER3 were then prepared using peptides corresponding to the target regions as immunogens to raise specific monoclonal antibodies, and subsequent screening identified antibodies capable of binding to HER3 in the native state. This approach provides exquisite control over the antibody epitope.

[0076] The antigen-binding molecules of the present disclosure may be defined by reference to the region of HER3 to which they bind. The antigen-binding molecules of the present disclosure may bind to a particular region of interest of HER3. In some aspects the antigen-binding molecule may bind to a linear epitope of HER3, consisting of a contiguous sequence of amino acids (i.e. an amino acid primary sequence). In some aspects, the antigen-binding molecule may bind to a conformational epitope of HER3, consisting of a discontinuous sequence of amino acids of the amino acid sequence.

[0077] In some aspects, the antigen-binding molecule of the present disclosure binds to HER3. In some aspects, the antigen-binding molecule binds to the extracellular region of HER3 (e.g. the region shown in SEQ ID NO:9). In some aspects, the antigen-binding molecule binds to subdomain II of the

extracellular region of HER3 (e.g. the region shown in SEQ ID NO:16).

[0078] In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:229. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:229. In some aspects, the antigen-binding molecule binds to the regions of HER3 shown in SEQ ID NOs:230 and 231. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the regions of HER3 shown in SEQ ID NOs:230 and 231. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:230. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:230. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:231. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:231.

[0079] In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:23. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:23. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:21. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:21. In some aspects the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:19. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:19. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:22. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:22.

[0080] In some aspects, the antigen-binding molecule does not bind to the region of HER3 corresponding to positions 260 to 279 of SEQ ID NO:1. In some aspects the antigen-binding molecule does not contact an amino acid residue of the region of HER3 corresponding to positions 260 to 279 of SEQ ID NO:1. In some aspects, the antigen-binding molecule does not bind to the region of HER3 shown in SEQ ID NO:23. In some aspects the antigen-binding molecule does not contact an amino acid residue of the region of HER3 shown in SEQ ID NO:23.

[0081] The region of a peptide/polypeptide to which an antibody binds can be determined by the skilled person using various methods well known in the art, including X-ray co-crystallography analysis of antibody-antigen complexes, peptide scanning, mutagenesis mapping, hydrogen-deuterium exchange analysis by mass spectrometry, phage display, competition ELISA and proteolysis-based 'protection' methods. Such methods are described, for example, in Gershoni et al., BioDrugs, 2007, 21(3):145-156.

[0082] In some aspects the antigen-binding molecule is capable of binding the same region of HER3, or an overlapping region of HER3, to the region of HER3 which is bound by an antibody comprising the VH and VL sequences of one of antibody clones 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93, 10A6, 4-35-B2 or 4-35-B4 described herein. In some aspects the antigen-binding molecule is capable of binding the same region of HER3, or an overlapping region of HER3, to the region of HER3 which is bound by an antibody comprising the VH and VL sequences of one of antibody clones 10D1_c89, 10D1_c90 or 10D1_c91. In some aspects the antigen-binding molecule is capable of binding the same region of

HER3, or an overlapping region of HER3, to the region of HER3 which is bound by an antibody comprising the VH and VL sequences of antibody clone 10D1_c89.

[0083] As used herein, a "peptide" refers to a chain of two or more amino acid monomers linked by peptide bonds. A peptide typically has a length in the region of about 2 to 50 amino acids. A "polypeptide" is a polymer chain of two or more peptides. Polypeptides typically have a length greater than about 50 amino acids.

[0084] In some aspects, the antigen-binding molecule of the present disclosure is capable of binding to a polypeptide comprising, or consisting of, the amino acid sequence of one of SEQ ID NOs:1, 3, 4, 6 or 8.

[0085] In some aspects, the antigen-binding molecule is capable of binding to a polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:9. In some aspects, the antigen-binding molecule is capable of binding to a polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:16.

[0086] In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:229. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequences of SEQ ID NOs:230 and 231. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:230. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:231. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:23. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:21. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:19. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:22.

[0087] In some aspects, the antigen-binding molecule is not capable of binding to a peptide consisting of the amino acid sequence corresponding to positions 260 to 279 of SEQ ID NO:1. In some aspects, the antigen-binding molecule is not capable of binding to a peptide consisting of the amino acid sequence of SEQ ID NO:23.

[0088] The ability of an antigen-binding molecule to bind to a given peptide/polypeptide can be analysed by methods well known to the skilled person, including analysis by ELISA, immunoblot (e.g. western blot), immunoprecipitation, Surface Plasmon Resonance (SPR; see e.g. Hearty et al., Methods Mol Biol (2012) 907:411-442) or Bio-Layer Interferometry (see e.g. Lad et al., (2015) J Biomol Screen 20(4): 498-507).

[0089] In aspects where the antigen binding molecule is capable of binding to a peptide/polypeptide comprising a reference amino acid sequence, the peptide/polypeptide may comprise one or more additional amino acids at one or both ends of the reference amino acid sequence. In some aspects the peptide/polypeptide comprises e.g. 1-5, 1-10, 1-20, 1-30, 1-40, 1-50, 5-10, 5-20, 5-30, 5-40, 5-50,

10-20, 10-30, 10-40, 10-50, 20-30, 20-40 or 20-50 additional amino acids at one or both ends of the reference amino acid sequence.

[0090] In some aspects the additional amino acid(s) provided at one or both ends (i.e. the N-terminal and C-terminal ends) of the reference sequence correspond to the positions at the ends of the reference sequence in the context of the amino acid sequence of HER3. By way of example, where the antigen-binding molecule is capable of binding to a peptide comprising the sequence of SEQ ID NO:23 and an additional two amino acids at the C-terminal end of SEQ ID NO:23, the additional two amino acids may be threonine and lysine, corresponding to positions 278 and 279 of SEQ ID NO:1.

[0091] In some aspects the antigen-binding molecule is capable of binding to a peptide/polypeptide which is bound by an antibody comprising the VH and VL sequences of one of antibody clones 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93, 10A6, 4-35-B2 or 4-35-B4 described herein. In some aspects the antigen-binding molecule is capable of binding to a peptide/polypeptide which is bound by an antibody comprising the VH and VL sequences of one of antibody clones 10D1_c89, 10D1_c90 or 10D1_c91. In some aspects the antigen-binding molecule is capable of binding to a peptide/polypeptide which is bound by an antibody comprising the VH and VL sequences of antibody clone 10D1_c89.

Antigen-binding molecules

[0092] The present disclosure provides antigen-binding molecules capable of binding to HER3.

[0093] An "antigen-binding molecule" refers to a molecule which is capable of binding to a target antigen, and encompasses monoclonal antibodies, polyclonal antibodies, monospecific and multispecific antibodies (e.g., bispecific antibodies), and antibody fragments (e.g. Fv, scFv, Fab, scFab, $F(ab')_2$, Fab_2, diabodies, triabodies, scFv-Fc, minibodies, single domain antibodies (e.g. VhH), etc.), as long as they display binding to the relevant target molecule(s).

[0094] The antigen-binding molecule of the present disclosure comprises a moiety capable of binding to a target antigen(s). In some aspects, the moiety capable of binding to a target antigen comprises an antibody heavy chain variable region (VH) and an antibody light chain variable region (VL) of an antibody capable of specific binding to the target antigen. In some aspects, the moiety capable of binding to a target antigen comprises or consists of an aptamer capable of binding to the target antigen, e.g. a nucleic acid aptamer (reviewed, for example, in Zhou and Rossi Nat Rev Drug Discov. 2017 16(3):181-202). In some aspects, the moiety capable of binding to a target antigen comprises or consists of a antigen-binding peptide/polypeptide, e.g. a peptide aptamer, thioredoxin, monobody, anticalin, Kunitz domain, avimer, knottin, fynomer, atrimer, DARPin, affibody, nanobody (i.e. a single-domain antibody (sdAb)) affilin, armadillo repeat protein (ArmRP), OBody or fibronectin - reviewed e.g. in Reverdatto et al., Curr Top Med Chem. 2015; 15(12): 1082-1101 (see also e.g. Boersma et al., J Biol Chem (2011) 286:41273-85 and Emanuel et al., Mabs (2011) 3:38-48).

[0095] The antigen-binding molecules of the present disclosure generally comprise an antigen-binding domain comprising a VH and a VL of an antibody capable of specific binding to the target antigen. The antigen-binding domain formed by a VH and a VL may also be referred to herein as an

Fv region.

[0096] An antigen-binding molecule may be, or may comprise, an antigen-binding polypeptide, or an antigen-binding polypeptide complex. An antigen-binding molecule may comprise more than one polypeptide which together form an antigen-binding domain. The polypeptides may associate covalently or non-covalently. In some aspects the polypeptides form part of a larger polypeptide comprising the polypeptides (e.g. in the case of scFv comprising VH and VL, or in the case of scFab comprising VH-CH1 and VL-CL).

[0097] An antigen-binding molecule may refer to a non-covalent or covalent complex of more than one polypeptide (e.g. 2, 3, 4, 6, or 8 polypeptides), e.g. an IgG-like antigen-binding molecule comprising two heavy chain polypeptides and two light chain polypeptides.

[0098] The antigen-binding molecules of the present disclosure may be designed and prepared using the sequences of monoclonal antibodies (mAbs) capable of binding to HER3. Antigen-binding regions of antibodies, such as single chain variable fragment (scFv), Fab and $F(ab')_2$ fragments may also be used/provided. An "antigen-binding region" is any fragment of an antibody which is capable of binding to the target for which the given antibody is specific.

[0099] Antibodies generally comprise six complementarity-determining regions CDRs; three in the heavy chain variable (VH) region: HC-CDR1, HC-CDR2 and HC-CDR3, and three in the light chain variable (VL) region: LC-CDR1, LC-CDR2, and LC-CDR3. The six CDRs together define the paratope of the antibody, which is the part of the antibody which binds to the target antigen.

[0100] The VH region and VL region comprise framework regions (FRs) either side of each CDR, which provide a scaffold for the CDRs. From N-terminus to C-terminus, VH regions comprise the following structure: N term-[HC-FR1]-[HC-CDR1]-[HC-FR2]-[HC-CDR2]-[HC-FR3]-[HC-CDR3]-[HC-FR4]-C term; and VL regions comprise the following structure: N term-[LC-FR1]-[LC-CDR1]-[LC-FR2]-[LC-CDR2]-[LC-FR3]-[LC-CDR3]-[LC-FR4]-C term.

[0101] There are several different conventions for defining antibody CDRs and FRs, such as those described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991), Chothia et al., J. Mol. Biol. 196:901-917 (1987), and VBASE2, as described in Retter et al., Nucl. Acids Res. (2005) 33 (suppl 1): D671-D674. The CDRs and FRs of the VH regions and VL regions of the antibody clones described herein were defined according to the international IMGT (ImMunoGeneTics) information system (LeFranc et al., Nucleic Acids Res. (2015) 43 (Database issue):D413-22), which uses the IMGT V-DOMAIN numbering rules as described in Lefranc et al., Dev. Comp. Immunol. (2003) 27:55-77.

[0102] In some aspects, the antigen-binding molecule comprises the CDRs of an antigen-binding molecule which is capable of binding to HER3. In some aspects, the antigen-binding molecule comprises the FRs of an antigen-binding molecule which is capable of binding to HER3. In some aspects, the antigen-binding molecule comprises the CDRs and the FRs of an antigen-binding molecule which is capable of binding to HER3. That is, in some aspects the antigen-binding molecule comprises the VH region and the VL region of an antigen-binding molecule which is capable of binding to HER3.

[0103] In some aspects the antigen-binding molecule comprises a VH region and a VL region which is, or which is derived from, the VH/VL region of a HER3-binding antibody clone described herein (i.e. anti-HER3 antibody clones 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93, 10D1, 10A6, 4-35-B2 or 4-35-B4; e.g. 10D1_c89, 10D1_c90 or 10D1_c91; e.g. 10D1_c89).

[0104] In some aspects the antigen-binding molecule comprises a VH region according to one of (1) to (10) below:

1. (1) (10D1 derived) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:43

   HC-CDR2 having the amino acid sequence of SEQ ID NO:46

   HC-CDR3 having the amino acid sequence of SEQ ID NO:51,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

2. (2) (10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c87, 10D1_c92, 10D1_c93) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:44

   HC-CDR3 having the amino acid sequence of SEQ ID NO:47,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

3. (3) (10D1_c85v1, 10D1_c85v2) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:47,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

4. (4) (10D1_c85o1) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:49,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

5. (5) (10D1_c85o2) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:50,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

6. (6) (10D1_c89, 10D1_c90) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:41

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:48,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

7. (7) (10D1_c91) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:42

   HC-CDR2 having the amino acid sequence of SEQ ID NO:45

   HC-CDR3 having the amino acid sequence of SEQ ID NO:48,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

8. (8) (10A6) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:158

   HC-CDR2 having the amino acid sequence of SEQ ID NO:159

   HC-CDR3 having the amino acid sequence of SEQ ID NO:160,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

9. (9) (4-35-B2) a VH region incorporating the following CDRs:

   HC-CDR1 having the amino acid sequence of SEQ ID NO:128

   HC-CDR2 having the amino acid sequence of SEQ ID NO:129

   HC-CDR3 having the amino acid sequence of SEQ ID NO:130,

   or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

10. (10) (4-35-B4) a VH region incorporating the following CDRs:

HC-CDR1 having the amino acid sequence of SEQ ID NO:144

HC-CDR2 having the amino acid sequence of SEQ ID NO:145

HC-CDR3 having the amino acid sequence of SEQ ID NO:146,

or a variant thereof in which one or two or three amino acids in one or more of HC-CDR1, HC-CDR2, or HC-CDR3 are substituted with another amino acid.

[0105] In some aspects the antigen-binding molecule comprises a VH region according to one of (11) to (24) below:

(11) (10D1) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:55

HC-FR2 having the amino acid sequence of SEQ ID NO:58

HC-FR3 having the amino acid sequence of SEQ ID NO:69

HC-FR4 having the amino acid sequence of SEQ ID NO:73,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(12) (10D1_c75, 10D1_c92) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:52

HC-FR2 having the amino acid sequence of SEQ ID NO:56

HC-FR3 having the amino acid sequence of SEQ ID NO:61

HC-FR4 having the amino acid sequence of SEQ ID NO:70,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(13) (10D1_c76, 10D1_c77, 10D1_c78v1) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:52

HC-FR2 having the amino acid sequence of SEQ ID NO:56

HC-FR3 having the amino acid sequence of SEQ ID NO:62

HC-FR4 having the amino acid sequence of SEQ ID NO:70,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(14) (10D1_c78v2) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:52

HC-FR2 having the amino acid sequence of SEQ ID NO:57

HC-FR3 having the amino acid sequence of SEQ ID NO:62

HC-FR4 having the amino acid sequence of SEQ ID NO:70,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(15) (10D1_11B) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:224

HC-FR2 having the amino acid sequence of SEQ ID NO:60

HC-FR3 having the amino acid sequence of SEQ ID NO:63

HC-FR4 having the amino acid sequence of SEQ ID NO:70,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(16) (10D1_c85v1) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:52

HC-FR2 having the amino acid sequence of SEQ ID NO:56

HC-FR3 having the amino acid sequence of SEQ ID NO:64

HC-FR4 having the amino acid sequence of SEQ ID NO:70,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(17) (10D1_c85v2, 10D1_c85o1, 10D1_c85o2) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:52

HC-FR2 having the amino acid sequence of SEQ ID NO:57

HC-FR3 having the amino acid sequence of SEQ ID NO:64

HC-FR4 having the amino acid sequence of SEQ ID NO:70,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(18) (10D1_c87, 10D1_c93) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:52

HC-FR2 having the amino acid sequence of SEQ ID NO:56

HC-FR3 having the amino acid sequence of SEQ ID NO:65

HC-FR4 having the amino acid sequence of SEQ ID NO:70,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(19) (10D1_c89) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:53

HC-FR2 having the amino acid sequence of SEQ ID NO:59

HC-FR3 having the amino acid sequence of SEQ ID NO:66

HC-FR4 having the amino acid sequence of SEQ ID NO:71,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(20) (10D1_c90) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:54

HC-FR2 having the amino acid sequence of SEQ ID NO:59

HC-FR3 having the amino acid sequence of SEQ ID NO:67

HC-FR4 having the amino acid sequence of SEQ ID NO:71,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(21) (10D1_c91) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:53

HC-FR2 having the amino acid sequence of SEQ ID NO:59

HC-FR3 having the amino acid sequence of SEQ ID NO:68

HC-FR4 having the amino acid sequence of SEQ ID NO:72,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(22) (10A6) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:161

HC-FR2 having the amino acid sequence of SEQ ID NO:162

HC-FR3 having the amino acid sequence of SEQ ID NO:163

HC-FR4 having the amino acid sequence of SEQ ID NO:73,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(23) (4-35-B2) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:131

HC-FR2 having the amino acid sequence of SEQ ID NO:132

HC-FR3 having the amino acid sequence of SEQ ID NO:133

HC-FR4 having the amino acid sequence of SEQ ID NO:134,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

(24) (4-35-B4) a VH region incorporating the following FRs:

HC-FR1 having the amino acid sequence of SEQ ID NO:147

HC-FR2 having the amino acid sequence of SEQ ID NO:148

HC-FR3 having the amino acid sequence of SEQ ID NO:149

HC-FR4 having the amino acid sequence of SEQ ID NO:73,

or a variant thereof in which one or two or three amino acids in one or more of HC-FR1, HC-FR2, HC-FR3, or HC-FR4 are substituted with another amino acid.

[0106] In some aspects the antigen-binding molecule comprises a VH region comprising the CDRs according to one of (1) to (10) above, and the FRs according to one of (11) to (24) above.

[0107] In some aspects the antigen-binding molecule comprises a VH region according to one of (25) to (41) below:

(25) a VH region comprising the CDRs according to (1) and the FRs according to (11), (12), (13), (14), (15), (16), (17), (18), (19), (20) or (21).

(26) a VH region comprising the CDRs according to (2) and the FRs according to (11).

(27) a VH region comprising the CDRs according to (2) and the FRs according to (12).

(28) a VH region comprising the CDRs according to (2) and the FRs according to (13).

(29) a VH region comprising the CDRs according to (2) and the FRs according to (14).

(30) a VH region comprising the CDRs according to (2) and the FRs according to (15).

(31) a VH region comprising the CDRs according to (2) and the FRs according to (18).

(32) a VH region comprising the CDRs according to (3) and the FRs according to (16).

(33) a VH region comprising the CDRs according to (3) and the FRs according to (17).

(34) a VH region comprising the CDRs according to (4) and the FRs according to (17).

(35) a VH region comprising the CDRs according to (5) and the FRs according to (17).

(36) a VH region comprising the CDRs according to (6) and the FRs according to (19).

(37) a VH region comprising the CDRs according to (6) and the FRs according to (20).

(38) a VH region comprising the CDRs according to (7) and the FRs according to (21).

(39) a VH region comprising the CDRs according to (8) and the FRs according to (22).

(40) a VH region comprising the CDRs according to (9) and the FRs according to (23).

(41) a VH region comprising the CDRs according to (10) and the FRs according to (24).

[0108] In some aspects the antigen-binding molecule comprises a VH region according to one of (42) to (61) below:

(42) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:24.

(43) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:25.

(44) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:26.

(45) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:27.

(46) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:28.

(47) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:29.

(48) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:30.

(49) a VH region comprising an amino acid sequence having at least 70% sequence identity more

preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:31.

(50) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:32.

(51) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:33.

(52) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:34.

(53) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:35.

(54) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:36.

(55) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:37.

(56) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:38.

(57) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:39.

(58) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:40.

(59) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:127.

(60) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:143.

(61) a VH region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:157.

[0109] In some aspects the antigen-binding molecule comprises a VL region according to one of (62) to (71) below:

(62) (10D1 derived) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:91

LC-CDR2 having the amino acid sequence of SEQ ID NO:94

LC-CDR3 having the amino acid sequence of SEQ ID NO:99;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(63) (10D1, 10D1_c75, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c87, 10D1_c89, 10D1_c91, 10D1_c93) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:95;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(64) (10D1_c76) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:89

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:95;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(65) (10D1_c77) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:90

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:96;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(66) (10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:93

LC-CDR3 having the amino acid sequence of SEQ ID NO:95;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(67) (10D1_c90) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:97;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(68) (10D1_c92) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:88

LC-CDR2 having the amino acid sequence of SEQ ID NO:92

LC-CDR3 having the amino acid sequence of SEQ ID NO:98;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(69) (10A6) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:165

LC-CDR2 having the amino acid sequence of SEQ ID NO:166

LC-CDR3 having the amino acid sequence of SEQ ID NO:167;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(70) (4-35-B2) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:136

LC-CDR2 having the amino acid sequence of SEQ ID NO:137

LC-CDR3 having the amino acid sequence of SEQ ID NO:138;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

(71) (4-35-B4) a VL region incorporating the following CDRs:

LC-CDR1 having the amino acid sequence of SEQ ID NO:151

LC-CDR2 having the amino acid sequence of SEQ ID NO:152

LC-CDR3 having the amino acid sequence of SEQ ID NO:153;

or a variant thereof in which one or two or three amino acids in one or more of LC-CDR1, LC-CDR2 or LC-CDR3 are substituted with another amino acid.

[0110] In some aspects the antigen-binding molecule comprises a VL region according to one of (72) to (86) below:

(72) (10D1) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:106

LC-FR2 having the amino acid sequence of SEQ ID NO:113

LC-FR3 having the amino acid sequence of SEQ ID NO:123

LC-FR4 having the amino acid sequence of SEQ ID NO:126,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(73) (10D1_c75) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:100

LC-FR2 having the amino acid sequence of SEQ ID NO:107

LC-FR3 having the amino acid sequence of SEQ ID NO:114

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(74) (10D1_c76) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:101

LC-FR2 having the amino acid sequence of SEQ ID NO:108

LC-FR3 having the amino acid sequence of SEQ ID NO:115

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(75) (10D1_c77) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:102

LC-FR2 having the amino acid sequence of SEQ ID NO:108

LC-FR3 having the amino acid sequence of SEQ ID NO:116

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(76) (10D1_c78v1, 10D1_c78v2, 10D1_11B) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:103

LC-FR2 having the amino acid sequence of SEQ ID NO:108

LC-FR3 having the amino acid sequence of SEQ ID NO:117

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(77) (10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:103

LC-FR2 having the amino acid sequence of SEQ ID NO:108

LC-FR3 having the amino acid sequence of SEQ ID NO:118

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(78) (10D1_c87) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:103

LC-FR2 having the amino acid sequence of SEQ ID NO:109

LC-FR3 having the amino acid sequence of SEQ ID NO:119

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(79) (10D1_c89) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:104

LC-FR2 having the amino acid sequence of SEQ ID NO:110

LC-FR3 having the amino acid sequence of SEQ ID NO:120

LC-FR4 having the amino acid sequence of SEQ ID NO:125,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(80) (10D1_c90) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:105

LC-FR2 having the amino acid sequence of SEQ ID NO:110

LC-FR3 having the amino acid sequence of SEQ ID NO:121

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(81) (10D1_c91) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:104

LC-FR2 having the amino acid sequence of SEQ ID NO:111

LC-FR3 having the amino acid sequence of SEQ ID NO:122

LC-FR4 having the amino acid sequence of SEQ ID NO:125,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(82) (10D1_c92) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:100

LC-FR2 having the amino acid sequence of SEQ ID NO:112

LC-FR3 having the amino acid sequence of SEQ ID NO:114

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(83) (10D1_c93) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:103

LC-FR2 having the amino acid sequence of SEQ ID NO:108

LC-FR3 having the amino acid sequence of SEQ ID NO:119

LC-FR4 having the amino acid sequence of SEQ ID NO:124,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(84) (10A6) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:168

LC-FR2 having the amino acid sequence of SEQ ID NO:169

LC-FR3 having the amino acid sequence of SEQ ID NO:170

LC-FR4 having the amino acid sequence of SEQ ID NO:142,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(85) (4-35-B2) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:139

LC-FR2 having the amino acid sequence of SEQ ID NO:140

LC-FR3 having the amino acid sequence of SEQ ID NO:141

LC-FR4 having the amino acid sequence of SEQ ID NO:142,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

(86) (4-35-B4) a VL region incorporating the following FRs:

LC-FR1 having the amino acid sequence of SEQ ID NO:154

LC-FR2 having the amino acid sequence of SEQ ID NO:155

LC-FR3 having the amino acid sequence of SEQ ID NO:156

LC-FR4 having the amino acid sequence of SEQ ID NO:142,

or a variant thereof in which one or two or three amino acids in one or more of LC-FR1, LC-FR2, LC-FR3, or LC-FR4 are substituted with another amino acid.

[0111] In some aspects the antigen-binding molecule comprises a VL region comprising the CDRs according to one of (62) to (71) above, and the FRs according to one of (72) to (86) above.

[0112] In some aspects the antigen-binding molecule comprises a VL region according to one of (87) to (102) below:

(87) a VL region comprising the CDRs according to (62) and the FRs according to (72), (73), (74), (75), (76), (77), (78), (79), (80), (81), (82), or (83).

(88) a VL region comprising the CDRs according to (63) and the FRs according to (72).

(89) a VL region comprising the CDRs according to (63) and the FRs according to (73).

(90) a VL region comprising the CDRs according to (63) and the FRs according to (76).

(91) a VL region comprising the CDRs according to (63) and the FRs according to (78).

(92) a VL region comprising the CDRs according to (63) and the FRs according to (79).

(93) a VL region comprising the CDRs according to (63) and the FRs according to (81).

(94) a VL region comprising the CDRs according to (63) and the FRs according to (83).

(95) a VL region comprising the CDRs according to (64) and the FRs according to (74).

(96) a VL region comprising the CDRs according to (65) and the FRs according to (75).

(97) a VL region comprising the CDRs according to (66) and the FRs according to (77).

(98) a VL region comprising the CDRs according to (67) and the FRs according to (80).

(99) a VL region comprising the CDRs according to (68) and the FRs according to (82).

(100) a VL region comprising the CDRs according to (69) and the FRs according to (84).

(101) a VL region comprising the CDRs according to (70) and the FRs according to (85).

(102) a VL region comprising the CDRs according to (71) and the FRs according to (86).

[0113] In some aspects the antigen-binding molecule comprises a VL region according to one of (103) to (119) below:

(103) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:74.

(104) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:75.

(105) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:76.

(106) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:77.

(107) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:78.

(108) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:79.

(109) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:80.

(110) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:81.

(111) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:82.

(112) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:83.

(113) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:84.

(114) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:85.

(115) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:86.

(116) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:87.

(117) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:135.

(118) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:150.

(119) a VL region comprising an amino acid sequence having at least 70% sequence identity more preferably one of at least 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, sequence identity to the amino acid sequence of SEQ ID NO:164.

[0114] In some aspects the antigen-binding molecule comprises a VH region according to any one of (1) to (61) above, and a VL region according to any one of (62) to (119) above.

[0115] In aspects in accordance with the present disclosure in which one or more amino acids are substituted with another amino acid, the substitutions may be conservative substitutions, for example

according to the following Table. In some aspects, amino acids in the same block in the middle column are substituted. In some aspects, amino acids in the same line in the rightmost column are substituted:

ALIPHATIC	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
	Polar - charged	D E
		K R
AROMATIC		H F W Y

[0116] In some aspects, substitution(s) may be functionally conservative. That is, in some aspects the substitution may not affect (or may not substantially affect) one or more functional properties (e.g. target binding) of the antigen-binding molecule comprising the substitution as compared to the equivalent unsubstituted molecule.

[0117] The VH and VL region of an antigen-binding region of an antibody together constitute the Fv region. In some aspects, the antigen-binding molecule according to the present disclosure comprises, or consists of, an Fv region which binds to HER3. In some aspects the VH and VL regions of the Fv are provided as single polypeptide joined by a linker region, i.e. a single chain Fv (scFv).

[0118] In some aspects the antigen-binding molecule of the present disclosure comprises one or more regions of an immunoglobulin heavy chain constant sequence. In some aspects the immunoglobulin heavy chain constant sequence is, or is derived from, the heavy chain constant sequence of an IgG (e.g. IgG1, IgG2, IgG3, IgG4), IgA (e.g. IgA1, IgA2), IgD, IgE or IgM.

[0119] In some aspects the immunoglobulin heavy chain constant sequence is human immunoglobulin G 1 constant (IGHG1; UniProt: P01857-1, v1; SEQ ID NO:171). Positions 1 to 98 of SEQ ID NO:171 form the CH1 region (SEQ ID NO:172). Positions 99 to 110 of SEQ ID NO:171 form a hinge region between CH1 and CH2 regions (SEQ ID NO:173). Positions 111 to 223 of SEQ ID NO:171 form the CH2 region (SEQ ID NO:174). Positions 224 to 330 of SEQ ID NO:171 form the CH3 region (SEQ ID NO:175).

[0120] The exemplified antigen-binding molecules may be prepared using pFUSE-CHIg-hG1, which comprises the substitutions D356E, L358M (positions numbered according to EU numbering) in the CH3 region. The amino acid sequence of the CH3 region encoded by pFUSE-CHIg-hG1 is shown in SEQ ID NO:176. It will be appreciated that CH3 regions may be provided with further substitutions in accordance with modification to an Fc region of the antigen-binding molecule as described herein.

[0121] In some aspects a CH1 region comprises or consists of the sequence of SEQ ID NO:172, or a sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO:172. In some aspects a CH1-CH2 hinge region comprises or consists of the sequence of SEQ ID NO:173, or a sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid

sequence of SEQ ID NO:173. In some aspects a CH2 region comprises or consists of the sequence of SEQ ID NO:174, or a sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO:174. In some aspects a CH3 region comprises or consists of the sequence of SEQ ID NO:175 or 176, or a sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO:175 or 176.

[0122] In some aspects the antigen-binding molecule of the present disclosure comprises one or more regions of an immunoglobulin light chain constant sequence. In some aspects the immunoglobulin light chain constant sequence is human immunoglobulin kappa constant (IGKC; Cκ; UniProt: P01834-1, v2; SEQ ID NO:177). In some aspects the immunoglobulin light chain constant sequence is a human immunoglobulin lambda constant (IGLC; Cλ), e.g. IGLC1, IGLC2, IGLC3, IGLC6 or IGLC7. In some aspects a CL region comprises or consists of the sequence of SEQ ID NO:177, or a sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO:177.

[0123] The VL and light chain constant (CL) region, and the VH region and heavy chain constant 1 (CH1) region of an antigen-binding region of an antibody together constitute the Fab region. In some aspects the antigen-binding molecule comprises a Fab region comprising a VH, a CH1, a VL and a CL (e.g. Cκ or CA). In some aspects the Fab region comprises a polypeptide comprising a VH and a CH1 (e.g. a VH-CH1 fusion polypeptide), and a polypeptide comprising a VL and a CL (e.g. a VL-CL fusion polypeptide). In some aspects the Fab region comprises a polypeptide comprising a VH and a CL (e.g. a VH-CL fusion polypeptide) and a polypeptide comprising a VL and a CH (e.g. a VL-CH1 fusion polypeptide); that is, in some aspects the Fab region is a CrossFab region. In some aspects the VH, CH1, VL and CL regions of the Fab or CrossFab are provided as single polypeptide joined by linker regions, i.e. as a single chain Fab (scFab) or a single chain CrossFab (scCrossFab).

[0124] In some aspects, the antigen-binding molecule of the present disclosure comprises, or consists of, a Fab region which binds to HER3.

[0125] In some aspects, the antigen-binding molecule described herein comprises, or consists of, a whole antibody which binds to HER3. As used herein, "whole antibody" refers to an antibody having a structure which is substantially similar to the structure of an immunoglobulin (Ig). Different kinds of immunoglobulins and their structures are described e.g. in Schroeder and Cavacini J Allergy Clin Immunol. (2010) 125(202): S41-S52.

[0126] Immunoglobulins of type G (i.e. IgG) are ~150 kDa glycoproteins comprising two heavy chains and two light chains. From N- to C-terminus, the heavy chains comprise a VH followed by a heavy chain constant region comprising three constant domains (CH1, CH2, and CH3), and similarly the light chain comprise a VL followed by a CL. Depending on the heavy chain, immunoglobulins may be classed as IgG (e.g. IgG1, IgG2, IgG3, IgG4), IgA (e.g. IgA1, IgA2), IgD, IgE, or IgM. The light chain may be kappa (κ) or lambda (A).

[0127] In some aspects, the antigen-binding molecule described herein comprises, or consists of, an IgG (e.g. IgG1, IgG2, IgG3, IgG4), IgA (e.g. IgA1, IgA2), IgD, IgE, or IgM which binds to HER3.

[0128] In some aspects, the antigen-binding molecule of the present disclosure is at least monovalent binding for HER3. Binding valency refers to the number of binding sites in an antigen-binding molecule for a given antigenic determinant. Accordingly, in some aspects the antigen-binding molecule comprises at least one binding site for HER3.

[0129] In some aspects the antigen-binding molecule comprises more than one binding site for HER3, e.g. 2, 3 or 4 binding sites. The binding sites may be the same or different. In some aspects the antigen-binding molecule is e.g. bivalent, trivalent or tetravalent for HER3.

[0130] Aspects of the present disclosure relate to multispecific antigen-binding molecules. By "multispecific" it is meant that the antigen-binding molecule displays specific binding to more than one target. In some aspects the antigen-binding molecule is a bispecific antigen-binding molecule. In some aspects the antigen-binding molecule comprises at least two different antigen-binding domains (i.e. at least two antigen-binding domains, e.g. comprising non-identical VHs and VLs).

[0131] In some aspects the antigen-binding molecule binds to HER3 and another target (e.g. an antigen other than HER3), and so is at least bispecific. The term "bispecific" means that the antigen-binding molecule is able to bind specifically to at least two distinct antigenic determinants.

[0132] It will be appreciated that an antigen-binding molecule according to the present disclosure (e.g. a multispecific antigen-binding molecule) may comprise antigen-binding molecules capable of binding to the targets for which the antigen-binding molecule is specific. For example, an antigen-binding molecule which is capable of binding to HER3 and an antigen other than HER3 may comprise: (i) an antigen-binding molecule which is capable of binding to HER3, and (ii) an antigen-binding molecule which is capable of binding to an antigen other than HER3.

[0133] It will also be appreciated that an antigen-binding molecule according to the present disclosure (e.g. a multispecific antigen-binding molecule) may comprise antigen-binding polypeptides or antigen-binding polypeptide complexes capable of binding to the targets for which the antigen-binding molecule is specific. For example, an antigen-binding molecule according to the present disclosure may comprise e.g. (i) an antigen-binding polypeptide complex capable of binding to HER3, comprising a light chain polypeptide (comprising the structure VL-CL) and a heavy chain polypeptide (comprising the structure VH-CH1-CH2-CH3), and (ii) an antigen-binding polypeptide complex capable of binding to an antigen other than HER3, comprising a light chain polypeptide (comprising the structure VL-CL) and a heavy chain polypeptide (comprising the structure VH-CH1-CH2-CH3).

[0134] In some aspects, a component antigen-binding molecule of a larger antigen-binding molecule (e.g. a multispecific antigen-biding molecule) may be referred to e.g. as an "antigen-binding domain" or "antigen-binding region" of the larger antigen-binding molecule.

[0135] In some aspects the antigen-binding molecule comprises an antigen-binding molecule capable of binding to HER3, and an antigen-binding molecule capable of binding to an antigen other than HER3. In some aspects, the antigen other than HER3 is an immune cell surface molecule. In some aspects, the antigen other than HER3 is a cancer cell antigen. In some aspects the antigen other than HER3 is a receptor molecule, e.g. a cell surface receptor. In some aspects the antigen other than HER3 is a cell signalling molecule, e.g. a cytokine, chemokine, interferon, interleukin or lymphokine. In some aspects the antigen other than HER3 is a growth factor or a hormone.

[0136] A cancer cell antigen is an antigen which is expressed or over-expressed by a cancer cell. A cancer cell antigen may be any peptide/polypeptide, glycoprotein, lipoprotein, glycan, glycolipid, lipid, or fragment thereof. A cancer cell antigen's expression may be associated with a cancer. A cancer cell antigen may be abnormally expressed by a cancer cell (e.g. the cancer cell antigen may be expressed with abnormal localisation), or may be expressed with an abnormal structure by a cancer cell. A cancer cell antigen may be capable of eliciting an immune response. In some aspects, the antigen is expressed at the cell surface of the cancer cell (i.e. the cancer cell antigen is a cancer cell surface antigen). In some aspects, the part of the antigen which is bound by the antigen-binding molecule described herein is displayed on the external surface of the cancer cell (i.e. is extracellular). The cancer cell antigen may be a cancer-associated antigen. In some aspects the cancer cell antigen is an antigen whose expression is associated with the development, progression or severity of symptoms of a cancer. The cancer-associated antigen may be associated with the cause or pathology of the cancer, or may be expressed abnormally as a consequence of the cancer. In some aspects, the cancer cell antigen is an antigen whose expression is upregulated (e.g. at the RNA and/or protein level) by cells of a cancer, e.g. as compared to the level of expression by comparable non-cancerous cells (e.g. non-cancerous cells derived from the same tissue/cell type). In some aspects, the cancer-associated antigen may be preferentially expressed by cancerous cells, and not expressed by comparable non-cancerous cells (e.g. non-cancerous cells derived from the same tissue/cell type). In some aspects, the cancer-associated antigen may be the product of a mutated oncogene or mutated tumor suppressor gene. In some aspects, the cancer-associated antigen may be the product of an overexpressed cellular protein, a cancer antigen produced by an oncogenic virus, an oncofetal antigen, or a cell surface glycolipid or glycoprotein.

[0137] In some aspects the antigen other than HER3 is an antigen expressed by cells of a HER3-associated cancer. A HER3-associated cancer may be a cancer expressing HER3 (e.g. expressing HER3 protein at the cell surface); such cancers may be referred to as "HER3-positive" cancers. HER3-associated cancers include cancers for which HER3 gene/protein expression is a risk factor for, and/or is positively associated with, the onset, development, progression or severity of symptoms of the cancer, and/or metastasis. HER3-associated cancers include those described in Zhang et al., Acta Biochimica et Biophysica Sinica (2016) 48(1):39-48 and Sithanandam and Anderson Cancer Gene Ther (2008) 15(7):413-448. In some aspects a HER3-associated cancer may be a lung cancer (e.g. NSCLC), melanoma, breast cancer, pancreatic cancer, prostate cancer, ovarian cancer, gastric cancer, colon cancer or oral cavity cancer.

[0138] An immune cell surface molecule may be any peptide/polypeptide, glycoprotein, lipoprotein, glycan, glycolipid, lipid, or fragment thereof expressed at or on the cell surface of an immune cell. In some aspects, the part of the immune cell surface molecule which is bound by the antigen-binding molecule of the present disclosure is on the external surface of the immune cell (i.e. is extracellular). The immune cell surface molecule may be expressed at the cell surface of any immune cell. In some aspects, the immune cell may be a cell of hematopoietic origin, e.g. a neutrophil, eosinophil, basophil, dendritic cell, lymphocyte, or monocyte. The lymphocyte may be e.g. a T cell, B cell, natural killer (NK) cell, NKT cell or innate lymphoid cell (ILC), or a precursor thereof (e.g. a thymocyte or pre-B cell). In some aspects the immune cell surface molecule may be a costimulatory molecule (e.g. CD28, OX40, 4-1BB, ICOS or CD27) or a ligand thereof. In some aspects the immune cell surface molecule may be a checkpoint molecule (e.g. PD-1, CTLA-4, LAG-3, TIM-3, VISTA, TIGIT or BTLA) or a ligand thereof.

[0139] Multispecific antigen-binding molecules according to the present disclosure may be provided in any suitable format, such as those formats described in described in Brinkmann and Kontermann MAbs (2017) 9(2): 182-212. Suitable formats include those shown in Figure 2 of Brinkmann and Kontermann MAbs (2017) 9(2): 182-212: antibody conjugates, e.g. IgG_2, $F(ab')_2$ or CovX-Body; IgG or IgG-like molecules, e.g. IgG, chimeric IgG, κλ-body common HC; CH1/CL fusion proteins, e.g. scFv2-CH1/CL, VHH2-CH1/CL; 'variable domain only' bispecific antigen-binding molecules, e.g. tandem scFv (taFV), triplebodies, diabodies (Db), dsDb, Db(kih), DART, scDB, dsFv-dsFv, tandAbs, triple heads, tandem dAb/VHH, tertravalent dAb.VHH; Non-Ig fusion proteins, e.g. $scFv_2$-albumin, scDb-albumin, taFv-albumin, taFv-toxin, miniantibody, DNL-Fab_2, DNL-Fab_2-scFv, DNL-Fab_2-IgG-$cytokine_2$, ImmTAC (TCR-scFv); modified Fc and CH3 fusion proteins, e.g. scFv-Fc(kih), scFv-Fc(CH3 charge pairs), scFv-Fc (EW-RVT), scFv-fc (HA-TF), scFv-Fc (SEEDbody), taFv-Fc(kih), scFv-Fc(kih)-Fv, Fab-Fc(kih)-scFv, Fab-scFv-Fc(kih), Fab-scFv-Fc(BEAT), Fab-scFv-Fc (SEEDbody), DART-Fc, scFv-CH3(kih), TriFabs; Fc fusions, e.g. Di-diabody, scDb-Fc, taFv-Fc, scFv-Fc-scFv, HCAb-VHH, Fab-scFv-Fc, $scFv_4$-Ig, $scFv_2$-Fcab; CH3 fusions, e.g. Dia-diabody, scDb-CH3; IgE/IgM CH2 fusions, e.g. scFv-EHD2-scFv, scFvMHD2-scFv; Fab fusion proteins, e.g. Fab-scFv (bibody), Fab-$scFv_2$ (tribody), Fab-Fv, Fab-dsFv, Fab-VHH, orthogonal Fab-Fab; non-Ig fusion proteins, e.g. DNL-Fab_3, DNL-Fab_2-scFv, DNL-Fab_2-IgG-$cytokine_2$; asymmetric IgG or IgG-like molecules, e.g. IgG(kih), IgG(kih) common LC, ZW1 IgG common LC, Biclonics common LC, CrossMab, CrossMab(kih), scFab-IgG(kih), Fab-scFab-IgG(kih), orthogonal Fab IgG(kih), DuetMab, CH3 charge pairs + CH1/CL charge pairs, hinge/CH3 charge pairs, SEED-body, Duobody, four-in-one-CrossMab(kih), LUZ-Y common LC; LUZ-Y scFab-IgG, FcFc*; appended and Fc-modified IgGs, e.g. IgG(kih)-Fv, IgG HA-TF-Fv, IgG(kih)scFab, scFab-Fc(kih)-scFv2, scFab-Fc(kih)-scFv, half DVD-Ig, DVI-Ig (four-in-one), CrossMab-Fab; modified Fc and CH3 fusion proteins, e.g. Fab-Fc(kih)-scFv, Fab-scFv-Fc(kih), Fab-scFv-Fc(BEAT), Fab-scFv-Fc-SEEDbody, TriFab; appended IgGs - HC fusions, e.g. IgG-HC, scFv, IgG-dAb, IgG-taFV, IgG-CrossFab, IgG-orthogonal Fab, IgG-(CαCβ) Fab, scFv-HC-IgG, tandem Fab-IgG (orthogonal Fab) Fab-IgG(CαCβ Fab), Fab-IgG(CR3), Fab-hinge-IgG(CR3); appended IgGs - LC fusions, e.g. IgG-scFv(LC), scFv(LC)-IgG, dAb-IgG; appended IgGs - HC and LC fusions, e.g. DVD-Ig, TVD-Ig, CODV-Ig, $scFv_4$-IgG, Zybody; Fc fusions, e.g. Fab-scFv-Fc, $scFv_4$-Ig; F(ab')2 fusions, e.g. $F(ab')_2$-$scFv_2$; CH1/CL fusion proteins e.g. $scFv_2$-CH1-hinge/CL; modified IgGs, e.g. DAF (two-in one-IgG), DutaMab, Mab^2; and non-Ig fusions, e.g. DNL-Fab_4-IgG.

[0140] The skilled person is able to design and prepare bispecific antigen-binding molecules. Methods for producing bispecific antigen-binding molecules include chemically crosslinking of antigen-binding molecules or antibody fragments, e.g. with reducible disulphide or non-reducible thioether bonds, for example as described in Segal and Bast, 2001. Production of Bispecific Antigen-binding molecules. Current Protocols in Immunology. 14:IV:2.13:2.13.1-2.13.16. For example, *N*-succinimidyl-3-(-2-pyridyldithio)-propionate (SPDP) can be used to chemically crosslink e.g. Fab fragments via hinge region SH- groups, to create disulfide-linked bispecific $F(ab)_2$ heterodimers.

[0141] Other methods for producing bispecific antigen-binding molecules include fusing antibody-producing hybridomas e.g. with polyethylene glycol, to produce a quadroma cell capable of secreting bispecific antibody, for example as described in D. M. and Bast, B. J. 2001. Production of Bispecific Antigen-binding molecules. Current Protocols in Immunology. 14:IV:2.13:2.13.1-2.13.16.

[0142] Bispecific antigen-binding molecules according to the present disclosure can also be produced

recombinantly, by expression from e.g. a nucleic acid construct encoding polypeptides for the antigen-binding molecules, for example as described in Antibody Engineering: Methods and Protocols, Second Edition (Humana Press, 2012), at Chapter 40: Production of Bispecific Antigen-binding molecules: Diabodies and Tandem scFv (Hornig and Färber-Schwarz), or French, How to make bispecific antigen-binding molecules, Methods Mol. Med. 2000; 40:333-339. For example, a DNA construct encoding the light and heavy chain variable domains for the two antigen-binding fragments (i.e. the light and heavy chain variable domains for the antigen-binding fragment capable of binding HER3, and the light and heavy chain variable domains for the antigen-binding fragment capable of binding to another target protein), and including sequences encoding a suitable linker or dimerization domain between the antigen-binding fragments can be prepared by molecular cloning techniques. Recombinant bispecific antibody can thereafter be produced by expression (e.g. *in vitro*) of the construct in a suitable host cell (e.g. a mammalian host cell), and expressed recombinant bispecific antibody can then optionally be purified.

Fc regions

[0143] In some aspects the antigen-binding molecules of the present disclosure comprise an Fc region.

[0144] In IgG, IgA and IgD isotypes an Fc region is composed of CH2 and CH3 regions from one polypeptide, and CH2 and CH3 regions from another polypeptide. The CH2 and CH3 regions from the two polypeptides together form the Fc region. In IgM and IgE isotypes the Fc regions contain three constant domains (CH2, CH3 and CH4), and CH2 to CH4 from the two polypeptides together form the Fc region.

[0145] In preferred aspects in accordance with the various aspects of the present disclosure an Fc region comprises two polypeptides, each polypeptide comprising a CH2 region and a CH3 region.

[0146] In some aspects, the antigen-binding molecule of the present disclosure comprises an Fc region comprising modification in one or more of the CH2 and CH3 regions promoting association of the Fc region. Recombinant co-expression of constituent polypeptides of an antigen-binding molecule and subsequent association leads to several possible combinations. To improve the yield of the desired combinations of polypeptides in antigen-binding molecules in recombinant production, it is advantageous to introduce in the Fc regions modification(s) promoting association of the desired combination of heavy chain polypeptides. Modifications may promote e.g. hydrophobic and/or electrostatic interaction between CH2 and/or CH3 regions of different polypeptide chains. Suitable modifications are described e.g. in Ha et al., Front. Immnol (2016) 7:394.

[0147] In some aspects the antigen-binding molecule of the present disclosure comprises an Fc region comprising paired substitutions in the CH3 regions of the Fc region according to one of the following formats, as shown in Table 1 of Ha et al., Front. Immnol (2016) 7:394: KiH, KiH_{S-S}, HA-TF, ZW1, 7.8.60, DD-KK, EW-RVT, $EW\text{-}RVT_{S-S}$, SEED or A107.

[0148] In some aspects, the Fc region comprises the "knob-into-hole" or "KiH" modification, e.g. as described e.g. in US 7,695,936 and Carter, J Immunol Meth 248, 7-15 (2001). In such aspects, one of the CH3 regions of the Fc region comprises a "knob" modification, and the other CH3 region

comprises a "hole" modification. The "knob" and "hole" modifications are positioned within the respective CH3 regions so that the "knob" can be positioned in the "hole" in order to promote heterodimerisation (and inhibit homodimerisation) of the polypeptides and/or stabilise heterodimers. Knobs are constructed by substituting amino acids having small chains with those having larger side chains (e.g. tyrosine or tryptophan). Holes are created by substituting amino acids having large side chains with those having smaller side chains (e.g. alanine or threonine).

[0149] In some aspects, one of the CH3 regions of the Fc region of the antigen-binding molecule of the present disclosure comprises the substitution (numbering of positions/substitutions in the Fc, CH2 and CH3 regions herein is according to the EU numbering system as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD, 1991) T366W, and the other CH3 region of the Fc region comprises the substitution Y407V. In some aspects, one of the CH3 regions of the Fc region of the antigen-binding molecule comprises the substitution T366W, and the other CH3 region of the Fc region comprises the substitutions T366S and L368A. In some aspects, one of the CH3 regions of the Fc region of the antigen-binding molecule comprises the substitution T366W, and the other CH3 region of the Fc region comprises the substitutions Y407V, T366S and L368A.

[0150] In some aspects, the Fc region comprises the "DD-KK" modification as described e.g. in WO 2014/131694 A1. In some aspects, one of the CH3 regions comprises the substitutions K392D and K409D, and the other CH3 region of the Fc region comprises the substitutions E356K and D399K. The modifications promote electrostatic interaction between the CH3 regions.

[0151] In some aspects, the antigen-binding molecule of the present disclosure comprises an Fc region modified as described in Labrijn et al., Proc Natl Acad Sci U S A. (2013) 110(13):5145-50, referred to as 'Duobody' format. In some aspects one of the CH3 regions comprises the substitution K409R, and the other CH3 region of the Fc region comprises the substitution K405L.

[0152] In some aspects, the antigen-binding molecule of the present disclosure comprises an Fc region comprising the "EEE-RRR" modification as described in Strop et al., J Mol Biol. (2012) 420(3):204-19. In some aspects one of the CH3 regions comprises the substitutions D221E, P228E and L368E, and the other CH3 region of the Fc region comprises the substitutions D221R, P228R and K409R.

[0153] In some aspects, the antigen-binding molecule comprises an Fc region comprising the "EW-RVT" modification described in Choi et al., Mol Cancer Ther (2013) 12(12):2748-59. In some aspects one of the CH3 regions comprises the substitutions K360E and K409W, and the other CH3 region of the Fc region comprises the substitutions Q347R, D399V and F405T.

[0154] In some aspects, one of the CH3 regions comprises the substitution S354C, and the other CH3 region of the Fc region comprises the substitution Y349C. Introduction of these cysteine residues results in formation of a disulphide bridge between the two CH3 regions of the Fc region, further stabilizing the heterodimer (Carter (2001), J Immunol Methods 248, 7-15).

[0155] In some aspects, the Fc region comprises the "KiH$_{S-S}$" modification. In some aspects one of the CH3 regions comprises the substitutions T366W and S354C, and the other CH3 region of the Fc region comprises the substitutions T366S, L368A, Y407V and Y349C.

[0156] In some aspects, the antigen-binding molecule of the present disclosure comprises an Fc region comprising the "SEED" modification as described in Davis et al., Protein Eng Des Sel (2010) 23(4):195-202, in which β-strand segments of human IgG1 CH3 and IgA CH3 are exchanged.

[0157] In some aspects, one of the CH3 regions comprises the substitutions S364H and F405A, and the other CH3 region of the Fc region comprises the substitutions Y349T and T394F (see e.g. Moore et al., MAbs (2011) 3(6):546-57).

[0158] In some aspects, one of the CH3 regions comprises the substitutions T350V, L351Y, F405A and Y407V, and the other CH3 region of the Fc region comprises the substitutions T350V, T366L, K392L and T394W (see e.g. Von Kreudenstein et al., MAbs (2013) 5(5):646-54).

[0159] In some aspects, one of the CH3 regions comprises the substitutions K360D, D399M and Y407A, and the other CH3 region of the Fc region comprises the substitutions E345R, Q347R, T366V and K409V (see e.g. Leaver-Fay et al., Structure (2016) 24(4):641-51).

[0160] In some aspects, one of the CH3 regions comprises the substitutions K370E and K409W, and the other CH3 region of the Fc region comprises the substitutions E357N, D399V and F405T (see e.g. Choi et al., PLoS One (2015) 10(12):e0145349).

[0161] Fc-mediated functions include Fc receptor binding, antibody-dependent cellular cytotoxicity (ADCC), antibody-dependent cell-mediated phagocytosis (ADCP), complement-dependent cytotoxicity (CDC), formation of the membrane attack complex (MAC), cell degranulation, cytokine and/or chemokine production, and antigen processing and presentation.

[0162] Modifications to antibody Fc regions that influence Fc-mediated functions are known in the art, such as those described e.g. in Wang et al., Protein Cell (2018) 9(1):63-73. Exemplary Fc region modifications known to influence antibody effector function are summarised in Table 1 of Wang et al., Protein Cell (2018) 9(1):63-73.

[0163] The combination of substitutions F243L/R292P/Y300L/V305I/P396L is described in Stavenhagen et al. Cancer Res. (2007) to increase binding to FcγRIIIa, and thereby enhance ADCC. The combination of substitutions S239D/I332E or S239D/I332E/A330L is described in Lazar et al., Proc Natl Acad Sci USA. (2006)103:4005-4010 to increase binding to FcγRIIIa, and thereby increase ADCC. The combination of substitutions S239D/I332E/A330L is also described to decrease binding to FcγRIIb, and thereby increase ADCC. The combination of substitutions S298A/E333A/K334A is described in Shields et al., J Biol Chem. (2001) 276:6591-6604 to increase binding to FcγRIIIa, and thereby increase ADCC. The combination of substitutions L234Y/L235Q/G236W/S239M/H268D/D270E/S298A in one heavy chain, and the combination of substitutions D270E/K326D/A330M/K334E in the other heavy chain, is described in Mimoto et al., MAbs. (2013): 5:229-236 to increase binding to FcγRIIIa, and thereby increase ADCC. The combination of substitutions G236A/S239D/I332E is described in Richards et al., Mol Cancer Ther. (2008) 7:2517-2527 to increase binding to FcγRIIa and to increase binding to FcγRIIIa, and thereby increase ADCP.

[0164] The combination of substitutions K326W/E333S is described in Idusogie et al. J Immunol. (2001) 166(4):2571-5 to increase binding to C1q, and thereby increase CDC. The combination of

substitutions S267E/H268F/S324T is described in Moore et al. MAbs. (2010) 2(2):181-9 to increase binding to C1q, and thereby increase CDC. The combination of substitutions described in Natsume et al., Cancer Res. (2008) 68(10):3863-72 is reported to increase binding to C1q, and thereby increase CDC. The combination of substitutions E345R/E430G/S440Y is described in Diebolder et al. Science (2014) 343(6176):1260-3 to increase hexamerisation, and thereby increase CDC.

[0165] The combination of substitutions M252Y/S254T/T256E is described in Dall'Acqua et al. J Immunol. (2002) 169:5171-5180 to increase binding to FcRn at pH 6.0, and thereby increase antigen-binding molecule half-life. The combination of substitutions M428L/N434S is described in Zalevsky et al. Nat Biotechnol. (2010) 28:157-159 to increase binding to FcRn at pH 6.0, and thereby increase antigen-binding molecule half-life.

[0166] Where a heavy chain constant region/Fc region/CH2-CH3 region/CH2 region/CH3 region is described herein as comprising position(s)/substitution(s) "corresponding to" reference position(s)/substitution(s), equivalent position(s)/substitution(s) in homologous heavy chain constant regions/Fc regions/CH2-CH3 regions/CH2 regions/CH3 regions are contemplated.

[0167] Where an Fc region is described as comprising specific position(s)/substitution(s), the position(s)/substitution(s) may be present in one or both of the polypeptide chains which together form the Fc region.

[0168] Unless otherwise specified, positions herein refer to positions of human immunoglobulin constant region amino acid sequences numbered according to the EU numbering system as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD, 1991. By way of illustration, the substitutions L242C and K334C in human IgG1 correspond to L>C substitution at position 125, and K>C substitution at position 217 of the human IgG1 constant region numbered according to SEQ ID NO:171.

[0169] Homologous heavy chain constant regions are heavy chain constant regions comprising an amino acid sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the heavy chain constant region of Human IgG1 (i.e. the amino acid sequence shown in SEQ ID NO:171). Homologous Fc regions are Fc regions comprised of polypeptides comprising an amino acid sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to CH2-CH3 region of Human IgG1 (i.e. the amino acid sequences shown in SEQ ID NO:174 and 175). Homologous CH2 regions are CH2 regions comprising an amino acid sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to CH2 region of Human IgG1 (i.e. the amino acid sequence shown in SEQ ID NO:174). Homologous CH3 regions are CH3 regions comprising an amino acid sequence having at least 60%, preferably one of 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to CH3 region of Human IgG1 (i.e. the amino acid sequence shown in SEQ ID NO:175).

[0170] Corresponding positions to those identified in human IgG1 can be identified by sequence alignment which can be performed e.g. using sequence alignment software such as ClustalOmega

(Söding, J. 2005, Bioinformatics 21, 951-960).

[0171] In some aspects the antigen-binding molecule of the present disclosure comprises an Fc region comprising modification to increase an Fc-mediated function. In some aspects the Fc region comprises modification to increase ADCC. In some aspects the Fc region comprises modification to increase ADCP. In some aspects the Fc region comprises modification to increase CDC. An antigen-binding molecule comprising an Fc region comprising modification to increase an Fc-mediated function (e.g. ADCC, ADCP, CDC) induces an increased level of the relevant effector function as compared to an antigen-binding molecule comprising the corresponding unmodified Fc region.

[0172] In some aspects, the antigen-binding molecule of the present disclosure comprises an Fc region comprising modification to increase affinity for one or more Fc receptors (e.g. FcγRIIa, FcγRIIIa). Modifications increasing affinity for Fc receptors can increase Fc-mediated effector function such as antibody-dependent cellular cytotoxicity (ADCC) and/or antibody-dependent cellular phagocytosis (ADCP). In some aspects, the antigen-binding molecule of the present disclosure comprises an Fc region comprising modification to reduce affinity for C1q; such modification reducing complement-dependent cytotoxicity (CDC), which can be desirable. In some aspects, the antigen-binding molecule of the present disclosure comprises an Fc region comprising modification to increase hexamer formation. Modifications to the Fc region capable of increasing affinity for one or more Fc receptors, reducing affinity for C1q and/or increasing hexamer formation are described e.g. in Saxena and Wu Front Immunol. (2016) 7:580. In some aspects the antigen-binding molecule of the present disclosure comprises an Fc region comprising CH2/CH3 comprising one or more of the substitutions shown in Table 1 of Saxena and Wu Front Immunol. (2016) 7:580.

[0173] In some aspects the antigen-binding molecule of the present disclosure comprises an Fc comprising modification to increase binding to an Fc receptor. In some aspects the Fc region comprises modification to increase binding to an Fcγ receptor. In some aspects the Fc region comprises modification to increase binding to one or more of FcγRI, FcγRIIa, FcγRIIb, FcγRIIc, FcγRIIIa and FcγRIIIb. In some aspects the Fc region comprises modification to increase binding to FcγRIIIa. In some aspects the Fc region comprises modification to increase binding to FcγRIIa. In some aspects the Fc region comprises modification to increase binding to FcγRIIb. In some aspects the Fc region comprises modification to increase binding to FcRn. In some aspects the Fc region comprises modification to increase binding to a complement protein. In some aspects the Fc region comprises modification to increase or reduce binding to C1q. In some aspects the Fc region comprises modification to promote hexamerisation of the antigen-binding molecule. In some aspects the Fc region comprises modification to increase antigen-binding molecule half-life. In some aspects the Fc region comprises modification to increase co-engagement.

[0174] In this specification an "Fcγ receptor" may be from any species, and includes isoforms, fragments, variants (including mutants) or homologues from any species. Similarly, "FcγRI", "FcγRIIa", "FcγRIIb", "FcγRIIc", "FcγRIIIa" and "FcγRIIIb" refer respectively to FcγRI/FcγRIIa/FcγRIIb/FcγRIIc/FcγRIIIa/FcγRIIIb from any species, and include isoforms, fragments, variants (including mutants) or homologues from any species. Humans have six different classes of Fc y receptor (mouse orthologues are shown in brackets): FcγRI (mFcγRI), FcγRIIa (mFcγRIII), FcγRIIb (mFcγRIIb), FcγRIIc, FcγRIIIa (mFcγRIV) and FcγRIIIb. Variant Fc y receptors include e.g. the 158V and 158F polymorphs of human FcγRIIIa, and the 167H and 167R polymorphs of human FcγRIIa.

[0175] In some aspects the antigen-binding molecule of the present disclosure comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, or a CH2-CH3 region, comprising) one or more (e.g. 1, 2, 3, 4, 5, 6, 7 or 8) of the following: C at the position corresponding to position 242; C at the position corresponding to position 334; A at the position corresponding to position 236; D at the position corresponding to position 239; E at the position corresponding to position 332; L at the position corresponding to position 330; K at the position corresponding to position 345; and G at the position corresponding to position 430.

[0176] In some aspects the antigen-binding molecule of the present disclosure comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, or a CH2-CH3 region, comprising) one or more (e.g. 1, 2, 3, 4, 5, 6, 7 or 8) of the following substitutions (or corresponding substitutions): L242C, K334C, G236A, S239D, I332E, A330L, E345K, and E430G.

[0177] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) a C at the position corresponding to position 242. In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) a C at the position corresponding to position 334. In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) a C at the position corresponding to position 242 and a C at the position corresponding to position 334.

[0178] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) an A at the position corresponding to position 236. In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) a D at the position corresponding to position 239. In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) an A at the position corresponding to position 236, and a D at the position corresponding to position 239.

[0179] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) an E at the position corresponding to position 332. In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) an A at the position corresponding to position 236, a D at the position corresponding to position 239, and an E at the position corresponding to position 332.

[0180] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) an L at the position corresponding to position 330. In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) an A at the position corresponding to position 236, a D at the position corresponding to position 239, an E at the position corresponding to position 332, and an L at the position corresponding to position 330.

[0181] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH3 region, comprising) a K at the position corresponding to position 345. In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH3 region, comprising) a G at the position corresponding to position 430. In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) a K at the position corresponding to position 345, and a G at the position corresponding to position 430.

[0182] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) a C at the position corresponding to position 242, a C at the position corresponding to position 334, an A at the position corresponding to position 236, and a D at the position corresponding to position 239.

[0183] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) a C at the position corresponding to position 242, a C at the position corresponding to position 334, an A at the position corresponding to position 236, a D at the position corresponding to position 239, and an E at the position corresponding to position 332.

[0184] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) a C at the position corresponding to position 242, a C at the position corresponding to position 334, an A at the position corresponding to position 236, a D at the position corresponding to position 239, an E at the position corresponding to position 332, and an L at the position corresponding to position 330.

[0185] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, or a CH2-CH3 region, comprising) a C at the position corresponding to position 242, a C at the position corresponding to position 334, a K at the position corresponding to position 345, and a G at the position corresponding to position 430.

[0186] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution L242C (or an equivalent substitution). In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution K334C (or an equivalent substitution). In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution L242C (or an equivalent substitution) and the substitution K334C (or an equivalent substitution).

[0187] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution G236A (or an equivalent substitution). In some aspects the

Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution S239D (or an equivalent substitution). In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution G236A (or an equivalent substitution), and the substitution S239D (or an equivalent substitution).

[0188] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution I332E (or an equivalent substitution). In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution G236A (or an equivalent substitution), the substitution S239D (or an equivalent substitution), and the substitution I332E (or an equivalent substitution).

[0189] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution A330L (or an equivalent substitution). In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution G236A (or an equivalent substitution), the substitution S239D (or an equivalent substitution), the substitution I332E (or an equivalent substitution), and the substitution A330L (or an equivalent substitution).

[0190] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH3 region, comprising) the substitution E345K (or an equivalent substitution). In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH3 region, comprising) the substitution E430G (or an equivalent substitution). In some aspects the Fc region comprises (e.g. comprises one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution E345K (or an equivalent substitution), and the substitution E430G (or an equivalent substitution).

[0191] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution L242C (or an equivalent substitution), the substitution K334C (or an equivalent substitution), the substitution G236A (or an equivalent substitution), and the substitution S239D (or an equivalent substitution).

[0192] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a CH2 region, comprising) the substitution L242C (or an equivalent substitution), the substitution K334C (or an equivalent substitution), the substitution G236A (or an equivalent substitution), the substitution S239D (or an equivalent substitution), and the substitution I332E (or an equivalent substitution).

[0193] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, a CH2-CH3 region, or a

CH2 region, comprising) the substitution L242C (or an equivalent substitution), the substitution K334C (or an equivalent substitution), the substitution G236A (or an equivalent substitution), the substitution S239D (or an equivalent substitution), the substitution I332E (or an equivalent substitution), and the substitution A330L (or an equivalent substitution).

[0194] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, or a CH2-CH3 region, comprising) the substitution L242C (or an equivalent substitution), the substitution K334C (or an equivalent substitution), the substitution E345K (or an equivalent substitution), and the substitution E430G (or an equivalent substitution).

[0195] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, or a CH2-CH3 region, comprising) one or more (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12) of the following: L at the position corresponding to position 243, P at the position corresponding to position 292, L at the position corresponding to position 300, I at the position corresponding to position 305 and L at the position corresponding to position 396; D at the position corresponding to position 239 and E at the position corresponding to position 332; D at the position corresponding to position 239, E at the position corresponding to position 332 and L at the position corresponding to position 330; A at the position corresponding to position 298, A at the position corresponding to position 333 and A at the position corresponding to position 334; Y at the position corresponding to position 234, Q at the position corresponding to position 235, W at the position corresponding to position 236, M at the position corresponding to position 239, D at the position corresponding to position 268, E at the position corresponding to position 270 and A at the position corresponding to position 298; E at the position corresponding to position 270, D at the position corresponding to position 326, M at the position corresponding to position 330 and E at the position corresponding to position 334; A at the position corresponding to position 236, D at the position corresponding to position 239 and E at the position corresponding to position 332; W at the position corresponding to position 326 and S at the position corresponding to position 333; E at the position corresponding to position 267, F at the position corresponding to position 268 and T at the position corresponding to position 324; R at the position corresponding to position 345, G at the position corresponding to position 430 and Y at the position corresponding to position 440; Y at the position corresponding to position 252, T at the position corresponding to position 254 and E at the position corresponding to position 256; and L at the position corresponding to position 428 and S at the position corresponding to position 434.

[0196] In some aspects the antigen-binding molecule comprises an Fc region comprising (e.g. comprising one more polypeptides comprising a heavy chain constant region, or a CH2-CH3 region, comprising) one or more (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12) of the following combinations of substitutions (or corresponding substitutions): F243L/R292P/Y300L/V305I/P396L; S239D/I332E; S239D/I332E/A330L; S298A/E333A/K334A; L234Y/L235Q/G236W/S239M/H268D/D270E/S298A; D270E/K326D/A330M/K334E; G236A/S239D/I332E; K326W/E333S; S267E/H268F/S324T; E345R/E430G/S440Y; M252Y/S254T/T256E; and M428L/N434S.

Polypeptides

[0197] The present disclosure also provides polypeptide constituents of antigen-binding molecules.

The polypeptides may be provided in isolated or substantially purified form.

[0198] The antigen-binding molecule of the present disclosure may be, or may comprise, a complex of polypeptides.

[0199] In the present specification where a polypeptide comprises more than one domain or region, it will be appreciated that the plural domains/regions are preferably present in the same polypeptide chain. That is, the polypeptide comprises more than one domain or region is a fusion polypeptide comprising the domains/regions.

[0200] In some aspects a polypeptide according to the present disclosure comprises, or consists of, a VH as described herein. In some aspects a polypeptide according to the present disclosure comprises, or consists of, a VL as described herein.

[0201] In some aspects, the polypeptide additionally comprises one or more antibody heavy chain constant regions (CH). In some aspects, the polypeptide additionally comprises one or more antibody light chain constant regions (CL).In some aspects, the polypeptide comprises a CH1, CH2 region and/or a CH3 region of an immunoglobulin (Ig).

[0202] In some aspects the polypeptide comprises one or more regions of an immunoglobulin heavy chain constant sequence. In some aspects the polypeptide comprises a CH1 region as described herein. In some aspects the polypeptide comprises a CH1-CH2 hinge region as described herein. In some aspects the polypeptide comprises a CH2 region as described herein. In some aspects the polypeptide comprises a CH3 region as described herein. In some aspects the polypeptide comprises a CH2-CH3 region as described herein.

[0203] In some aspects the polypeptide comprises a CH3 region comprising any one of the following amino acid substitutions/combinations of amino acid substitutions (shown e.g. in Table 1 of Ha et al., Front. Immnol (2016) 7:394): T366W; T366S, L368A and Y407V; T366W and S354C; T366S, L368A, Y407V and Y349C; S364H and F405A; Y349T and T394F; T350V, L351Y, F405A and Y407V; T350V, T366L, K392L and T394W; K360D, D399M and Y407A; E345R, Q347R, T366V and K409V; K409D and K392D; D399K and E356K; K360E and K409W; Q347R, D399V and F405T; K360E, K409W and Y349C; Q347R, D399V, F405T and S354C; K370E and K409W; and E357N, D399V and F405T.

[0204] In some aspects the CH2 and/or CH3 regions of the polypeptide comprise one or more amino acid substitutions for promoting association of the polypeptide with another polypeptide comprising a CH2 and/or CH3 region.

[0205] In some aspects the polypeptide comprises one or more regions of an immunoglobulin light chain constant sequence. In some aspects the polypeptide comprises a CL region as described herein.

[0206] In some aspects, the polypeptide according to the present disclosure comprises a structure from N- to C-terminus according to one of the following:

1. (i) VH
2. (ii) VL
3. (iii) VH-CH1

4. (iv) VL-CL
5. (v) VL-CH1
6. (vi) VH-CL
7. (vii) VH-CH1-CH2-CH3
8. (viii) VL-CL-CH2-CH3
9. (ix) VL-CH1-CH2-CH3
10. (x) VH-CL-CH2-CH3

[0207] Also provided by the present disclosure are antigen-binding molecules composed of the polypeptides of the present disclosure. In some aspects, the antigen-binding molecule of the present disclosure comprises one of the following combinations of polypeptides:

1. (A) VH + VL
2. (B) VH-CH1 + VL-CL
3. (C) VL-CH1 + VH-CL
4. (D) VH-CH1-CH2-CH3 + VL-CL
5. (E) VH-CL-CH2-CH3 + VL-CH1
6. (F) VL-CH1-CH2-CH3 + VH-CL
7. (G) VL-CL-CH2-CH3 + VH-CH1
8. (H) VH-CH1-CH2-CH3 + VL-CL-CH2-CH3
9. (I) VH-CL-CH2-CH3 + VL-CH1-CH2-CH3

[0208] In some aspects the antigen-binding molecule comprises more than one of a polypeptide of the combinations shown in (A) to (I) above. By way of example, with reference to (D) above, in some aspects the antigen-binding molecule comprises two polypeptides comprising the structure VH-CH1-CH2-CH3, and two polypeptides comprising the structure VL-CL.

[0209] In some aspects, the antigen-binding molecule of the present disclosure comprises one of the following combinations of polypeptides:

(J) VH (anti-HER3) + VL (anti-HER3)

(K) VH (anti-HER3)-CH1 + VL (anti-HER3)-CL

(L) VL (anti-HER3)-CH1 + VH (anti-HER3)-CL

(M) VH (anti-HER3)-CH1-CH2-CH3 + VL (anti-HER3)-CL

(N) VH (anti-HER3)-CL-CH2-CH3 + VL (anti-HER3)-CH1

(O) VL (anti-HER3)-CH1-CH2-CH3 + VH (anti-HER3)-CL

(P) VL (anti-HER3)-CL-CH2-CH3 + VH (anti-HER3)-CH1

(Q) VH (anti-HER3)-CH1-CH2-CH3 + VL (anti-HER3)-CL-CH2-CH3

(R) VH (anti-HER3)-CL-CH2-CH3 + VL (anti-HER3)-CH1-CH2-CH3

[0210] Wherein: "VH(anti-HER3)" refers to the VH of an antigen-binding molecule capable of binding to HER3 as described herein, e.g. as defined in one of (1) to (61) above; "VL(anti-HER3)" refers to the VL of an antigen-binding molecule capable of binding to HER3 as described herein, e.g. as defined in one of (62) to (119) above.

[0211] In some aspects the polypeptide comprises or consists of an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of one of SEQ ID NOs:187 to 223.

Linkers and additional sequences

[0212] In some aspects the antigen-binding molecules and polypeptides of the present disclosure comprise a hinge region. In some aspects a hinge region is provided between a CH1 region and a CH2 region. In some aspects a hinge region is provided between a CL region and a CH2 region. In some aspects the hinge region comprises, or consists of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of SEQ ID NO:173.

[0213] In some aspects the antigen-binding molecules and polypeptides of the present disclosure comprise one or more linker sequences between amino acid sequences. A linker sequence may be provided at one or both ends of one or more of a VH, VL, CH1-CH2 hinge region, CH2 region and a CH3 region of the antigen-binding molecule/polypeptide.

[0214] Linker sequences are known to the skilled person, and are described, for example in Chen et al., Adv Drug Deliv Rev (2013) 65(10): 1357-1369. In some aspects, a linker sequence may be a flexible linker sequence. Flexible linker sequences allow for relative movement of the amino acid sequences which are linked by the linker sequence. Flexible linkers are known to the skilled person, and several are identified in Chen et al., Adv Drug Deliv Rev (2013) 65(10): 1357-1369. Flexible linker sequences often comprise high proportions of glycine and/or serine residues.

[0215] In some aspects, the linker sequence comprises at least one glycine residue and/or at least one serine residue. In some aspects the linker sequence consists of glycine and serine residues. In some aspects, the linker sequence has a length of 1-2, 1-3, 1-4, 1-5 or 1-10 amino acids.

[0216] The antigen-binding molecules and polypeptides of the present disclosure may additionally comprise further amino acids or sequences of amino acids. For example, the antigen-binding molecules and polypeptides may comprise amino acid sequence(s) to facilitate expression, folding, trafficking, processing, purification or detection of the antigen-binding molecule/polypeptide. For example, the antigen-binding molecule/polypeptide may comprise a sequence encoding a His, (e.g. 6XHis), Myc, GST, MBP, FLAG, HA, E, or Biotin tag, optionally at the N- or C- terminus of the antigen-binding molecule/polypeptide. In some aspects the antigen-binding molecule/polypeptide comprises a detectable moiety, e.g. a fluorescent, lunminescent, immuno-detectable, radio, chemical, nucleic acid or enzymatic label.

[0217] The antigen-binding molecules and polypeptides of the present disclosure may additionally comprise a signal peptide (also known as a leader sequence or signal sequence). Signal peptides normally consist of a sequence of 5-30 hydrophobic amino acids, which form a single alpha helix. Secreted proteins and proteins expressed at the cell surface often comprise signal peptides.

[0218] The signal peptide may be present at the N-terminus of the antigen-binding molecule/polypeptide, and may be present in the newly synthesised antigen-binding molecule/polypeptide. The signal peptide provides for efficient trafficking and secretion of the antigen-binding molecule/polypeptide. Signal peptides are often removed by cleavage, and thus are not comprised in the mature antigen-binding molecule/polypeptide secreted from the cell expressing the antigen-binding molecule/polypeptide.

[0219] Signal peptides are known for many proteins, and are recorded in databases such as GenBank, UniProt, Swiss-Prot, TrEMBL, Protein Information Resource, Protein Data Bank, Ensembl, and InterPro, and/or can be identified/predicted e.g. using amino acid sequence analysis tools such as SignalP (Petersen et al., 2011 Nature Methods 8: 785-786) or Signal-BLAST (Frank and Sippl, 2008 Bioinformatics 24: 2172-2176).

[0220] In some aspects, the signal peptide of the antigen-binding molecule/polypeptide of the present disclosure comprises, or consists of, an amino acid sequence having at least 80%, 85% 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of one of SEQ ID NOs:178 to 186.

Labels and conjugates

[0221] In some aspects the antigen-binding molecules of the present disclosure additionally comprise a detectable moiety.

[0222] In some aspects the antigen-binding molecule comprises a detectable moiety, e.g. a fluorescent label, phosphorescent label, luminescent label, immuno-detectable label (e.g. an epitope tag), radiolabel, chemical, nucleic acid or enzymatic label. The antigen-binding molecule may be covalently or non-covalently labelled with the detectable moiety.

[0223] Fluorescent labels include e.g. fluorescein, rhodamine, allophycocyanin, eosine and NDB, green fluorescent protein (GFP) chelates of rare earths such as europium (Eu), terbium (Tb) and samarium (Sm), tetramethyl rhodamine, Texas Red, 4-methyl umbelliferone, 7-amino-4-methyl coumarin, Cy3, and Cy5. Radiolabels include radioisotopes such as Iodine^{123}, Iodine^{125}, Iodine^{126}, Iodine^{131}, Iodine^{133}, Bromine^{77}, Technetium^{99m}, Indium^{111}, Indium^{113m}, Gallium^{67}, Gallium^{68}, Ruthenium^{95}, Ruthenium^{97}, Ruthenium^{103}, Ruthenium^{105}, Mercury^{207}, Mercury^{203}, Rhenium^{99m}, Rhenium^{101}, Rhenium^{105}, Scandium^{47}, Tellurium^{121m}, Tellurium^{122m}, Tellurium^{125m}, Thulium^{165}, Thuliuml^{167}, Thulium^{168}, Copper^{67}, Fluorine^{18}, Yttrium^{90}, Palladium^{100}, Bismuth^{217} and Antimony^{211}. Luminescent labels include as radioluminescent, chemiluminescent (e.g. acridinium ester, luminol, isoluminol) and bioluminescent labels. Immuno-detectable labels include haptens, peptides/polypeptides, antibodies, receptors and ligands such as biotin, avidin, streptavidin or digoxigenin. Nucleic acid labels include aptamers. Enzymatic labels include e.g. peroxidase, alkaline

phosphatase, glucose oxidase, beta-galactosidase and luciferase.

[0224] In some aspects the antigen-binding molecules of the present disclosure are conjugated to a chemical moiety. The chemical moiety may be a moiety for providing a therapeutic effect. Antibody-drug conjugates are reviewed e.g. in Parslow et al., Biomedicines. 2016 Sep; 4(3):14. In some aspects, the chemical moiety may be a drug moiety (e.g. a cytotoxic agent). In some aspects, the drug moiety may be a chemotherapeutic agent. In some aspects, the drug moiety is selected from calicheamicin, DM1, DM4, monomethylauristatin E (MMAE), monomethylauristatin F (MMAF), SN-38, doxorubicin, duocarmycin, D6.5 and PBD.

Particular exemplary aspects of the antigen-binding molecules

[0225] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:187; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:188.

[0226] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:189; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91 %, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:190.

[0227] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91 %, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:191; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91 %, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:192.

[0228] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%,

preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:193; and

2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:195.

[0229] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:194; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:195.

[0230] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:196; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:195.

[0231] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:197; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:199.

[0232] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:198; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:199.

[0233] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:200; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:201.

[0234] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:202; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:203.

[0235] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:204; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:205.

[0236] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:206; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:207.

[0237] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:208; and

2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:209.

[0238] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:210; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:211.

[0239] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:212; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:213.

[0240] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:214; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:215.

[0241] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:216; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:217.

[0242] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:218; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:219.

[0243] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:220; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:221.

[0244] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:222; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:223.

[0245] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:225; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:207.

[0246] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:226; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%,

preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:207.

[0247] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:227; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:217.

[0248] In some aspects the antigen-binding molecule comprises, or consists of:

1. (i) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:228; and
2. (ii) two polypeptides comprising, or consisting of, an amino acid sequence having at least 70%, preferably one of 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the amino acid sequence of NO:217.

Functional properties of the antigen-binding molecules

[0249] The antigen-binding molecules described herein may be characterised by reference to certain functional properties. In some aspects, the antigen-binding molecule described herein may possess one or more of the following properties:

binds to HER3 (e.g. human, mouse, rat or cynomolgus macaque HER3);

does not bind to EGFR and/or HER2;

binds to HER3-expressing cells;

binds to subdomain II of the extracellular region of HER3;

binds to HER3 when HER3 is in open and closed conformations;

binds to HER3 independently of NRG;

does not compete with MM-121 and/or LJM-716 for binding to HER3;

does not compete with M-05-74 and/or M-08-11 for binding to HER3;

inhibits interaction between HER3 and an interaction partner for HER3 (e.g. HER3, HER2, EGFR, HER4, HGFR, IGF1R and/or cMet);

inhibits HER3-mediated signalling;

inhibits proliferation of HER3-expressing cells (e.g. in response to stimulation with NRG);

inhibits PI3K/AKT/mTOR and/or MAPK signalling by HER3-expressing cells (e.g. in response to stimulation with NRG);

binds to an activatory Fcγ receptor (e.g. FcγRIIIa);

increased binding to an activatory Fcγ receptor;

increased binding to an activatory Fcγ receptor as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

decreased binding to an inhibitory Fcγ receptor as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

increased binding to an activatory Fcγ receptor over an inhibitory Fcγ receptor as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

increased or decreased binding to a complement protein (e.g. C1q) as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

increased hexamerisation as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

increased ADCC activity as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

increased ADCP activity as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

increased or decreased CDC activity as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

similar or increased thermostability as compared to an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175;

increases killing of HER3-expressing cells;

reduces the number/proportion of HER3-expressing cells;

and

inhibits the development and/or progression of cancer *in vivo.*

[0250] The antigen-binding molecules described herein preferably display specific binding to HER3. As used herein, "specific binding" refers to binding which is selective for the antigen, and which can be discriminated from non-specific binding to non-target antigen. An antigen-binding molecule that specifically binds to a target molecule preferably binds the target with greater affinity, and/or with greater duration than it binds to other, non-target molecules.

[0251] The ability of a given polypeptide to bind specifically to a given molecule can be determined by analysis according to methods known in the art, such as by ELISA, Surface Plasmon Resonance (SPR; see e.g. Hearty et al., Methods Mol Biol (2012) 907:411-442), Bio-Layer Interferometry (see e.g. Lad et al., (2015) J Biomol Screen 20(4): 498-507), flow cytometry, or by a radiolabeled antigen-binding assay (RIA) enzyme-linked immunosorbent assay. Through such analysis binding to a given molecule can be measured and quantified. In some aspects, the binding may be the response detected in a given assay.

[0252] In some aspects, the extent of binding of the antigen-binding molecule to an non-target molecule is less than about 10% of the binding of the antibody to the target molecule as measured, e.g. by ELISA, SPR, Bio-Layer Interferometry or by RIA. Alternatively, binding specificity may be reflected in terms of binding affinity where the antigen-binding molecule binds with a dissociation constant (K_D) that is at least 0.1 order of magnitude (i.e. 0.1×10^n, where n is an integer representing the order of magnitude) greater than the K_D of the antigen-binding molecule towards a non-target molecule. This may optionally be one of at least 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.5, or 2.0.

[0253] In some aspects, the antigen-binding molecule displays binding to human HER3, mouse HER3, rat HER3 and/or cynomolgus macaque (*Macaca fascicularis*) HER3. That is, in some aspects the antigen-binding molecule is cross-reactive for human HER3, mouse HER3, rat HER3 and/or cynomolgus macaque HER3. In some aspects the antigen-binding molecule of the present disclosure displays cross-reactivity with HER3 of a non-human primate. Cross-reactivity to HER3 in model species allows *in vivo* exploration of efficacy in syngeneic models without relying on surrogate molecules.

[0254] In some aspects the antigen-binding molecule binds to human HER3, mouse HER3, rat HER3 and/or cynomolgus macaque HER3; and does not bind to HER2 and/or EGFR (e.g. human HER2 and/or human EGFR).

[0255] In some aspects, the antigen-binding molecule does not display specific binding to EGFR (e.g. human EGFR). In some aspects, the antigen-binding molecule does not display specific binding to HER2 (e.g. human HER2). In some aspects, the antigen-binding molecule does not display specific binding to (i.e. does not cross-react with) a member of the EGFR family of proteins other than HER3. In some aspects, the antigen-binding molecule does not display specific binding to EGFR, HER2 and/or HER4.

[0256] In some aspects, the antigen-binding molecule of the present disclosure binds to HER3 (e.g. human HER3) with a K_D of 10 μM or less, preferably one of ≤5 μM, ≤2 μM, ≤1 μM, ≤500 nM, ≤400 nM, ≤300 nM, ≤200 nM, ≤100 nM, ≤95 nM, ≤90 nM, ≤85 nM, ≤80 nM, ≤75 nM, ≤70 nM, ≤65 nM, ≤60 nM, ≤55 nM, ≤50 nM, ≤45 nM, ≤40 nM, ≤35 nM, ≤30 nM, ≤25 nM, ≤20 nM, ≤15 nM, ≤12.5 nM, ≤10 nM, ≤9 nM, ≤8 nM, ≤7 nM, ≤6 nM, <5 nM, ≤4 nM ≤3 nM, ≤2 nM, ≤1 nM, ≤900 pM, ≤800 pM, ≤700 pM, ≤600 pM, ≤500 pM, ≤400 pM, ≤300 pM, ≤200 pM, ≤100 pM, ≤90 pM, ≤80 pM, ≤70 pM, ≤60 pM, ≤50

pM, ≤40 pM, ≤30 pM, ≤20 pM, ≤10 pM, ≤9 pM, ≤8 pM, ≤7 pM, ≤6 pM, ≤5 pM, ≤4 pM, ≤3 pM, ≤2 pM, ≤1 pM.

[0257] The antigen-binding molecules of the present disclosure may bind to a particular region of interest of HER3. The antigen-binding region of an antigen-binding molecule according to the present disclosure may bind to a linear epitope of HER3, consisting of a contiguous sequence of amino acids (i.e. an amino acid primary sequence). In some aspects, the antigen-binding molecule may bind to a conformational epitope of HER3, consisting of a discontinuous sequence of amino acids of the amino acid sequence.

[0258] In some aspects, the antigen-binding molecule of the present disclosure binds to HER3. In some aspects, the antigen-binding molecule binds to the extracellular region of HER3 (e.g. the region shown in SEQ ID NO:9). In some aspects, the antigen-binding molecule binds to subdomain II of the extracellular region of HER3 (e.g. the region shown in SEQ ID NO:16).

[0259] In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:229. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:229. In some aspects, the antigen-binding molecule binds to the regions of HER3 shown in SEQ ID NOs:230 and 231. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the regions of HER3 shown in SEQ ID NOs:230 and 231. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:230. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:230. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:231. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:231. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:23. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:23. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:21. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:21. In some aspects the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:19. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:19. In some aspects, the antigen-binding molecule binds to the region of HER3 shown in SEQ ID NO:22. In some aspects the antigen-binding molecule contacts one or more amino acid residues of the region of HER3 shown in SEQ ID NO:22.

[0260] In some aspects, the antigen-binding molecule of the present disclosure is capable of binding to a polypeptide comprising, or consisting of, the amino acid sequence of one of SEQ ID NOs:1, 3, 4, 6 or 8. In some aspects, the antigen-binding molecule is capable of binding to a polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:9. In some aspects, the antigen-binding molecule is capable of binding to a polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:16. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:229. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequences of SEQ ID NO:230 and 231. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:230. In some aspects, the antigen-binding molecule is

capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:231. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:23. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:21. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:19. In some aspects, the antigen-binding molecule is capable of binding to a peptide/polypeptide comprising, or consisting of, the amino acid sequence of SEQ ID NO:22.

[0261] In some aspects, the antigen-binding molecule does not bind to the region of HER3 corresponding to positions 260 to 279 of SEQ ID NO:1. In some aspects the antigen-binding molecule does not contact an amino acid residue of the region of HER3 corresponding to positions 260 to 279 of SEQ ID NO:1. In some aspects, the antigen-binding molecule does not bind to the region of HER3 shown in SEQ ID NO:23. In some aspects the antigen-binding molecule does not contact an amino acid residue of the region of HER3 shown in SEQ ID NO:23. In some aspects, the antigen-binding molecule is not capable of binding to a peptide consisting of the amino acid sequence corresponding to positions 260 to 279 of SEQ ID NO:1. In some aspects, the antigen-binding molecule is not capable of binding to a peptide consisting of the amino acid sequence of SEQ ID NO:23.

[0262] As used herein, a "peptide" refers to a chain of two or more amino acid monomers linked by peptide bonds. A peptide typically has a length in the region of about 2 to 50 amino acids. A "polypeptide" is a polymer chain of two or more peptides. Polypeptides typically have a length greater than about 50 amino acids.

[0263] The ability of an antigen-binding molecule to bind to a given peptide/polypeptide can be analysed by methods well known to the skilled person, including analysis by ELISA, immunoblot (e.g. western blot), immunoprecipitation, surface plasmon resonance and biolayer interferometry.

[0264] Ligand binding to HER3 promotes conformational changes that enables HER3 to homo- or heterodimerise, resulting in activation of downstream pathways. HER3 demonstrates 'closed' and 'open' conformations. By closed conformation it is meant that HER3 is in a tethered conformation and is unavailable for receptor homo- or heterodimerisation. By open conformation it is meant that HER3 is in an extended conformation and is available for receptor homo- or heterodimerisation.

[0265] In some aspects the antigen-binding molecule is capable of binding to HER3 when HER3 is in the open conformation. In some aspects the antigen-binding molecule is capable of binding to HER3 when HER3 is in the closed conformation. In some aspects the antigen-binding molecule is capable of binding to HER3 when HER3 is in the open and/or closed conformation. In some aspects the antigen-binding molecule is capable of binding to the HER3 ectodomain when HER3 is in the open and/or closed conformation. In some aspects the antigen-binding molecule is capable of binding to the HER3 dimerisation arm when HER3 is in the open and/or closed conformation. Binding to the dimerisation arm enables an antigen-binding molecule to prevent interaction between HER3 and an interaction partner for HER3, e.g. as described herein.

[0266] In some aspects the antigen-binding molecule is capable of binding to HER3 in the presence and/or absence of a ligand for HER3. In some aspects the antigen-binding molecule is capable of binding to HER3 independently of a ligand for HER3. In some aspects the ligand is NRG, NRG-1

and/or NRG-2. HER3 is activated by ligand binding to its extracellular domain which promotes conformational changes that enables HER3 to homo- or heterodimerise. Binding of an antigen-binding molecule to HER3 independently of ligand binding allows the antigen-binding molecule to inhibit the action of HER3 in both ligand-absent and ligand-present conformational states. In some aspects the antigen-binding molecule does not compete with ligand binding to HER3. In some aspects the antigen-binding molecule does not bind to HER3 at the ligand binding site.

[0267] In some aspects the antigen-binding molecule is capable of binding the same region of HER3, or an overlapping region of HER3, to the region of HER3 which is bound by an antibody comprising the VH and VL sequences of one of clones 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93, 10A6, 4-35-B2 or 4-35-B4. In some aspects the antigen-binding molecule is capable of binding the same region of HER3, or an overlapping region of HER3, to the region of HER3 which is bound by an antibody comprising the VH and VL sequences of one of clones 10D1_c89, 10D1_c90 or 10D1_c91. In some aspects the antigen-binding molecule is capable of binding the same region of HER3, or an overlapping region of HER3, to the region of HER3 which is bound by an antibody comprising the VH and VL sequences of clone 10D1_c89.

[0268] The region of a peptide/polypeptide to which an antibody binds can be determined by the skilled person using various methods well known in the art, including X-ray co-crystallography analysis of antibody-antigen complexes, peptide scanning, mutagenesis mapping, hydrogen-deuterium exchange analysis by mass spectrometry, phage display, competition ELISA and proteolysis-based 'protection' methods. Such methods are described, for example, in Gershoni et al., BioDrugs, 2007, 21(3):145-156. Such methods can also be used to determine whether an antigen-binding molecule is capable of binding to proteins in different conformations.

[0269] In some aspects the antigen-binding molecule of the present disclosure does not bind to HER3 in the same region of HER3, or an overlapping region of HER3, as an antibody comprising the VH and VL sequences of anti-HER3 antibody clone MM-121 (described e.g. in Schoeberl et al., Sci. Signal. (2009) 2(77): ra31) and/or LJM-716 (described e.g. Garner et al., Cancer Res (2013) 73: 6024-6035). In some aspects the antigen-binding molecule of the present disclosure does not display competition with an antibody comprising the VH and VL sequences of anti-HER3 antibody clone MM-121 and/or LJM-716 for binding to HER3, e.g. as determined by SPR analysis.

[0270] In some aspects the antigen-binding molecule of the present disclosure binds to HER3 in a region which is accessible to an antigen-binding molecule (i.e., an extracellular antigen-binding molecule) when HER3 is expressed at the cell surface (i.e. in or at the cell membrane). In some aspects the antigen-binding molecule is capable of binding to HER3 expressed at the cell surface of a cell expressing HER3. In some aspects the antigen-binding molecule is capable of binding to HER3-expressing cells (e.g. HER3+ cells, e.g. HER3+ cancer cells).

[0271] The ability of an antigen-binding molecule to bind to a given cell type can be analysed by contacting cells with the antigen-binding molecule, and detecting antigen-binding molecule bound to the cells, e.g. after a washing step to remove unbound antigen-binding molecule. The ability of an antigen-binding molecule to bind to immune cell surface molecule-expressing cells and/or cancer cell antigen-expressing cells can be analysed by methods such as flow cytometry and immunofluorescence microscopy.

[0272] The antigen-binding molecule of the present disclosure may be an antagonist of HER3. In some aspects, the antigen-binding molecule is capable of inhibiting a function or process (e.g. interaction, signalling or other activity) mediated by HER3 and/or a binding partner for HER3 (e.g. HER3 (i.e. in the case of homodimerisation), HER2, EGFR, HER4, HGFR, IGF1 R and/or cMet). Herein, 'inhibition' refers to a reduction, decrease or lessening relative to a control condition.

[0273] In some aspects the antigen-binding molecule of the present disclosure is capable of inhibiting interaction between HER3 and an interaction partner for HER3. An interaction partner for HER3 may be expressed by the same cell as the HER3. An interaction partner or HER3 may be expressed at the cell surface (i.e. in or at the cell membrane). In some aspects an interaction partner for HER3 may be a member of the EGFR family of proteins, e.g. HER3, HER2, EGFR, HER4, HGFR, IGF1 R and/or cMet. In some aspects an interaction partner for HER3 may be IGF1 R and/or cMet. Interaction between HER3 and an interaction partner for HER3 may result in the formation of a polypeptide complex. Interaction between HER3 and an interaction partner for HER3 to form a polypeptide complex may be referred to as multimerisation. Where multimerisation is between polypeptide monomers multimerisation may be referred to as dimerisation.

[0274] In some aspects the antigen-binding molecule is capable of inhibiting interaction between HER3 monomers. In some aspects the antigen-binding molecule is capable of inhibiting interaction between HER3 and HER2. In some aspects the antigen-binding molecule is capable of inhibiting interaction between HER3 and EGFR. In some aspects the antigen-binding molecule is capable of inhibiting interaction between HER3 and HER4. In some aspects the antigen-binding molecule is capable of inhibiting interaction between HER3 and HGFR. In some aspects the antigen-binding molecule is capable of inhibiting interaction between HER3 and IGF1R. In some aspects the antigen-binding molecule is capable of inhibiting interaction between HER3 and cMet.

[0275] Inhibition of interaction may be achieved by binding of the antigen-binding molecule to a region of HER3 required for interaction between HER3 and an interaction partner for HER3 (e.g. the dimerisation loop of HER3 shown in SEQ ID NO:19). In some aspects the antigen-binding molecule contacts one or more residues of HER3 necessary for interaction between HER3 and an interaction partner for HER3; in this way the antigen-binding molecule makes the region unavailable, thereby inhibiting interaction. In some aspects the antigen-binding molecule binds to HER3 in a manner which inhibits/prevents interaction between HER3 and an interaction partner for HER3. In some aspects the antigen-binding molecule inhibits/prevents access of the interaction partner for HER3 to the region of HER3 required for interaction between HER3 and the interaction partner for HER3; this may be achieved in cases even where the antigen-binding molecule does not contact the region of HER3 required for interaction between HER3 and the interaction partner for HER3, e.g. through steric inhibition of access of the interaction partner for HER3 to the region of HER3 required for interaction between HER3 and the interaction partner.

[0276] In some aspects the antigen-binding molecule is capable of inhibiting homodimerisation of HER3 monomers. In some aspects the antigen-binding molecule is capable of inhibiting dimerisation between HER3 and HER2. In some aspects the antigen-binding molecule is capable of inhibiting dimerisation between HER3 and EGFR. In some aspects the antigen-binding molecule is capable of inhibiting dimerisation between HER3 and HER4. In some aspects the antigen-binding molecule is capable of inhibiting dimerisation between HER3 and HGFR. In some aspects the antigen-binding molecule is capable of inhibiting dimerisation between HER3 and IGF1R. In some aspects the

antigen-binding molecule is capable of inhibiting dimerisation between HER3 and cMet.

[0277] The ability of an antigen-binding molecule to inhibit interaction between two factors can be determined for example by analysis of interaction in the presence of, or following incubation of one or both of the interaction partners with, the antibody/fragment. Assays for determining whether a given antigen-binding molecule is capable of inhibiting interaction between two interaction partners include competition ELISA assays and analysis by SPR. In some aspects the antigen-binding molecule is a competitive inhibitor of interaction between HER3 and an interaction partner for HER3.

[0278] In some aspects, the antigen-binding molecule of the present disclosure is capable of inhibiting interaction between HER3 and an interaction partner for HER3 (e.g. HER3, HER2, EGFR, HER4, HGFR, IGF1 R and/or cMet) to less than less than 1 times, e.g. ≤0.99 times, ≤0.95 times, ≤0.9 times, ≤0.85 times, ≤0.8 times, ≤0.75 times, ≤0.7 times, ≤0.65 times, ≤0.6 times, ≤0.55 times, ≤0.5 times, ≤0.45 times, ≤0.4 times, ≤0.35 times, ≤0.3 times, ≤0.25 times, ≤0.2 times, ≤0.15 times, ≤0.1 times, ≤0.05 times, or ≤0.01 times the level of interaction between HER3 and the interaction partner for HER3 in the absence of the antigen-binding molecule (or in the presence of an appropriate control antigen-binding molecule), in a suitable assay.

[0279] The ability of an antigen-binding molecule to inhibit interaction between interaction partners can also be determined by analysis of the downstream functional consequences of such interaction. For example, downstream functional consequences of interaction between HER3 and interaction partners for HER3 include PI3K/AKT/mTOR and/or MAPK signalling. For example, the ability of an antigen-binding molecule to inhibit interaction of HER3 and an interaction partner for HER3 may be determined by analysis of PI3K/AKT/mTOR and/or MAPK signalling following treatment with NRG in the presence of the antigen-binding molecule. PI3K/AKT/mTOR and/or MAPK signalling can be detected and quantified e.g. using antibodies capable of detecting phosphorylated members of the signal transduction pathways.

[0280] The ability of an antigen-binding molecule to inhibit interaction of HER3 and an interaction partner for HER3 can also be determined by analysing proliferation of cells expressing HER3 following treatment with NRG in the presence of the antigen-binding molecule. Cell proliferation can be determined e.g. by detecting changes in number of cells over time, or by *in vitro* analysis of incorporation of ^{3}H-thymidine or by CFSE dilution assay, e.g. as described in Fulcher and Wong, Immunol Cell Biol (1999) 77(6): 559-564.

[0281] In some aspects, the antigen-binding molecule of the present disclosure is capable of inhibiting proliferation of cells harbouring mutation to BRAF V600, e.g. cells comprising the BRAF V600E or V600K mutation (see Example 10).

[0282] In some aspects the antigen-binding molecule inhibits HER3-mediated signalling. HER3-mediated signalling can be analysed e.g. using an assay of a correlate of HER3-mediated signalling, e.g. cell proliferation, and/or phosphorylation of one or more signal transduction molecules of the PI3K/AKT/mTOR and/or MAPK signal transduction pathways.

[0283] In some aspects, the antigen-binding molecule of the present disclosure is capable of inhibiting PI3K/AKT/mTOR and/or MAPK signalling by HER3-expressing cells. The level of PI3K/AKT/mTOR and/or MAPK signalling may be analysed by detection and quantification of the level of

phosphorylation of one or more of the components of the PI3K/AKT/mTOR and/or MAPK pathways, e.g. following stimulation with NRG (see Example 4.3).

[0284] In some aspects, the antigen-binding molecule of the present disclosure is capable of inhibiting proliferation of HER3-expressing cells, e.g. in response to stimulation with NRG. In some aspects, the antigen-binding molecule of the present disclosure is capable of inhibiting proliferation of HER3-expressing cells to less than less than 1 times, e.g. ≤0.99 times, ≤0.95 times, ≤0.9 times, ≤0.85 times, ≤0.8 times, ≤0.75 times, ≤0.7 times, ≤0.65 times, ≤0.6 times, ≤0.55 times, ≤0.5 times, ≤0.45 times, ≤0.4 times, ≤0.35 times, ≤0.3 times, ≤0.25 times, ≤0.2 times, ≤0.15 times, ≤0.1 times, ≤0.05 times, or ≤0.01 times the level of proliferation of HER3-expressing cells in the absence of the antigen-binding molecule (or in the presence of an appropriate control antigen-binding molecule), in a suitable assay.

[0285] In some aspects, the antigen-binding molecule of the present disclosure is capable of inhibiting PI3K/AKT/mTOR and/or MAPK signalling by HER3-expressing cells to less than less than 1 times, e.g. ≤0.99 times, ≤0.95 times, ≤0.9 times, ≤0.85 times, ≤0.8 times, ≤0.75 times, ≤0.7 times, ≤0.65 times, ≤0.6 times, ≤0.55 times, ≤0.5 times, ≤0.45 times, ≤0.4 times, ≤0.35 times, ≤0.3 times, ≤0.25 times, ≤0.2 times, ≤0.15 times, ≤0.1 times, ≤0.05 times, or ≤0.01 times the level of signalling by HER3-expressing cells in the absence of the antigen-binding molecule (or in the presence of an appropriate control antigen-binding molecule), in a suitable assay.

[0286] HER3-mediated signalling can be investigated *in vitro,* e.g. as described in Example 8.9, or *in vivo,* e.g. as described in Example 11.

[0287] ADCC activity can be analysed e.g. according to the methods described in Yamashita et al., Scientific Reports (2016) 6:19772, or by ^{51}Cr release assay as described e.g. in Jedema et al., Blood (2004) 103: 2677-82. ADCC activity can also be analysed using the Pierce LDH Cytotoxicity Assay Kit, in accordance with the manufacturer's instructions (as described in Example 5 herein).

[0288] ADCP can be analysed e.g. according to the method described in Kamen et al., J Immunol (2017) 198 (1 Supplement) 157.17.

[0289] The ability to induce CDC can be analysed e.g. using a C1q binding assay, e.g. as described in Schlothauer et al., Protein Engineering, Design and Selection (2016), 29(10):457-466.

[0290] Thermostability of antigen-binding molecules can be analysed by methods well known to the skilled person, including Differential Scanning Fuorimetry and Differential Scanning Calorimetry (DSC), which are described e.g. in He et al., J Pharm Sci. (2010). Thermostability may be reflected in terms of a melting temperature (T_m), unfolding temperature or disassembly temperature (expressed e.g. in °C or F°).

[0291] In some aspects, an antigen-binding molecule comprising an Fc region as described herein binds to an activatory Fcγ receptor (e.g. hFcγRIIa (e.g. hFcγRIIa167H, hFcγRIIa167R), hFcγRIIIa (e.g. hFcγRIIIa158V, hFcγRIIIa158F), mFcγRIV, mFcγRIII) with an affinity of binding which is greater than 1 times, e.g. greater than 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or greater than 20 times the affinity of binding to the activatory Fcγ receptor by an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175. In some aspects the K_D of the antigen-binding molecule comprising an Fc region described herein for binding to the

activatory Fcγ receptor is less than 1 times, e.g. less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, 0.1, 0.09, 0.08, 0.07, 0.06 or less than 0.05 times the K_D of an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175 for the activatory Fcγ receptor.

[0292] In some aspects, the antigen-binding molecule comprising an Fc region as described herein binds to an activatory Fcγ receptor (e.g. hFcγRIIa (e.g. hFcγRIIa167H, hFcγRIIa167R), hFcγRIIIa (e.g. hFcγRIIIa158V, hFcγRIIIa158F), mFcγRIV, mFcγRIII) with a K_D of 1000 nM or less, preferably one of ≤500 nM, ≤100 nM, ≤75 nM, ≤50 nM, ≤40 nM, ≤30 nM, ≤20 nM, ≤15 nM, ≤12.5 nM, ≤10 nM, ≤9 nM, ≤8 nM, ≤7 nM, ≤6 nM, ≤5 nM, ≤4 nM ≤3 nM, ≤2 nM or ≤1 nM.

[0293] In some aspects, an antigen-binding molecule comprising an Fc region as described herein binds to an FcRn (e.g. hFcRn, mFcRn) with an affinity of binding which is greater than 1 times, e.g. greater than 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or greater than 20 times the affinity of binding to the FcRn by an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175. In some aspects the K_D of the antigen-binding molecule comprising an Fc region described herein for binding to the FcRn is less than 1 times, e.g. less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, 0.1, 0.09, 0.08, 0.07, 0.06 or less than 0.05 times the K_D of an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175 for the FcRn.

[0294] In some aspects, the antigen-binding molecule comprising an Fc region as described herein binds to an FcRn (e.g. hFcRn, mFcRn) with a K_D of 1000 nM or less, preferably one of ≤500 nM, ≤100 nM, ≤75 nM, ≤50 nM, ≤40 nM, ≤30 nM, ≤20 nM, ≤15 nM, ≤12.5 nM, <10 nM, ≤9 nM, ≤8 nM, ≤7 nM, ≤6 nM, ≤5 nM, ≤4 nM ≤3 nM, ≤2 nM or ≤1 nM.

[0295] In some aspects, an antigen-binding molecule comprising an Fc region as described herein binds to an inhibitory Fcγ receptor (e.g. hFcγRIIb mFcγRIIb) with an affinity of binding which is less than 1 times, e.g. less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, or less than 0.1 times the affinity of binding to the inhibitory Fcγ receptor by an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175. In some aspects the K_D of the antigen-binding molecule comprising an Fc region described herein for binding to the inhibitory Fcγ receptor is greater than 1 times, e.g. greater than 2, 3, 4, 5, 6, 7, 8, 9 or greater than 10 times the K_D of an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175 for the inhibitory Fcγ receptor.

[0296] In some aspects, the antigen-binding molecule comprising an Fc region as described herein binds to an inhibitory Fcγ receptor (e.g. hFcγRIIb mFcγRIIb) with a K_D 1 nM or greater, preferably one of ≥ 5 nM, ≥ 10 nM, ≥ 50 nM, ≥ 100 nM, ≥ 500 nM, ≥ 1000 nM, ≥ 2000 nM, ≥ 3000 nM, ≥ 4000 nM or ≥ 5000 nM.

[0297] In some aspects the selectivity of binding for an activatory Fcγ receptor (e.g. hFcγRIIa) relative to an inhibitory Fcγ receptor (e.g. hFcγRIIb) for an antigen-binding molecule comprising an Fc region as described herein is greater than 1 times, e.g. greater than 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or greater than 20 times selectivity of binding displayed by an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175.

[0298] In some aspects, an antigen-binding molecule comprising an Fc region as described herein displays ADCC which is greater than 1 times, e.g. greater than 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or greater than 20 times the ADCC displayed by an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175.

[0299] In some aspects, the EC50 (ng/ml) determined for an antigen-binding molecule comprising an Fc region as described herein in an assay of ADCC activity less than 1 times, e.g. less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, or less than 0.1 times the EC50 (ng/ml) determined for an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175.

[0300] In some aspects, the EC50 (ng/ml) for an antigen-binding molecule comprising an Fc region as described herein in an assay of ADCC activity is 500 ng/ml or less, preferably one of ≤400 ng/ml, ≤300 ng/ml, ≤200 ng/ml, ≤100 ng/ml, ≤90 ng/ml, ≤80 ng/ml, ≤70 ng/ml, ≤60 ng/ml, ≤50 ng/ml, ≤40 ng/ml, ≤30 ng/ml, ≤20 ng/ml, or ≤10 ng/ml.

[0301] In some aspects, an antigen-binding molecule comprising an Fc region as described herein may have a melting temperature, unfolding temperature or disassembly temperature which is which is ≥ 0.75 times and ≤ 1.25 times, e.g. ≥ 0.8 times and ≤ 1.2 times, ≥ 0.85 times and ≤ 1.15 times, ≥ 0.9 times and ≤ 1.1 times, ≥ 0.91 times and ≤ 1.09 times, ≥ 0.92 times and ≤ 1.08 times, ≥ 0.93 times and ≤ 1.07 times, ≥ 0.94 times and ≤ 1.06 times, ≥ 0.95 times and ≤ 1.05 times, ≥ 0.96 times and ≤ 1.04 times, ≥ 0.97 times and ≤ 1.03 times, ≥ 0.98 times and ≤ 1.02 times, or ≥ 0.99 times and ≤ 1.01 times the melting temperature, unfolding temperature or disassembly temperature of an equivalent antigen-binding molecule having an Fc region comprised of CH2-CH3 having the amino acid sequence of SEQ ID NO:174-175.

[0302] In some aspects, the antigen-binding molecule of the present disclosure is capable of increasing killing of HER3-expressing cells. Killing of HER3-expressing cells may be increased through an effector function of the antigen-binding molecule. In aspects wherein antigen-binding molecule comprises an Fc region the antigen-binding molecule may increasing killing of HER3-expressing cells through one or more of complement dependent cytotoxicity (CDC), antibody-dependent cell-mediated cytotoxicity (ADCC) and antibody-dependent cellular phagocytosis (ADCP).

[0303] An antigen-binding molecule which is capable of increasing killing of HER3-expressing cells can be identified by observation of an increased level of killing of HER3-expressing cells in the presence of - or following incubation of the HER3-expressing cells with - the antigen-binding molecule, as compared to the level of cell killing detected in the absence of the antigen-binding molecule (or in the presence of an appropriate control antigen-binding molecule), in an appropriate assay. Assays of CDC, ADCC and ADCP are well known the skilled person. The level of killing of HER3-expressing cells can also be determined by measuring the number/proportion of viable and/or non-viable HER3-expressing cells following exposure to different treatment conditions.

[0304] In some aspects, the antigen-binding molecule of the present disclosure is capable of increasing killing of HER3-expressing cells (e.g. HER3-expressing cancer cells) to more than 1 times, e.g. ≥1.01 times, ≥1.02 times, ≥1.03 times, ≥1.04 times, ≥1.05 times, ≥1.1 times, ≥1.2 times, ≥1.3 times, ≥1.4 times, ≥1.5 times, ≥1.6 times, ≥1.7 times, ≥1.8 times, ≥1.9 times, ≥2 times, ≥3 times, ≥4 times, ≥5 times, ≥6 times, ≥7 times, ≥8 times, ≥9 times or ≥10 times the level of killing observed in the

absence of the antigen-binding molecule (or in the presence of an appropriate control antigen-binding molecule).

[0305] In some aspects, the antigen-binding molecule of the present disclosure is capable of reducing the number of HER3-expressing cells (e.g. HER3-expressing cancer cells) to less than less than 1 times, e.g. ≤0.99 times, ≤0.95 times, ≤0.9 times, ≤0.85 times, ≤0.8 times, ≤0.75 times, ≤0.7 times, ≤0.65 times, ≤0.6 times, ≤0.55 times, ≤0.5 times, ≤0.45 times, ≤0.4 times, ≤0.35 times, ≤0.3 times, ≤0.25 times, ≤0.2 times, ≤0.15 times, ≤0.1 times, ≤0.05 times, or ≤0.01 times the number of HER3-expressing cells (e.g. HER3-expressing cancer cells) detected following incubation in the absence of the antigen-binding molecule (or following incubation in the presence of an appropriate control antigen-binding molecule), in a comparable assay.

[0306] In some aspects, the antigen-binding molecule of the present disclosure inhibits the development and/or progression of cancer *in vivo.*

[0307] In some aspects the antigen-binding molecule causes an increase in the killing of cancer cells, e.g. by effector immune cells. In some aspects the antigen-binding molecule causes a reduction in the number of cancer cells *in vivo,* e.g. as compared to an appropriate control condition. In some aspects the antigen-binding molecule inhibits tumor growth, e.g. as determined by measuring tumor size/volume over time.

[0308] The antigen-binding molecule of the present disclosure may be analysed for the ability to inhibit development and/or progression of cancer in an appropriate *in vivo* model, e.g. cell line-derived xenograft model. The cell line-derived xenograft model may be derived from HER3-expressing cancer cells. In some aspects the model is an N87 cell-derived model, a SNU16 cell-derived model, a FaDu cell-derived model, an OvCAR8 cell-derived model, a HCC95 cell-derived model, an A549 cell-derived model, an ACHN cell-derived model or a HT29 cell-derived model.

[0309] The cancer may be a HER3-associated cancer as described herein (i.e. cancers for which HER3 gene/protein expression is a risk factor for, and/or is positively associated with, the onset, development, progression or severity of symptoms of the cancer, and/or metastasis). The cancer may comprise HER3-expressing cells. In some aspects the cancer comprises a HER3+ tumor.

[0310] In some aspects, administration of an antigen-binding molecule according to the present disclosure may cause one or more of: inhibition of the development/progression of the cancer, a delay to/prevention of onset of the cancer, a reduction in/delay to/prevention of tumor growth, a reduction in/delay to/prevention of metastasis, a reduction in the severity of the symptoms of the cancer, a reduction in the number of cancer cells, a reduction in tumour size/volume, and/or an increase in survival (e.g. progression free survival), e.g. as determined in an appropriate HER3-expressing cancer cell line-derived xenograft model.

[0311] In some aspects, the antigen-binding molecule of the present disclosure is capable of inhibiting tumor growth in a HER3-expressing cancer cell line-derived xenograft model to less than less than 1 times, e.g. ≤0.99 times, ≤0.95 times, ≤0.9 times, ≤0.85 times, ≤0.8 times, ≤0.75 times, ≤0.7 times, ≤0.65 times, ≤0.6 times, ≤0.55 times, ≤0.5 times, ≤0.45 times, ≤0.4 times, ≤0.35 times, ≤0.3 times, ≤0.25 times, ≤0.2 times, ≤0.15 times, ≤0.1 times, ≤0.05 times, or ≤0.01 times the tumor growth observed in the absence of treatment with the antigen-binding molecule (or following treatment with

an appropriate negative control antigen-binding molecule).

Chimeric antigen receptors (CARs)

[0312] The present disclosure also provides Chimeric Antigen Receptors (CARs) comprising the antigen-binding molecules or polypeptides of the present disclosure.

[0313] CARs are recombinant receptors that provide both antigen-binding and T cell activating functions. CAR structure and engineering is reviewed, for example, in Dotti et al., Immunol Rev (2014) 257(1). CARs comprise an antigen-binding region linked to a cell membrane anchor region and a signalling region. An optional hinge region may provide separation between the antigen-binding region and cell membrane anchor region, and may act as a flexible linker.

[0314] The CAR of the present disclosure comprises an antigen-binding region which comprises or consists of the antigen-binding molecule of the present disclosure, or which comprises or consists of a polypeptide according to the present disclosure.

[0315] The cell membrane anchor region is provided between the antigen-binding region and the signalling region of the CAR and provides for anchoring the CAR to the cell membrane of a cell expressing a CAR, with the antigen-binding region in the extracellular space, and signalling region inside the cell. In some aspects, the CAR comprises a cell membrane anchor region comprising or consisting of an amino acid sequence which comprises, consists of, or is derived from, the transmembrane region amino acid sequence for one of CD3-ζ, CD4, CD8 or CD28. As used herein, a region which is 'derived from' a reference amino acid sequence comprises an amino acid sequence having at least 60%, e.g. one of at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the reference sequence.

[0316] The signalling region of a CAR allows for activation of the T cell. The CAR signalling regions may comprise the amino acid sequence of the intracellular domain of CD3-ζ, which provides immunoreceptor tyrosine-based activation motifs (ITAMs) for phosphorylation and activation of the CAR-expressing T cell. Signalling regions comprising sequences of other ITAM-containing proteins such as FcγRI have also been employed in CARs (Haynes et al., 2001 J Immunol 166(1):182-187). Signalling regions of CARs may also comprise co-stimulatory sequences derived from the signalling region of co-stimulatory molecules, to facilitate activation of CAR-expressing T cells upon binding to the target protein. Suitable co-stimulatory molecules include CD28, OX40, 4-1BB, ICOS and CD27. In some cases CARs are engineered to provide for co-stimulation of different intracellular signalling pathways. For example, signalling associated with CD28 costimulation preferentially activates the phosphatidylinositol 3-kinase (P13K) pathway, whereas the 4-1BB-mediated signalling is through TNF receptor associated factor (TRAF) adaptor proteins. Signalling regions of CARs therefore sometimes contain co-stimulatory sequences derived from signalling regions of more than one co-stimulatory molecule. In some aspects, the CAR of the present disclosure comprises one or more co-stimulatory sequences comprising or consisting of an amino acid sequence which comprises, consists of, or is derived from, the amino acid sequence of the intracellular domain of one or more of CD28, OX40, 4-1BB, ICOS and CD27.

[0317] An optional hinge region may provide separation between the antigen-binding domain and the

transmembrane domain, and may act as a flexible linker. Hinge regions may be derived from IgG1. In some aspects, the CAR of the present disclosure comprises a hinge region comprising or consisting of an amino acid sequence which comprises, consists of, or is derived from, the amino acid sequence of the hinge region of IgG1.

[0318] Also provided is a cell comprising a CAR according to the present disclosure. The CAR according to the present disclosure may be used to generate CAR-expressing immune cells, e.g. CAR-T or CAR-NK cells. Engineering of CARs into immune cells may be performed during culture, *in vitro.*

[0319] The antigen-binding region of the CAR of the present disclosure may be provided with any suitable format, e.g. scFv, scFab, etc.

Nucleic acids and vectors

[0320] The present disclosure provides a nucleic acid, or a plurality of nucleic acids, encoding an antigen-binding molecule, polypeptide or CAR according to the present disclosure.

[0321] In some aspects, the nucleic acid is purified or isolated, e.g. from other nucleic acid, or naturally-occurring biological material. In some aspects the nucleic acid(s) comprise or consist of DNA and/or RNA.

[0322] The present disclosure also provides a vector, or plurality of vectors, comprising the nucleic acid or plurality of nucleic acids according to the present disclosure.

[0323] The nucleotide sequence may be contained in a vector, e.g. an expression vector. A "vector" as used herein is a nucleic acid molecule used as a vehicle to transfer exogenous nucleic acid into a cell. The vector may be a vector for expression of the nucleic acid in the cell. Such vectors may include a promoter sequence operably linked to the nucleotide sequence encoding the sequence to be expressed. A vector may also include a termination codon and expression enhancers. Any suitable vectors, promoters, enhancers and termination codons known in the art may be used to express a peptide or polypeptide from a vector according to the present disclosure.

[0324] The term "operably linked" may include the situation where a selected nucleic acid sequence and regulatory nucleic acid sequence (e.g. promoter and/or enhancer) are covalently linked in such a way as to place the expression of nucleic acid sequence under the influence or control of the regulatory sequence (thereby forming an expression cassette). Thus a regulatory sequence is operably linked to the selected nucleic acid sequence if the regulatory sequence is capable of effecting transcription of the nucleic acid sequence. The resulting transcript(s) may then be translated into a desired peptide(s)/po lypeptide(s).

[0325] Suitable vectors include plasmids, binary vectors, DNA vectors, mRNA vectors, viral vectors (e.g. gammaretroviral vectors (e.g. murine Leukemia virus (MLV)-derived vectors), lentiviral vectors, adenovirus vectors, adeno-associated virus vectors, vaccinia virus vectors and herpesvirus vectors), transposon-based vectors, and artificial chromosomes (e.g. yeast artificial chromosomes).

[0326] In some aspects, the vector may be a eukaryotic vector, e.g. a vector comprising the elements necessary for expression of protein from the vector in a eukaryotic cell. In some aspects, the vector may be a mammalian vector, e.g. comprising a cytomegalovirus (CMV) or SV40 promoter to drive protein expression.

[0327] Constituent polypeptides of an antigen-binding molecule according to the present disclosure may be encoded by different nucleic acids of the plurality of nucleic acids, or by different vectors of the plurality of vectors.

Cells comprising/expressing the antigen-binding molecules and polypeptides

[0328] The present disclosure also provides a cell comprising or expressing an antigen-binding molecule, polypeptide or CAR according to the present disclosure. Also provided is a cell comprising or expressing a nucleic acid, a plurality of nucleic acids, a vector or a plurality of vectors according to the present disclosure.

[0329] The cell may be a eukaryotic cell, e.g. a mammalian cell. The mammal may be a primate (rhesus, cynomolgous, non-human primate or human) or a non-human mammal (e.g. rabbit, guinea pig, rat, mouse or other rodent (including any animal in the order Rodentia), cat, dog, pig, sheep, goat, cattle (including cows, e.g. dairy cows, or any animal in the order Bos), horse (including any animal in the order Equidae), donkey, and non-human primate).

[0330] The present disclosure also provides a method for producing a cell comprising a nucleic acid(s) or vector(s) according to the present disclosure, comprising introducing a nucleic acid, a plurality of nucleic acids, a vector or a plurality of vectors according to the present disclosure into a cell. In some aspects, introducing an isolated nucleic acid(s) or vector(s) according to the present disclosure into a cell comprises transformation, transfection, electroporation or transduction (e.g. retroviral transduction).

[0331] The present disclosure also provides a method for producing a cell expressing/comprising an antigen-binding molecule, polypeptide or CAR according to the present disclosure, comprising introducing a nucleic acid, a plurality of nucleic acids, a vector or a plurality of vectors according to the present disclosure in a cell. In some aspects, the methods additionally comprise culturing the cell under conditions suitable for expression of the nucleic acid(s) or vector(s) by the cell. In some aspects, the methods are performed *in vitro.*

[0332] The present disclosure also provides cells obtained or obtainable by the methods according to the present disclosure.

Producing the antigen-binding molecules and polypeptides

[0333] Antigen-binding molecules and polypeptides according to the present disclosure may be prepared according to methods for the production of polypeptides known to the skilled person.

[0334] Polypeptides may be prepared by chemical synthesis, e.g. liquid or solid phase synthesis. For

example, peptides/polypeptides can by synthesised using the methods described in, for example, Chandrudu et al., Molecules (2013), 18: 4373-4388.

[0335] Alternatively, antigen-binding molecules and polypeptides may be produced by recombinant expression. Molecular biology techniques suitable for recombinant production of polypeptides are well known in the art, such as those set out in Green and Sambrook, Molecular Cloning: A Laboratory Manual (4th Edition), Cold Spring Harbor Press, 2012, and in Nat Methods. (2008); 5(2): 135-146. Methods for the recombinant production of antigen-binding molecules are also described in Frenzel et al., Front Immunol. (2013); 4: 217 and Kunert and Reinhart, Appl Microbiol Biotechnol. (2016) 100: 3451-3461.

[0336] In some cases the antigen-binding molecule of the present disclosure are comprised of more than one polypeptide chain. In such cases, production of the antigen-binding molecules may comprise transcription and translation of more than one polypeptide, and subsequent association of the polypeptide chains to form the antigen-binding molecule.

[0337] For recombinant production according to the present disclosure, any cell suitable for the expression of polypeptides may be used. The cell may be a prokaryote or eukaryote. In some aspects the cell is a prokaryotic cell, such as a cell of archaea or bacteria. In some aspects the bacteria may be Gram-negative bacteria such as bacteria of the family Enterobacteriaceae, for example Escherichia coli. In some aspects, the cell is a eukaryotic cell such as a yeast cell, a plant cell, insect cell or a mammalian cell, e.g. CHO, HEK (e.g. HEK293), HeLa or COS cells. In some aspects, the cell is a CHO cell that transiently or stably expresses the polypeptides.

[0338] In some cases the cell is not a prokaryotic cell because some prokaryotic cells do not allow for the same folding or post-translational modifications as eukaryotic cells. In addition, very high expression levels are possible in eukaryotes and proteins can be easier to purify from eukaryotes using appropriate tags. Specific plasmids may also be utilised which enhance secretion of the protein into the media.

[0339] In some aspects polypeptides may be prepared by cell-free-protein synthesis (CFPS), e.g. according using a system described in Zemella et al. Chembiochem (2015) 16(17): 2420-2431.

[0340] Production may involve culture or fermentation of a eukaryotic cell modified to express the polypeptide(s) of interest. The culture or fermentation may be performed in a bioreactor provided with an appropriate supply of nutrients, air/oxygen and/or growth factors. Secreted proteins can be collected by partitioning culture media/fermentation broth from the cells, extracting the protein content, and separating individual proteins to isolate secreted polypeptide(s). Culture, fermentation and separation techniques are well known to those of skill in the art, and are described, for example, in Green and Sambrook, Molecular Cloning: A Laboratory Manual (4th Edition).

[0341] Bioreactors include one or more vessels in which cells may be cultured. Culture in the bioreactor may occur continuously, with a continuous flow of reactants into, and a continuous flow of cultured cells from, the reactor. Alternatively, the culture may occur in batches. The bioreactor monitors and controls environmental conditions such as pH, oxygen, flow rates into and out of, and agitation within the vessel such that optimum conditions are provided for the cells being cultured.

[0342] Following culturing the cells that express the antigen-binding molecule/polypeptide(s), the polypeptide(s) of interest may be isolated. Any suitable method for separating proteins from cells known in the art may be used. In order to isolate the polypeptide it may be necessary to separate the cells from nutrient medium. If the polypeptide(s) are secreted from the cells, the cells may be separated by centrifugation from the culture media that contains the secreted polypeptide(s) of interest. If the polypeptide(s) of interest collect within the cell, protein isolation may comprise centrifugation to separate cells from cell culture medium, treatment of the cell pellet with a lysis buffer, and cell disruption e.g. by sonification, rapid freeze-thaw or osmotic lysis.

[0343] It may then be desirable to isolate the polypeptide(s) of interest from the supernatant or culture medium, which may contain other protein and non-protein components. A common approach to separating protein components from a supernatant or culture medium is by precipitation. Proteins of different solubilities are precipitated at different concentrations of precipitating agent such as ammonium sulfate. For example, at low concentrations of precipitating agent, water soluble proteins are extracted. Thus, by adding different increasing concentrations of precipitating agent, proteins of different solubilities may be distinguished. Dialysis may be subsequently used to remove ammonium sulfate from the separated proteins.

[0344] Other methods for distinguishing different proteins are known in the art, for example ion exchange chromatography and size chromatography. These may be used as an alternative to precipitation, or may be performed subsequently to precipitation.

[0345] Once the polypeptide(s) of interest have been isolated from culture it may be desired or necessary to concentrate the polypeptide(s). A number of methods for concentrating proteins are known in the art, such as ultrafiltration or lyophilisation.

Compositions

[0346] The present disclosure also provides compositions comprising the antigen-binding molecules, polypeptides, CARs, nucleic acids, expression vectors and cells described herein.

[0347] The antigen-binding molecules, polypeptides, CARs, nucleic acids, expression vectors and cells described herein may be formulated as pharmaceutical compositions or medicaments for clinical use and may comprise a pharmaceutically acceptable carrier, diluent, excipient or adjuvant. The composition may be formulated for topical, parenteral, systemic, intracavitary, intravenous, intra-arterial, intramuscular, intrathecal, intraocular, intraconjunctival, intratumoral, subcutaneous, intradermal, intrathecal, oral or transdermal routes of administration which may include injection or infusion.

[0348] Suitable formulations may comprise the antigen-binding molecule in a sterile or isotonic medium. Medicaments and pharmaceutical compositions may be formulated in fluid, including gel, form. Fluid formulations may be formulated for administration by injection or infusion (e.g. via catheter) to a selected region of the human or animal body.

[0349] In some aspects the composition is formulated for injection or infusion, e.g. into a blood vessel or tumor.

[0350] In accordance with the present disclosure methods are also provided for the production of pharmaceutically useful compositions, such methods of production may comprise one or more steps selected from: producing an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof) or cell described herein; isolating an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof) or cell described herein; and/or mixing an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof) or cell described herein with a pharmaceutically acceptable carrier, adjuvant, excipient or diluent.

[0351] For example, a further aspect the present disclosure relates to a method of formulating or producing a medicament or pharmaceutical composition for use in the treatment of a disease/condition (e.g. a cancer), the method comprising formulating a pharmaceutical composition or medicament by mixing an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof) or cell described herein with a pharmaceutically acceptable carrier, adjuvant, excipient or diluent.

Therapeutic and prophylactic applications

[0352] The antigen-binding molecules, polypeptides, CARs, nucleic acids, expression vectors, cells and compositions described herein find use in therapeutic and prophylactic methods.

[0353] The present disclosure provides an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof), cell or composition described herein for use in a method of medical treatment or prophylaxis. Also provided is the use of an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof), cell or composition described herein in the manufacture of a medicament for treating or preventing a disease or condition. Also provided is a method of treating or preventing a disease or condition, comprising administering to a subject a therapeutically or prophylactically effective amount of an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof), cell or composition described herein.

[0354] The methods may be effective to reduce the development or progression of a disease/condition, alleviation of the symptoms of a disease/condition or reduction in the pathology of a disease/condition. The methods may be effective to prevent progression of the disease/condition, e.g. to prevent worsening of, or to slow the rate of development of, the disease/condition. In some aspects the methods may lead to an improvement in the disease/condition, e.g. a reduction in the symptoms of the disease/condition or reduction in some other correlate of the severity/activity of the disease/condition. In some aspects the methods may prevent development of the disease/condition a later stage (e.g. a chronic stage or metastasis).

[0355] It will be appreciated that the articles of the present disclosure may be used for the treatment/prevention of any disease/condition that would derive therapeutic or prophylactic benefit from a reduction in the number and/or activity of cells expressing HER3. For example, the disease/condition may be a disease/condition in which cells expressing HER3 are pathologically implicated, e.g. a disease/condition in which an increased number/proportion of cells expressing

HER3 is positively associated with the onset, development or progression of the disease/condition, and/or severity of one or more symptoms of the disease/condition, or for which an increased number/proportion of cells expressing HER3, is a risk factor for the onset, development or progression of the disease/condition.

[0356] In some aspects, the disease/condition to be treated/prevented in accordance with the present disclosure is a disease/condition characterised by an increase in the number/proportion/activity of cells expressing HER3, e.g. as compared to the number/proportion/activity of cells expressing HER3 in the absence of the disease/condition.

[0357] In some aspects the disease/condition to be treated/prevented is a cancer.

[0358] The cancer may be any unwanted cell proliferation (or any disease manifesting itself by unwanted cell proliferation), neoplasm or tumor. The cancer may be benign or malignant and may be primary or secondary (metastatic). A neoplasm or tumor may be any abnormal growth or proliferation of cells and may be located in any tissue. The cancer may be of tissues/cells derived from e.g. the adrenal gland, adrenal medulla, anus, appendix, bladder, blood, bone, bone marrow, brain, breast, cecum, central nervous system (including or excluding the brain) cerebellum, cervix, colon, duodenum, endometrium, epithelial cells (e.g. renal epithelia), gallbladder, oesophagus, glial cells, heart, ileum, jejunum, kidney, lacrimal glad, larynx, liver, lung, lymph, lymph node, lymphoblast, maxilla, mediastinum, mesentery, myometrium, nasopharynx, omentum, oral cavity, ovary, pancreas, parotid gland, peripheral nervous system, peritoneum, pleura, prostate, salivary gland, sigmoid colon, skin, small intestine, soft tissues, spleen, stomach, testis, thymus, thyroid gland, tongue, tonsil, trachea, uterus, vulva, and/or white blood cells.

[0359] Tumors to be treated may be nervous or non-nervous system tumors. Nervous system tumors may originate either in the central or peripheral nervous system, e.g. glioma, medulloblastoma, meningioma, neurofibroma, ependymoma, Schwannoma, neurofibrosarcoma, astrocytoma and oligodendroglioma. Non-nervous system cancers/tumors may originate in any other non-nervous tissue, examples include melanoma, mesothelioma, lymphoma, myeloma, leukemia, Non-Hodgkin's lymphoma (NHL), Hodgkin's lymphoma, chronic myelogenous leukemia (CML), acute myeloid leukemia (AML), myelodysplastic syndrome (MDS), cutaneous T-cell lymphoma (CTCL), chronic lymphocytic leukemia (CLL), hepatoma, epidermoid carcinoma, prostate carcinoma, breast cancer, lung cancer, colon cancer, ovarian cancer, pancreatic cancer, thymic carcinoma, NSCLC, hematologic cancer and sarcoma.

[0360] HER3 and its association with and role in cancer is reviewed e.g. in Karachaliou et al., BioDrugs. (2017) 31(1):63-73 and Zhang et al., Acta Biochimica et Biophysica Sinica (2016) 48(1): 39-48.

[0361] In some aspects, a cancer is selected from: a cancer comprising cells expressing HER3, a solid tumor, breast cancer, breast carcinoma, ductal carcinoma, gastric cancer, gastric carcinoma, gastric adenocarcinoma, colorectal cancer, colorectal carcinoma, colorectal adenocarcinoma, head and neck cancer, squamous cell carcinoma of the head and neck (SCCHN), lung cancer, lung adenocarcinoma, squamous cell lung carcinoma, ovarian cancer, ovarian carcinoma, ovarian serous adenocarcinoma, kidney cancer, renal cell carcinoma, renal clear cell carcinoma, renal cell adenocarcinoma, renal papillary cell carcinoma, pancreatic cancer, pancreatic adenocarcinoma,

pancreatic ductal adenocarcinoma, cervical cancer, cervical squamous cell carcinoma, skin cancer, melanoma, esophageal cancer, esophageal adenocarcinoma, liver cancer, hepatocellular carcinoma, cholangiocarcinoma, uterine cancer, uterine corpus endometrial carcinoma, thyroid cancer, thyroid carcinoma, pheochromocytoma, paraganglioma, bladder cancer, bladder urothelial carcinoma, prostate cancer, prostate adenocarcinoma, sarcoma and thymoma.

[0362] In some aspects the cancer to be treated in accordance with the present disclosure is selected from: a HER3-expressing cancer, gastric cancer (e.g. gastric carcinoma, gastric adenocarcinoma, gastrointestinal adenocarcinoma), head and neck cancer (e.g. head and neck squamous cell carcinoma), breast cancer, ovarian cancer (e.g. ovarian carcinoma), lung cancer (e.g. NSCLC, lung adenocarcinoma, squamous lung cell carcinoma), melanoma, prostate cancer, oral cavity cancer (e.g. oropharyngeal cancer), renal cancer (e.g. renal cell carcinoma) or colorectal cancer (e.g. colorectal carcinoma), oesophageal cancer, pancreatic cancer, a solid cancer and/or a liquid cancer.

[0363] The treatment/prevention may be aimed at one or more of: delaying/preventing the onset/progression of symptoms of the cancer, reducing the severity of symptoms of the cancer, reducing the survival/growth/invasion/metastasis of cells of the cancer, reducing the number of cells of the cancer and/or increasing survival of the subject.

[0364] In some aspects, the cancer to be treated/prevented comprises cells expressing an EGFR family member (e.g. HER3, EGFR, HER2 or HER4), and/or cells expressing a ligand for an EGFR family member. In some aspects, the cancer to be treated/prevented is a cancer which is positive for an EGFR family member. In some aspects, the cancer over-expresses an EGFR family member and/or a ligand for an EGFR family member. Overexpression of can be determined by detection of a level of expression which is greater than the level of expression by equivalent non-cancerous cells/non-tumor tissue.

[0365] Expression may be determined by any suitable means. Expression may be gene expression or protein expression. Gene expression can be determined e.g. by detection of mRNA encoding HER3, for example by quantitative real-time PCR (qRT-PCR). Protein expression can be determined e.g. by for example by antibody-based methods, for example by western blot, immunohistochemistry, immunocytochemistry, flow cytometry, or ELISA.

[0366] In some aspects, the cancer to be treated/prevented comprises cells expressing HER3. In some aspects, the cancer to be treated/prevented is a cancer which is positive for HER3. In some aspects, the cancer over-expresses HER3. Overexpression of HER3 can be determined by detection of a level of expression of HER3 which is greater than the level of expression by equivalent non-cancerous cells/non-tumor tissue.

[0367] In some aspects, a patient may be selected for treatment described herein based on the detection of a cancer expressing HER3, or overexpressing HER3, e.g. in a sample obtained from the subject.

[0368] In some aspects, the cancer to be treated/prevented comprises cells expressing a ligand for HER3 (e.g. NRG1 and/or NRG2). In some aspects, the cancer to be treated/prevented comprises cells expressing a level of expression of NRG1 and/or NRG2 which is greater than the level of expression by equivalent non-cancerous cells/non-tumor tissue.

[0369] Administration of the articles of the present disclosure is preferably in a "therapeutically effective" or "prophylactically effective" amount, this being sufficient to show therapeutic or prophylactic benefit to the subject. The actual amount administered, and rate and time-course of administration, will depend on the nature and severity of the disease/condition and the particular article administered. Prescription of treatment, e.g. decisions on dosage etc., is within the responsibility of general practitioners and other medical doctors, and typically takes account of the disease/disorder to be treated, the condition of the individual subject, the site of delivery, the method of administration and other factors known to practitioners. Examples of the techniques and protocols mentioned above can be found in Remington's Pharmaceutical Sciences, 20th Edition, 2000, pub. Lippincott, Williams & Wilkins.

[0370] Administration may be alone or in combination with other treatments, either simultaneously or sequentially dependent upon the condition to be treated. The antigen-binding molecule or composition described herein and a therapeutic agent may be administered simultaneously or sequentially.

[0371] In some aspects, the methods comprise additional therapeutic or prophylactic intervention, e.g. for the treatment/prevention of a cancer. In some aspects, the therapeutic or prophylactic intervention is selected from chemotherapy, immunotherapy, radiotherapy, surgery, vaccination and/or hormone therapy. In some aspects, the therapeutic or prophylactic intervention comprises leukapheresis. In some aspects the therapeutic or prophylactic intervention comprises a stem cell transplant.

[0372] In some aspects the antigen-binding molecule is administered in combination with an agent capable of inhibiting signalling mediated by an EGFR family member.

[0373] Accordingly, the present disclosure provides compositions comprising an article according to the present disclosure (e.g. an antigen-binding molecule according to the present disclosure) and another agent capable of inhibiting signalling mediated by an EGFR family member (e.g. EGFR, HER2, HER3 or HER4). Also provided is the use of such compositions in methods of medical treatment and prophylaxis of diseases/conditions described herein.

[0374] Also provided are methods for treating/preventing diseases/conditions described herein comprising administering articles of the present disclosure an article according to the present disclosure (e.g. an antigen-binding molecule according to the present disclosure) and another agent capable of inhibiting signalling mediated by an EGFR family member.

[0375] Agents capable of inhibiting signalling mediated by EGFR family members are known in the art, and include e.g. small molecule inhibitors (e.g. tyrosine kinase inhibitors), monoclonal antibodies (and antigen-binding fragments thereof), peptide/polypeptide inhibitors (e.g. decoy ligands/receptors or peptide aptamers) and nucleic acids (e.g. antisense nucleic acid, splice-switching nucleic acids or nucleic acid aptamers). Inhibitors of signalling mediated by EGFR family members include agents that inhibit signalling through a direct effect on an EGFR family member, an interaction partner therefore, and/or a downstream factor involved in signalling mediated by the EGFR family member.

[0376] In some aspects the antagonist of signalling mediated by an EGFR family member inhibits signalling mediated by one or more of EGFR, HER2, HER4 and HER3. Inhibitors of signalling

mediated by EGFR family members are described e.g. in Yamaoka et al., Int. J. Mol. Sci. (2018), 19, 3491. In some aspects the antagonist is a pan-ErbB inhibitor. In some aspects the antagonist is an inhibitor of signalling mediated by EGFR (e.g. cetuximab, panitumumab, gefitinib, erlotinib, lapatinib, afatinib, brigatinib, icotinib, osimertinib, zalutumumab, vandetanib, necitumumab, nimotuzumab, dacomitinib, duligotuzumab or matuzumab). In some aspects the antagonist is an inhibitor of signalling mediated by HER2 (e.g. trastuzumab, pertuzumab, lapatinib, neratinib, afatinib, dacomitinib, MM-111, MCLA-128 or margetuximab). In some aspects the antagonist is an inhibitor of signalling mediated by HER3 (e.g. seribantumab, lumretuzumab, elgemtumab, KTN3379, AV-203, GSK2849330, REGN1400, MP-RM-1, EV20, duligotuzumab, MM-111, istiratumab, MCLA-128, patritumab, EZN-3920, RB200 or U3-1402). In some aspects the antagonist is an inhibitor of signalling mediated by HER4 (e.g. lapatinib, ibrutinib, afatinib, dacomitinib or neratinib).

[0377] In some aspects the antagonist of signalling mediated by an EGFR family member inhibits a downstream effector of signalling by an EGFR family member. Downstream effectors of signalling by an EGFR family members include e.g. PI3K, AKT, KRAS, BRAF, MEK/ERK and mTOR. In some aspects, the antagonist of signalling mediated by an EGFR family member is an inhibitor of the MAPK/ERK pathway. In some aspects, the antagonist of signalling mediated by an EGFR family member is an inhibitor of the PI3K/ATK/mTOR pathway. In some aspects the antagonist is a PI3K inhibitor (e.g. pictilisib, buparlisib, idelalisib, copanlisib or duvelisib). In some aspects the antagonist is an AKT inhibitor (e.g. MK-2206, AZD5363, ipatasertib, VQD-002, perifosine or miltefosine). In some aspects the antagonist is a BRAF inhibitor (e.g. vemurafenib, dabrafenib, SB590885, XL281, RAF265, encorafenib, GDC-0879, PLX-4720, sorafenib, or LGX818). In some aspects the antagonist is a MEK/ERK inhibitor (e.g. trametinib, cobimetinib, binimetinib, selumetinib, PD-325901, CI-1040, PD035901, or TAK-733). In some aspects the antagonist is a mTOR inhibitor (e.g. rapamycin, deforolimus, temsirolimus, everolimus, ridaforolimus or sapanisertib).

[0378] In some aspects, the cancer to be treated in accordance with an aspect of the present disclosure (including monotherapy or combination therapy) is a cancer which is resistant to treatment with an antagonist of signalling mediated by an EGFR family member (e.g. EGFR, HER2, HER4 and/or HER3), e.g. an antagonist as described in the preceding three paragraphs. In some aspects the subject to be treated has a cancer which is resistant to treatment with an antagonist of signalling mediated by an EGFR family member. In some aspects the subject to be treated has a cancer which has developed resistance to treatment with an antagonist of signalling mediated by an EGFR family member. In some aspects the subject to be treated has a cancer which previously responded to treatment with an antagonist of signalling mediated by an EGFR family member, and which is now resistant to treatment with the antagonist. In some aspects the subject to be treated has a cancer which has relapsed and/or progressed following treatment with an antagonist of signalling mediated by an EGFR family member. In some aspects the subject to be treated has a cancer which initially responded to treatment with an antagonist of signalling mediated by an EGFR family member, but later progressed on said treatment.

[0379] The skilled person is readily able to identify cancers and subjects according to the preceding paragraph. Such cancers and subjects may be identified e.g. through monitoring of the development/progression of the cancer (and/or correlates thereof) overtime e.g. during the course of treatment with an antagonist of signalling mediated by an EGFR family member. In some aspects, identification of such subjects/cancers may comprise analysis of a sample (e.g. a biopsy), e.g. *in vitro.* In some aspects the cancer may be determined to comprise cells having a mutation which is

associated with reduced susceptibility and/or resistance to treatment with the antagonist. In some aspects the cancer may be determined to comprise cells having upregulated expression of an EGFR family member.

[0380] In particular aspects, the cancer to be treated is a cancer which is resistant to treatment with an antagonist of signalling mediated by EGFR and/or HER2. In some aspects the subject to be treated has a cancer which is resistant to treatment with an antagonist of signalling mediated by EGFR and/or HER2. In some aspects the subject to be treated has a cancer which has developed resistance to treatment with an antagonist of signalling mediated by EGFR and/or HER2. In some aspects the subject to be treated has a cancer which previously responded to treatment with an antagonist of signalling mediated by EGFR and/or HER2, and which is now resistant to treatment with the antagonist. In some aspects the subject to be treated has a cancer which has relapsed and/or progressed following treatment with an antagonist of signalling mediated by EGFR and/or HER2. In some aspects the subject to be treated has a cancer which initially responded to treatment with an antagonist of signalling mediated by EGFR and/or HER2, but later progressed on said treatment.

[0381] In particular aspects, the cancer to be treated comprises mutation conferring resistance to treatment with an inhibitor of BRAF. In some aspects, the mutation is mutation at BRAF V600. In some aspects, the mutation is BRAF V600E or V600K.

[0382] In particular aspects, the cancer to be treated comprises mutation conferring resistance to treatment with an inhibitor of BRAF (e.g. mutation at BRAF V600), and the treatment comprises administration of vemurafenib or darafenib.

[0383] In some aspects the antigen-binding molecule is administered in combination with an agent capable of inhibiting signalling mediated by an immune checkpoint molecule. In some aspects the immune checkpoint molecule is e.g. PD-1, CTLA-4, LAG-3, VISTA, TIM-3, TIGIT or BTLA. In some aspects the antigen-binding molecule is administered in combination with an agent capable of promoting signalling mediated by a costimulatory receptor. In some aspects the costimulatory receptor is e.g. CD28, CD80, CD40L, CD86, OX40, 4-1BB, CD27 or ICOS.

[0384] Accordingly, the present disclosure provides compositions comprising an article according to the present disclosure (e.g. an antigen-binding molecule according to the present disclosure) and an agent capable of inhibiting signalling mediated by an immune checkpoint molecule. Also provided are compositions comprising the articles of the present disclosure and an agent capable of promoting signalling mediated by a costimulatory receptor. Also provided is the use of such compositions in methods of medical treatment and prophylaxis of diseases/conditions described herein.

[0385] Also provided are methods for treating/preventing diseases/conditions described herein comprising administering articles of the present disclosure an article according to the present disclosure (e.g. an antigen-binding molecule according to the present disclosure) and an agent capable of inhibiting signalling mediated by an immune checkpoint molecule. Also provided are methods for treating/preventing diseases/conditions described herein comprising administering articles of the present disclosure an article according to the present disclosure (e.g. an antigen-binding molecule according to the present disclosure) and an agent capable of promoting signalling mediated by a costimulatory receptor.

[0386] Agents capable of inhibiting signalling mediated by immune checkpoint molecules are known in the art, and include e.g. antibodies capable of binding to immune checkpoint molecules or their ligands, and inhibiting signalling mediated by the immune checkpoint molecule. Other agents capable of inhibiting signalling mediated by an immune checkpoint molecule include agents capable of reducing gene/protein expression of the immune checkpoint molecule or a ligand for the immune checkpoint molecule (e.g. through inhibiting transcription of the gene(s) encoding the immune checkpoint molecule/ligand, inhibiting post-transcriptional processing of RNA encoding the immune checkpoint molecule/ligand, reducing stability of RNA encoding the immune checkpoint molecule/ligand, promoting degradation of RNA encoding the immune checkpoint molecule/ligand, inhibiting post-translational processing of the immune checkpoint molecule/ligand, reducing stability the immune checkpoint molecule/ligand, or promoting degradation of the immune checkpoint molecule/ligand), and small molecule inhibitors.

[0387] Agents capable of promoting signalling mediated by costimulatory receptors are known in the art, and include e.g. agonist antibodies capable of binding to costimulatory receptors and triggering or increasing signalling mediated by the costimulatory receptor. Other agents capable of promoting signalling mediated by costimulatory receptors include agents capable of increasing gene/protein expression of the costimulatory receptor or a ligand for the costimulatory receptor (e.g. through promoting transcription of the gene(s) encoding the costimulatory receptor/ligand, promoting post-transcriptional processing of RNA encoding the costimulatory receptor/ligand, increasing stability of RNA encoding the costimulatory receptor/ligand, inhibiting degradation of RNA encoding the costimulatory receptor/ligand, promoting post-translational processing of the costimulatory receptor/ligand, increasing stability the costimulatory receptor/ligand, or inhibiting degradation of the costimulatory receptor/ligand), and small molecule agonists.

[0388] In particular aspects the antigen-binding molecule of the present disclosure is administered in combination with an agent capable of inhibiting signalling mediated by PD-1. The agent capable of inhibiting signalling mediated by PD-1 may be a PD-1- or PD-L1-targeted agent. The agent capable of inhibiting signalling mediated by PD-1 may e.g. be an antibody capable of binding to PD-1 or PD-L1 and inhibiting PD-1-mediated signalling.

[0389] In some aspects, the antigen-binding molecule of the present disclosure is administered in combination with an agent capable of inhibiting signalling mediated by CTLA-4. The agent capable of inhibiting signalling mediated by CTLA-4 may be a CTLA-4-targeted agent, or an agent targeted against a ligand for CTLA-4 such as CD80 or CD86. In some aspects, the agent capable of inhibiting signalling mediated by CTLA-4 may e.g. be an antibody capable of binding to CTLA-4, CD80 or CD86 and inhibiting CTLA-4-mediated signalling.

[0390] In some aspects, the antigen-binding molecule of the present disclosure is administered in combination with an agent capable of inhibiting signalling mediated by LAG-3. The agent capable of inhibiting signalling mediated by LAG-3 may be a LAG-3-targeted agent, or an agent targeted against a ligand for LAG-3 such as MHC class II. In some aspects, the agent capable of inhibiting signalling mediated by LAG-3 may e.g. be an antibody capable of binding to LAG-3 or MHC class II and inhibiting LAG-3-mediated signalling.

[0391] In some aspects, the antigen-binding molecule of the present disclosure is administered in combination with an agent capable of inhibiting signalling mediated by VISTA. The agent capable of

inhibiting signalling mediated by VISTA may be a VISTA-targeted agent, or an agent targeted against a ligand for VISTA such as VSIG-3 or VSIG-8. In some aspects, the agent capable of inhibiting signalling mediated by VISTA may e.g. be an antibody capable of binding to VISTA, VSIG-3 or VSIG-8 and inhibiting VISTA-mediated signalling.

[0392] In some aspects, the antigen-binding molecule of the present disclosure is administered in combination with an agent capable of inhibiting signalling mediated by TIM-3. The agent capable of inhibiting signalling mediated by TIM-3 may be a TIM-3-targeted agent, or an agent targeted against a ligand for TIM-3 such as Galectin 9. In some aspects, the agent capable of inhibiting signalling mediated by TIM-3 may e.g. be an antibody capable of binding to TIM-3 or Galectin 9 and inhibiting TIM-3-mediated signalling.

[0393] In some aspects, the antigen-binding molecule of the present disclosure is administered in combination with an agent capable of inhibiting signalling mediated by TIGIT. The agent capable of inhibiting signalling mediated by TIGIT may be a TIGIT-targeted agent, or an agent targeted against a ligand for TIGIT such as CD113, CD112 or CD155. In some aspects, the agent capable of inhibiting signalling mediated by TIGIT may e.g. be an antibody capable of binding to TIGIT, CD113, CD112 or CD155 and inhibiting TIGIT-mediated signalling.

[0394] In some aspects, the antigen-binding molecule of the present disclosure is administered in combination with an agent capable of inhibiting signalling mediated by BTLA. The agent capable of inhibiting signalling mediated by BTLA may be a BTLA-targeted agent, or an agent targeted against a ligand for BTLA such as HVEM. In some aspects, the agent capable of inhibiting signalling mediated by BTLA may e.g. be an antibody capable of binding to BTLA or HVEM and inhibiting BTLA -mediated signalling.

[0395] In some aspects methods employing a combination of an antigen-binding molecule of the present disclosure and an agent capable of inhibiting signalling mediated by an immune checkpoint molecule (e.g. PD-1) provide an improved treatment effect as compared to the effect observed when either agent is used as a monotherapy. In some aspects the combination of an antigen-binding molecule of the present disclosure and an agent capable of inhibiting signalling mediated by an immune checkpoint molecule (e.g. PD-1) provide a synergistic (i.e. super-additive) treatment effect.

[0396] Simultaneous administration refers to administration of the antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof), cell or composition and therapeutic agent together, for example as a pharmaceutical composition containing both agents (combined preparation), or immediately after each other and optionally via the same route of administration, e.g. to the same artery, vein or other blood vessel. Sequential administration refers to administration of one of the antigen-binding molecule/composition or therapeutic agent followed after a given time interval by separate administration of the other agent. It is not required that the two agents are administered by the same route, although this is the case in some aspects. The time interval may be any time interval.

[0397] Chemotherapy and radiotherapy respectively refer to treatment of a cancer with a drug or with ionising radiation (e.g. radiotherapy using X-rays or γ-rays). The drug may be a chemical entity, e.g. small molecule pharmaceutical, antibiotic, DNA intercalator, protein inhibitor (e.g. kinase inhibitor), or a biological agent, e.g. antibody, antibody fragment, aptamer, nucleic acid (e.g. DNA, RNA), peptide,

polypeptide, or protein. The drug may be formulated as a pharmaceutical composition or medicament. The formulation may comprise one or more drugs (e.g. one or more active agents) together with one or more pharmaceutically acceptable diluents, excipients or carriers.

[0398] A treatment may involve administration of more than one drug. A drug may be administered alone or in combination with other treatments, either simultaneously or sequentially dependent upon the condition to be treated. For example, the chemotherapy may be a co-therapy involving administration of two drugs, one or more of which may be intended to treat the cancer.

[0399] The chemotherapy may be administered by one or more routes of administration, e.g. parenteral, intravenous injection, oral, subcutaneous, intradermal or intratumoral.

[0400] The chemotherapy may be administered according to a treatment regime. The treatment regime may be a pre-determined timetable, plan, scheme or schedule of chemotherapy administration which may be prepared by a physician or medical practitioner and may be tailored to suit the patient requiring treatment. The treatment regime may indicate one or more of: the type of chemotherapy to administer to the patient; the dose of each drug or radiation; the time interval between administrations; the length of each treatment; the number and nature of any treatment holidays, if any etc. For a co-therapy a single treatment regime may be provided which indicates how each drug is to be administered.

[0401] Chemotherapeutic drugs may be selected from: Abemaciclib, Abiraterone Acetate, Abitrexate (Methotrexate), Abraxane (Paclitaxel Albumin-stabilized Nanoparticle Formulation), ABVD, ABVE, ABVE-PC, AC, Acalabrutinib, AC-T, Adcetris (Brentuximab Vedotin), ADE, Ado-Trastuzumab Emtansine, Adriamycin (Doxorubicin Hydrochloride), Afatinib Dimaleate, Afinitor (Everolimus), Akynzeo (Netupitant and Palonosetron Hydrochloride), Aldara (Imiquimod), Aldesleukin, Alecensa (Alectinib), Alectinib, Alemtuzumab, Alimta (Pemetrexed Disodium), Aliqopa (Copanlisib Hydrochloride), Alkeran for Injection (Melphalan Hydrochloride), Alkeran Tablets (Melphalan), Aloxi (Palonosetron Hydrochloride), Alunbrig (Brigatinib), Ambochlorin (Chlorambucil), Amboclorin (Chlorambucil), Amifostine, Aminolevulinic Acid, Anastrozole, Aprepitant, Aredia (Pamidronate Disodium), Arimidex (Anastrozole), Aromasin (Exemestane), Arranon (Nelarabine), Arsenic Trioxide, Arzerra (Ofatumumab), Asparaginase Erwinia chrysanthemi, Atezolizumab, Avastin (Bevacizumab), Avelumab, Axicabtagene Ciloleucel, Axitinib, Azacitidine, Bavencio (Avelumab), BEACOPP, Becenum (Carmustine), Beleodaq (Belinostat), Belinostat, Bendamustine Hydrochloride, BEP, Besponsa (Inotuzumab Ozogamicin) , Bevacizumab, Bexarotene, Bexxar (Tositumomab and Iodine I 131 Tositumomab), Bicalutamide, BiCNU (Carmustine), Bleomycin, Blinatumomab, Blincyto (Blinatumomab), Bortezomib, Bosulif (Bosutinib), Bosutinib, Brentuximab Vedotin, Brigatinib, BuMel, Busulfan, Busulfex (Busulfan), Cabazitaxel, Cabometyx (Cabozantinib-S-Malate), Cabozantinib-S-Malate, CAF, Calquence (Acalabrutinib), Campath (Alemtuzumab), Camptosar (Irinotecan Hydrochloride), Capecitabine, CAPOX, Carac (Fluorouracil--Topical), Carboplatin, CARBOPLATIN-TAXOL, Carfilzomib, Carmubris (Carmustine), Carmustine, Carmustine Implant, Casodex (Bicalutamide), CEM, Ceritinib, Cerubidine (Daunorubicin Hydrochloride), Cervarix (Recombinant HPV Bivalent Vaccine), Cetuximab, CEV, Chlorambucil, CHLORAMBUCIL-PREDNISONE, CHOP, Cisplatin, Cladribine, Clafen (Cyclophosphamide), Clofarabine, Clofarex (Clofarabine), Clolar (Clofarabine), CMF, Cobimetinib, Cometriq (Cabozantinib-S-Malate), Copanlisib Hydrochloride, COPDAC, COPP, COPP-ABV, Cosmegen (Dactinomycin), Cotellic (Cobimetinib), Crizotinib, CVP, Cyclophosphamide, Cyfos (Ifosfamide), Cyramza (Ramucirumab), Cytarabine, Cytarabine Liposome, Cytosar-U

(Cytarabine), Cytoxan (Cyclophosphamide), Dabrafenib, Dacarbazine, Dacogen (Decitabine), Dactinomycin, Daratumumab, Darzalex (Daratumumab), Dasatinib, Daunorubicin Hydrochloride, Daunorubicin Hydrochloride and Cytarabine Liposome, Decitabine, Defibrotide Sodium, Defitelio (Defibrotide Sodium), Degarelix, Denileukin Diftitox, Denosumab, DepoCyt (Cytarabine Liposome), Dexamethasone, Dexrazoxane Hydrochloride, Dinutuximab, Docetaxel, Doxil (Doxorubicin Hydrochloride Liposome), Doxorubicin Hydrochloride, Doxorubicin Hydrochloride Liposome, Dox-SL (Doxorubicin Hydrochloride Liposome), DTIC-Dome (Dacarbazine), Durvalumab, Efudex (Fluorouracil--Topical), Elitek (Rasburicase), Ellence (Epirubicin Hydrochloride), Elotuzumab, Eloxatin (Oxaliplatin), Eltrombopag Olamine, Emend (Aprepitant), Empliciti (Elotuzumab), Enasidenib Mesylate, Enzalutamide, Epirubicin Hydrochloride, EPOCH, Erbitux (Cetuximab), Eribulin Mesylate, Erivedge (Vismodegib), Erlotinib Hydrochloride, Erwinaze (Asparaginase Erwinia chrysanthemi), Ethyol (Amifostine), Etopophos (Etoposide Phosphate), Etoposide, Etoposide Phosphate, Evacet (Doxorubicin Hydrochloride Liposome), Everolimus, Evista (Raloxifene Hydrochloride), Evomela (Melphalan Hydrochloride), Exemestane, 5-FU (Fluorouracil Injection), 5-FU (Fluorouracil--Topical), Fareston (Toremifene), Farydak (Panobinostat), Faslodex (Fulvestrant), FEC, Femara (Letrozole), Filgrastim, Fludara (Fludarabine Phosphate), Fludarabine Phosphate, Fluoroplex (Fluorouracil--Topical), Fluorouracil Injection, Fluorouracil--Topical, Flutamide, Folex (Methotrexate), Folex PFS (Methotrexate), FOLFIRI, FOLFIRI-BEVACIZUMAB, FOLFIRI-CETUXIMAB, FOLFIRINOX, FOLFOX, Folotyn (Pralatrexate), FU-LV, Fulvestrant, Gardasil (Recombinant HPV Quadrivalent Vaccine), Gardasil 9 (Recombinant HPV Nonavalent Vaccine), Gazyva (Obinutuzumab), Gefitinib, Gemcitabine Hydrochloride, GEMCITABINE-CISPLATIN, GEMCITABINE-OXALIPLATIN, Gemtuzumab Ozogamicin, Gemzar (Gemcitabine Hydrochloride), Gilotrif (Afatinib Dimaleate), Gleevec (Imatinib Mesylate), Gliadel (Carmustine Implant), Gliadel wafer (Carmustine Implant), Glucarpidase, Goserelin Acetate, Halaven (Eribulin Mesylate), Hemangeol (Propranolol Hydrochloride), Herceptin (Trastuzumab), HPV Bivalent Vaccine, Recombinant, HPV Nonavalent Vaccine, Recombinant, HPV Quadrivalent Vaccine, Recombinant, Hycamtin (Topotecan Hydrochloride), Hydrea (Hydroxyurea), Hydroxyurea, Hyper-CVAD, Ibrance (Palbociclib), Ibritumomab Tiuxetan, Ibrutinib, ICE, Iclusig (Ponatinib Hydrochloride), Idamycin (Idarubicin Hydrochloride), Idarubicin Hydrochloride, Idelalisib, Idhifa (Enasidenib Mesylate), Ifex (Ifosfamide), Ifosfamide, Ifosfamidum (Ifosfamide), IL-2 (Aldesleukin), Imatinib Mesylate, Imbruvica (Ibrutinib), Imfinzi (Durvalumab), Imiquimod, Imlygic (Talimogene Laherparepvec), Inlyta (Axitinib), Inotuzumab Ozogamicin, Interferon Alfa-2b, Recombinant, Interleukin-2 (Aldesleukin), Intron A (Recombinant Interferon Alfa-2b), Iodine I 131 Tositumomab and Tositumomab, Ipilimumab, Iressa (Gefitinib), Irinotecan Hydrochloride, Irinotecan Hydrochloride Liposome, Istodax (Romidepsin), Ixabepilone, Ixazomib Citrate, Ixempra (Ixabepilone), Jakafi (Ruxolitinib Phosphate), JEB, Jevtana (Cabazitaxel), Kadcyla (Ado-Trastuzumab Emtansine), Keoxifene (Raloxifene Hydrochloride), Kepivance (Palifermin), Keytruda (Pembrolizumab), Kisqali (Ribociclib), Kymriah (Tisagenlecleucel), Kyprolis (Carfilzomib), Lanreotide Acetate, Lapatinib Ditosylate, Lartruvo (Olaratumab), Lenalidomide, Lenvatinib Mesylate, Lenvima (Lenvatinib Mesylate), Letrozole, Leucovorin Calcium, Leukeran (Chlorambucil), Leuprolide Acetate, Leustatin (Cladribine), Levulan (Aminolevulinic Acid), Linfolizin (Chlorambucil), LipoDox (Doxorubicin Hydrochloride Liposome), Lomustine, Lonsurf (Trifluridine and Tipiracil Hydrochloride), Lupron (Leuprolide Acetate), Lupron Depot (Leuprolide Acetate), Lupron Depot-Ped (Leuprolide Acetate), Lynparza (Olaparib), Marqibo (Vincristine Sulfate Liposome), Matulane (Procarbazine Hydrochloride), Mechlorethamine Hydrochloride, Megestrol Acetate, Mekinist (Trametinib), Melphalan, Melphalan Hydrochloride, Mercaptopurine, Mesna, Mesnex (Mesna), Methazolastone (Temozolomide), Methotrexate, Methotrexate LPF (Methotrexate), Methylnaltrexone Bromide, Mexate (Methotrexate), Mexate-AQ (Methotrexate), Midostaurin, Mitomycin C, Mitoxantrone Hydrochloride, Mitozytrex (Mitomycin C), MOPP, Mozobil (Plerixafor), Mustargen (Mechlorethamine

Hydrochloride), Mutamycin (Mitomycin C), Myleran (Busulfan), Mylosar (Azacitidine), Mylotarg (Gemtuzumab Ozogamicin), Nanoparticle Paclitaxel (Paclitaxel Albumin-stabilized Nanoparticle Formulation), Navelbine (Vinorelbine Tartrate), Necitumumab, Nelarabine, Neosar (Cyclophosphamide), Neratinib Maleate, Nerlynx (Neratinib Maleate), Netupitant and Palonosetron Hydrochloride, Neulasta (Pegfilgrastim), Neupogen (Filgrastim), Nexavar (Sorafenib Tosylate), Nilandron (Nilutamide), Nilotinib, Nilutamide, Ninlaro (Ixazomib Citrate), Niraparib Tosylate Monohydrate, Nivolumab, Nolvadex (Tamoxifen Citrate), Nplate (Romiplostim), Obinutuzumab, Odomzo (Sonidegib), OEPA, Ofatumumab, OFF, Olaparib, Olaratumab, Omacetaxine Mepesuccinate, Oncaspar (Pegaspargase), Ondansetron Hydrochloride, Onivyde (Irinotecan Hydrochloride Liposome), Ontak (Denileukin Diftitox), Opdivo (Nivolumab), OPPA, Osimertinib, Oxaliplatin, Paclitaxel, Paclitaxel Albumin-stabilized Nanoparticle Formulation, PAD, Palbociclib, Palifermin, Palonosetron Hydrochloride, Palonosetron Hydrochloride and Netupitant, Pamidronate Disodium, Panitumumab, Panobinostat, Paraplat (Carboplatin), Paraplatin (Carboplatin), Pazopanib Hydrochloride, PCV, PEB, Pegaspargase, Pegfilgrastim, Peginterferon Alfa-2b, PEG-Intron (Peginterferon Alfa-2b), Pembrolizumab, Pemetrexed Disodium, Perjeta (Pertuzumab), Pertuzumab, Platinol (Cisplatin), Platinol-AQ (Cisplatin), Plerixafor, Pomalidomide, Pomalyst (Pomalidomide), Ponatinib Hydrochloride, Portrazza (Necitumumab), Pralatrexate, Prednisone, Procarbazine Hydrochloride, Proleukin (Aldesleukin), Prolia (Denosumab), Promacta (Eltrombopag Olamine), Propranolol Hydrochloride, Provenge (Sipuleucel-T), Purinethol (Mercaptopurine), Purixan (Mercaptopurine), [No Entries], Radium 223 Dichloride, Raloxifene Hydrochloride, Ramucirumab, Rasburicase, R-CHOP, R-CVP, Recombinant Human Papillomavirus (HPV) Bivalent Vaccine, Recombinant Human Papillomavirus (HPV) Nonavalent Vaccine, Recombinant Human Papillomavirus (HPV) Quadrivalent Vaccine, Recombinant Interferon Alfa-2b, Regorafenib, Relistor (Methylnaltrexone Bromide), R-EPOCH, Revlimid (Lenalidomide), Rheumatrex (Methotrexate), Ribociclib, R-ICE, Rituxan (Rituximab), Rituxan Hycela (Rituximab and Hyaluronidase Human), Rituximab, Rituximab and Hyaluronidase Human, Rolapitant Hydrochloride, Romidepsin, Romiplostim, Rubidomycin (Daunorubicin Hydrochloride), Rubraca (Rucaparib Camsylate), Rucaparib Camsylate, Ruxolitinib Phosphate, Rydapt (Midostaurin), Sclerosol Intrapleural Aerosol (Talc), Siltuximab, Sipuleucel-T, Somatuline Depot (Lanreotide Acetate), Sonidegib, Sorafenib Tosylate, Sprycel (Dasatinib), STANFORD V, Sterile Talc Powder (Talc), Steritalc (Talc), Stivarga (Regorafenib), Sunitinib Malate, Sutent (Sunitinib Malate), Sylatron (Peginterferon Alfa-2b), Sylvant (Siltuximab), Synribo (Omacetaxine Mepesuccinate), Tabloid (Thioguanine), TAC, Tafinlar (Dabrafenib), Tagrisso (Osimertinib), Talc, Talimogene Laherparepvec, Tamoxifen Citrate, Tarabine PFS (Cytarabine), Tarceva (Erlotinib Hydrochloride), Targretin (Bexarotene), Tasigna (Nilotinib), Taxol (Paclitaxel), Taxotere (Docetaxel), Tecentriq (Atezolizumab), Temodar (Temozolomide), Temozolomide, Temsirolimus, Thalidomide, Thalomid (Thalidomide), Thioguanine, Thiotepa, Tisagenlecleucel, Tolak (Fluorouracil--Topical), Topotecan Hydrochloride, Toremifene, Torisel (Temsirolimus), Tositumomab and Iodine I 131 Tositumomab, Totect (Dexrazoxane Hydrochloride), TPF, Trabectedin, Trametinib, Trastuzumab, Treanda (Bendamustine Hydrochloride), Trifluridine and Tipiracil Hydrochloride, Trisenox (Arsenic Trioxide), Tykerb (Lapatinib Ditosylate), Unituxin (Dinutuximab), Uridine Triacetate, VAC, Valrubicin, Valstar (Valrubicin), Vandetanib, VAMP, Varubi (Rolapitant Hydrochloride), Vectibix (Panitumumab), VeIP, Velban (Vinblastine Sulfate), Velcade (Bortezomib), Velsar (Vinblastine Sulfate), Vemurafenib, Venclexta (Venetoclax), Venetoclax, Verzenio (Abemaciclib), Viadur (Leuprolide Acetate), Vidaza (Azacitidine), Vinblastine Sulfate, Vincasar PFS (Vincristine Sulfate), Vincristine Sulfate, Vincristine Sulfate Liposome, Vinorelbine Tartrate, VIP, Vismodegib, Vistogard (Uridine Triacetate), Voraxaze (Glucarpidase), Vorinostat, Votrient (Pazopanib Hydrochloride), Vyxeos (Daunorubicin Hydrochloride and Cytarabine Liposome), Wellcovorin (Leucovorin Calcium), Xalkori (Crizotinib), Xeloda (Capecitabine), XELIRI, XELOX, Xgeva

(Denosumab), Xofigo (Radium 223 Dichloride), Xtandi (Enzalutamide), Yervoy (Ipilimumab), Yescarta (Axicabtagene Ciloleucel), Yondelis (Trabectedin), Zaltrap (Ziv-Aflibercept), Zarxio (Filgrastim), Zejula (Niraparib Tosylate Monohydrate), Zelboraf (Vemurafenib), Zevalin (Ibritumomab Tiuxetan), Zinecard (Dexrazoxane Hydrochloride), Ziv-Aflibercept, Zofran (Ondansetron Hydrochloride), Zoladex (Goserelin Acetate), Zoledronic Acid, Zolinza (Vorinostat), Zometa (Zoledronic Acid), Zydelig (Idelalisib), Zykadia (Ceritinib) and Zytiga (Abiraterone Acetate).

[0402] In some aspects the antigen-binding molecule of the present disclosure is administered in combination with one or more of: trastuzumab, cetuximab, cisplatin, 5-FU or capecitabine. In some aspects the antigen-binding molecule of the present disclosure is administered in combination with trastuzumab and cisplatin, and 5-FU or capecitabine.

[0403] In some aspects the antigen-binding molecule of the present disclosure is administered in combination with cetuximab. Administration in combination with cetuximab is contemplated in particular for the treatment of head and neck cancer (e.g. head and neck squamous cell carcinoma).

[0404] Multiple doses of the antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof), cell or composition may be provided. One or more, or each, of the doses may be accompanied by simultaneous or sequential administration of another therapeutic agent.

[0405] Multiple doses may be separated by a predetermined time interval, which may be selected to be one of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31 days, or 1, 2, 3, 4, 5, or 6 months. By way of example, doses may be given once every 7, 14, 21 or 28 days (plus or minus 3, 2, or 1 days).

Methods of detection

[0406] The present disclosure also provides the articles of the present disclosure for use in methods for detecting, localizing or imaging HER3, or cells expressing HER3.

[0407] The antigen-binding molecules described herein may be used in methods that involve the antigen-binding molecule to HER3. Such methods may involve detection of the bound complex of the antigen-binding molecule and HER3.

[0408] As such, a method is provided, comprising contacting a sample containing, or suspected to contain, HER3, and detecting the formation of a complex of the antigen-binding molecule and HER3. Also provided is a method comprising contacting a sample containing, or suspected to contain, a cell expressing HER3, and detecting the formation of a complex of the antigen-binding molecule and a cell expressing HER3.

[0409] Suitable method formats are well known in the art, including immunoassays such as sandwich assays, e.g. ELISA. The methods may involve labelling the antigen-binding molecule, or target(s), or both, with a detectable moiety, e.g. a fluorescent label, phosphorescent label, luminescent label, immuno-detectable label, radiolabel, chemical, nucleic acid or enzymatic label as described herein. Detection techniques are well known to those of skill in the art and can be selected to correspond with

the labelling agent.

[0410] Methods of this kind may provide the basis of methods for the diagnostic and/or prognostic evaluation of a disease or condition, e.g. a cancer. Such methods may be performed *in vitro* on a patient sample, or following processing of a patient sample. Once the sample is collected, the patient is not required to be present for the *in vitro* method to be performed, and therefore the method may be one which is not practised on the human or animal body. In some aspects the method is performed *in vivo.*

[0411] Detection in a sample may be used for the purpose of diagnosis of a disease/condition (e.g. a cancer), predisposition to a disease/condition, or for providing a prognosis (prognosticating) for a disease/condition, e.g. a disease/condition described herein. The diagnosis or prognosis may relate to an existing (previously diagnosed) disease/ condition.

[0412] Such methods may involve detecting or quantifying HER3 or cells expressing HER3, e.g. in a patient sample. Where the method comprises quantifying the relevant factor, the method may further comprise comparing the determined amount against a standard or reference value as part of the diagnostic or prognostic evaluation. Other diagnostic/prognostic tests may be used in conjunction with those described herein to enhance the accuracy of the diagnosis or prognosis or to confirm a result obtained by using the tests described herein.

[0413] A sample may be taken from any tissue or bodily fluid. The sample may comprise or may be derived from: a quantity of blood; a quantity of serum derived from the individual's blood which may comprise the fluid portion of the blood obtained after removal of the fibrin clot and blood cells; a tissue sample or biopsy; pleural fluid; cerebrospinal fluid (CSF); or cells isolated from said individual. In some aspects, the sample may be obtained or derived from a tissue or tissues which are affected by the disease/condition (e.g. tissue or tissues in which symptoms of the disease manifest, or which are involved in the pathogenesis of the disease/condition).

[0414] The present disclosure also provides methods for selecting/stratifying a subject for treatment with a HER3-targeted agent. In some aspects a subject is selected for treatment/prevention in accordance with the present disclosure, or is identified as a subject which would benefit from such treatment/prevention, based on detection/quantification of HER3, or cells expressing HER3, e.g. in a sample obtained from the individual.

Subjects

[0415] The subject in accordance with aspects the present disclosure may be any animal or human. The subject is preferably mammalian, more preferably human. The subject may be a non-human mammal, but is more preferably human. The subject may be male or female. The subject may be a patient. A subject may have been diagnosed with a disease or condition requiring treatment (e.g. a cancer), may be suspected of having such a disease/condition, or may be at risk of developing/contracting such a disease/condition.

[0416] In aspects according to the present disclosure the subject is preferably a human subject. In some aspects, the subject to be treated according to a therapeutic or prophylactic method of the

present disclosure herein is a subject having, or at risk of developing, a cancer. In aspects according to the present disclosure, a subject may be selected for treatment according to the methods based on characterisation for certain markers of such disease/condition.

Kits

[0417] In some aspects of the present disclosure a kit of parts is provided. In some aspects the kit may have at least one container having a predetermined quantity of an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof), cell or composition described herein.

[0418] In some aspects, the kit may comprise materials for producing an antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof), cell or composition described herein.

[0419] The kit may provide the antigen-binding molecule, polypeptide, CAR, nucleic acid (or plurality thereof), expression vector (or plurality thereof), cell or composition together with instructions for administration to a patient in order to treat a specified disease/condition.

[0420] In some aspects the kit may further comprise at least one container having a predetermined quantity of another therapeutic agent (e.g. anti-infective agent or chemotherapy agent). In such aspects, the kit may also comprise a second medicament or pharmaceutical composition such that the two medicaments or pharmaceutical compositions may be administered simultaneously or separately such that they provide a combined treatment for the specific disease or condition. The therapeutic agent may also be formulated so as to be suitable for injection or infusion to a tumor or to the blood.

Sequence identity

[0421] As used herein, "sequence identity" refers to the percent of nucleotides/amino acid residues in a subject sequence that are identical to nucleotides/amino acid residues in a reference sequence, after aligning the sequences and, if necessary, introducing gaps, to achieve the maximum percent sequence identity between the sequences. Pairwise and multiple sequence alignment for the purposes of determining percent sequence identity between two or more amino acid or nucleic acid sequences can be achieved in various ways known to a person of skill in the art, for instance, using publicly available computer software such as ClustalOmega (Söding, J. 2005, Bioinformatics 21, 951-960), T-coffee (Notredame et al. 2000, J. Mol. Biol. (2000) 302, 205-217), Kalign (Lassmann and Sonnhammer 2005, BMC Bioinformatics, 6(298)) and MAFFT (Katoh and Standley 2013, Molecular Biology and Evolution, 30(4) 772-780 software. When using such software, the default parameters, e.g. for gap penalty and extension penalty, are preferably used.

Sequences

[0422]

SEQ ID NO:	DESCRIPTION	SEQUENCE
1	Human HER3 isoform 1 (UniProt: P21860-1, v1)	MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLE IVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHA LRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCW GPGSEDCQTLTKTICAPQCNGHCFGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVP RCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMC EPCGGLCPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNV FRTVREITGYLNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGR IYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGPGPGQC LSCRNYSRGGVCVTHCNFLNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFR DGPHCVSSCPHGVLGAKGPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLTM ALTVIAGLVVIFMMLGGTFLYWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIFKETELRK LKVLGSGVFGTVHKGVWIPEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIGSLDHAHIVRLLGLC PGSSLQLVTQYLPLGSLLDHVRQHRGALGPQLLLNWGVQIAKGMYYLEEHGMVHRNLAARNVLL KSPSQVQVADFGVADLLPPDDKQLLYSEAKTPIKWMALESIHFGKYTHQSDVWSYGVTVWELMT FGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYMVMVKCWMIDENIRPTFKELANEFTRMARDP PRYLVIKRESGPGIAPGPEPHGLTNKKLEEVELEPELDLDLDLEAEEDNLATTTLGSALSLPVGTLN RPRGSQSLLSPSSGYMPMNQGNLGESCQESAVSGSSERCPRPVSLHPMPRGCLASESSEGHVT GSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVMPDTHL KGTPSSREGTLSSVGLSSVLGTEEEDEDEEYEYMNRRRRHSPPHPPRPSSLEELGYEYMDVGSD LSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYMNRQRDGGGPGGDYAAMGACPASEQGYEEMR AFQGPGHQAPHVHYARLKTLRSLEATDSAFDNPDYWHSRLFPKANAQRT
2	Human HER3 isoform 2 (UniProt: P21860-2)	MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLE IVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHA LRQLRLTQLTGQFPMVPSGLTPQPAQDWYLLDDDPRLLTLSASSKVPVTLAAV
3	Human HER3 isoform 3 (UniProt: P21860-3)	MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLE IVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHA LRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCW GPGSEDCQTLTKTICAPQCNGHCFGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVP RCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMC EPCGGLCPKAF
4	Human HER3 isoform 4 (UniProt: P21860-4)	MGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNT NSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRDAEIVVKDNGRSCPPCHEVCK GRCWGPGSEDCQTLTKTICAPQCNGHCFGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSG ACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNG LKMCEPCGGLCPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDP EKLNVFRTVREITGYLNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKE ISAGRIYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCA QCAHFRDGPHCVSSCPHGVLGAKGPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIG KTHLTMALTVIAGLVVIFMMLGGTFLYWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIF KETELRKLKVLGSGVFGTVHKGVWIPEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIGSLDHAHI VRLLGLCPGSSLQLVTQYLPLGSLLDHVRQHRGALGPQLLLNWGVQIAKGMYYLEEHGMVHRNL AARNVLLKSPSQVQVADFGVADLLPPDDKQLLYSEAKTPIKWMALESIHFGKYTHQSDVWSYGVT
		VWELMTFGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYMVMVKCWMIDENIRPTFKELANEFT RMARDPPRYLVIKRESGPGIAPGPEPHGLTNKKLEEVELEPELDLDLDLEAEEDNLATTTLGSALS LPVGTLNRPRGSQSLLSPSSGYMPMNQGNLGESCQESAVSGSSERCPRPVSLHPMPRGCLASE SSEGHVTGSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGY VMPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDEDEEYEYMNRRRRHSPPHPPRPSSLEELGYE YMDVGSDLSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYMNRQRDGGGPGGDYAAMGACPASE QGYEEMRAFQGPGHQAPHVHYARLKTLRSLEATDSAFDNPDYWHSRLFPKANAQRT
	Human HER3	MALTVIAGLVVIFMMLGGTFLYWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIFKETEL RKLKVLGSGVFGTVHKGVWIPEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIGSLDHAHIVRLLG LCPGSSLQLVTQYLPLGSLLDHVRQHRGALGPQLLLNWGVQIAKGMYYLEEHGMVHRNLAARNV LLKSPSQVQVADFGVADLLPPDDKQLLYSEAKTPIKWMALESIHFGKYTHQSDVWSYGVTVWEL

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5	isoform 5 (UniProt: P21860-5)	MTFGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYMVMVKCWMIDENIRPTFKELANEFTRMA RDPPRYLVIKRESGPGIAPGPEPHGLTNKKLEEVELEPELDLDLDLEAEEDNLATTTLGSALSLPVG TLNRPRGSQSLLSPSSGYMPMNQGNLGESCQESAVSGSSERCPRPVSLHPMPRGCLASESSEG HVTGSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVMP DTHLKGTPSSREGTLSSVGLSSVLGTEEEDEDEEYEYMNRRRRHSPPHPPRPSSLEELGYEYMD VGSDLSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYMNRQRDGGGPGGDYAAMGACPASEQGY EEMRAFQGPGHQAPHVHYARLKTLRSLEATDSAFDNPDYWHSRLFPKANAQRT
6	Mature human HER3 isoform 1 (UniProt: P21860-1, v1 positions 20 to 1342)	SEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGHNADLSFLQWIREVT GYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIE KNDKLCHMDTIDWRDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQC NGHCFGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNP HTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCGGLCPKACEGTGSGS RFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLNIQSWPPH MHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSLNWTK VLRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNF LNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCPHGVLGAK GPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLTMALTVIAGLVVIFMMLGGTF LYWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIFKETELRKLKVLGSGVFGTVHKGVWI PEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIGSLDHAHIVRLLGLCPGSSLQLVTQYLPLGSLLD HVRQHRGALGPQLLLNWGVQIAKGMYYLEEHGMVHRNLAARNVLLKSPSQVQVADFGVADLLPP DDKQLLYSEAKTPIKWMALESIHFGKYTHQSDVWSYGVTVWELMTFGAEPYAGLRLAEVPDLLEK GERLAQPQICTIDVYMVMVKCWMIDENIRPTFKELANEFTRMARDPPRYLVIKRESGPGIAPGPEP HGLTNKKLEEVELEPELDLDLDLEAEEDNLATTTLGSALSLPVGTLNRPRGSQSLLSPSSGYMPM NQGNLGESCQESAVSGSSERCPRPVSLHPMPRGCLASESSEGHVTGSEAELQEKVSMCRSRSR SRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVMPDTHLKGTPSSREGTLSSVGLSS VLGTEEEDEDEEYEYMNRRRRHSPPHPPRPSSLEELGYEYMDVGSDLSASLGSTQSCPLHPVPI MPTAGTTPDEDYEYMNRQRDGGGPGGDYAAMGACPASEQGYEEMRAFQGPGHQAPHVHYAR LKTLRSLEATDSAFDNPDYWHSRLFPKANAQRT
7	Mature human HER3 isoform 2 (UniProt: P21860-2 positions 20 to 183)	SEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGHNADLSFLQWIREVT GYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTGQFPMVPSG LTPQPAQDWYLLDDDPRLLTLSASSKVPVTLAAV
8	Mature human HER3 isoform 3 (UniProt: P21860-3 positions 20 to 331)	SEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGHNADLSFLQWIREVT GYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIE KNDKLCHMDTIDWRDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQC NGHCFGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNP HTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCGGLCPKAF
9	Human HER3 isoform 1 extracellular region (UniProt: P21860-1, v1 positions 20 to 643)	SEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGHNADLSFLQWIREVT GYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIE KNDKLCHMDTIDWRDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQC NGHCFGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNP HTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCGGLCPKACEGTGSGS RFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLNIQSWPPH MHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSLNWTK VLRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNF LNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCPHGVLGAK GPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLT
10	Human HER3 isoform 1 transmembrane domain (UniProt: P21860-1, v1 positions 644 to	MALTVIAGLVVIFMMLGGTFL

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	664)	
11	Human HER3 isoform 1 cytoplasmic domain (UniProt: P21860-1, v1 positions 665 to 1342)	YWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIFKETELRKLKVLGSGVFGTVHKGVWI PEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIGSLDHAHIVRLLGLCPGSSLQLVTQYLPLGSLLD HVRQHRGALGPQLLLNWGVQIAKGMYYLEEHGMVHRNLAARNVLLKSPSQVQVADFGVADLLPP DDKQLLYSEAKTPIKWMALESIHFGKYTHQSDVWSYGVTVWELMTFGAEPYAGLRLAEVPDLLEK
		GERLAQPQICTIDVYMVMVKCWMIDENIRPTFKELANEFTRMARDPPRYLVIKRESGPGIAPGPEP HGLTNKKLEEVELEPELDLDLDLEAEEDNLATTTLGSALSLPVGTLNRPRGSQSLLSPSSGYMPM NQGNLGESCQESAVSGSSERCPRPVSLHPMPRGCLASESSEGHVTGSEAELQEKVSMCRSRSR SRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVMPDTHLKGTPSSREGTLSSVGLSS VLGTEEEDEDEEYEYMNRRRRHSPPHPPRPSSLEELGYEYMDVGSDLSASLGSTQSCPLHPVPI MPTAGTTPDEDYEYMNRQRDGGGPGGDYAAMGACPASEQGYEEMRAFQGPGHQAPHVHYAR LKTLRSLEATDSAFDNPDYWHSRLFPKANAQRT
12	Human HER3 isoform 1 juxtamembrane segment (UniProt: P21860-1, v1 positions 665 to 708)	YWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIFKETE
13	Human HER3 isoform 1 protein kinase domain (UniProt: P21860-1, v1 positions 709 to 966)	LRKLKVLGSGVFGTVHKGVWIPEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIGSLDH AHIVRLLGLCPGSSLQLVTQYLPLGSLLDHVRQHRGALGPQLLLNWGVQIAKGMYYLEEH GMVHRNLAARNVLLKSPSQVQVADFGVADLLPPDDKQLLYSEAKTPIKWMALESIHFGKY THQSDVWSYGVTVWELMTFGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYMVMVKCW MIDENIRPTFKELANEFT
14	Human HER3 isoform 1 C terminal segment (UniProt: P21860-1, v1 positions 967 to 1342)	RMARDPPRYLVIKRESGPGIAPGPEPHGLTNKKLEEVELEPELDLDLDLEAEEDNLATTTLGSALS LPVGTLNRPRGSQSLLSPSSGYMPMNQGNLGESCQESAVSGSSERCPRPVSLHPMPRGCLASE SSEGHVTGSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGY VMPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDEDEEYEYMNRRRRHSPPHPPRPSSLEELGYE YMDVGSDLSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYMNRQRDGGGPGGDYAAMGACPASE QGYEEMRAFQGPGHQAPHVHYARLKTLRSLEATDSAFDNPDYWHSRLFPKANAQRT
15	Human HER3 extracellular region subdomain I (UniProt: P21860-1, v1 positions 20 to 183)	SEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGHNADLSFLQWIREVT GYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIE KNDKLCHMDTIDWRDIVRDRDAEIVVKDNGRSC
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16	extracellular region subdomain II (UniProt: P21860-1, v1 positions 184 to 329)	PPCHEVCKGRCWGPGSEDCQTLTKTICAPQCNGHCFGPNPNQCCHDECAGGCSGPQDTDCFA CRHFNDSGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPD KMEVDKNGLKMCEPCGGLCPK
17	Human HER3 extracellular region subdomain III (UniProt: P21860-1, v1 positions 330 to 495)	ACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGY LNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLC YHHSLNWTKVLRGPTEERLDIKHNRPRRDCVA
18	Human HER3 extracellular region subdomain IV (UniProt: P21860-1, v1 positions 496 to 643)	EGKVCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEPREFAHEAECFSCHPECQ PMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCPHGVLGAKGPIYKYPDVQNECRPCHENCTQ GCKGPELQDCLGQTLVLIGKTHLT
19	Human HER3 extracellular region subdomain II dimerisation loop (UniProt: P21860-1, v1 positions 261 to 278)	QPLVYNKLTFQLEPNPH
20	Rhesus macaque HER3 (UniProt: F7HEH3-1, v2)	MGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNT NSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWKDIVRDQDAEIVVKDNGRSCPLCHEVCK GRCWGPGPEDCQTLTKTICAPQCNGHCFGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSG ACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNG LKMCEPCGGLCPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDP EKLNVFRTVREITGYLNIQSWPPHMYNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKE ISAGRIYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCA QCAHFRDGPHCVSSCPHGVLGAKGPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIG KTHLTMALTVIAGLVVIFMMLGGTFLYWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIF KETELRKLKVLGSGVFGTVHKGVWIPEGESIKIPVCIKIIEDKSGRQSFQAVTDHMLAIGSLDHAHIV RLLGLCPGSSLQLVTQYLPLGSLLDHVRQHRGALGPQLLLNWGVQIAKGMYYLEEHGMVHRNLA
		ARNVLLKSPSQVQVADFGVADLLPPDDKQLLYSEAKTPIKWMALESIHFGKYTHQSDVWSYGVTV WELMTFGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYMVMVKCWMIDENIRPTFKELANEFTR MARDPPRYLVIKRESGPGIAPGPEPHGLTNKKLEEVELEPELDLDLDLEAEEDNLATTTLGSALSLP VGTLNRPRGSQSLLSPSSGYMPMNQGNLGEAFQESAVSGSSEWCPRPVSLHPMPRGCLASESS EGHVTGSEAELQEKVSTCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVM PDTHLKGTPSSREGTLSSVGLSSVLGTEEEDEDEEYEYMNRRRRHSPPRPPRPSSLEELGYEYM DVGSDLSASLGSTQSCPLHPVPVMPTAGTTPDEDYEYMNRQRGGSGPGGDYAAMGACPASEQ GYEEMRAFQGPGHQAPHVHYAHLKTLRSLEATDSAFDNPDYWHSRLFPKANAQRT

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21	Epitope recognised by anti-HER3 antibody clone 10A6	YNKLTFQLEPNPH
22	Epitope recognised by anti-HER3 antibody clone 4-35-B2 and 4-35-B4	PRCPQPLVYNKLTF
23	Composite sequence of epitopes recognised by anti-HER3 antibody clones 4-35-B2, 4-35-B4 and 10A6	PRCPQPLVYNKLTFQLEPNPH
24	10D1 heavy chain variable region	DVQLQESGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQFPGNKLEWMGSIHYSGGTNYNPSL KSRISITRDTSKNQFFLQLNSVTTEDTATYFCARMTTAPRYPFDYWGQGTTLTVSS
25	10D1_c75 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPTLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
26	10D1_c76 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
27	10D1_c77 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
28	10D1_c78v1 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
29	10D1_c78v2 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGkGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
30	10D1_11 B heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVYGYSITSGYSWHWIRQPPGKGLEWIGSIHYSGGTNYNPSLK SRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMTTAPRYPFDYWGQGTLVTVSS
31	10D1_c85v1 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIRYSGGTNYNPSLK SRITISRDTSKNQFSLKLGSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS

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32	10D1_c85v2 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGKGLEWIGSIRYSGGTNYNPSLK SRITISRDTSKNQFSLKLGSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
33	10D1_c85o1 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGKGLEWIGSIRYSGGTNYNPSLK SRITISRDTSKNQFSLKLGSVTAADTAVYFCARETTAPRYPFDYWGQGTLVTVSS
34	10D1_c85o2 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGKGLEWIGSIRYSGGTNYNPSLK SRITISRDTSKNQFSLKLGSVTAADTAVYFCARGTTAPRYPFDYWGQGTLVTVSS
35	10D1_c87 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLRLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
36	10D1_c89 heavy chain variable region	QVQLQESGPGLVKPSQTLSLTCTVSGYSITSGYSWHWIRQHPGKGLEWIGSIRYSGGTDYNPSLK SLVTISADTSKNQFSLKLSSVTAADTAVYYCARMTTAPWYPFDYWGQGTTVTVSS
37	10D1_c90 heavy chain variable region	QVQLQESGPGLVKPSQTLFLTCTVSGYSITSGYSWHWIRQHPGKGLEWIGSIRYSGGTDYNPSLK SLVTISVDTSKNQFSLKLSSVTAADTAVYYCARMTTAPWYPFDYWGQGTTVTVSS
38	10D1_c91 heavy chain variable region	QVQLQESGPGLVKPSQTLSLTCTVSGYYITSGYSWHWIRQHPGKGLEWIGSIRYSGGTDYNPSLK SLATISADTSKNQFSLKLSSVTAADTAVYYCARMTTAPWYPFDYWGQGTAVTVSS
39	10D1_c92 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPTLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
40	10D1_c93 heavy chain variable region	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLRLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSS
41	10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c92, 10D1_c93 heavy chain	GYSITSGYS

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	CDR1	
42	10D1_c91 heavy chain CDR1	GYYITSGYS
43	10D1 derived consensus heavy chain CDR1	$GYX_1ITSGYS$
		wherein X_1 = S or Y
44	10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain CDR2	IHYSGGT
45	10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c89, 10D1_c90, 10D1_c91 heavy chain CDR2	IRYSGGT
46	10D1 derived consensus heavy chain CDR2	IX_2YSGGT
		wherein X_2 = H or R
47	10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain CDR3	ARMTTAPRYPFDY
	10D1_c89,	ARMTTAPWYPFDY

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48	10D1_c90, 10D1_c91 heavy chain CDR3	
49	10D1_c85o1 heavy chain CDR3	ARETTAPRYPFDY
50	10D1_c85o2 heavy chain CDR3	ARGTTAPRYPFDY
51	10D1 derived consensus heavy chain CDR3	ARX_3TTAPX_4YPFDY
		wherein X_3 = M, E or G; X_4 = R or W
52	10D1_c75 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain FR1	DVQLQEWGAGLLKPSETLSLTCAVT
53	110D1_c89, 10D1_c91 heavy chain FR1	QVQLQESGPGLVKPSQTLSLTCTVS
54	10D1_c90 heavy chain FR1	QVQLQESGPGLVKPSQTLFLTCTVS
55	10D1 heavy chain FR1	DVQLQESGPDLVKPSQSLSLTCTVT
56	10D1_c75 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c85v1, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain FR2	WHWIRQFPGNGLEWIGS
	10D1_c78v2,	WHWIRQFPGKGLEWIGS

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57	10D1_c85v2, 10D1_c85o1, 10D1_c85o2 heavy chain FR2	
58	10D1 heavy chain FR2	WHWIRQFPGNKLEWMGS
59	10D1_c89, 10D1_c90, 10D1_c91 heavy chain FR2	WHWIRQHPGKGLEWIGS
60	10D1_11B heavy chain FR2	WHWIRQPPGKGLEWIGS
61	10D1_c75, 10D1_c92 heavy chain FR3	NYNPTLKSRITISRDTSKNQFSLKLSSVTAADTAVYFC
62	10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2 heavy chain FR3	NYNPSLKSRITISRDTSKNQFSLKLSSVTAADTAVYFC
63	10D1_11B heavy chain FR3	NYNPSLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYC
64	10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2 heavy chain FR3	NYNPSLKSRITISRDTSKNQFSLKLGSVTAADTAVYFC
65	10D1_c87, 10D1_c93 heavy chain FR3	NYNPSLKSRITISRDTSKNQFSLRLSSVTAADTAVYFC
66	10D1_c89 heavy chain FR3	DYNPSLKSLVTISADTSKNQFSLKLSSVTAADTAVYYC
67	10D1_c90 heavy chain FR3	DYNPSLKSLVTISVDTSKNQFSLKLSSVTAADTAVYYC
68	10D1_c91 heavy chain FR3	DYNPSLKSLATISADTSKNQFSLKLSSVTAADTAVYYC

SEQ ID NO:	DESCRIPTION	SEQUENCE
69	10D1 heavy chain FR3	NYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYFC
70	10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain FR4	WGQGTLVTVSS
71	10D1_c89, 10D1_c90 heavy chain FR4	WGQGTTVTVSS
72	10D1_c91 heavy chain FR4	WGQGTAVTVSS
73	10D1, 4-35-B4, 10A6 heavy chain FR4	WGQGTTLTVSS
74	10D1 light chain variable region	DIVMTQSQKFMSTSVGDRVSVTCKASQIVGSNVAWYQQKPGQSPKPLIYSASYRYSGVPDRFTA SGSGTDFTLTITNVQSEDLAEYFCQQYSSHPLTFGAGTKLELK
75	10D1_c75 light chain variable region	DIVMTQSPSSLSASVGDLVTITCKASQIVGSNVAWYQMKPGKSPKPLIYSASYLYFGVPSRFSGSG SGTDFTLTISSLQPEDVAEYFCQQYSSHPLTFGPGTKVEIK
76	10D1_c76 light chain variable region	DIVMTQSPSSLSASGGDRVTITCKASQIVGYNVAWYQQKPGKSPKPLIYSASYLYSDVPSRFSAS GSGTDFTLTISSLQPEDVAEYFCQQYSSHPLTFGPGTKVEIK
77	10D1_c77 light chain variable region	VIVMTQSPSSLSASVGDRVTITCKASQIVGPNVAWYQQKPGKSPKPLIYSASYGYSDVPSRFSGS GSGTDFTLTISSLQPEDVAEYFCQQYSTHPLTFGPGTKVEIK
78	10D1_c78v1, 10D1_c78v2, 10D1_11B light chain variable region	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSASYGYSDVPSRFSGS GSGTDFTLTISSLRPEDVATYYCQQYSSHPLTFGPGTKVEIK
	10D1_c85v1,	

SEQ ID NO:	DESCRIPTION	SEQUENCE
79	10D1_c85v2 light chain variable region	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSARYQYSGVPFRFSGS GSGTDFTLTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIK
80	10D1_c85o1 light chain variable region	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSARYQYSGVPFRFSGS GSGTDFTLTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIK
81	10D1_c85o2 light chain variable region	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSARYQYSGVPFRFSGS GSGTDFTLTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIK
82	10D1_c87 light chain variable region	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQMPGKSPEPLIYSASYLYSDVPSRFSGS GSGTDFTMTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIK
83	10D1_c89 light chain variable region	DIQMTQSPSSVSASVGDRVTITCKASQIVGSNVAWYQQKPGKAPEPLIYSASYLYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQYSSHPLTFGQGTKLEIK
84	10D1_c90 light chain variable region	DIQMTQSPSSVSASVGDRVTFTCKASQIVGSNVAWYQQKPGKAPEPLIYSASYLYSSVPSRFSGS GSGTEFTMTISSLEPEDFATYYCQQYTTHPLTFGPGTKVEIK
85	10D1_c91 light chain variable region	DIQMTQSPSSVSASVGDRVTITCKASQIVGSNVAWYQQKPGKAPMPLIYSASYGYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQYSSHPLTFGQGTKLEIK
86	10D1_c92 light chain variable region	DIVMTQSPSSLSASVGDLVTITCKASQIVGSNVAWYQMKLGKSPKPLIYSASYLYFGVPSRFSGSG SGTDFTLTISSLQPEDVAEYFCQQYFSHPLTFGPGTKVEIK
87	10D1_c93 light chain variable region	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSASYLYSDVPSRFSGS GSGTDFTMTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIK
88	10D1, 10D1_c75, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 light chain CDR1	QIVGSN

SEQ ID NO:	DESCRIPTION	SEQUENCE
89	10D1_c76 light chain CDR1	QIVGYN
90	10D1_c77 light chain CDR1	QIVGPN
91	10D1 derived consensus light chain CDR1	QIVGX_5N
		wherein X_5 = S, Y or P
92	10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 light chain CDR2	SAS
93	10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2 light chain CDR2	SAR
94	10D1 derived consensus light chain CDR2	SAX$_6$
		wherein X_6 = S or R
95	10D1, 10D1_c75, 10D1_c76, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c91, 10D1_c93 light chain CDR3	QQYSSHPLT
96	10D1_c77 light chain CDR3	QQYSTHPLT

SEQ ID NO:	DESCRIPTION	SEQUENCE
97	10D1_c90 light chain CDR3	QQYTTHPLT
98	10D1_c92 light chain CDR3	QQYFSHPLT
99	10D1 derived consensus light chain CDR3	QQYX_7X_8HPLT
		wherein X_7 = S, T or F; X_8 = S or T
100	10D1_c75, 10D1_c92 light chain FR1	DIVMTQSPSSLSASVGDLVTITCKAS
101	10D1_c76 light chain FR1	DIVMTQSPSSLSASGGDRVTITCKAS
102	10D1_c77 light chain FR1	VIVMTQSPSSLSASVGDRVTITCKAS
103	10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c93 light chain FR1	DIVMTQSPSSLSASVGDRVTITCKAS
104	10D1_c89, 10D1_c91 light chain FR1	DIQMTQSPSSVSASVGDRVTITCKAS
105	10D1_c90 light chain FR1	DIQMTQSPSSVSASVGDRVTFTCKAS
106	10D1 light chain FR1	DIVMTQSQKFMSTSVGDRVSVTCKAS
107	10D1_c75 light chain FR2	VAWYQMKPGKSPKPLIY
108	10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c93 light chain FR2	VAWYQQKPGKSPKPLIY
109	10D1_c87 light chain FR2	VAWYQQMPGKSPEPLIY

SEQ ID NO:	DESCRIPTION	SEQUENCE
110	10D1_c89, 10D1_c90 light chain FR2	VAWYQQKPGKAPEPLIY
111	10D1_c91 light chain FR2	VAWYQQKPGKAPMPLIY
112	10D1_c92 light chain FR2	VAWYQMKLGKSPKPLIY
113	10D1 light chain FR2	VAWYQQKPGQSPKPLIY
114	10D1_c75, 10D1_c92 light chain FR3	YLYFGVPSRFSGSGSGTDFTLTISSLQPEDVAEYFC
115	10D1_c76 light chain FR3	YLYSDVPSRFSASGSGTDFTLTISSLQPEDVAEYFC
116	10D1_c77 light chain FR3	YGYSDVPSRFSGSGSGTDFTLTISSLQPEDVAEYFC
117	10D1_c78v1, 10D1_c78v2, 10D1_11B light chain FR3	YGYSDVPSRFSGSGSGTDFTLTISSLRPEDVATYYC
118	10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2 light chain FR3	YQYSGVPFRFSGSGSGTDFTLTISSLQPEDVATYYC
119	10D1_c87, 10D1_c93 light chain FR3	YLYSDVPSRFSGSGSGTDFTMTISSLQPEDVATYYC
120	10D1_c89 light chain FR3	YLYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
121	10D1_c90 light chain FR3	YLYSSVPSRFSGSGSGTEFTMTISSLEPEDFATYYC
122	10D1_c91 light chain FR3	YGYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
123	10D1 light chain FR3	YRYSGVPDRFTASGSGTDFTLTITNVQSEDLAEYFC
124	10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1,	FGPGTKVEIK

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	10D1_c85o2, 10D1_c87, 10D1_c90, 10D1_c92, 10D1_c93 light chain FR4	
125	10D1_c89, 10D1_c91 light chain FR4	FGQGTKLEIK
126	10D1 light chain FR4	FGAGTKLELK
127	4-35-B2 heavy chain variable region	EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGHINPYNGGTTYNQKF KGRATLTVDKSSSTAFMHLNSLTSEDSAVYFCVSLRWGAMDYWGQGTSVTVSS
128	4-35-B2 heavy chain CDR1	GYSFTDYN
129	4-35-B2 heavy chain CDR2	INPYNGGT
130	4-35-B2 heavy chain CDR3	VSLRWGAMDY
131	4-35-B2 heavy chain FR1	EIQLQQSGPELVKPGASVKVSCKAS
132	4-35-B2 heavy chain FR2	MYWVKQSHGKSLEWIGH
133	4-35-B2 heavy chain FR3	TYNQKFKGRATLTVDKSSSTAFMHLNSLTSEDSAVYFC
134	4-35-B2 heavy chain FR4	WGQGTSVTVSS
135	4-35-B2 light chain variable region	QIVLTQSPALMSASPGEKVTMTCSASSSVSYMYWYQQKPRSSPKPWIYLTSNLASGVPARFSGS GSGTSYSLTISSMEAEDAATYYCQQWNSNPYTFGGGTKLEIK
136	4-35-B2 light chain CDR1	SSVSY
137	4-35-B2 light chain CDR2	LTS
138	4-35-B2 light chain CDR3	QQWNSNPYT
139	4-35-B2 light chain FR1	QIVLTQSPALMSASPGEKVTMTCSAS
140	4-35-B2 light chain FR2	MYWYQQKPRSSPKPWIY
141	4-35-B2 light chain FR3	NLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYC

SEQ ID NO:	DESCRIPTION	SEQUENCE
142	4-35-B2,4-35-B4, 10A6 light chain FR4	FGGGTKLEIK
143	4-35-B4 heavy chain variable region	EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHWVKQRPDQGLEWIGKIIDPANGNTNYDPKF QGKATITADTSSNTAYLQLSSLSSEDTAVYFCARGLHWGQGTTLTVSS
144	4-35-B4 heavy chain CDR1	GFNIKDTY
145	4-35-B4 heavy chain CDR2	IDPANGNT
146	4-35-B4 heavy chain CDR3	ARGLH
147	4-35-B4 heavy chain FR1	EVQLQQSGAELVKPGASVKLSCTAS
148	4-35-B4 heavy chain FR2	IHWVKQRPDQGLEWIGK
149	4-35-B4 heavy chain FR3	NYDPKFQGKATITADTSSNTAYLQLSSLSSEDTAVYFC
150	4-35-B4 light chain variable region	DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARF SGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPYTFGGGTKLEIK
151	4-35-B4 light chain CDR1	KSVSTSGYSY
152	4-35-B4 light chain CDR2	LAS
153	4-35-B4 light chain CDR3	QHSRELPYT
154	4-35-B4 light chain FR1	DIVLTQSPASLAVSLGQRATISCRAS
155	4-35-B4 light chain FR2	MHWYQQKPGQPPKLLIY
156	4-35-B4 light chain FR3	NLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYC
157	10A6 heavy chain variable region	DVQLQESGPGLVKPSQSLSLTCSVTGNFITSGYFWNWIRQFPGNKLEWMGFISYDGSNNYKPSL KNRISITRDTSKNQFFLKLNSVTTEDTATYYCARENYGFGFDYWGQGTTLTVSS
158	10A6 heavy chain CDR1	GNFITSGYF
159	10A6 heavy chain CDR2	ISYDGSN
160	10A6 heavy chain CDR3	ARENYGFGFDY

SEQ ID NO:	DESCRIPTION	SEQUENCE
161	10A6 heavy chain FR1	DVQLQESGPGLVKPSQSLSLTCSVT
162	10A6 heavy chain FR2	WNWIRQFPGNKLEWMGF
163	10A6 heavy chain FR3	NYKPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYC
164	10A6 light chain variable region	DIVLTQSPSSLPVSIGEKVTMSCKSSQSLLYSDNQKNYLAWYQQKPGQSPKLLIYWASTWKSGVP DRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYFTFPWTFGGGTKLEIK
165	10A6 light chain CDR1	QSLLYSDNQKNY
166	10A6 light chain CDR2	WAS
167	10A6 light chain CDR3	QQYFTFPWT
168	10A6 light chain FR1	DIVLTQSPSSLPVSIGEKVTMSCKSS
169	10A6 light chain FR2	LAWYQQKPGQSPKLLIY
170	10A6 light chain FR3	TWKSGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYC
171	Human IgG1 constant region (IGHG1; UniProt:P01857-1, v1)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
172	CH1 IgG1 (positions 1-98 of P01857-1, v1)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV
173	Hinge IgG1 (positions 99-110 of P01857-1, v1)	EPKSCDKTHTCP
174	CH2 IgG1 (positions 111-223 of P01857-1, v1)	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
175	CH3 IgG1 (positions 224-330 of P01857-1, v1)	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
	CH3 (D356E, L358M;	GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF

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176	positions numbered according to EU numbering)	FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
177	Cκ CL (IGCK; UniProt: P01834-1, v2)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
178	10A6 heavy chain SignalP	MKVLSLLYLLTAIPGILS
179	10D1 heavy chain SignalP	MRVLILLCLFTAFPGILS
180	10D1 light chain SignalP	MESQTQVFVYMLLWLSGVDG
181	4-35-B2 heavy chain SignalP	MEWSWIFLFLLSGTTGVHS
182	4-35-B2 light chain SignalP	MDFQVQIFSFLLMSASVMMSRG
183	4-35-B4 heavy chain SignalP	MKCSWVIFFLMAVVTGVNS
184	4-35-B4 light chain SignalP	METDTLLLWVLLLWVPGSTG
185	10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 heavy chain SignalP	MELGLRWVFLIATLAGARC
	10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2,	MDMRVPAQLLGLLLLWLRGARC

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186	10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 light chain SignalP	
187	10D1_c75 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPTLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
188	10D1_c75 VL-Cκ	DIVMTQSPSSLSASVGDLVTITCKASQIVGSNVAWYQMKPGKSPKPLIYSASYLYFGVPSRFSGSG SGTDFTLTISSLQPEDVAEYFCQQYSSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
189	10D1_c76 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL
		GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
190	10D1_c76 VL-Cκ	DIVMTQSPSSLSASGGDRVTITCKASQIVGYNVAWYQQKPGKSPKPLIYSASYLYSDVPSRFSAS GSGTDFTLTISSLQPEDVAEYFCQQYSSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
191	10D1_c77 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
192	10D1_c77 VL-Cκ	VIVMTQSPSSLSASVGDRVTITCKASQIVGPNVAWYQQKPGKSPKPLIYSASYGYSDVPSRFSGS GSGTDFTLTISSLQPEDVAEYFCQQYSTHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC
	10D1_c78v1	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL

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193	VH-CH1-CH2-CH3	GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
194	10D1_c78v2 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGkGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
195	10D1_c78v1, 10D1_c78v2, 10D1_11B VL-Cκ	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSASYGYSDVPSRFSGS GSGTDFTLTISSLRPEDVATYYCQQYSSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC
196	10D1_11B VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVYGYSITSGYSWHWIRQPPGKGLEWIGSIHYSGGTNYNPSLK SRVTISRDTSKNQFSLKLSSVTAADTAVYYCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
197	10D1_c85v1 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIRYSGGTNYNPSLK SRITISRDTSKNQFSLKLGSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
198	10D1_c85v2 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGKGLEWIGSIRYSGGTNYNPSLK SRITISRDTSKNQFSLKLGSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
199	10D1_c85v1, 10D1_c85v2 VL-Cκ	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSARYQYSGVPFRFSGS GSGTDFTLTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
200	10D1_c85o1 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGKGLEWIGSIRYSGGTNYNPSLK SRITISRDTSKNQFSLKLGSVTAADTAVYFCARETTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
		DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSARYQYSGVPFRFSGS

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201	10D1_c85o1 VL-Cκ	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSARYQTSGVPTRFSGS GSGTDFTLTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
202	10D1_c85o2 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGKGLEWIGSIRYSGGTNYNPSLK SRITISRDTSKNQFSLKLGSVTAADTAVYFCARGTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
203	10D1_c85o2 VL-Cκ	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSARYQYSGVPFRFSGS GSGTDFTLTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
204	10D1_c87 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLRLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
205	10D1_c87 VL-Cκ	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQMPGKSPEPLIYSASYLYSDVPSRFSGS GSGTDFTMTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
206	10D1_c89 VH-CH1-CH2-CH3	QVQLQESGPGLVKPSQTLSLTCTVSGYSITSGYSWHWIRQHPGKGLEWIGSIRYSGGTDYNPSLK SLVTISADTSKNQFSLKLSSVTAADTAVYYCARMTTAPWYPFDYWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
207	10D1_c89 VL-Cκ	DIQMTQSPSSVSASVGDRVTITCKASQIVGSNVAWYQQKPGKAPEPLIYSASYLYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQYSSHPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC
208	10D1_c90 VH-CH1-CH2-CH3	QVQLQESGPGLVKPSQTLFLTCTVSGYSITSGYSWHWIRQHPGKGLEWIGSIRYSGGTDYNPSLK SLVTISVDTSKNQFSLKLSSVTAADTAVYYCARMTTAPWYPFDYWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
209	10D1_c90 VL-Cκ	DIQMTQSPSSVSASVGDRVTFTCKASQIVGSNVAWYQQKPGKAPEPLIYSASYLYSSVPSRFSGS GSGTEFTMTISSLEPEDFATYYCQQYTTHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC

SEQ ID NO:	DESCRIPTION	SEQUENCE
210	10D1_c91 VH-CH1-CH2-CH3	QVQLQESGPGLVKPSQTLSLTCTVSGYYITSGYSWHWIRQHPGKGLEWIGSIRYSGGTDYNPSLK SLATISADTSKNQFSLKLSSVTAADTAVYYCARMTTAPWYPFDYWGQGTAVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
211	10D1_c91 VL-Cκ	DIQMTQSPSSVSASVGDRVTITCKASQIVGSNVAWYQQKPGKAPMPLIYSASYGYSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQYSSHPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV THQGLSSPVTKSFNRGEC
212	10D1_c92 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPTLK SRITISRDTSKNQFSLKLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
213	10D1_c92 VL-Cκ	DIVMTQSPSSLSASVGDLVTITCKASQIVGSNVAWYQMKLGKSPKPLIYSASYLYFGVPSRFSGSG SGTDFTLTISSLQPEDVAEYFCQQYFSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVT
		HQGLSSPVTKSFNRGEC
214	10D1_c93 VH-CH1-CH2-CH3	DVQLQEWGAGLLKPSETLSLTCAVTGYSITSGYSWHWIRQFPGNGLEWIGSIHYSGGTNYNPSLK SRITISRDTSKNQFSLRLSSVTAADTAVYFCARMTTAPRYPFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
215	10D1_c93 VL-Cκ	DIVMTQSPSSLSASVGDRVTITCKASQIVGSNVAWYQQKPGKSPKPLIYSASYLYSDVPSRFSGS GSGTDFTMTISSLQPEDVATYYCQQYSSHPLTFGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC
216	10D1 VH-CH1-CH2-CH3	DVQLQESGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQFPGNKLEWMGSIHYSGGTNYNPSL KSRISITRDTSKNQFFLQLNSVTTEDTATYFCARMTTAPRYPFDYWGQGTTLTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
217	10D1 VL-CK	DIVMTQSQKFMSTSVGDRVSVTCKASQIVGSNVAWYQQKPGQSPKPLIYSASYRYSGVPDRFTA SGSGTDFTLTITNVQSEDLAEYFCQQYSSHPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC

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218	4-35-B2 VH-CH1-CH2-CH3	EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGHINPYNGGTTYNQKF KGRATLTVDKSSSTAFMHLNSLTSEDSAVYFCVSLRWGAMDYWGQGTSVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
219	4-35-B2 VL-CK	QIVLTQSPALMSASPGEKVTMTCSASSSVSYMYWYQQKPRSSPKPWIYLTSNLASGVPARFSGS GSGTSYSLTISSMEAEDAATYYCQQWNSNPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC
220	4-35-B4 VH-CH1-CH2-CH3	EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHWVKQRPDQGLEWIGKIIDPANGNTNYDPKF QGKATITADTSSNTAYLQLSSLSSEDTAVYFCARGLHWGQGTTLTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
221	4-35-B4 VL-CK	DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLESGVPARF SGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
222	10A6 VH-CH1-CH2-CH3	DVQLQESGPGLVKPSQSLSLTCSVTGNFITSGYFWNWIRQFPGNKLEWMGFISYDGSNNYKPSL KNRISITRDTSKNQFFLKLNSVTTEDTATYYCARENYGFGFDYWGQGTTLTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
223	10A6 VL-CK	DIVLTQSPSSLPVSIGEKVTMSCKSSQSLLYSDNQKNYLAWYQQKPGQSPKLLIYWASTWKSGVP DRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYFTFPWTFGGGTKLEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC
224	10D1_11 B heavy chain FR1	DVQLQEWGAGLLKPSETLSLTCAVY
225	10D1F VH-CH1-CH2-CH3 (GASDALIE; LCKC) (10D1 F.FcB)	QVQLQESGPGLVKPSQTLSLTCTVSGYSITSGYSWHWIRQHPGKGLEWIGSIRYSGGTDYNPSLK SLVTISADTSKNQFSLKLSSVTAADTAVYYCARMTTAPWYPFDYWGQGTTVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLAGPDVFCFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPLPEECTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
226	10D1FVH-CH1-CH2-CH3	QVQLQESGPGLVKPSQTLSLTCTVSGYSITSGYSWHWIRQHPGKGLEWIGSIRYSGGTDYNPSLK SLVTISADTSKNQFSLKLSSVTAADTAVYYCARMTTAPWYPFDYWGQGTTVTVSSASTKGPSVFP

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	(N297Q)	LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
		LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
227	10D1 VH-CH1-CH2-CH3 (GASDALIE; LCKC)	DVQLQESGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQFPGNKLEWMGSIHYSGGTNYNPSL KSRISITRDTSKNQFFLQLNSVTTEDTATYFCARMTTAPRYPFDYWGQGTTLTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLAGPDVFCFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPLPEECTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
228	10D1 VH-CH1-CH2-CH3 (GASD)	DVQLQESGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQFPGNKLEWMGSIHYSGGTNYNPSL KSRISITRDTSKNQFFLQLNSVTTEDTATYFCARMTTAPRYPFDYWGQGTTLTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLAGPDVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
229	HER3 binding site for 10D1-derived clones	CFGPNPNQCCHDECAGGC
230	Binding site motif 1	PNPNQ
231	Binding site motif 2	DECAG

[0423] The present disclosure includes the combination of the aspects and preferred features described except where such a combination is clearly impermissible or expressly avoided.

[0424] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0425] Aspects and aspects of the present disclosure will now be illustrated, by way of example, with reference to the accompanying figures. Further aspects and aspects will be apparent to those skilled in the art.

[0426] Throughout this specification, including the claims which follow, unless the context requires otherwise, the word "comprise," and variations such as "comprises" and "comprising," will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

[0427] It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. Ranges may

be expressed herein as from "about" one particular value, and/or to "about" another particular value. When such a range is expressed, another embodiment includes from the one particular value and/or to the other particular value. Similarly, when values are expressed as approximations, by the use of the antecedent "about," it will be understood that the particular value forms another embodiment.

[0428] Where a nucleic acid sequence is disclosed herein, the reverse complement thereof is also expressly contemplated.

[0429] Methods described herein may preferably performed *in vitro.* The term *"in vitro"* is intended to encompass procedures performed with cells in culture whereas the term *"in vivo"* is intended to encompass procedures with/on intact multi-cellular organisms.

Brief Description of the Figures

[0430] Aspects and experiments illustrating the principles of the invention will now be discussed with reference to the accompanying figures.

Figures 1A and 1B. Histograms showing staining of cells by anti-HER3 antibodies as determined by flow cytometry. Histograms show staining of HEK293 cells (which do not express HER3), or HEK293 HER3 overexpressing cells (HEK293 HER3 O/E) by (**1A, 1B**) anti-HER3 antibody clone 10D1 and (**1B**) anti-HER3 antibody clone LJM716.

Figures 2A and 2B. Histograms showing staining of cells by anti-HER3 antibodies as determined by flow cytometry. Histograms show staining of HEK293 cells (which do not express HER3), or HEK293 HER3 overexpressing cells (HEK293 HER3 O/E) by (**2A, 2B**) anti-HER3 antibody clone 4-35-B2 and (**2B**) anti-HER3 antibody clone LJM716.

Figures 3A and 3B. Histograms showing staining of cells by anti-HER3 antibodies as determined by flow cytometry. Histograms show staining of HEK293 cells (which do not express HER3), or HEK293 HER3 overexpressing cells (HEK293 HER3 O/E) by (**3A, 3B**) anti-HER3 antibody clone 4-35-B4 and (**3B**) anti-HER3 antibody clone LJM716.

Figure 4. Histograms showing staining of cells by anti-HER3 antibodies as determined by flow cytometry. Histograms show staining of HEK293 cells (which do not express HER3), or HEK293 HER3 overexpressing cells (HEK293 HER3 O/E) by anti-HER3 antibody clone 10A6.

Figures 5A and 5B. Graphs showing the results of ELISA analysis of binding of anti-HER3 antibody clone 10D1 to (**5A**) human, mouse, rat and cynomolgus macaque HER3, and (**5B**) human EGFR and human HER2. EC_{50} values are shown.

Figures 6A and 6B. Graphs showing the results of ELISA analysis of binding of anti-HER3 antibody clone 4-35-B2 to (**6A**) human, mouse, rat and cynomolgus macaque HER3, and (**6B**) human EGFR and human HER2.

Figures 7A and 7B. Graphs showing the results of ELISA analysis of binding of anti-HER3 antibody clone 4-35-B4 to (**7A**) human HER3, human EGFR and human HER2, and (**7B**) human, mouse, rat and cynomolgus macaque HER3.

Figure 8. Representative sensorgram showing the results of analysis of affinity of binding of anti-HER3 antibody clone 10D1 to human HER3. Kon, Koff and K_D are shown.

Figure 9. Representative sensorgram showing the results of analysis of affinity of binding of anti-HER3 antibody clone 4-35-B2 to human HER3.

Figure 10. Representative sensorgram showing the results of analysis of affinity of binding of anti-HER3 antibody clone 4-35-B4 to human HER3.

Figure 11. Graph showing the results of analysis of stability of anti-HER3 antibody clone 10D1 by Differential Scanning Fluorimetry analysis.

Figure 12. Graph showing the results of the analysis of recombinantly-expressed anti-HER3 antibody clone 10D1 by size exclusion chromatography.

Figure 13. Images showing the results of the analysis of anti-HER3 antibody clone 10D1 expression by SDS-PAGE and western blot. Lanes: M1 = TaKaRa protein marker Cat. No. 3452; M2 = GenScript protein marker Cat. No. M00521; 1 = reducing conditions; 2 = non-reducing conditions; P = positive control: human IgG1, Kappa (Sigma Cat. No. 15154). For western blot, the primary antibodies used were goat anti-human IgG-HRP (GenScript Cat No. A00166) and goat anti-human kappa-HRP (SouterhnBiotech Cat No. 2060-05).

Figure 14A and 14B. Representative sensorgram and table showing the results of analysis of competition between different anti-HER3 antibody clones for binding to HER3.

Figure 15. Graph showing the results of analysis of the inhibition of interaction between HER3 and HER2 by anti-HER3 antibody clone 10D1 as determined by ELISA.

Figures 16A and 16B. Table and histograms showing gene and protein expression of EGFR protein family members and their ligands by different cancer cell lines.

Figure 17. Images showing the results of analysis of the effect of anti-HER3 antibody clone 10D1 treatment on the HER3-medated signalling in N87 and FaDu cells by phospho-western blot. UN = untreated; T = treated with anti-HER3 antibody clone 10D1.

Figure 18. Images and graph showing the results of analysis of the effect of anti-HER3 antibody clone 10D1 treatment on the HER3-medated signalling in FaDu cells using the Phosphoprotein Antibody Array assay kit. Untreated = untreated FaDu cells; Treated = FaDu cells treated with anti-HER3 antibody clone 10D1.

Figures 19A and 19B. Graphs showing the percent confluence of cells relative to an untreated control condition (100%), for the indicated cells lines as determined by CCK8 assay, following incubation in the presence of anti-HER3 antibody clone 10D1. (**19A**) Shows the results obtained for N87 cells, and (**19B**) shows the results obtained for FaDu cells.

Figure 20. Graph showing the results of analysis of tumour volume over time in a N87 cell-line derived mouse gastric carcinoma model. Anti-HER3 antibody clone 10D1 was administered IP, biweekly at 500 µg per dose for a total of 10 doses. A control treatment group received an equal volume of PBS (vehicle).

Figure 21. Graph showing the results of analysis of tumour volume over time in a N87 cell-line

derived mouse gastric carcinoma model. Anti-HER3 antibody clone 4-35-B2 was administered IP, weekly at 11 mg/kg per dose for a total of 4 doses. A control treatment group received an equal amount of isotype control antibody (isotype).

Figure 22. Graph showing the results of analysis of tumour volume over time in a SNU16 cell-line derived mouse gastric carcinoma model. Anti-HER3 antibody clone 10D1 was administered IP, biweekly at 500 µg per dose for a total of 9 doses. A control treatment group received an equal volume of PBS (vehicle).

Figure 23. Graph showing the results of analysis of tumour volume over time in a FaDu cell-line derived mouse model of head and neck squamous cell carcinoma. Anti-HER3 antibody clone 10D1 was administered IP, weekly at 500 µg per dose for a total of 4 doses. Control treatment groups received an equal volume of PBS (vehicle), or the same dose of an isotype control antibody (isotype).

Figure 24. Graph showing the results of analysis of tumour volume over time in a FaDu cell-line derived mouse model of head and neck squamous cell carcinoma. Anti-HER3 antibody clone 10D1 was administered IP, biweekly at 500 µg per dose for a total of 8 doses. A control treatment group received an equal volume of PBS (vehicle).

Figure 25. Graph showing the results of analysis of tumour volume over time in an OvCAR8 cell-line derived mouse model of ovarian carcinoma. Anti-HER3 antibody clone 10D1 was administered IP, biweekly at 500 µg per dose for a total of 9 doses. A control treatment group received an equal volume of PBS (vehicle).

Figure 26. Graph showing the results of analysis of tumour volume over time in a HCC-95 cell-line derived mouse model of squamous lung cell carcinoma. Anti-HER3 antibody clone 10D1 was administered IP, biweekly at 500 µg per dose for a total of 4 doses. A control treatment group received an equal volume of PBS (vehicle).

Figure 27. Graph showing the results of analysis of tumour volume over time in an A549 cell-line derived mouse model of lung adenocarcinoma. Anti-HER3 antibody clone 10D1 was administered IP, biweekly at 500 µg per dose for a total of 10 doses. A control treatment group received an equal volume of PBS (vehicle).

Figure 28. Graph showing the results of analysis of tumour volume over time in an A549 cell-line derived mouse model of lung adenocarcinoma. Anti-HER3 antibody clone 4-35-B2 was administered IP, biweekly at 500 µg per dose for a total of 4 doses. A control treatment group received an equal volume of PBS (vehicle).

Figure 29. Graph showing the results of analysis of tumour volume over time in an ACHN cell-line derived mouse model of renal cell carcinoma. Anti-HER3 antibody clone 10D1 was administered IP, biweekly at 500 µg per dose for a total of 7 doses. A control treatment group received an equal volume of PBS (vehicle).

Figure 30. Histogram showing staining of cells by anti-HER3 antibody clone 10D1_c89 as determined by flow cytometry. Histograms show staining of HEK293 cells (which do not express HER3), or HEK293 HER3 overexpressing cells (HEK293 HER3 O/E).

Figure 31. Histogram showing staining of cells by anti-HER3 antibody clone 10D1_c90 as determined by flow cytometry. Histograms show staining of HEK293 cells (which do not express HER3), or HEK293 HER3 overexpressing cells (HEK293 HER3 O/E).

Figure 32. Histogram showing staining of cells by anti-HER3 antibody clone 10D1_c91 as determined by flow cytometry. Histograms show staining of HEK293 cells (which do not express HER3), or HEK293 HER3 overexpressing cells (HEK293 HER3 O/E).

Figures 33A and 33B. Graphs showing the results of ELISA analysis of binding of anti-HER3 antibody 10D1 variant clones to human HER3. (**33A**) shows binding of anti-HER3 antibody clones 10D1 (referred to as 10D1P), 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78, 10D1_11B (referred to as v11b78L), 10D1_c85, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c93, LJM716 and hIgG (negative control). (**33B**) shows the same data as 33A, but for clones 10D1_c89, 10D1_c90, 10D1_c91 and LJM716 only.

Figures 34A and 34B. Graphs showing the results of the analysis of recombinantly-expressed anti-HER3 antibody 10D1 variant clones by size exclusion chromatography. (**34A**) shows results for anti-HER3 antibody clones 10D1_c93, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78, 10D1_11B (referred to as C78 v11b), 10D1_c85, 10D1_c85o1, 10D1_c85o2, 10D1_c89, 10D1_c90, 10D1_c91 and 10D1_c93. (**34B**) shows the same data as 33A, but for clones 10D1_c89, 10D1_c90, 10D1_c91 and only.

Figures 35A to 35C. Graphs showing the results analysis of stability of anti-HER3 antibody 10D1 variant clones by Differential Scanning Fluorimetry analysis. (**35A**) shows results for anti-HER3 antibody clones LJM716 (also referred to as Elgemtumab), 10D1 (referred to as 10D1 (parental)), 10D1_c75, 10D1_c76, 10D1_c77 and 10D1_c78. (**35B**) shows results for 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_11B (referred to as c78_V11B), 10D1_c85 and 10D1_c85o1. (35C) shows results for 10D1_c90, 10D1_c91 and 10D1_c93.

Figures 36A to 36M. Representative sensorgrams showing the results of analysis of affinity of anti-HER3 antibody 10D1 variant clones to human HER3. Kon, Koff and K_D are shown. (**36A**) shows results for clone 10D1_c89, (**36B**) shows results for clone 10D1_c90, (**36C**) shows results for clone 10D1_c91, (**36D**) shows results for clone 10D1_c11B, (**36E**) shows results for clone 10D1_c85o2, (**36F**) shows results for clone 10D1_c87, (**36G**) shows results for clone 10D1_c93, (**36H**) shows results for clone 10D1_c76, (**36I**) shows results for clone 10D1_c77, (**36J**) shows results for clone 10D1_c78, (**36K**) shows results for clone 10D1_c75, (**36L**) shows results for clone 10D1_c85, and (**36M**) shows results for clone 10D1_c85o1.

Figure 37. Table summarising properties of anti-HER3 antibody 10D1 variant clones relevant to safety and developability.

Figures 38A and 38B. Bio-Layer Interferometry (**38A**) and thermostability (**38B**) analysis of Fc-modified anti-HER3 antibody clone 10D1 comprising GASDALIE and LCKC substitutions in CH2 region. (**38A**) BLI shows a representative sensorgram showing the results of analysis of affinity of binding to FcγRIIIa by Fc-modified anti-HER3 antibody clone 10D1. Kon, Koff and K_D are shown.

Figures 39A and 39B. Representative sensorgrams showing results of analysis of affinity of binding to FcγRIIIa by (**39A**) non-Fc-modified anti-HER3 antibody clone 10D1 and (**39B**) Fc-modified anti-HER3 antibody clone 10D1 comprising GASD substitutions in CH2 region. Kon, Koff and K_D are shown.

Figure 40. Graph showing the results of analysis of stability of anti-HER3 antibody clone 10D1 GASD variant by Differential Scanning Fluorimetry analysis.

Figures 41A and 41B. Tables showing the binding affinity for mouse and human Fc receptors of anti-HER3 antibody clones 10D1F.FcA and 10D1F.FcB (GASDALIE-LCKC variant) compared to silent variant N297Q, isoform variants, and commercially available antibodies. ND = K_D Not Determined due to low binding affinity.

Figures 42A and 42B. Histograms showing staining of cells by anti-HER3 antibodies as determined by flow cytometry. Histograms show staining of HEK293 cells (which do not express HER3), or HEK293 HER3 overexpressing cells (HEK293 HER3 O/E) by (**42A**) anti-HER3 antibody clone 10D1F.FcA and (**42B**) anti-HER3 antibody clones 10D1 and LJM-716.

Figure 43. Graph showing the results of ELISA analysis of binding of anti-HER3 antibody clone 10D1F.FcA to human EGFR (HER1) and human HER2. EC_{50} values are shown.

Figure 44. Histogram showing staining of cells by anti-HER3 and anti-HER4 antibodies as determined by flow cytometry. Histogram shows staining of HEK293 HER4 overexpressing cells by anti-HER3 antibody clone 10D1F.FcA, anti-HER3 antibodies LJM-716 and MM-121, and commercial anti-HER4 antibody.

Figure 45. Graph showing the results of ELISA analysis of binding of anti-HER3 antibody clone 10D1F.FcA to human, mouse, rat and cynomolgus macaque HER3. EC_{50} values are shown.

Figures 46A and 46B. Representative sensorgrams showing the results of analysis of affinity of binding of anti-HER3 antibody clones (**46A**) 10D1F.FcA and (**46B**) 10D1F.FcB to human HER3. Kon, Koff and K_D are shown.

Figures 47A and 47B. Graph showing the results of analysis of stability of anti-HER3 antibody clones (**47A**) 10D1F.FcA and (**47B**) 10D1F.FcB by Differential Scanning Fluorimetry analysis.

Figures 48A and 48B. Graph showing the results of purity analysis of anti-HER3 antibody clones (**48A**) 10D1F.FcA and (**48B**) 10D1F.FcB by size exclusion chromatography.

Figures 49A and 49B. Representative sensorgram and table showing the results of analysis of competition for binding to HER3 between anti-HER3 antibody clone 10D1F.FcA and anti-HER3 antibodies M-05-74 and M-08-11.

Figure 50. Graph and tables showing the results of pharmacokinetic analysis of anti-HER3 antibody clone 10D1 in mice.

Figures 51A to 51F. Graphs showing the effect of anti-HER3 antibody clone 10D1 treatment on blood cell counts (**51A**), electrolyte indices (**51B**) and indices of hepatoxicity, nephrotoxicity and pancreatic toxicity (**51C-51F**) in mice. Left bars represent vehicle control, right bars represent 10D1 treatment. Dotted lines indicate the end points of the Charles River reference range. Indices of hepatoxicity, nephrotoxicity and pancreatic toxicity include alanine aminotransferase (ALT), aspartate transaminase (AST), blood urea nitrogen (BUN), creatinine (CREA), alkaline phosphatase (ALP), glucose (GLU), calcium (CAL), total bilirubin (BIL), total protein (TPR) and albumin (ALB).

Figure 52. Graph and table showing the results of analysis of the inhibition of interaction between HER2 and HER3 by anti-HER3 antibody clone 10D1F.FcA and antibodies MM-121, LJM-716 and Roche M05 as determined by ELISA.

Figure 53. Graph and table showing the results of analysis of the inhibition of interaction between EGFR and HER3 by anti-HER3 antibody clone 10D1F.FcA and antibodies MM-121 and LJM716, as determined by ELISA.

Figure 54. Graph and table showing the results of analysis of the ability of anti-HER3 antibody clones 10D1F.FcA (10D1F.A), 10D1F.FcB (10D1F.B), 10D1F-hIgG1(N297Q) and anti-HER3 antibodies LJM-716 and Seribantumab (MM-121), to induce antibody-dependent cell-mediated cytotoxicity (ADCC). EC_{50} values are shown.

Figures 55A to 55C. Images showing the results of analysis of the effect of anti-HER3 antibody treatment on HER3-medated signalling in (**55A**) N87, (**55B**) FaDu and (**55C**) OvCar8 cells by phospho-western blot.

Figures 56A and 56B. Graph and tables showing the results of pharmacokinetic analysis of anti-HER3 antibody clones (**56A**) 10D1F.FcA and (**56B**) 10D1F.FcB in mice. Parameters: maximum concentration (C_{max}), T_{max}, AUC (0-336hr), AUC (0-infinity), Half-life (t½), Clearance (CL), Volume of distribution at steady state (Vss).

Figures 57A to 57D. Graph and tables showing the results of pharmacokinetic analysis of anti-HER3 antibody clones 10D1F.FcA and 10D1F.FcB at (**57A**) 10 mg/kg, (**57B**) 25 mg/kg, (**57C**) 100 mg/kg and (**57D**) 250 mg/kg in rats. Parameters: maximum concentration (C_{max}), T_{max}, AUC (0-336hr), AUC (0-infinity), Half-life (t½), Clearance (CL), Volume of distribution at steady state (V_{ss}).

Figures 58A to 58F. Graphs showing the effect of treatment of anti-HER3 antibody clone 10D1 F.FcA or 10D1 F.FcB at 200 ug (~10 mg/kg), 500 ug (~25 mg/kg), 2 mg (-100 mg/kg), or 5 mg (~250 mg/kg) on (**58A, 58B**) red blood cell indices, (**58C**) white blood cell indices, (**58D**) hepatotoxicity, (**58E**) kidney and pancreatic indices, and (**58F**) electrolyte indices.

Figures 59A to 59D. Graphs showing the effect of treatment anti-HER3 antibody clone 10D1 F.FcA on percentage tumour inhibition in *in vitro* mouse cancer models using N87 cells (gastric cancer), HCC95 cells (lung cancer), FaDu cells (head and neck cancer), SNU-16 cells (gastric cancer), A549 cells (lung cancer), OvCar8 cells (ovarian cancer), ACHN cells (kidney cancer) and HT29 cells (colorectal cancer) in comparison to (**59A & 59B**) anti-HER3 antibodies seribantumab and LJM-716 and (**59C & 59D**) EGFR family therapies cetuximab, trastuzumab and pertuzumab.

Figure 60. Graph showing the results of analysis of tumour volume over time in an A549 cell-line derived mouse model of lung adenocarcinoma after biweekly treatment with the indicated concentrations of antibodies for six weeks (n=6, vehicle control n=8). Antibody administration is indicated by triangles along x-axis.

Figure 61. Graph showing the results of analysis of tumour volume over time in a FaDu cell-line derived mouse model of head and neck squamous cell carcinoma after weekly treatment with the indicated concentrations of antibodies for six weeks (n=6). Antibody administration is indicated by triangles along x-axis.

Figure 62. Graph showing the results of analysis of tumour volume over time in a OvCAR8 cell-line derived mouse model of ovarian carcinoma after weekly treatment with the indicated concentrations of antibodies for six weeks (n=6). Antibody administration is indicated by triangles along x-axis.

Figures 63A to 63D. Box plots showing the results of analysis of pathway activation by gene set

enrichment analysis, for cancer cell lines treated with 10D1 F.FcA, LJM-716 or seribantumab in *in vitro* phosphorylation assays. **63A** shows the results obtained from N87 cells, **63B** shows the results obtained from A549 cells, **63C** shows the results obtained from OvCar8 cells and **63D** shows the results obtained from FaDu cells.

Figure 64. Images showing the results of analysis of the effect of anti-HER3 antibody treatment on HER3-medated signalling in A549 cells by phospho-western blot, at the indicated time points.

Figure 65. Graph showing the results of analysis of inhibiting of HER2:HER3 interaction by 10D1 F.FcA or pertuzumab, as determined by PathHunter Pertuzumab Bioassay. IC50 (M) values are shown.

Figures 66A to 66C. Histograms showing the results of analysis of expression of EGFR, HER2 and HER3 by (**66A**) BCPAP (**66B**) BHT101 and (**66C**) SW1736 cells. 1 = unstained cells, 2 = isotype control, 3 = cetuximab, 4 = trastuzumab, and 5 = 10D1 F.FcA.

Figures 67A to 67C. Graphs showing the results of analysis of the ability of different anti-ErbB antibodies to inhibit proliferation of $BRAF^{V600E}$ mutant thyroid cancer cell lines *in vitro.* **67A** shows the results obtained for BHT101 cells, **687** shows the results obtained for BCPAP cells, and **67C** shows the results obtained for SW1736 cells.

Figures 68A to 68C. Graphs showing the results of analysis of the ability of 10D1 F.FcA alone, or in combation with vemurafenib, to inhibit proliferation of $BRAF^{V600E}$ mutant thyroid cancer cell lines *in vitro.* **68A** shows the results obtained for BHT101 cells, **68B** shows the results obtained for SW1736 cells, and **68C** shows the results obtained for BCPAP cells.

Figures 69A to 69C. Tables showing representative hematological profiles of BALB/c mice following administration of 10 mg/kg, 25 mg/kg, 100 mg/kg or 250 mg/kg of 10D1 F.FcA or an equal volume of PBS. **69A** shows results of analysis of the red blood cell compartment, **69B** shows results of analysis of the white blood cell compartment, and **69C** shows results of analysis of correlates of liver, kidney and pancreas function, and levels of electrolytes. RBC = red blood cell, MVC = mean corpuscular volume, MCH = mean corpuscular haemoglobin, MCHC = mean corpuscular haemoglobin concentration, WBC = white blood cell, ALT = alanine aminotransferase, ALP = alkaline phosphatase, CREA = creatinine, BUN = blood urea nitrogen, GLU = glucagon, AMY = amylase, NA = sodium, K = potassium, P = phosphorus and CA = calcium.

Figures 70A to 70C. Tables showing representative hematological profiles of SD rats at the indicated time points, following administration of 250 mg/kg 10D1 F.FcA or an equal volume of PBS. **70A** shows results of analysis of the red blood cell compartment, **70B** shows results of analysis of the white blood cell compartment, and **70C** shows results of analysis of correlates of liver, kidney and pancreas function, and levels of electrolytes. RBC = red blood cell, MVC = mean corpuscular volume, MCH = mean corpuscular haemoglobin, MCHC = mean corpuscular haemoglobin concentration, WBC = white blood cell, ALT = alanine aminotransferase, ALP = alkaline phosphatase, CREA = creatinine, BUN = blood urea nitrogen, GLU = glucagon, AMY = amylase, NA = sodium, K = potassium, P = phosphorus and CA = calcium.

Figure 71. Images showing the results of analysis of the effect of 10D1 F.FcA treatment on HER3-medated signalling *in vivo* in cells of FaDu or OvCar8 cell-derived tumors, as determined by phospho-western blot.

Figure 72. Box blot showing the results of analysis of internalisation of different anti-ErbB antibodies by the indicated cell lines.

Figures 73A and 73B. Histograms and tables showing the results of analysis of internalisation of 10D1F.FcA or trastuzumab by the indicated cell lines at different time points, as determined by flow cytometry. **73B** shows median fluorescence intensity and percentages of PE-positive cells determined from the histograms shown in **73A.**

Figure 74. Graph showing the results of analysis of tumour volume over time in a N87 cell-line derived mouse model of gastric cancer after biweekly treatment with the indicated concentrations of the indicated anti-ErbB antibodies, for six weeks (n=6). Antibody administration is indicated by triangles along x-axis.

Figures 75A and 75B. Images showing immunohistochemical staining of malignant and normal human tissues using 10D1 F.FcA. **75A** and **75B** shows staining of different tissues.

Figure 76. Images showing immunohistochemical staining of A549 tumor xenograft cryosections by 10D1F or a rabbit polyclonal anti-HER3 antibody, at the indicated magnifications. Secondary-only control stainings are shown.

Figures 77A and 77B. Bar charts showing the results of analysis of the ability of the indicated anti-ErbB antibodies to inhibit *in vitro* proliferation of the indicated cancer cell lines at the serum concentrations the antibodies reach at C_{max} following IP administration to mice at 25 mg/kg. **77A** and **77B** show results obtained using different cell lines.

Examples

[0431] In the following Examples, the inventors describe the generation of novel anti-HER3 antibody clones targeted to specific regions of interest in the HER3 molecule, and the biophysical and functional characterisation and therapeutic evaluation of these antigen-binding molecules.

Example 1: HER3 target design and anti-HER3 antibody hybridoma production

[0432] The inventors selected two regions in the extracellular region of human HER3 (SEQ ID NO:9) for raising HER3-binding monoclonal antibodies.

1.1 Hybridoma production

[0433] Approximately 6 week old female BALB/c mice were obtained from InVivos (Singapore). Animals were housed under specific pathogen-free conditions and were treated in compliance with the Institutional Animal Care and Use Committee (IACUC) guidelines.

[0434] For hybridoma production, mice were immunized with proprietary mixtures of antigenic

peptide, recombinant target protein or cells expressing the target protein.

[0435] Prior to harvesting the spleen for fusion, mice were either boosted with antigen mixture for three consecutive days or only for a single day. 24 h after the final boost total splenocytes were isolated and fused with the myeloma cell line P3X63.Ag8.653 (ATCC, USA), with PEG using ClonaCell-HY Hybridoma Cloning Kit, in accordance with the manufacturer's instructions (Stemcell Technologies, Canada).

[0436] Fused cells were cultured in ClonaCell-HY Medium C (Stemcell Technologies, Canada) overnight at 37°C in a 5% CO_2 incubator. The next day, fused cells were centrifuged and resuspended in 10 ml of ClonaCell-HY Medium C and then gently mixed with 90 ml of semisolid methylcellulose-based ClonaCell-HY Medium D (StemCell Technologies, Canada) containing HAT components, which combines the hybridoma selection and cloning into one step.

[0437] The fused cells were then plated into 96 well plates and allowed to grow at 37 °C in a 5% CO_2 incubator. After 7-10 days, single hybridoma clones were isolated and antibody producing hybridomas were selected by screening the supernatants by Enzyme-linked immunosorbent assay (ELISA) and Fluorescence-activated cell sorting (FACs).

1.2 Antibody variable region amplification and sequencing

[0438] Total RNA was extracted from hybridoma cells using TRIzol reagent (Life Technologies, Inc., USA) using manufacturer's protocol. Double-stranded cDNA was synthesized using SMARTer RACE 5'/3' Kit (Clontech™, USA) in accordance with the manufacturer's instructions. Briefly, 1 µg total RNA was used to generate full-length cDNA using 5'-RACE CDS primer (provided in the kit), and the 5' adaptor (SMARTer II A primer) was then incorporated into each cDNA according to manufacturer's instructions. cDNA synthesis reactions contained: 5X First-Strand Buffer, DTT (20 mM), dNTP Mix (10 mM), RNase Inhibitor (40 U/µl) and SMARTScribe Reverse Transcriptase (100 U/µl).

[0439] The race-ready cDNAs were amplified using SeqAmp DNA Polymerase (Clontech™, USA). Amplification reactions contained SeqAmp DNA Polymerase, 2X Seq AMP buffer, 5' universal primer provided in the 5' SMARTer Race kit, that is complement to the adaptor sequence, and 3' primers that anneal to respective heavy chain or light chain constant region primer. The 5' constant region were designed based on previously reported primer mix either by Krebber et al. J. Immunol. Methods 1997; 201: 35-55, Wang et al. Journal of Immunological Methods 2000, 233; 167-177 or Tiller et al. Journal of Immunological Methods 2009; 350:183-193. The following thermal protocol was used: pre-denature cycle at 94°C for 1 min; 35 cycles of 94°C, 30 s, 55°C, 30 s and 72°C, 45 s; final extension at 72°C for 3 min.

[0440] The resulting VH and VL PCR products, approximately 550 bp, were cloned into pJET1.2/blunt vector using CloneJET PCR Cloning Kit (Thermo Scientific, USA) and used to transform highly competent *E.coli* DH5α. From the resulting transformants, plasmid DNA was prepared using Miniprep Kit (Qiagene, Germany) and sequenced. DNA sequencing was carried out by AITbiotech. These sequencing data were analyzed using the international IMGT (ImMunoGeneTics) information system (LeFranc et al., Nucleic Acids Res. (2015) 43 (Database issue):D413-22) to characterize the individual CDRs and framework sequences. The signal peptide at 5' end of the VH and VL was identified by

SignalP (v 4.1; Nielsen, in Kihara, D (ed): Protein Function Prediction (Methods in Molecular Biology vol. 1611) 59-73, Springer 2017).

[0441] Four monoclonal anti-HER3 antibody clones were selected for further development: 10D1, 10A6, 4-35-B2, and 4-35-B4.

[0442] Humanised versions of 10D1 were designed *in silico* by grafting of complementarity determining regions (CDRs) into VH and VL comprising human antibody framework regions, and were further optimized for antigen binding by yeast display method.

[0443] For yeast display, humanized sequences were converted into single-chain fragment variable (scFv) format by polymerase chain reaction (PCR) and used as templates to generate mutant libraries by random mutagenesis. Mutant PCR libraries were then electroporated into yeast together with linearized pCTcon2 vector to generate yeast libraries. The libraries were stained with human HER3 antigen and sorted for top binders. After 4-5 rounds of sorting, individual yeast clones were sequenced to identify unique antibody sequences.

Antibody clone	**VH/VL sequence**	
10A6	VH = SEQ ID NO:157	
	VL = SEQ ID NO:164	
10D1	VH = SEQ ID NO:24	
	VL = SEQ ID NO:74	
10D1_c75	VH = SEQ ID NO:25	
	VL = SEQ ID NO:75	
10D1_c76	VH = SEQ ID NO:26	
	VL = SEQ ID NO:76	
10D1_c77	VH = SEQ ID NO:27	
	VL = SEQ ID NO:77	
10D1_c78v1	VH = SEQ ID NO:28	
	VL = SEQ ID NO:78	
10D1_c78v2	VH = SEQ ID NO:29	
	VL = SEQ ID NO:78	
10D1_11B	VH = SEQ ID NO:30	
	VL = SEQ ID NO:78	
10D1_c85v1	VH = SEQ ID NO:31	
	VL = SEQ ID NO:79	
10D1_c85v2	VH = SEQ ID NO:32	
	VL = SEQ ID NO:79	
10D1_c85o1	VH = SEQ ID NO:33	
	VL = SEQ ID NO:80	
10D1_c85o2	VH = SEQ ID NO:34	
	VL = SEQ ID NO:81	

Antibody clone	VH/VL sequence	
10D1_c87	VH = SEQ ID NO:35	
	VL = SEQ ID NO:82	
10D1_c89	VH = SEQ ID NO:36	
	VL = SEQ ID NO:83	
10D1_c90	VH = SEQ ID NO:37	
	VL = SEQ ID NO:84	
10D1_c91	VH = SEQ ID NO:38	
	VL = SEQ ID NO:85	
10D1_c92	VH = SEQ ID NO:39	
	VL = SEQ ID NO:86	
10D1_c93	VH = SEQ ID NO:40	
	VL = SEQ ID NO:87	
4-35-B2	VH = SEQ ID NO:127	
	VL = SEQ ID NO:135	
4-35-B4	VH = SEQ ID NO:143	
	VL = SEQ ID NO:150	

Example 2: Antibody production and purification

2.1 Cloning VH and VL into Expression Vectors:

[0444] DNA sequences encoding the heavy and light chain variable regions of the anti-HER3 antibody clones were subcloned into the pmAbDZ_lgG1_CH and pmAbDZ_lgG1_CL (InvivoGen, USA) eukaryotic expression vectors for construction of human-mouse chimeric antibodies.

[0445] Alternatively, DNA sequence encoding the heavy and light chain variable regions of the anti-HER3 antibody clones were subcloned into the pFUSE-CHIg-hG1 and pFUSE2ss-CLIg-hk (InvivoGen, USA) eukaryotic expression vectors for construction of human-mouse chimeric antibodies. Human IgG1 constant region encoded by pFUSE-CHIg-hG1 comprises the substitutions D356E, L358M (positions numbered according to EU numbering) in the CH3 region relative to Human IgG1 constant region (IGHG1; UniProt:P01857-1, v1; SEQ ID NO:176). pFUSE2ss-CLIg-hk encodes human IgG1 light chain kappa constant region (IGCK; UniProt: P01834-1, v2).

[0446] Variable regions along with the signal peptides were amplified from the cloning vector using SeqAmp enzyme (Clontech™, USA) following the manufacturer's protocol. Forward and reverse primers having 15-20bp overlap with the appropriate regions within VH or VL plus 6 bp at 5' end as restriction sites were used. The DNA insert and the vector were digested with restriction enzyme recommended by the manufacturer to ensure no frameshift was introduced and ligated into its respective plasmid using T4 ligase enzyme (Thermo Scientific, USA). The molar ratio of 3:1 of DNA

insert to vector was used for ligation.

2.2 Expression of antibodies in mammalian cells

[0447] Antibodies were expressed using either 1) Expi293 Transient Expression System Kit (Life Technologies, USA), or 2) HEK293-6E Transient Expression System (CNRC-NRC, Canada) following the manufacturer's instructions.

1) Expi293 Transient Expression System:

Cell line maintenance:

[0448] HEK293F cells (Expi293F) were obtained from Life Technologies, Inc (USA). Cells were cultured in serum-free, protein-free, chemically defined medium (Expi293 Expression Medium, Thermo Fisher, USA), supplemented with 50 IU/ml penicillin and 50 µg/ml streptomycine (Gibco, USA) at 37°C, in 8% CO_2 and 80% humidified incubators with shaking platform.

Transfection:

[0449] Expi293F cells were transfected with expression plasmids using ExpiFectamine 293 Reagent kit (Gibco, USA) according to its manufacturer's protocol. Briefly, cells at maintenance were subjected to a media exchange to remove antibiotics by spinning down the culture, cell pellets were re-suspended in fresh media without antibiotics at 1 day before transfection. On the day of transfection, 2.5 x 10^6/ml of viable cells were seeded in shaker flasks for each transfection. DNA-ExpiFectamine complexes were formed in serum-reduced medium, Opti-MEM (Gibco, USA), for 25 min at room temperature before being added to the cells. Enhancers were added to the transfected cells at 16-18 h post transfection. An equal amount of media was topped up to the transfectants at day 4 post-transfection to prevent cell aggregation. Transfectants were harvested at day 7 by centrifugation at 4000 x *g* for 15 min, and filtered through 0.22 µm sterile filter units.

2) HEK293-6E Transient Expression System

Cell line maintenance:

[0450] HEK293-6E cells were obtained from National Research Council Canada. Cells were cultured in serum-free, protein-free, chemically defined Freestyle F17 Medium (Invitrogen, USA), supplemented with 0.1% Kolliphor-P188 and 4 mM L-Glutamine (Gibco, USA) and 25 µg/ml G-418 at 37°C, in 5% CO_2 and 80% humidified incubators with shaking platform.

Transfection:

[0451] HEK293-6E cells were transfected with expression plasmids using PEIproTM (Polyplus, USA) according to its manufacturer's protocol. Briefly, cells at maintenance were subjected to a media exchange to remove antibiotics by centrifugation, cell pellets were re-suspended with fresh media without antibiotics at 1 day before transfection. On the day of transfection, 1.5-2 x 10^6 cells/ml of viable cells were seeded in shaker flasks for each transfection. DNA and PEIproTM were mixed to a ratio of 1:1 and the complexes were allowed to form in F17 medium for 5 min at RT before adding to the cells. 0.5% (w/v) of Tryptone N1 was fed to transfectants at 24-48 h post transfection. Transfectants were harvested at day 6-7 by centrifugation at 4000 x *g* for 15 min and the supernatant was filtered through 0.22 µm sterile filter units.

[0452] Cells were transfected with vectors encoding the following combinations of polypeptides:

Antigen-biding molecule	**Polypeptides**	**Antibody**
[1]	10D1 VH-CH1-CH2-CH3 (SEQ ID NO:216) + 10D1 VL-Cκ (SEQ ID NO:217)	anti-HER3 clone 10D1 IgG1
[2]	10A6 VH-CH1-CH2-CH3 (SEQ ID NO:222) + 10A6 VL-Cκ (SEQ ID NO:223)	anti-HER3 clone 10A6 IgG1
[3]	4-35-B2 VH-CH1-CH2-CH3 (SEQ ID NO:218) + 4-35-B2 VL-Cκ (SEQ ID NO:219)	anti-HER3 clone 4-35-B2 IgG1
[4]	4-35-B4 VH-CH1-CH2-CH3 (SEQ ID NO:220) + 4-35-B4 VL-Cκ (SEQ ID NO:221)	anti-HER3 clone 4-35-B4 IgG1
[5]	10D1_c75 VH-CH1-CH2-CH3 (SEQ ID NO:187) + 10D1_c75 VL-Cκ (SEQ ID NO:188)	anti-HER3 clone 10D1_c75 IgG1
[6]	10D1_c76 VH-CH1-CH2-CH3 (SEQ ID NO:189) + 10D1_c76 VL-Cκ (SEQ ID NO:190)	anti-HER3 clone 10D1_c76 IgG1
[7]	10D1_c77 VH-CH1-CH2-CH3 (SEQ ID NO:191) + 10D1_c77 VL-Cκ (SEQ ID NO:192)	anti-HER3 clone 10D1_c77 IgG1
[8]	10D1_c78v1 VH-CH1-CH2-CH3 (SEQ ID NO:193) + 10D1_c78v1 VL-Cκ (SEQ ID NO:195)	anti-HER3 clone 10D1_c78v1 IgG1
[9]	10D1_c78v1 VH-CH1-CH2-CH3 (SEQ ID NO:194) + 10D1_c78v2 VL-Cκ (SEQ ID NO:195)	anti-HER3 clone 10D1_c78v2 IgG1
[10]	10D1_11B VH-CH1-CH2-CH3 (SEQ ID NO:196) + 10D1_11B VL-Cκ (SEQ ID NO:195)	anti-HER3 clone 10D1_11 B IgG1
[11]	10D1_c85v1 VH-CH1-CH2-CH3 (SEQ ID NO:197) + 10D1_c85v1 VL-Cκ (SEQ ID NO:199)	anti-HER3 clone 10D1_c85v1 IgG1

Antigen-biding molecule	Polypeptides	Antibody
[12]	10D1_c85v2 VH-CH1-CH2-CH3 (SEQ ID NO:198) + 10D1_c85v2 VL-Cκ (SEQ ID NO:199)	anti-HER3 clone 10D1_c85v2 IgG1
[13]	10D1_c85o1 VH-CH1-CH2-CH3 (SEQ ID NO:200) + 10D1_c85o1 VL-Cκ (SEQ ID NO:201)	anti-HER3 clone 10D1_c85o1 IgG1
[14]	10D1_c85o2 VH-CH1-CH2-CH3 (SEQ ID NO:202) + 10D1_c85o2 VL-Cκ (SEQ ID NO:203)	anti-HER3 clone 10D1_c85o2 IgG1
[15]	10D1_c87 VH-CH1-CH2-CH3 (SEQ ID NO:204) + 10D1_c87 VL-Cκ (SEQ ID NO:205)	anti-HER3 clone 10D1_c87 IgG1
[16]	10D1_c89 VH-CH1-CH2-CH3 (SEQ ID NO:206) + 10D1_c89 VL-Cκ (SEQ ID NO:207)	anti-HER3 clone 10D1_c89 IgG1
[17]	10D1_c90 VH-CH1-CH2-CH3 (SEQ ID NO:208) + 10D1_c90 VL-Cκ (SEQ ID NO:209)	anti-HER3 clone 10D1_c90 IgG1
[18]	10D1_c91 VH-CH1-CH2-CH3 (SEQ ID NO:210) + 10D1_c91 VL-Cκ (SEQ ID NO:211)	anti-HER3 clone 10D1_c91 IgG1
[19]	10D1_c92 VH-CH1-CH2-CH3 (SEQ ID NO:212) + 10D1_c92 VL-Cκ (SEQ ID NO:213)	anti-HER3 clone 10D1_c92 IgG1
[20]	10D1_c93 VH-CH1-CH2-CH3 (SEQ ID NO:214) + 10D1_c93 VL-Cκ (SEQ ID NO:215)	anti-HER3 clone 10D1_c93 IgG1

2.3 Antibody Purification

Affinity purification, buffer exchange and storage:

[0453] Antibodies secreted by the transfected cells into the culture supernatant were purified using liquid chromatography system AKTA Start (GE Healthcare, UK). Specifically, supernatants were loaded onto HiTrap Protein G column (GE Healthcare, UK) at a binding rate of 5 ml/min, followed by washing the column with 10 column volumes of washing buffer (20 mM sodium phosphate, pH 7.0). Bound mAbs were eluted with elution buffer (0.1 M glycine, pH 2.7) and the eluents were fractionated to collection tubes which contain appropriate amount of neutralization buffer (1 M Tris, pH 9). Neutralised elution buffer containing purified mAb were exchanged into PBS using 30K MWCO protein concentrators (Thermo Fisher, USA) or 3.5K MWCO dialysis cassettes (Thermo Fisher, USA). Monoclonal antibodies were sterilized by passing through 0.22 µm filter, aliquoted and snap-frozen in -80°C for storage.

2.4 Antibody-purity analysis

Size exclusion chromatography (SEC):

[0454] Antibody purity was analysed by size exclusion chromatography (SEC) using Superdex 200 10/30 GL columns (GE Healthcare, UK) in PBS running buffer, on a AKTA Explorer liquid chromatography system (GE Healthcare, UK). 150 µg of antibody in 500 µl PBS pH 7.2 was injected to the column at a flow rate of 0.75 ml/min at room temperature. Proteins were eluted according to their molecular weights.

[0455] The result for anti-HER3 antibody clone 10D1 ([1] of Example 2.2) is shown in Figure 12.

[0456] The results obtained for the different 10D1 variant clones are shown in Figure 34.

Sodium-Dodecyl Sulfate Polyacrylamide gel electrophoresis (SDS-PAGE):

[0457] Antibody purity was also analysed by SDS-PAGE under reducing and non-reducing conditions according to standard methods. Briefly, 4%-20% TGX protein gels (Bio-Rad, USA) were used to resolve proteins using a Mini-Protean Electrophoresis System (Bio-Rad, USA). For non-reducing condition, protein samples were denatured by mixing with 2x Laemmli sample buffer (Bio-Rad, USA) and boiled at 95°C for 5-10 min before loading to the gel. For reducing conditions, 2x sample buffer containing 5% of β-mercaptoethanol (βME), or 40 mM DTT (dithiothreitol) was used. Electrophoresis was carried out at a constant voltage of 150V for 1 h in SDS running buffer (25 mM Tris, 192 mM glycine, 1% SDS, pH 8.3).

Western Blot:

[0458] Protein samples (30 µg) were fractionated by SDS-PAGE as described above and transferred to nitrocellulose membranes. Membranes were then blocked and immunoblotted with antibodies overnight at 4°C. After washing three times in PBS-Tween the membranes were then incubated for 1 h at room temperature with horseradish peroxidase (HRP)-conjugated secondary antibodies. The results were visualized via a chemiluminescent Pierce ECL Substrate Western blot detection system (Thermo Scientific, USA) and exposure to autoradiography film (Kodak XAR film).

[0459] The primary antibodies used for detection were goat anti-human IgG-HRP (GenScript Cat No. A00166) and goat anti-human kappa-HRP (SouterhnBiotech Cat No. 2060-05).

[0460] The result for anti-HER3 antibody clone 10D1 ([1] of Example 2.2) is shown in Figure 13. 10D1 was easily expressed, purified and processed at high concentrations.

Example 3: Biophysical characterisation

3.1 Analysis of cell surface antigen-binding by flow cytometry

[0461] Wildtype HEK293 cells (which do not express high levels of HER3) and HEK293 cells transfected with vector encoding human HER3 (i.e. HEK 293 HER O/E cells) were incubated with 20 µg/ml of anti-HER3 antibody or isotype control antibody at 4°C for 1.5 hr. The anti-HER3 antibody clone LJM716 (described e.g. in Garner et al., Cancer Res (2013) 73: 6024-6035) was included in the analysis as a positive control.

[0462] The cells were washed thrice with FACS buffer (PBS with 5mM EDTA and 0.5% BSA) and resuspended in FITC-conjugated anti-FC antibody (Invitrogen, USA) for 40 min at 2-8°C. Cells were washed again and resuspended in 200 µL of FACS flow buffer (PBS with 5mM EDTA) for flow cytometric analysis using MACSQuant 10 (Miltenyi Biotec, Germany). After acquisition, all raw data were analyzed using Flowlogic software. Cells were gated using forward and side scatter profile percentage of positive cells was determined for native and overexpressing cell populations.

[0463] The results are shown in Figures 1 to 4 and 30 to 32. The anti-HER3 antibodies were shown to bind to human HER3 with high specificity. 10D1 and LJM716 were shown to bind to human HER3-expressing cells to a similar extent.

3.2 ELISAs for determining antibody specificity and cross-reactivity

[0464] ELISAs were used to determine the binding specificity of the antibodies. The antibodies were analysed for binding to human HER3 polypeptide, as well as respective mouse, rat and monkey homologues of HER3 (Sino Biological Inc., China). The antibodies were also analysed for their ability to bind to human EGFR and human HER2 (Sino Biological Inc., China).

[0465] ELISAs were carried out according to standard protocols. Briefly, 96-well plates (Nunc, Denmark) were coated with 0.1 µg/ml of target polypeptide in phosphate-buffered saline (PBS) for 16 h at 4°C. After blocking for 1 h with 1 % BSA in Tris buffer saline (TBS) at room temperature, the anti-HER3 antibody was serially diluted with the highest concentration being 10 µg/ml, and added to the plate. Post 1 h incubation at room temperature, plates were washed three times with TBS containing 0.05% Tween 20 (TBS-T) and were then incubated with a HRP-conjugated anti-His antibody (Life Technologies, Inc., USA) for 1 h at room temperature. After washing, plates were developed with colorimetric detection substrate 3,3',5,5'-tetramethylbenzidine (Turbo-TMB; Pierce, USA) for 10 min. The reaction was stopped with 2M H_2SO_4, and OD was measured at 450 nM.

[0466] The results of the ELISAs are shown in Figures 5 to 7 and Figure 33.

[0467] Anti-HER3 antibody clone 10D1 was found not to bind to human HER2 or human EGFR even at high concentrations of the antibody (Figure 5A). Anti-HER3 antibody clone 10D1 was also found to display substantial cross-reactivity with mouse HER3, rat HER3 and cynomolgus macaque HER3 (Figure 5B).

[0468] Anti-HER3 antibody clone 4-35-B2 was found to bind to human HER2 and human EGFR (Figure 6A). Anti-HER3 antibody clone 4-35-B2 also displayed substantial cross-reactivity with mouse HER3, rat HER3 and cynomolgus macaque HER3 (Figure 6B).

[0469] Anti-HER3 antibody clone 4-35-B4 was found to bind to human HER2 and human EGFR (Figure 7A). Anti-HER3 antibody clone 4-35-B4 also displayed substantial cross-reactivity with mouse HER3, rat HER3 and cynomolgus macaque HER3 (Figure 7B).

[0470] All of the 10D1 variants were demonstrated to bind to human HER3 (Figures 33A and 33B).

3.3 Global affinity study using Octet QK384 system

[0471] The anti-HER3 antibody clones in IgG1 format were analysed for binding affinity to human HER3.

[0472] Bio-Layer Interferometry (BLI) experiments were performed using the Octet QK384 system (ForteBio). anti-Human IgG Capture (AHC) Octet sensor tips (Pall ForteBio, USA) were used to anti-HER3 antibodies (25 nM). All measurements were performed at 25°C with agitation at 1000 rpm. Kinetic measurements for antigen binding were performed by loading His-tagged human HER3 antigens at different concentrations for 120 s, followed by a 120 s dissociation time by transferring the biosensors into assay buffer containing wells. Sensograms were referenced for buffer effects and then fitted using the Octet QK384 user software (Pall ForteBio, USA). Kinetic responses were subjected to a global fitting using a one site binding model to obtain values for association (K_{on}), dissociation (K_{off}) rate constants and the equilibrium dissociation constant (K_D). Only curves that could be reliably fitted with the software (R^2>0.90) were included in the analysis.

[0473] A representative sensorgram for the analysis of clone 10D1 is shown in Figure 8. Clone 10D1 was found to bind to human HER3 with an affinity of K_D = 9.58 nM.

[0474] The humanised/optimized 10D1 variants bind to human HER3 with very high affinity. Representative sensorgrams are shown in Figures 36A to 36M.

[0475] The affinities determined for 10D1 clone variants are shown below:

Antibody clone	**Affinity (K_D)**
10D1_c89	72.6 pM
10D1_c90	< 1 pM
10D1_c91	176 pM
10D1_11B	0.41 nM
10D1_c85o	17.3 nM
10D1_c87	< 1 pM
10D1_c93	< 1 pM
10D1_c76	< 1 pM

Antibody clone	Affinity (K_D)
10D1_c77	1.93 nM
10D1_c78	< 1 pM
10D1_c75	< 1 pM
10D1_c85	7.58 nM
10D1_c85o1	18.2 nM

[0476] Clone 4-35-B2 was found to bind to human HER3 with an affinity of K_D = 80.9 nM (Figure 9), and clone 4-35-B4 was found to bind to human HER3 with an affinity of K_D = 50.3 nM (Figure 10).

3.4 Analysis of thermostability by Differential Scanning Fluorimetry

[0477] Briefly, triplicate reaction mixes of antibodies at 0.2 mg/mL and SYPRO Orange dye (ThermoFisher) were prepared in 25 µL of PBS, transferred to wells of MicroAmp Optical 96-Well Reaction Plates (ThermoFisher), and sealed with MicroAmp Optical Adhesive Film (ThermoFisher). Melting curves were run in a 7500 fast Real-Time PCR system (Applied Biosystems) selecting TAMRA as reporter and ROX as passive reference. The thermal profile included an initial step of 2 min at 25°C and a final step of 2 min at 99°C, with a ramp rate of 1.2%. The first derivative of the raw data was plotted as a function of temperature to obtain the derivative melting curves. Melting temperatures (Tm) of the antibodies were extracted from the peaks of the derivative curves.

[0478] The first derivative of the raw data obtained for Differential Scanning Fluorimetry analysis of the thermostability of antibody clone 10D1 is shown in Figure 11. Three different samples of the antibody were analysed. The Tm was determined to be 70.3°C.

[0479] The analysis was also performed for the 10D1 variant clones and LJM716. The first derivative of the raw data and the determined Tms are shown in Figures 35A to 35C.

3.5 Analysis of anti-HER3 antibody 10D1 epitope

[0480] Anti-HER3 antibody 10D1 was analysed to determine whether it competes with anti-HER3 antibodies MM-121 and/or LJM-716 for binding to HER3. The epitope for MM-121 has been mapped in domain I of HER3; it blocks the NRG ligand binding site. The epitope for LJM-716 has been mapped to conformational epitope distributed across domains II and IV, and it locks HER3 in an inactive conformation.

[0481] Bio-Layer Interferometry (BLI) experiments were performed using the Octet QK384 system (ForteBio). anti-Penta-HIS (HIS1K) coated biosensor tips (ForteBio, USA) were used to capture His-tagged human HER3 (75 nM; 300 s). Binding by saturating antibody (400 nm; 600 s) was detected, followed by a dissociation step (120s), followed by detection of binding with competing antibody (300 nM; 300 s), followed by a dissociation step (120s). The variable region of MM-121 antibody was cloned in the PDZ vector having human IgG2 and IgKappa Fc backbone. The variable region of LJM-

716 antibody was cloned in the PDZ vector having human IgG1 and IgKappa Fc backbone.

[0482] The results of the analysis are shown in Figures 14A and 14B. Anti-HER3 antibody was found not to compete with MM-121 and/or LJM-716 for binding to HER3.

[0483] 10D1 was found to bind a distinct and topologically distant epitope of HER3 than MM-121 and/or LJM-716.

[0484] The epitope for 10D1 was mapped using overlapping 15-mer amino acids to cover the entire HER3 extracellular domain. Each unique 15-mer was elongated by a GS linker at C and N-terminals, conjugated to a unique well in 384 well plates, and the plates were incubated with 0.1, 1, 10 and 100 ug/ml of 10D1 antibody for 16hrs at 4°C. The plates were washed and then incubated for 1hr at 20°C with POD-conjugated goat anti-human IgG. Finally POD substrate solution was added to the wells for 20 min. before binding was assessed by measurement of chemiluminescence at 425nm using a LI-COR Odyssey Imaging System, and quantification and analysis was performed using the PepSlide Analyzer software package. The experiment was performed in duplicate.

[0485] The 10D1 epitope was found not to be directly located at a β-hairpin structure of the HER3 dimerisation arm located at domain II, but instead at a dimerisation interface N-terminal to the β-hairpin.

[0486] The site of HER3 to which 10D1 and 10D1-derived clones was determined to bind corresponds to positions 218 to 235 of the amino acid sequence of human HER3 (as shown e.g. in SEQ ID NO:1); the amino acid sequence for this region of HER3 is shown in SEQ ID NO:229. Within this region, two consensus binding site motifs were identified, and are shown in SEQ ID NOs:230 and 231.

[0487] Binding to this location of HER3 acts to impede HER family heterodimerisation and consequent downstream signalling pathways (see Example 4). Binding is ligand (NRG) independent. The 10D1 binding site is solvent accessible in both the open and closed HER3 conformations, is not conserved between HER3 and other HER family members, and is 100% conserved between human, mouse, rat and monkey HER3 orthologs.

Example 4: Functional characterisation

4.1 Inhibition of dimerisation of HER2 and HER3

[0488] The anti-HER3 antibodies were analysed for their ability to inhibit heterodimerisation of HER3 and HER2.

[0489] Briefly, 96-well plates (Nunc, Denmark) were coated with 0.1 µg/ml His-tagged HER2 protein in PBS for 16 h at 4°C. After blocking for 1 h with 1 % BSA in PBS at room temperature, recombinant biotinylated human HER3 protein was added in the presence of different concentrations of anti-HER3 antibody clone 10D1, and pates were incubated for 1 h at room temperature. Plates were subsequently washed three times, and then incubated with HRP-conjugated secondary antibody for 1

h at room temperature. After washing, plates were developed with colorimetric detection substrate 3,3',5,5'-tetramethylbenzidine (Turbo-TMB; Pierce, USA) for 10 min. The reaction was stopped with 2M H_2SO_4, and OD was measured at 450 nM.

[0490] The results are shown in Figure 15. Anti-HER3 antibody clone 10D1 was found to inhibit interaction between HER2 and HER3 in a dose-dependent fashion.

[0491] In further experiments, inhibition of HER2:HER3 dimerisation was analysed
In further experiments, inhibition of HER2:HER3 dimerisation was evaluated using the PathHunter Pertuzumab Bioassay Kit (DiscoverX) according to the manufacturer's instructions.

[0492] Briefly, HER2 and HER3 overexpressing U2OS cells were thawed using 1 ml of pre-warmed CP5 media and 5,000 cells were seeded per well and cultured at 37°C in 5% CO_2 atmosphere for 4 hr. Cells were then treated with an 8-point serial dilution of 10D1F.FcA or Pertuzumab, starting from 25 µg/ml.

[0493] After 4 hr incubation, 30 ng/ml of heregulin-β2 was added to each well and the cells were incubated for a further 16 hr. 10 µL of PathHunter bioassay detection reagent 1 was added to wells, and incubated for 15 min at room temperature in the dark. This was followed by addition of 40 µL PathHunter bioassay detection reagent 2, and incubation for 60 min at room temperature in the dark. Plates were then read using Synergy4 Biotek with 1 second delay.

[0494] The results are shown in Figure 65. 10D1F.FcA was found inhibit HER2:HER3 dimerisation with greater efficiency than pertuzumab, as reflected by its lower IC50.

4.2 Identification of cancer cell lines for analysis

[0495] The inventors characterised expression of EGFR protein family members by cancer cell lines to identify appropriate cells to investigate inhibition of HER3.

[0496] Figure 16A shows mRNA expression data EGFR family members and ligands by N87, SNU16, HT29, FaDu, A549, HCC95, OvCAR8 and AHCN cells according to the Cancer Cell Line Encyclopaedia (CCLE; Barretina et al., Nature (2012) 483: 603-607 and The Cancer Cell Line Encyclopedia Consortium & The Genomics of Drug Sensitivity in Cancer Consortium, Nature (2015) 528: 84-87). Figure 16A also shows protein expression data for EGFR, HER2 and HER3 as determined by FlowLogic.

[0497] Cell lines used in the experiments were purchased from ATCC and cultured as recommended. Briefly, cell lines maintained in the indicated cell culture medium, supplemented with 10% FBS and 1% Pen/Strep. Cells were cultured at 37°C, in 5% CO_2 incubators. Cultured cells were plated at the appropriate seeding density in a 96 well plate: HT29, HCC95, FADU and OvCar8 cells were seeded at 2000 cells/well, NCI-N87 cells were seeded at 5000 cells/well, SNU-16, ACHN and cells were seeded at 1500 cells/well, and A549 cells were seeded at 1200 cells/well.

[0498] Figure 16B shows surface expression of EGFR, HER2 and HER3 as determined by flow

cytometry. Briefly, 500,000 cells were stained in staining buffer containing 0.5% BSA and 2mM EDTA with primary antibodies (20 µg/ml) for 1.5 h at 4°C. The secondary Antibody used was anti-human Alexafluor488 at 10 µg/ml for 20 min at 4°C.

4.3 Inhibition of HER3-mediated signalling

[0499] Anti-HER3 antibody 10D1 was analysed for its ability to inhibit HER-3 mediated signalling *in vitro.*

[0500] Briefly, N87 and FaDu cells were seeded in wells of a 6 well plate with 10% serum at 37°C, 5% CO_2 After 16 hrs, cells were starved by culture overnight in 1% FBS cell culture medium (to reduce signalling elicited by growth factors in the serum). On the following day cells were treated with 50 µg/ml anti-HER3 antibody 10D1 for 4 hrs, followed by 15 min stimulation with NRG (100 ng/ml). Proteins were then extracted, quantified using standard Bradford protein assay, fractionated by SDS-PAGE, and transferred to nitrocellulose membranes. The membranes were then blocked and immunoblotted with the following antibodies overnight at 4°C anti-pHER3, anti-pAKT, pan anti-HER3, pan anti-AKT and anti-beta-actin. The blots were visualized via Bio-Rad Clarity Western ECL substrate, and bands were quantified using densiometric analysis; data were normalized to beta actin controls.

[0501] The results are shown in Figure 17. Anti-HER3 antibody 10D1 was found to inhibit HER3 phosphorylation and downstream signalling.

[0502] In further experiments the inventors investigated the intracellular signalling pathways affected by anti-HER3 antibody-mediated inhibition of HER3.

[0503] FaDu cells were seeded in wells of a 6 well plate with 10% serum at 37°C, 5% CO_2 After 16 hrs, cells were starved by culture overnight in 1% FBS cell culture medium. On the following day cells were treated with 50 µg/ml anti-HER3 antibody 10D1 for 4 hrs, followed by 15 min stimulation with NRG (100 ng/ml). Proteins were then extracted, quantified using standard Bradford protein assay, and incubated overnight with pre-blocked Phosphoprotein Antibody Array membrane (Ray Biotech) at 4°C. The membrane was then washed with washing buffer and incubated with detection antibody cocktail for 2 hrs at room temperature, followed by washing and incubation with HRP-Conjugated anti-IgG. After 2 hrs the membrane was washed and probed using the kit detection buffer. Images were captured with Syngene Gbox imaging system, the intensity of each dot/phosphoprotein was measured and percent inhibition was calculated by comparison with intensity measured for cells treated in the same way in the absence of the antibody.

[0504] The results are shown in Figure 18. Anti-HER3 antibody 10D1 was found to inhibit PI3K/AKT/mTOR and MAPK signalling.

[0505] In further experiments the inventors investigated the effect of treatment with anti-HER3 antibody 10D1 on proliferation of HER3-expressing cells.

[0506] Briefly, N87 and FaDu cells were treated with serially diluted concentrations of anti-HER3 antibody 10D1, starting from 100 µg/ml with a 9-point half log dilution. Cell proliferation was

measuring using the CCK-8 proliferation assay (Dojindo, Japan) after a period of 5 days, in accordance with the manufacturer's instructions. Briefly 1x CCK-8 solution was added to each well followed by incubation for 2 h at 37°C. The OD was then measured at 450 nm.

[0507] Figures 19A and 19B shows the percent cell confluence relative to untreated control cells (data points are averages of three replicates).

[0508] Anti-HER3 antibody 10D1 displayed dose-dependent inhibition of cell proliferation by N87 and FaDu cells.

Example 5: Analysis *in vivo*

5.1 Pharmacokinetic analysis

[0509] Female NCr nude mice approximately 6-8 weeks old were housed under specific pathogen-free conditions and treated in compliance with the Institutional Animal Care and Use Committee (IACUC) guidelines.

[0510] 500 µg anti-HER3 antibody was administered and blood was obtained from 3 mice by cardiac puncture at baseline (- 2 hr), 0.5 hr, 6 hr, 24 hr, 96 hr, 168 hr and 336 hr after administration. Antibody in the serum was quantified by ELISA.

[0511] The results are shown in Figure 50. Anti-HER3 antibody clone 10D1 was found to have a half-life of 16.3 days in NCr nude mice.

5.2 Safety immunotoxicity

[0512] Anti-HER3 antibody clone 10D1 was analysed *in silico* for safety and immunogenicity using IMGT DomainGapAlign (Ehrenmann et al., Nucleic Acids Res., 38, D301-307 (2010)) and IEDB deimmunization (Dhanda et al., Immunology. (2018) 153(1):118-132) tools.

[0513] Anti-HER3 antibody clone 10D1 had numbers of potential immunogenic peptides few enough to be considered safe, and did not possess any other properties that could cause potential developability issues.

[0514] The Table of Figure 37 provides an overview of the properties of the 10D1 variant clones relevant to safety and developability.

[0515] Mice treated with anti-HER3 antibodies in the experiments described in Example 5.3 were monitored for changes in weight and gross necroscopy. No differences were detected in these mice as compared to mice treated with vehicle only.

[0516] Hemotoxicity was investigated in an experiment in which 6-8 week old female BALB/c mice

(20-25 g) were injected intraperitoneally with a single dose of 1000 µg anti-HER3 10D1 antibody or an equal volume of PBS. Blood samples were obtained at 96 hours post injection and analysed for numbers of different types of white blood cells by flow cytometry and electrolyte indices for NA^+, K^+, and Cl^-.

[0517] Figures 51A and 51B show that the numbers of the different cell types and electrolyte indices were found to be within the Charles River reference range (3 mice) and did not differ significantly from the PBS-treated group (3 mice). Left bars represent vehicle, right bars represent 10D1 treatment, end points of the Charles River reference range indicated with dotted lines. No differences in clinical signs, gross necroscopy or weight were detected between the different groups.

[0518] Mice were also analysed for correlates hepatotoxicity, nephrotoxicity and pancreatic toxicity at 96 hours post injection. The levels of alanine aminotransferase (ALT), aspartate transaminase (AST), blood urea nitrogen (BUN), creatinine (CREA), alkaline phosphatase (ALP), glucose (GLU), calcium (CAL), total bilirubin (BIL), total protein (TPR) and albumin (ALB) detected following administration of a single dose of 1000 µg anti-HER3 antibody were found to be within the Charles River reference range and do not differ significantly from the levels of these markers in the PBS-treated group. These are shown in Figures 51C to 51F. Left bars represent vehicle, right bars represent 10D1 treatment, end points of the Charles River reference range indicated with dotted lines. 10D1 treatment has no effect on the kidney, liver or pancreatic indices and thus does not affect normal kidney, liver or pancreatic functions.

5.3 Analysis of efficacy to treat cancer in vivo

[0519] Female NCr nude mice approximately 6-8 weeks old were purchased from InVivos (Singapore). Animals were housed under specific pathogen-free conditions and were treated in compliance with the Institutional Animal Care and Use Committee (IACUC) guidelines.

[0520] Cell lines used included N87 cells (gastric cancer), FaDu cells (head and neck cancer), OvCAR8 cells (ovarian cancer), SNU16 cells (gastric cancer), HT29 cells (colorectal cancer), A549 cells (lung cancer), HCC95 cells (lung cancer) and AHCN cells (kidney cancer).

[0521] Tumor volumes were measured 3 times a week using a digital caliper and calculated using the formula [L x W2/2]. Study End point was considered to have been reaches once the tumors of the control arm measured >1.5 cm in length.

5.3.1 N87 model

[0522] Figure 20 shows the results obtained in an experiment wherein the anti-cancer effect of anti-HER3 antibody 10D1 ([1] of Example 2.2) was investigated in a N87 cell-line derived mouse gastric carcinoma model. The model was established by subcutaneous injection of 1×10^6 N87 cells into the right flank (n = 6 mice per treatment group).

[0523] 10D1 was administered IP, biweekly at 500 µg per dose (for a total of 10 doses); a control

treatment group received an equal volume of PBS.

[0524] Anti-HER3 antibody clone 10D1 was found to be highly potent in this model, and capable of inhibiting tumor growth by ~76%.

[0525] Figure 21 shows the results obtained in a similar experiment in wherein anti-HER3 antibody clone 4-35-B4 was administered weekly IP at a dose of 11 mg/kg (total of 4 doses). Anti-HER3 antibody clone 4-35-B4 was similarly found to be highly potent in this model, and capable of inhibiting tumor growth by ~60%.

5.3.2 SNU16 model

[0526] Figure 22 shows the results obtained in an experiment wherein the anti-cancer effect of anti-HER3 antibody 10D1 ([1] of Example 2.2) was investigated in a SNU16 cell-line derived mouse gastric carcinoma model. The model was established by subcutaneous injection of 1 x 10^6 SNU16 cells into the right flank (n = 6 mice per treatment group).

[0527] 10D1 was administered IP, biweekly at 500 µg per dose (for a total of 9 doses); a control treatment group received an equal volume of PBS.

[0528] Anti-HER3 antibody clone 10D1 was found to be highly potent in this model, and capable of inhibiting tumor growth by ~68%.

5.3.3 FaDu model

[0529] Figure 23 shows the results obtained in an experiment wherein the anti-cancer effect of anti-HER3 antibody 10D1 ([1] of Example 2.2) was investigated in a FaDu cell-line derived mouse model of head and neck squamous cell carcinoma. The model was established by subcutaneous injection of 1 x 10^6 FaDu cells into the right flanks of female NPG mice (NOD scid gamma phenotype; n = 6 mice per treatment group).

[0530] 10D1 was administered IP, weekly at 500 µg per dose (for a total of 4 doses). Control treatment groups received an equal volume of PBS, or the same dose of an isotype control antibody.

[0531] Anti-HER3 antibody clone 10D1 was found to be highly potent in this model, and capable of inhibiting tumor growth by ~85%.

[0532] Figure 24 shows the results obtained in an experiment wherein the anti-cancer effect of anti-HER3 antibody 10D1 ([1] of Example 2.2) was investigated in a FaDu cell-line derived mouse model of head and neck squamous cell carcinoma. The model was established by subcutaneous injection of 1 x 10^6 FaDu cells into the right flanks of female NCr nude mice (n = 6 mice per treatment group).

[0533] 10D1 was administered IP, biweekly at 500 µg per dose (for a total of 8 doses); a control treatment group received an equal volume of PBS.

[0534] Anti-HER3 antibody clone 10D1 was found to be highly potent in this model, and capable of inhibiting tumor growth by ~86%.

5.3.4 OvCAR8 model

[0535] Figure 25 shows the results obtained in an experiment wherein the anti-cancer effect of anti-HER3 antibody 10D1 ([1] of Example 2.2) was investigated in an OvCAR8 cell-line derived mouse model of ovarian carcinoma. The model was established by subcutaneous injection of 1 x 10^6 OvCAR8 cells into the right flanks of female NCr nude mice (n = 6 mice per treatment group).

[0536] 10D1 was administered IP, biweekly at 500 µg per dose (for a total of 9 doses); a control treatment group received an equal volume of PBS.

[0537] Anti-HER3 antibody clone 10D1 was found to be highly potent in this model, and capable of inhibiting tumor growth by ~74%.

5.3.5 HCC-95 model

[0538] Figure 26 shows the results obtained in an experiment wherein the anti-cancer effect of anti-HER3 antibody 10D1 ([1] of Example 2.2) was investigated in a HCC-95 cell-line derived mouse model of squamous cell lung carcinoma. The model was established by subcutaneous injection of 1 x 10^6 HCC-95 cells into the right flanks of female NCr nude mice (n = 6 mice per treatment group).

[0539] 10D1 was administered IP, biweekly at 500 µg per dose (for a total of 4 doses); a control treatment group received an equal volume of PBS.

[0540] Anti-HER3 antibody clone 10D1 was found to be highly potent in this model, and capable of inhibiting tumor growth by ~90%.

5.3.6 A549 model

[0541] Figure 27 shows the results obtained in an experiment wherein the anti-cancer effect of anti-HER3 antibody 10D1 ([1] of Example 2.2) was investigated in an A549 cell-line derived mouse model of lung adenocarcinoma. The model was established by subcutaneous injection of 1 x 10^6 A549 cells into the right flanks of female NCr nude mice (n = 6 mice per treatment group).

[0542] 10D1 was administered IP, biweekly at 500 µg per dose (for a total of 10 doses); a control treatment group received an equal volume of PBS.

[0543] Anti-HER3 antibody clone 10D1 was found to be highly potent in this model, and capable of inhibiting tumor growth by ~91%.

[0544] Figure 28 shows the results obtained in a similar experiment in wherein the anti-cancer effect of anti-HER3 antibody clone 4-35-B2 was investigated in an A549 cell-line derived model established by injection of 1 x 10^6 A549 cells into the right flanks of female NPG mice (NOD scid gamma phenotype). Anti-HER3 antibody clone 4-35-B2 was administered IP weekly at a dose of 500 µg per dose (total of 4 doses). A control treatment group received an equal volume of PBS (6 mice per treatment group).

[0545] Anti-HER3 antibody clone 4-35-B2 was similarly found to be highly potent in this model, and capable of inhibiting tumor growth by ~63%.

5.3.6 ACHN model

[0546] Figure 29 shows the results obtained in an experiment wherein the anti-cancer effect of anti-HER3 antibody 10D1 ([1] of Example 2.2) was investigated in an ACHN cell-line derived mouse model of renal cell carcinoma. The model was established by subcutaneous injection of 1 x 10^6 ACHN cells into the right flanks of female NCr nude mice (n = 6 mice per treatment group).

[0547] 10D1 was administered IP, biweekly at 500 µg per dose (for a total of 7 doses); a control treatment group received an equal volume of PBS.

[0548] Anti-HER3 antibody clone 10D1 was found to be highly potent in this model, and capable of inhibiting tumor growth by ~61%.

5.4 Treatment of Gastric Carcinoma

First in human

[0549] Patients with HER2+ advanced gastric cancer who have failed or cannot receive trastuzumab are treated by intravenous injection of anti-HER3 antibody selected from: 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92 and 10D1_c93, at a dose calculated in accordance with safety-adjusted 'Minimal Anticipated Biological Effect Level' (MABEL) approach. Patients are monitored for 28 days post-administration.

[0550] The patients are then evaluated according to the Common Terminology Criteria for Adverse Events (CTCAE), to determine the safety and tolerability of the treatment, and to determine the pharmacokinetics of the molecules.

[0551] Treatment with the anti-HER3 antibodies is found to be safe and tolerable.

Dose escalation - monotherapy

[0552] 12-48 patients with HER2+ advanced gastric cancer who have failed or cannot receive trastuzumab are treated by intravenous injection of anti-HER3 antibody selected from: 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92 and 10D1_c93 (e.g. 10D1_c89, 10D1_c90 or 10D1_c91; e.g. 10D1_c89), in accordance with a 3+3 model based escalation with overdose control (EWOC) dose escalation.

[0553] The patients are then evaluated according to the Common Terminology Criteria for Adverse Events (CTCAE) to determine the safety and tolerability of the treatment, and the pharmacokinetics of the molecules and efficacy of the treatment is evaluated. The maximum tolerated dose (MTD) and maximum administered dose (MAD) are also determined.

Dose escalation - combination therapy

[0554] 9-18 patients with HER2+ advanced gastric cancer who have failed or trastuzumab are treated by intravenous injection of anti-HER3 antibody selected from: 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92 and 10D1_c93 (e.g. 10D1_c89, 10D1_c90 or 10D1_c91; e.g. 10D1_c89) in combination with trastuzumab, in accordance with a 3+3 model based escalation with anti-PD-L1 antibody (3 mg/kg).

[0555] The patients are then evaluated according to the Common Terminology Criteria for Adverse Events (CTCAE) to determine the safety and tolerability of the treatment, and the pharmacokinetics of the molecules and efficacy of the treatment is evaluated.

Dose expansion

[0556] Patients with HER2+ advanced gastric cancer who have recently failed trastuzumab, and whose tumours have been well-characterised genetically and histologically are treated with anti-HER3 antibody selected from: 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 (e.g. 10D1_c89, 10D1_c90 or 10D1_c91; e.g. 10D1_c89) in combination with trastuzumab, cisplatin, and either 5-FU or capecitabine

[0557] The anti-HER3 antibodies are found to be safe and tolerable, to be able to reduce the number/proportion of cancer cells, reduce tumor cell marker expression, increase progression-free survival and increase overall survival.

Example 6: Affinity matured and humanised clones

[0558] Humanization of the variable regions of the parental mouse antibody 10D1P was done by CDR grafting. Human framework sequences for grafting were identified by blasting the parental amino acid sequence against the human V domain database and the genes with highest identity to the parental

sequence were selected. Upon grafting the mouse CDRs into the selected human frameworks, residues in canonical positions of the framework were back mutated to the parental mouse sequence to preserve antigen binding. A total of 9 humanized variants of 10D1P were designed.

[0559] Affinity against human HER3 was increased by two rounds of affinity maturation using yeast display. In the first round, a mixed library of the 9 designed variants was constructed by random mutagenesis and screened by flow cytometry using biotinylated antigen. In the second round, one heavy chain and one light chain clones isolated in the first round were used as template to generate and screen a second library. A total of 10 humanized and affinity matured clones were isolated.

[0560] Potential liabilities (immunogenicity, glycosylation sites, exposed reactive residues, aggregation potential) in the variable regions of the designed and isolated humanized variants of 10D1P was assessed using in silico prediction tools. The sequences were deimmunised using IEDB deimmunisation tool. The final sequence of 10D1F was selected among the optimized variants based on its developability characteristics as well as in vitro physicochemical and functional properties.

[0561] Clone 10D1F comprises VH of SEQ ID NO:36 and VL of SEQ ID NO:83. 10D1F displays 89.9% homology with human heavy chain and 85.3% homology with human light chain.

[0562] The antigen-binding molecule comprising 10D1F variable regions and human IgG1 constant regions, and which is comprised of the polypeptides of SEQ ID NOs: 206 and 207, is designated 10D1F.FcA (also sometimes referred to herein as "10D1F.A" or "anti-HER3 clone 10D1_c89 IgG1" - see e.g. [16] of Example 2.2).

Example 7: Fc engineering

[0563] 10D1 and 10D1 variants were engineered to comprise mutations in CH2 and/or CH3 regions to increase the potency of the antibodies, e.g. optimise Fc effector function, enhance antibody-dependent cellular cytotoxicity (ADCC) and/or antibody-dependent cellular phagocytosis (ADCP), and improve half-life.

[0564] The Fc regions of clones 10D1 and 10D1F.FcA were modified to include modifications 'GASDALIE' (G236A, S239D, A330L, I332E) and 'LCKC' (L242C, K334C) in the CH2 region. The GASDALIE substitutions were found to increase affinity for the FcγRIIa (GA) and FcγRIIIa (SDALIE) receptors and enhance ADCP and NK-mediated ADCC (see Example 8.8), whilst decreasing affinity for C1q (AL) and reducing CDC. The LCKC substitutions were found to increase thermal stability of the Fc region by creating a new intramolecular disulphide bridge.

[0565] The modified version of 10D1F.FcA heavy chain polypeptide comprising the GASDALIE and LCKC mutations is shown in SEQ ID NO:225. The antigen-binding molecule comprised of the polypeptides of SEQ ID NOs: 225 and 207 is designated 10D1 F.FcB (also sometimes referred to herein as "10D1F.B").

[0566] A modified version of 10D1 comprising the GASDALIE and LCKC substitutions in CH2 region was prepared and its ability to bind Fc receptor FcγRIIIa was analysed by Bio-Layer Interferometry. The sequence for 10D1 VH-CH1-CH2-CH3 comprising substitutions GASDALIE and LCKC

corresponding to G236A, S239D, A330L, I332E and L242C, K334C is shown in SEQ ID NO:227.

[0567] Briefly, anti-Penta-HIS (HIS1K) coated biosensor tips (Pall ForteBio, USA) were used to capture His-tagged FcγRIIIa (V158) (270 nM) for 120 s. All measurements were performed at 25°C with agitation at 1000 rpm. Association kinetic measurements for antigen binding were performed by incubating anti-HER3 antibodies at different concentrations (500 nM to 15.6 nM) for 60 s, followed by a 120 s dissociation time by transferring the biosensors into assay buffer (pH 7.2) containing wells. Sensograms were referenced for buffer effects and then fitted using the Octet QK384 user software (Pall ForteBio, USA). Kinetic responses were subjected to a global fitting using a one site binding model to obtain values for association (K_{on}), dissociation (K_{off}) rate constants and the equilibrium dissociation constant (K_D). Only curves that could be reliably fitted with the software (R^2>0.90) were included in the analysis.

[0568] The thermostability of the variant was also analysed by Differential Scanning Fluorimetry analysis as described in Example 3.4.

[0569] Figures 38A and 38B show the BLI analysis and thermostability analysis, respectively, for 10D1 comprising GASDALIE and LCKC Fc substitutions. The Fc engineered 10D1 variant showed significantly improved binding to FcγRIIIa (~9 fold increase in affinity) compared to non-Fc-engineered 10D1 (see Figure 39A) with thermal stability maintained above 60°C.

[0570] A construct for 10D1 comprising the GASD substitutions in CH2 region was also prepared; a sequence of 10D1 VH-CH1-CH2-CH3 comprising substitutions corresponding to G236A and S239D is shown in SEQ ID NO:228.

[0571] The affinity of anti-HER3 antibody clone 10D1 ([1] of Example 2.2) and the GASD variant thereof were analysed by Bio-Layer Interferometry for affinity of binding to FcγRIIIa. BLI was performed as described above.

[0572] Figures 39A and 39B show representative sensorgrams, K_{on}, K_{off} and K_D values. As expected, the 10D1 GASD variant (39B) displayed dramatically increased affinity for FcγRIIIa compared to 10D1 (39A).

[0573] The thermostability of the 10D1 GASD variant was also analysed by Differential Scanning Fluorimetry analysis as described in Example 3.4. The results are shown in Figure 40.

Further 10D1F Fc variant

[0574] Another antibody variant was created comprising an N297Q substitution in the CH2 region. A representative sequence for 10D1F VH-CH1-CH2-CH3 comprising the N297Q substitution is shown in SEQ ID NO:226. This 'silent form' prevents both N-linked glycosylation of the Fc region and Fc binding to Fcγ receptors and is used as a negative control.

[0575] Figures 41A and 41B show the binding affinity of 10D1F hIgG1 Fc variants 10D1F.FcA and 10D1F.FcB to human and mouse Fc receptors, determined as described above. 10D1F.FcB was

found to show significantly improved binding to human and mouse Fcγ and FcRn receptors compared to non-modified 10D1F.FcA or commercially available antibodies. ND = K_D Not Determined due to low binding affinity.

Example 8: Characterisation of humanised and modified clones

8.1 Analysis of cell surface antigen-binding by flow cytometry

[0576] Wildtype (WT) HEK293 cells (which do not express high levels of HER3) and HEK293 cells transfected with vector encoding human HER3 (i.e. HEK293 HER O/E cells) were incubated with 10 µg/ml of humanised anti-HER3 antibody 10D1F.FcA (10D1F), anti-HER3 antibody 10D1 (10D1P) or isotype control antibody at 4°C for 1.5 hr. The anti-HER3 antibody clone LJM716 (described e.g. in Garner et al., Cancer Res (2013) 73: 6024-6035, and Example 3.5) was included in the analysis as a positive control.

[0577] The cells were washed with buffer (PBS with 2mM EDTA and 0.5% BSA) and resuspended in FITC-conjugated anti-FC antibody (Invitrogen, USA) at 10 µg/ml for 20 min at 4°C. Cells were washed again and resuspended in 200 µL of FACS flow buffer (PBS with 5mM EDTA) for flow cytometric analysis using MACSQuant 10 (Miltenyi Biotec, Germany). Unstained WT and transfected HEK293 cells were included in the analysis as negative controls. After acquisition, all raw data were analyzed using Flowlogic software. Cells were gated using forward and side scatter profile percentage of positive cells was determined for native and overexpressing cell populations.

[0578] The results are shown in Figures 42A and 42B. Anti-HER3 antibody 10D1F.FcA was shown to bind to human HER3 with high specificity (42A). 10D1F.FcA, 10D1P and LJM716 were shown to bind to human HER3-expressing cells to a similar extent (42B).

8.2 ELISAs for determining antibody specificity and cross-reactivity

[0579] ELISAs were used to confirm the binding specificity of the 10D1 F.FcA antibody. The antibodies were analysed for their ability to bind to human HER3 polypeptide as well as human HER1 (EGFR) and human HER2 (Sino Biological Inc., China). Human IgG isotype and an irrelevant antigen were included as negative controls.

[0580] ELISAs were carried out according to standard protocols. Plates were coated with 0.1 µg/ml of target polypeptide in phosphate-buffered saline (PBS) for 16 h at 4°C. After blocking for 1 h with 1 % BSA in Tris buffer saline (TBS) at room temperature, the anti-HER3 antibody was serially diluted with the highest concentration being 10 µg/ml, and added to the plate. Post 1 h incubation at room temperature, plates were washed three times with TBS containing 0.05% Tween 20 (TBS-T) and were then incubated with a HRP-conjugated anti-His antibody (Life Technologies, Inc., USA) for 1 h at room temperature. After washing, plates were developed with colorimetric detection substrate 3,3',5,5'-tetramethylbenzidine (Turbo-TMB; Pierce, USA) for 10 min. The reaction was stopped with 2M H_2SO_4, and OD was measured at 450 nM.

[0581] The results are shown in Figure 43. Anti-HER3 antibody 10D1F.FcA was found not to bind to human HER2 or human HER1 (EGFR) even at high concentrations of the antibody.

[0582] The ability of 10D1F.FcA to bind HER4 was analysed using flow cytometry. Wildtype (WT) HEK293 cells (which do not express high levels of HER4) and HEK293 cells transfected with vector encoding human HER4 (i.e. HEK293 HER O/E cells) were incubated with 10 µg/ml of anti-HER3 antibody 10D1F.FcA (10D1F) or isotype control antibody (negative control) at 4°C for 1.5 hr. The anti-HER3 antibody clones LJM716 (described e.g. in Garner et al., Cancer Res (2013) 73: 6024-6035) and MM-121 (seribantumab), as described in Example 3.5, were included in the analysis as positive control. Also included was a commercial anti-HER4 antibody (Novus, Cat: FAB11311P). Unstained HEK293 cells were included in the analysis as negative controls.

[0583] HEK293 cells were incubated with 10 µg/ml of each antibody for 1 hour at 4°C. Flow cytometry was performed as described above. Cells were contacted with FITC-conjugated anti-FC antibody (Invitrogen, USA) at for 30 min at 4°C.

[0584] The results are shown in Figure 44. Anti-HER3 antibody 10D1F.FcA was found not to bind to cell-surface expressed HER4.

[0585] In addition, antibody 10D1 F.FcA was analysed for its ability to bind to HER3 polypeptide homologues from mouse, rat and monkey (Sino Biological Inc., China). *M. musculus, R. norvegicus* and M. *cynomolgus* HER3 homologues share 91.1, 91.0 and 98.9% sequence identity respectively with human HER3 and the HER3 signalling pathways are conserved between the four species.

[0586] ELISAs were performed as above.

[0587] The results are shown in Figure 45. 10D1F.FcA antibody was found to bind with high affinity to HER3 cyno, mouse, rat and human orthologs, thus displaying substantial cross-reactivity between species.

8.3 Global affinity study using Octet QK384 system

[0588] The anti-HER3 antibody clones 10D1 F.FcA and 10D1F.FcB were analysed for binding affinity to human HER3.

[0589] Bio-Layer Interferometry (BLI) experiments were performed using the Octet QK384 system (ForteBio). Antibodies (25 nM) were coated onto anti-Human IgG Capture (AHC) Octet sensor tips (Pall ForteBio, USA). Binding was detected using titrated HIS-tagged human HER3 in steps of baseline (60 s), loading (120 s), baseline2 (60 s), association (120 s), dissociation (FcA 120 s, FcB 600 s) and regeneration (15 s). Antigen concentrations are shown in the table in Figures 46A and 46B. Sensorgrams were analysed as described in Example 3.3. Values were obtained for association (K_{on}), dissociation (K_{off}) rate constants and the equilibrium dissociation constant (K_D).

[0590] Representative sensorgrams for the analysis of clones 10D1 F.FcA and 10D1F.FcB are shown in Figures 46A and 46B. 10D1F.FcA binds to human HER3 with a high affinity of K_D = 72.6 pM (46A).

10D1F.FcB binds to human HER3 with a high affinity of K_D = 22.2 pM (46B).

8.4 Analysis of thermostability by Differential Scanning Fluorimetry

[0591] Differential Scanning Fluorimetry was performed for antibodies 10D1F.FcA and 10D1F.FcB as described in Example 3.4.

[0592] The first derivative of the raw data obtained for Differential Scanning Fluorimetry analysis of the thermostability of antibody clone 10D1 F.FcA is shown in Figure 47A. Three different samples of the antibody were analysed and the Tm was determined to be 70.0°C.

[0593] The first derivative of the raw data obtained for Differential Scanning Fluorimetry analysis of the thermostability of antibody clone 10D1 F.FcB is shown in Figure 47B. Three different samples of the antibody were analysed and the Tm was determined to be 62.7°C.

8.5 Antibody purity analysis

[0594] The purity of antibodies 10D1F.FcA and 10D1F.FcB was analysed by size exclusion chromatography (SEC). 150 µg of 10D1 F.FcA in 500 µl PBS pH 7.2 or 150 µg of 10D1F.FcB in 500 µl PBS pH 7.45 was injected on a Superdex 200 10/30 GL column in PBS running buffer at a flow rate of 0.75 min/ml or 0.5 min/ml, respectively, at room temperature and the A280 of flow through was recorded.

[0595] The results are shown in Figures 48A (10D1F.FcA) and 48B (10D1F.FcB).

8.6 Analysis of anti-HER3 antibody 10D1F.FcA epitope

[0596] Anti-HER3 antibody 10D1F.FcA was analysed to determine whether it competes with anti-HER3 antibodies M-05-74 or M-08-11 (Roche) for binding to HER3. Epitopes of M-05-74 and M-08-11 were both mapped to the β-hairpin structure of the HER3 dimerisation arm located at domain II. M-08-11 does not bind to HER4 whereas M-05-74 recognises the HER4 dimerisation arm. Binding of M-05-74 and M-08-11 to HER3 is ligand (NRG) independent.

[0597] BLI experiments were performed as described in Example 3.5 with one alteration: 400 nM of competing antibodies were used. The variable regions of M-05-74 and M-08-11 antibodies were cloned in the PDZ vector having human IgG1 and IgKappa Fc backbone.

[0598] The results of the analysis are shown in Figures 49A and 49B. Anti-HER3 10D1 F.FcA antibody was found not to compete with M-05-74 or M-08-11 for binding to HER3. 10D1F.FcA was found to bind a distinct and topologically distant epitope of HER3 compared to M-05-74 and M-08-11. Binding of 10D1F.FcA to HER3 is ligand (NRG) independent.

[0599] Conclusions:

- Binding of 10D1F.FcA to human HER3 can be achieved in a ligand-independent manner.
- 10D1F.FcA binding epitope is distinct and topologically distant from that of M-05-74 and M-08-11.

8.7 Inhibition of dimerisation of HER2-HER3 and EGFR-HER3

[0600] Anti-HER3 antibody 10D1F.FcA was analysed for its ability to inhibit heterodimerisation of HER3 and HER2.

[0601] Plate-based ELISA dimerisation assays were carried out according to standard protocols. Plates were coated with 1 µg/ml HER2-Fc protein. After blocking and washing, the plate was incubated with different concentrations of candidate antibodies 10D1F.FcA, MM-121, LJM716, Pertuzumab, Roche M05, Roche M08 or isotype control and constant HER3 His 2 µg/ml and NRG 0.1 µg/ml for 1 hour. Plates were then washed and incubated for 1 hour with secondary anti-HIS HRP antibody. Plates were washed, treated with TMB for 10 mins and the reaction was stopped using 2M H_2SO_4 stop solution. The absorbance was read at 450 nm.

[0602] The results are shown in Figure 52. Anti-HER3 antibody clone 10D1F.FcA was found to directly inhibit interaction between HER2 and HER3 in a dose dependent fashion.

[0603] In another assay, inhibition of dimerization was detected using PathHunter® Pertuzumab Bioassay Kit (DiscoverX, San Francisco, USA). HER2 and HER3 overexpressing U20S cells were thawed using 1 ml of pre-warmed CP5 media and 5K cells were seeded per at 37°C, 5% CO_2 for 4 hrs. Cells were treated with serially diluted concentrations of 10D1F.FcA, Seribantumab, or Pertuzumab starting from 25 µg/ml with an 8-point serial dilution. After 4 hrs incubation, 30 ng/ml of heregulin-β2 was added to each well and the plates were further incubated for 16 hrs. Following incubation, 10 µL PathHunter bioassay detection reagent 1 was added and incubated for 15 mins at room temperature in the dark, followed by addition of 40 µL PathHunter bioassay detection reagent 2 which was then incubated for 60 mins at room temperature in the dark. Plates were read using Synergy4 Biotek with 1 second delay.

[0604] 10D1F.FcA was found to have an EC_{50} value of 3.715e-11 for inhibition of HER2-HER3 heterodimerisation. In the same assay, the comparative EC_{50} value for Seribantumab/MM-121 was found to be 6.788e-10 and the comparative EC_{50} value for Pertuzumab was found to be 2.481e-10.

[0605] Anti-HER3 antibody 10D1F.FcA was analysed for its ability to inhibit heterodimerisation of EGFR and HER3.

[0606] Plate-based ELISA dimerisation assays were performed according to standard protocols. Plate was coated with 1 µg/ml human EGFR-His. After blocking and washing, the plate was incubated with different concentrations of candidate antibodies 10D1F.FcA, MM-121, LJM716, Pertuzumab, or isotype control with constant HER3-biotin 4 µg/ml and NRG 0.1 µg/ml for 1 hour. Plates were then washed and incubated for 1 hour with secondary anti-avidin HRP antibody. Plates were washed,

treated with TMB for 10 mins and the reaction was stopped using 2M H_2SO_4 stop solution. The absorbance was read at 450 nm.

[0607] The results are shown in Figure 53. Anti-HER3 antibody clone 10D1F.FcA was found to directly inhibit interaction between EGFR and HER3 in a dose dependent fashion.

8.8 Analysis of ability to induce ADCC

[0608] Anti-HER3 antibody clones 10D1 F.FcA and 10D1 F.FcB were analysed for their ability to induce antibody-dependent cell-mediated cytotoxicity (ADCC).

[0609] Target cells (HEK293 overexpressing HER3) were plated in U-bottom 96-well plates at a density of 20,000 cells/well. Cells were treated with a dilution series (50,000 ng/ml - 0.18 ng/ml) of one of 10D1F.FcA, 10D1F.FcB, 10D1F.FcA_N297Q (silent form), LJM-716, Seribantumab (MM-121) or left untreated, and incubated at 37°C and 5% CO_2 for 30 min. Effector cells (Human Natural Killer Cell Line No-GFP-CD16.NK-92; 176V) were added to the plate containing target cells at a density of 60,000 cells/well.

[0610] The following controls were included: Target cell maximal LDH release (target cells only), spontaneous release (target cells and effector cells without antibody), background (culture media only). Plates were spun down and incubated at 37°C and 5% CO_2 for 21 hrs.

[0611] LDH release assay (Pierce LDH Cytotoxicity Assay Kit): before the assay, 10 µl of Lysis Buffer (10X) were added to target cell maximal LDH release controls and incubated at 37°C and 5% CO_2 for 20 min. After incubation, plates were spun down and 50 µL of the supernatant were transferred to clear flat-bottom 96-well plates. Reactions were started by addition of 50 µl of LDH assay mix containing substrate to the supernatants and incubated at 37°C for 30 min. Reactions were stopped by addition of 50 µl of stop solution and absorbance was recorded at 490 nm and 680 nm with a BioTek Synergy HT microplate reader.

[0612] For data analysis, absorbance from test samples was corrected to background and spontaneous release from target cells and effector cells. Percent cytotoxicity of test samples was calculated relative to target cell maximal LDH release controls and plot as a function of antibody concentration.

[0613] The results are shown in Figure 54. Anti-HER3 antibody 10D1F.FcB was found to induce potent ADCC activity against HER3 overexpressing cells in a dose dependent fashion.

8.9 Inhibition of HER3-mediated signalling

[0614] Anti-HER3 antibody 10D1F.FcA was analysed for its ability to inhibit HER-3 mediated signalling *in vitro* in cancer cell lines.

[0615] N87, FaDu or OvCAR8 cells were seeded in wells in a 6 well plate with 10% serum overnight at

37°C with 5% CO_2. Cells were starved with 0.2% FBS culture medium for 16 hrs, and were then treated for 0.5 hours with different antibodies at IC50 corresponding to the cell line. Antibodies tested were: 10D1F.FcA (10D1), Seribantumab (SBT), Elegemtumab (LJM), Pertuzumab (PTM), Cetuximab (CTX), and Trastuzumab (TZ).

[0616] Before harvesting, cells were stimulated with 100 ng/ml of NRG1. Protein extracted from cell lines were quantified using standard Bradford protein assay. Protein samples (50 µg) were fractionated by SDS-PAGE and transferred to nitrocellulose membrane. Membranes were then blocked and immunoblotted with the indicated antibodies. The results were visualized via Bio-Rad Clarity Western ECL substrate. The blots were quantified using densiometric analysis and data was normalised to beta actin.

[0617] The results are shown in Figures 55A to 55C. Anti-HER3 antibody 10D1F.FcA was found to inhibit HER3 phosphorylation and downstream signalling in N87 (55A), FaDu (55B), OvCar8 (55C) and A549 (55D) cell lines.

[0618] For the experiments using N87 cells, A549 cells, OvCar8 cells and FaDu cells total RNA was extracted at 16 hrs post antibody treatment was analysed to determine pathway activation based on the level of expression of key signal transduction pathway proteins by gene set enrichment analysis. The results of the analysis are shown in Figures 63A to 63D. 10D1 F.FcA was the most effective inhibitor of downstream signalling.

[0619] In further experiments using A549 cells, *in vitro* phosphorylation assays were performed as above except that the cells were treated for 0.5 hours or 4 hours with the different antibodies. The results are shown in Figure 64.

Example 9: Analysis of humanised and modified clones *in vitro* and *in vivo*

9.1 Pharmacokinetic analysis

Mice

[0620] Female NCr nude mice approximately 6-8 weeks old were housed under specific pathogen-free conditions and treated in compliance with the Institutional Animal Care and Use Committee (IACUC) guidelines.

[0621] 500 µg anti-HER3 antibody 10D1F.FcA or 10D1F.FcB was administered and blood was obtained from 4 mice by cardiac puncture at baseline (- 2 hr), 6 hr, 24 hr, 96 hr, 168 hr and 336 hr after administration. Antibody in the serum was quantified by ELISA.

[0622] The parameters for the pharmacokinetic analysis were derived from a non-compartmental model: maximum concentration (C_{max}), AUC (0-336hr), AUC (0-infinity), Half-life ($t_{½}$), Clearance (CL), Volume of distribution at steady state (V_{ss}).

[0623] The results are shown in Figures 56A and 56B. Anti-HER3 antibody clone 10D1F.FcA was found to have a half-life of 253 hours (56A) and anti-HER3 antibody clone 10D1 F.FcB was found to have a half-life of 273 hours (56B) in NCr nude mice.

Rats

[0624] 10D1F variants were analysed to determine a single dose pharmacokinetic profile in female Sprague Dawley rats with mean weight of 320 g.

[0625] Antibody clones 10D1F.FcA and 10D1 F.FcB were administered in a single dose of 4 mg (~10 mg/kg), 10 mg (-25 mg/kg), 40 mg (~100 mg/kg) or 100 mg (-250 mg/kg) via tail vein slow i.v. injection. Vehicle was administered as a negative control. Blood from 2 rats per treatment was obtained at baseline (- 24 hr), 6 hr, 24 hr, 96 hr, 168 hr and 336 hr after administration. Antibody in the serum was quantified by ELISA.

[0626] The parameters for the pharmacokinetic analysis were derived from a non-compartmental model: maximum concentration (C_{max}), AUC (0-336hr), AUC (0-infinity), Half-life ($t_{½}$), Clearance (CL), Volume of distribution at steady state (V_d).

[0627] The results are shown in Figures 57A (10 mg/kg), 57B (25 mg/kg), 57C (100 mg/kg) and 57D (250 mg/kg).

9.2 Safety immunotoxicity

[0628] The toxicological effects of 10D1F.FcA and 10D1F.FcB were analysed.

Mice

[0629] 6-8 week old female BALB/c mice (20-25 g) were injected intraperitoneally with a single dose of either 10D1 F.FcA and 10D1 F.FcB at one of doses: 200 ug (-10 mg/kg), 500 ug (-25 mg/kg), 2 mg (~100 mg/kg), or 5 mg (-250 mg/kg), or an equal volume of PBS. 3 mice were injected with each treatment, 4 mice were injected with PBS control. Blood samples were obtained at 96 hours post injection and analysed for RBC indices (total RBC count, haematocrit, haemoglobin, platelet count, mean corpuscular volume, mean corpuscular haemoglobin, mean corpuscular haemoglobin concentration) and WBC indices (total WBC count, lymphocyte count, neutrophil count, monocyte count). Analysis was performed using a HM5 Hematology Analyser.

[0630] The results are shown in Figures 58A, 58B (RBC indices) and 58C (WBC indices). Anti-HER3 antibodies 10D1F.FcA and 10D1F.FcB had no effect on the RBC indices, but were found to have an effect on the WBC indices at higher doses (10D1F.FcA 250 mg/kg, 10D1 F.FcB 100 mg/kg, 10D1 F.FcB 250 mg/kg).

[0631] Hepatotoxicity, nephrotoxicity and pancreatic toxicity were also analysed 96 hours post injection. 10D1F.FcA and 10D1F.FcB had no effect on the levels of alanine aminotransferase, alkaline phosphatase, albumin, total protein (liver indices; Figure 58D), creatine, blood urea nitrogen, glucose or amylase (kidney and pancreatic indices; Figure 58E). Nor did 10D1F.FcA and 10D1 F.FcB have an effect on electrolyte indices sodium, potassium, calcium or phosphate (Figure 58F).

[0632] Mice treated with 10D1F.FcA or 10D1 F.FcB showed no abnormalities after 96 hours in weight, behaviour, skin condition, oral examination, stool and urine examination or eye examination. Enlarged spleen (splenomegaly) approximately 1.5 times the normal size was observed in mice treated with higher doses: 10D1F.FcA 250 mg/kg, 10D1F.FcB 100 mg/kg, 10D1F.FcB 250 mg/kg.

[0633] A further study was performed in the BALB/c mice to assess the toxicological effects of repeat doses of 500 µg (-25 mg/kg) 10D1F.FcA or 10D1 F.FcB. Antibody was administered once a week for four weeks. Blood was obtained 28 days after the first administration. There was no effect observed on RBC, liver, kidney, pancreatic or electrolyte indices for either antibody, no signs of clinical abnormalities and no differences detected in gross necroscopy. Total WBC count, lymphocyte count and neutrophil count was observed to be decreased in mice treated with 10D1F.FcA or 10D1F.FcB but this was not considered to be toxic.

[0634] In another study, BALB/c mice were administered with a single dose of 10D1F.FcA or an equal volume of PBS (vehicle control), and analysed after 336 hours. Representative results are shown in Figures 69A to 69C.

Rats

[0635] 6-8 week old female Sprague Dawley rats (400-450 g) were injected intraperitoneally with a single dose of either 10D1 F.FcA or 10D1 F.FcB antibody at one of doses: 4 mg (-10 mg/kg), 10 mg (-25 mg/kg), 40 mg (~100 mg/kg), 100 mg (~250 mg/kg). Blood was obtained at -24 hours, 6 hours, 24 hours, 96 hours, 168 hours and 336 hours. Up to 366 hours post injection there was no effect on RBC indices, no toxic effect on WBC indices, and no effect on liver, kidney, pancreatic or electrolyte indices. There were no signs of clinical abnormalities and no differences detected in gross necroscopy.

[0636] Representative results obtained from rats administered with 250 mg/kg 10D1F.FcA are shown in Figures 70A to 70C.
The absence of toxicity signals in rodent toxicology models indicates superior clinical safety for 10D1 and variants.

9.3 Analysis of efficacy to treat cancer in vitro

[0637] Anti-HER3 antibody 10D1F.FcA was analysed for its ability to inhibit tumour growth *in vitro* in a number of tumour models: N87 cells (gastric cancer), HCC95 cells (lung cancer), FaDu cells (head and neck cancer), SNU-16 cells (gastric cancer), A549 cells (lung cancer), OvCar8 cells (ovarian cancer), ACHN cells (kidney cancer) and HT29 cells (colorectal cancer). 10D1F.FcA efficacy was compared to other anti-HER3 antibodies seribantumab (MM-121) and LJM-716, and other EGFR

family therapies cetuximab, trastuzumab and pertuzumab.

[0638] Cells were treated with serially diluted concentrations of therapeutic antibodies, starting from 1500 ug/ml with a 9-point dilution. Cell viability was measured using CCK-8 cell proliferation assay, 3-5 days post treatment. The percentage of cell inhibition shown is relative to cells treated with only buffer (PBS). Data points indicates average of three replicates.

[0639] The results are shown in Figure 59A to 59D. Anti-HER3 antibody 10D1F.FcA demonstrates superior *in vitro* tumour inhibition in multiple tumour models compared to other HER3 antibodies (59A & 59B) and EGFR family therapies (59C & 59D).

[0640] Figures 77A and 77B show the ability of different anti-ErbB antibodies to inhibit proliferation of different cancer cell lines *in vitro,* at the C_{max} concentration they achieve in mice administered IP with 25 mg/kg of the relevant antibody. 10D1F.FcA displays outstanding ability to inhibit growth of a wide variety of different cancer cell types.

9.4 Analysis of efficacy to treat cancer in vivo

[0641] Anti-HER3 antibody clones 10D1 F.FcA and 10D1 F.FcB were assessed for their effect on tumour growth in *in vivo* cancer models.

9.4.1 A549 model

[0642] Tumour cells were inserted subcutaneously into the right flanks of female NCr nude mice. Antibodies (25 mg/kg 10D1F.FcA, 10D1F.FcB, Cetuximab, LJM-716 or MM-121; n=6 for each treatment) or vehicle (n=8) were administered biweekly for six weeks.

[0643] The results are shown in Figure 60. Anti-HER3 antibody clones 10D1 F.FcA and 10D1F.FcB both displayed potent efficacy in the A549 model of lung carcinoma. 10D1F.FcB was found to be particularly potent and made tumours regress.

9.4.2 FaDu model

[0644] Tumour cells were inserted with matrigel subcutaneously into the right flanks of female NCr nude mice. Antibodies (10 and 25 mg/kg 10D1F.FcA and 10D1F.FcB, or 25 mg/kg of Cetuximab, Trastuzumab, Pertuzumab, LJM-716 or MM-121; n=6 for each treatment) or vehicle (n=6) were administered once a week for six weeks.

[0645] The results are shown in Figure 61. Anti-HER3 antibody clones 10D1F.FcA and 10D1F.FcB were both found to be effective to prevent tumour growth in the FaDu model of head and neck cancer.

9.4.3 OvCar8 model

[0646] Tumour cells were inserted with matrigel subcutaneously into the right flanks of female NCr nude mice. Antibodies (10 and 25 mg/kg 10D1F.FcA, or 25 mg/kg Cetuximab, LJM-716 or MM-121; n=6) or vehicle (n=6) were administered once a week for six weeks.

[0647] The results are shown in Figure 62. Anti-HER3 antibody clone 10D1F.FcA was found to be effective at reducing tumour volume at higher dose.

9.4.4 N87 model

[0648] Tumour cells are inserted with matrigel subcutaneously into the right flanks of female NCr nude mice. Antibodies (25 mg/kg 10D1F.FcA, or 50 mg/kg of Trastuzumab, LJM-716 or MM-121; n=6 for each treatment) or vehicle (n=6) were administered biweekly for six weeks.

[0649] The results are shown in Figure 74. Anti-HER3 antibody 10D1F.FcA and was found to be effective to prevent tumour growth in the N87 model of gastric cancer.

Example 10: Analysis of inhibition of proliferation of BRAFV600E mutant thyroid cancer cell lines

[0650] The following cell lines were investigated:

Cell Line	Type of Cancer	Mutation
SW1736	Anaplastic thyroid cancer	BRAF V600E
BHT101	Anaplastic thyroid cancer	BRAF V600E
BCPAP	Papillary thyroid cancer	BRAF V600E and p53 mutation

[0651] The cells were investigated for surface expression of EGFR family members by flow cytometry. Briefly, 300,000 cells were incubated with 20 µg/ml of 10D1 F.FcA, cetuximab or trastuzumab for 1 hr at 4°C. Alexafluor 488-conjugated anti-human antibody was used at 10 µg/ml as a secondary antibody (40 min at 4°C).

[0652] The results are shown in Figure 66A to 66C. SW1736, BHT101 and BCPAP cells were shown to express EGFR, HER2 and HER3.

[0653] The inventors investigated the ability of different HER3-binding antibodies to inhibit *in vitro* proliferation of different thyroid cancer cell lines harbouring the V600E BRAF mutation.

[0654] Briefly, cells of the different cell lines were seeded at a density of 1.5 x 10^5 cells/well, and treated the next day with a 10 point serial dilution starting from 1000 µg/ml of 10D1F.FcA, seribantumab, LJM-716, pertuzumab or isotype control antibody. After 3 days, proliferation was measured using a CCK-8 cell proliferation assay. Percent inhibition of proliferation was calculated relative to cells treated with an equal volume of PBS instead of antibodies.

[0655] The results are shown in Figures 67A to 67C. 10D1F.FcA was found to be more effective at inhibiting proliferation of cell lines harbouring BRAF V600E mutation than any other of the anti-HER3 antibodies analysed.

[0656] In further experiments, the ability of a combination of 10D1F.FcA and vemurafenib to inhibit *in vitro* proliferation of different thyroid cancer cell lines harbouring the V600E BRAF mutation was investigated.

[0657] Cells were seeded at a density of 1.5 x 10^5 cells/well, and treated the next day with a 10 point serial dilution starting from 1000 µg/ml of 10D1F.FcA or isotype control antibody, in the presence or absence of 200 nM vemurafenib. After 3 days, proliferation was measured using a CCK-8 cell proliferation assay. Percent inhibition of proliferation was calculated relative to cells treated with an equal volume of PBS instead of antibodies.

[0658] The results are shown in Figures 68A to 68C. 10D1F.FcA was found to enhance the ability of vemurafenib to inhibit proliferation of SW1736 and BHT101 cells, which are susceptible to vemurafenib. 10D1 F.FcA was also found to be a potent inhibitor of proliferation of vemurafenib-resistant BCPAP cells.

Example 11: Analysis of inhibition of HER3-mediated signalling *in vivo*

[0659] The inventors investigated the ability of 10D1F.FcA to inhibit HER3-mediated signalling *in vivo.*

[0660] 1 x 10^6 FaDu or OvCar8 cells were introduced subcutaneously into NCr nude mice, to establish ectopic xenograft tumors.

[0661] Once tumors had reached a volume of greater than 100 mm3, mice were with treated by biweekly intraperitoneal injection of 10D1 F.FcA at a dose of 25 mg/kg, or an equal volume of vehicle (control). After 4 weeks, tumors were harvested. Protein extracts were prepared from the tumors and quantified via Bradford assay, 50 µg samples were fractionated by SDS-PAGE, and analysed by western blot using antibodies in order to determine in vivo phosphorylation of HER3 and AKT, as described in Example 4.3.

[0662] The results are shown in Figure 71. 10D1F.FcA was found to inhibit phosphorylation of HER3 and AKT in tumor cells *in vivo.*

Example 12: Analysis of internalisation of anti-HER3 antibodies

[0663] The inventors investigated internalisation of anti-HER3 antibodies by HER3-expressing cells.

[0664] Briefly, 100,000 HEK293 cells engineered to express HER3, HCC95, N87 or OVCAR8 cells were seeded in wells of 96-well tissue culture plates and cultured overnight at 37°C in 5% CO_2. Cells were then treated with 120 nM of 10D1F.FcA, LJM-716, seribantumab or trastuzumab, and 360 nM of

pHrodo iFL Green reagent, and incubated at 37°C in 5% CO_2. The cells in culture were imaged every 30 min for 24 hours, in 4 different fields of each well. The maximum signal intensity in the FITC channel of each field was quantified at 24 hours.

[0665] The results are shown in Figure 72. Modest to moderate internalization of LJM-716 and seribantumab was observed in OvCar8 cells, whereas modest internalization of trastuzumab was observed in N87 cells.

[0666] No significant internalization of 10D1F.FcA was observed in HCC95, N87, or OvCar8 cells.

[0667] As expected, significant internalization of 10D1F.FcA, LJM-716, and seribantumab was observed in HEK293 cells overexpressing HER3.

[0668] In further experiments, antibody internalisation was investigated by flow cytometry.

[0669] N87 cells were seeded in wells of 96-well tissue culture plates at a density of 50,000 cells/well, and allowed to adhere overnight (37°C, 5% CO_2). 10D1 F.FcA or trastuzumab were mixed with labelling reagent, and the labelled complexes were added to cells. Samples were harvested at 0 min, 10 min, 30 min, 1 hour, 2 hour and 4.5 hour time points, by aspiration of cell culture medium, washing with PBS and treatment with accutase. Accutase activity was neutralised, and cells were resuspended in FACs buffer and analysed by flow cytometry.

[0670] The results are shown in Figure 73A and 73B. The cells displayed minimal internalisation of 10D1F.FcA. By contrast, substantial internalisation of anti-HER2 antibody trastuzumab was observed.

Example 13: Use of HER3-binding antibodies in immunohistochemistry

[0671] Anti-HER3 antibody 10D1F in mIgG2a format was evaluated for its ability to be used in immunohistochemistry for the detection of human HER3 protein.

[0672] Processing of sections was performed using Bond reagents (Leica Biosystems). Arrays of commercially-available frozen tissue sections were obtained. Slides were dried in a desiccator for 10 min and then subjected to the following treatments, with water washes and/or TBS-T rinses between steps: (i) fixation by treatment with 100% acetone for 10 min at room temperature; (ii) endogenous peroxidase blocking by treatment with 3% (v/v) H_2O_2 for 15 min at room temperature; (iii) blocking by treatment with 10% goat serum for 30 min at room temperature, (iv) incubation with 10D1 F-mIgG2a at 1:250 dilution of a 6.2 mg/ml solution overnight at 4°C, (v) incubation with HRP-polymer conjugated goat anti-mouse antibody for 30 min at room temperature, and (vi) development with Bond Mixed DAB Refine for 5 min at room temperature, followed by rinsing with deionised water and 1x Bond Wash to stop the reaction.

[0673] Slides were then dehydrated, mounted in synthetic mounting media and scanned with high resolution.

[0674] The results are shown in Figures 75A and 75B. 10D1F preferentially stained malignant human tissue sections, with low cross-reactivity to normal tissue.

[0675] In further experiments, an A549 xenograft tumor was harvested in cold PBS, embedded in OCT cryoembedding medium, frozen in dry-ice and stored at -80 °C. 10 µm sections were obtained using a cryostat.

[0676] Slides were dried in a desiccator for 10 min and then subjected to the following treatments, with water washes and/or TBS-T rinses between steps: (i) fixation by treatment with 100% acetone for 10 min at room temperature; (ii) endogenous peroxidase blocking by treatment with 3% (v/v) H_2O_2 for 15 min at room temperature; (iii) blocking by treatment with 10% goat serum for 30 min at room temperature, (iv) incubation with 10D1F.FcA at 1:50 dilution of 8.8 mg/ml solution, or with 1:200 dilution of Sino Biological rabbit anti-HER3 (Cat. No. 10201-T24) overnight at 4°C, (v) incubation with Invitrogen F(ab')2-Goat anti-Human IgG (H+L) HRP (A24470) (1:500), or HRP-polymer conjugated goat anti-rabbit antibody for 30 min at room temperature, and (vi) development with Bond Mixed DAB Refine for 5 min at room temperature, followed by rinsing with deionised water and 1x Bond Wash to stop the reaction.

[0677] Slides were then counterstained with haematoxylin, dehydrated, mounted in synthetic mounting media and scanned with high resolution.

[0678] The results are shown in Figures 76. 10D1 F.FcA displayed specific membrane and cytoplasmic staining of A549 tumor xenograft cryosections.

SEQUENCE LISTING

[0679]

<110> Hummingbird Bioscience Holdings Pte. Ltd. (All States) Clegg, Richard (LS only)

<120> HER3 Antigen-Binding Molecules

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<150> PCT/EP2018/058259
<151> 2018-03-29

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Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
740 745 750

Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
755 760 765

Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
770 775 780

Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg
785 790 795 800

Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val
805 810 815

Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His
820 825 830

Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val
835 840 845

Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys
850 855 860

Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu
865 870 875 880

Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser
885 890 895

Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr
900 905 910

Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu
915 920 925

Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met
930 935 940

Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu
945 950 955 960

Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu
965 970 975

Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
980 985 990

His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu
995 1000 1005

Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala
1010 1015 1020

Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu
1025 1030 1035

Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly
1040 1045 1050

Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu
1055 1060 1065

Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser
1070 1075 1080

Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu
1085 1090 1095

Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val Ser
1100 1105 1110

Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly
1115 1120 1125

Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro Val
1130 1135 1140

Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly
1145 1150 1155

Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg
1160 1165 1170

Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr
1175 1180 1185

Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg
1190 1195 1200

Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu
1205 1210 1215

Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala
1220 1225 1230

Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile
1235 1240 1245

Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met
1250 1255 1260

Asn Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala
1265 1270 1275

1265 1270 1275

Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg
1280 1285 1290

Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala
1295 1300 1305

Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe
1310 1315 1320

Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala Asn
1325 1330 1335

Ala Gln Arg Thr
1340

<210> 2

<211> 183

<212> PRT

<213> Homo sapiens HER3 isoform 2

<400> 2

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
1 5 10 15

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
20 25 30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
85 90 95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Gly Gln Phe Pro
130 135 140

Met Val Pro Ser Gly Leu Thr Pro Gln Pro Ala Gln Asp Trp Tyr Leu
145 150 155 160

Leu Asp Asp Asp Pro Arg Leu Leu Thr Leu Ser Ala Ser Ser Lys Val
165 170 175

Pro Val Thr Leu Ala Ala Val
180

<210> 3

<211> 331

<212> PRT

<213> Homo sapiens HER3 isoform 3

<400> 3

```
Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
1               5                  10                  15

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
            20                  25                  30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
        35                  40                  45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
    50                  55                  60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65                  70                  75                  80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
                85                  90                  95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
            100                 105                 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
        115                 120                 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
    130                 135                 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145                 150                 155                 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
                165                 170                 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
            180                 185                 190

Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
        195                 200                 205

Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
    210                 215                 220

Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
225                 230                 235                 240

Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
                245                 250                 255

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
            260                 265                 270
```

Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
275 280 285

Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
290 295 300

Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305 310 315 320

Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Phe
325 330

<210> 4

<211> 1283

<212> PRT

<213> Homo sapiens HER3 isoform 4

<400> 4

Met Gly Asn Leu Glu Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser
1 5 10 15

Phe Leu Gln Trp Ile Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met
20 25 30

Asn Glu Phe Ser Thr Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly
35 40 45

Thr Gln Val Tyr Asp Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr
50 55 60

Asn Thr Asn Ser Ser His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu
65 70 75 80

Thr Glu Ile Leu Ser Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu
85 90 95

Cys His Met Asp Thr Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp
100 105 110

Ala Glu Ile Val Val Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His
115 120 125

Glu Val Cys Lys Gly Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln
130 135 140

Thr Leu Thr Lys Thr Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe
145 150 155 160

Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys
165 170 175

Ser Gly Pro Gln Asp Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp
180 185 190

Ser Gly Ala Cys Val Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys
195 200 205

Leu Thr Phe Gln Leu Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly
210 215 220

```
Gly Val Cys Val Ala Ser Cys Pro His Asn Phe Val Val Asp Gln Thr
225                 230                 235                 240

Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn
                245                 250                 255

Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys
            260                 265                 270

Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn
        275                 280                 285

Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe
    290                 295                 300

Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu
305                 310                 315                 320

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
                325                 330                 335

Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met His Asn Phe Ser Val
            340                 345                 350

Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly
        355                 360                 365

Phe Ser Leu Leu Ile Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe
    370                 375                 380

Arg Ser Leu Lys Glu Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn
385                 390                 395                 400

Arg Gln Leu Cys Tyr His His Ser Leu Asn Trp Thr Lys Val Leu Arg
                405                 410                 415

Gly Pro Thr Glu Glu Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg
            420                 425                 430

Asp Cys Val Ala Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly
        435                 440                 445

Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr
    450                 455                 460

Ser Arg Gly Gly Val Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu
465                 470                 475                 480

Pro Arg Glu Phe Ala His Glu Ala Glu Cys Phe Ser Cys His Pro Glu
                485                 490                 495

Cys Gln Pro Met Glu Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp
            500                 505                 510

Thr Cys Ala Gln Cys Ala His Phe Arg Asp Gly Pro His Cys Val Ser
        515                 520                 525

Ser Cys Pro His Gly Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr
    530                 535                 540

Pro Asp Val Gln Asn Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln
545                 550                 555                 560
```

Gly Cys Lys Gly Pro Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val
565 570 575

Leu Ile Gly Lys Thr His Leu Thr Met Ala Leu Thr Val Ile Ala Gly
580 585 590

Leu Val Val Ile Phe Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg
595 600 605

Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg
610 615 620

Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val
625 630 635 640

Leu Ala Arg Ile Phe Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu
645 650 655

Gly Ser Gly Val Phe Gly Thr Val His Lys Gly Val Trp Ile Pro Glu
660 665 670

Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys
675 680 685

Ser Gly Arg Gln Ser Phe Gln Ala Val Thr Asp His Met Leu Ala Ile
690 695 700

Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro
705 710 715 720

Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu
725 730 735

Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu
740 745 750

Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu
755 760 765

His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys
770 775 780

Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu
785 790 795 800

Pro Pro Asp Asp Lys Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile
805 810 815

Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln
820 825 830

Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe
835 840 845

Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu
850 855 860

Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp
865 870 875 880

```
Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg
                885                 890                 895

Pro Thr Phe Lys Glu Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp
            900                 905                 910

Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala
        915                 920                 925

Pro Gly Pro Glu Pro His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val

    930                 935                 940

Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu
945                 950                 955                 960

Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val
                965                 970                 975

Gly Thr Leu Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser
            980                 985                 990

Ser Gly Tyr Met Pro Met Asn Gln  Gly Asn Leu Gly Glu  Ser Cys Gln
        995                 1000                1005

Glu Ser  Ala Val Ser Gly Ser  Ser Glu Arg Cys Pro  Arg Pro Val
    1010                1015                1020

Ser Leu  His Pro Met Pro Arg  Gly Cys Leu Ala Ser  Glu Ser Ser
    1025                1030                1035

Glu Gly  His Val Thr Gly Ser  Glu Ala Glu Leu Gln  Glu Lys Val
    1040                1045                1050

Ser Met  Cys Arg Ser Arg Ser  Arg Ser Arg Ser Pro  Arg Pro Arg
    1055                1060                1065

Gly Asp  Ser Ala Tyr His Ser  Gln Arg His Ser Leu  Leu Thr Pro
    1070                1075                1080

Val Thr  Pro Leu Ser Pro Pro  Gly Leu Glu Glu Glu  Asp Val Asn
    1085                1090                1095

Gly Tyr  Val Met Pro Asp Thr  His Leu Lys Gly Thr  Pro Ser Ser
    1100                1105                1110

Arg Glu  Gly Thr Leu Ser Ser  Val Gly Leu Ser Ser  Val Leu Gly
    1115                1120                1125

Thr Glu  Glu Glu Asp Glu Asp  Glu Glu Tyr Glu Tyr  Met Asn Arg
    1130                1135                1140

Arg Arg  Arg His Ser Pro Pro  His Pro Pro Arg Pro  Ser Ser Leu
    1145                1150                1155

Glu Glu  Leu Gly Tyr Glu Tyr  Met Asp Val Gly Ser  Asp Leu Ser
    1160                1165                1170

Ala Ser  Leu Gly Ser Thr Gln  Ser Cys Pro Leu His  Pro Val Pro
    1175                1180                1185
```

```
Ile Met  Pro Thr Ala Gly Thr  Thr Pro Asp Glu Asp  Tyr Glu Tyr
    1190                 1195                 1200

Met Asn  Arg Gln Arg Asp Gly  Gly Gly Pro Gly Gly  Asp Tyr Ala
    1205                 1210                 1215

Ala Met  Gly Ala Cys Pro Ala  Ser Glu Gln Gly Tyr  Glu Glu Met
    1220                 1225                 1230

Arg Ala  Phe Gln Gly Pro Gly  His Gln Ala Pro His  Val His Tyr
    1235                 1240                 1245

Ala Arg  Leu Lys Thr Leu Arg  Ser Leu Glu Ala Thr  Asp Ser Ala
    1250                 1255                 1260

Phe Asp  Asn Pro Asp Tyr Trp  His Ser Arg Leu Phe  Pro Lys Ala
    1265                 1270                 1275

Asn Ala  Gln Arg Thr
    1280
```

<210> 5

<211> 699

<212> PRT

<213> Homo sapiens HER3 isoform 5

<400> 5

```
Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe Met Met Leu
1               5                  10                  15

Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg
            20                  25                  30

Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu Pro Leu Asp
        35                  40                  45

Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr
    50                  55                  60

Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val
65                  70                  75                  80

His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val
                85                  90                  95

Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala
            100                 105                 110

Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His Ala His Ile
        115                 120                 125

Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr
    130                 135                 140

Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg Gln His Arg
145                 150                 155                 160

Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala
                165                 170                 175
```

```
Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu
            180                 185                 190

Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala
        195                 200                 205

Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu
    210                 215                 220

Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile
225                 230                 235                 240

His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val
                245                 250                 255

Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu
            260                 265                 270

Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala
        275                 280                 285

Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys
    290                 295                 300

Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn
305                 310                 315                 320

Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys
                325                 330                 335

Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro His Gly Leu
            340                 345                 350

Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu
        355                 360                 365

Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr Thr Thr Leu
    370                 375                 380

Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu Asn Arg Pro Arg Gly
385                 390                 395                 400

Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro Met Asn Gln
                405                 410                 415

Gly Asn Leu Gly Glu Ser Cys Gln Glu Ser Ala Val Ser Gly Ser Ser
            420                 425                 430

Glu Arg Cys Pro Arg Pro Val Ser Leu His Pro Met Pro Arg Gly Cys
        435                 440                 445

Leu Ala Ser Glu Ser Ser Glu Gly His Val Thr Gly Ser Glu Ala Glu
    450                 455                 460

Leu Gln Glu Lys Val Ser Met Cys Arg Ser Arg Ser Arg Ser Arg Ser
465                 470                 475                 480

Pro Arg Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu
                485                 490                 495
```

```
Leu Thr Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp
            500                 505                 510

Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser
        515                 520                 525

Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly
    530                 535                 540

Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg
545                 550                 555                 560

Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu Glu
                565                 570                 575

Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala Ser Leu
            580                 585                 590

Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile Met Pro Thr
        595                 600                 605

Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg
    610                 615                 620

Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly Ala Cys Pro
625                 630                 635                 640

Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln Gly Pro Gly
                645                 650                 655

His Gln Ala Pro His Val His Tyr Ala Arg Leu Lys Thr Leu Arg Ser
            660                 665                 670

Leu Glu Ala Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser
        675                 680                 685

Arg Leu Phe Pro Lys Ala Asn Ala Gln Arg Thr
    690                 695
```

<210> 6

<211> 1323

<212> PRT

<213> Homo sapiens HER3 isoform 1

<400> 6

```
Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
1               5                   10                  15

Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
            20                  25                  30

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
        35                  40                  45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
    50                  55                  60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65                  70                  75                  80
```

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
85 90 95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
100 105 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
115 120 125

Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
130 135 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
145 150 155 160

Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp
165 170 175

Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala
180 185 190

Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys
195 200 205

His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys
210 215 220

Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val Pro Arg Cys
225 230 235 240

Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn
245 250 255

Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro
260 265 270

His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro
275 280 285

Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys
290 295 300

Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser Gly Ser Arg
305 310 315 320

Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val Asn Cys Thr
325 330 335

Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu Asn Gly Asp
340 345 350

Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu Asn Val Phe
355 360 365

Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln Ser Trp Pro
370 375 380

Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr Thr Ile Gly
385 390 395 400

```
Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile Met Lys Asn
                405                 410                 415

Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu Ile Ser Ala
            420                 425                 430

Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr His His Ser
        435                 440                 445

Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu Arg Leu Asp
    450                 455                 460

Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu Gly Lys Val
465                 470                 475                 480

Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly Pro Gly
                485                 490                 495

Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys Val Thr
            500                 505                 510

His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala His Glu Ala
        515                 520                 525

Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu Gly Thr Ala
    530                 535                 540

Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala His Phe
545                 550                 555                 560

Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly Val Leu Gly
                565                 570                 575

Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg
            580                 585                 590

Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln
        595                 600                 605

Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr His Leu Thr
    610                 615                 620

Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe Met Met Leu
625                 630                 635                 640

Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg
                645                 650                 655

Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu Pro Leu Asp
            660                 665                 670

Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr
        675                 680                 685

Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val
    690                 695                 700

His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val
705                 710                 715                 720
```

```
Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala
                725                 730                 735

Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His Ala His Ile
            740                 745                 750

Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr
        755                 760                 765

Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg Gln His Arg
    770                 775                 780

Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala
785                 790                 795                 800

Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu
                805                 810                 815

Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala
            820                 825                 830

Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu
        835                 840                 845

Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile
    850                 855                 860

His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val
865                 870                 875                 880

Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu
                885                 890                 895

Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala
            900                 905                 910

Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys
        915                 920                 925

Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn
    930                 935                 940

Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys
945                 950                 955                 960

Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro His Gly Leu
                965                 970                 975

Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu
            980                 985                 990

Asp Leu Asp Leu Glu Ala Glu Glu  Asp Asn Leu Ala Thr  Thr Thr Leu
        995                 1000                1005

Gly Ser  Ala Leu Ser Leu Pro  Val Gly Thr Leu Asn  Arg Pro Arg
    1010                1015                1020

Gly Ser  Gln Ser Leu Leu Ser  Pro Ser Ser Gly Tyr  Met Pro Met
    1025                1030                1035

Asn Gln  Gly Asn Leu Gly Glu  Ser Cys Gln Glu Ser  Ala Val Ser
    1040                1045                1050
```

```
Gly Ser  Ser Glu Arg Cys Pro  Arg Pro Val Ser Leu  His Pro Met
    1055                 1060                 1065

Pro Arg  Gly Cys Leu Ala Ser  Glu Ser Ser Glu Gly  His Val Thr
    1070                 1075                 1080

Gly Ser  Glu Ala Glu Leu Gln  Glu Lys Val Ser Met  Cys Arg Ser
    1085                 1090                 1095

Arg Ser  Arg Ser Arg Ser Pro  Arg Pro Arg Gly Asp  Ser Ala Tyr
    1100                 1105                 1110

His Ser  Gln Arg His Ser Leu  Leu Thr Pro Val Thr  Pro Leu Ser
    1115                 1120                 1125

Pro Pro  Gly Leu Glu Glu Glu  Asp Val Asn Gly Tyr  Val Met Pro
    1130                 1135                 1140

Asp Thr  His Leu Lys Gly Thr  Pro Ser Ser Arg Glu  Gly Thr Leu
    1145                 1150                 1155

Ser Ser  Val Gly Leu Ser Ser  Val Leu Gly Thr Glu  Glu Glu Asp
    1160                 1165                 1170

Glu Asp  Glu Glu Tyr Glu Tyr  Met Asn Arg Arg Arg  Arg His Ser
    1175                 1180                 1185

Pro Pro  His Pro Pro Arg Pro  Ser Ser Leu Glu Glu  Leu Gly Tyr
    1190                 1195                 1200

Glu Tyr  Met Asp Val Gly Ser  Asp Leu Ser Ala Ser  Leu Gly Ser
    1205                 1210                 1215

Thr Gln  Ser Cys Pro Leu His  Pro Val Pro Ile Met  Pro Thr Ala
    1220                 1225                 1230

Gly Thr  Thr Pro Asp Glu Asp  Tyr Glu Tyr Met Asn  Arg Gln Arg
    1235                 1240                 1245

Asp Gly  Gly Gly Pro Gly Gly  Asp Tyr Ala Ala Met  Gly Ala Cys
    1250                 1255                 1260

Pro Ala  Ser Glu Gln Gly Tyr  Glu Glu Met Arg Ala  Phe Gln Gly
    1265                 1270                 1275

Pro Gly  His Gln Ala Pro His  Val His Tyr Ala Arg  Leu Lys Thr
    1280                 1285                 1290

Leu Arg  Ser Leu Glu Ala Thr  Asp Ser Ala Phe Asp  Asn Pro Asp
    1295                 1300                 1305

Tyr Trp  His Ser Arg Leu Phe  Pro Lys Ala Asn Ala  Gln Arg Thr
    1310                 1315                 1320
```

<210> 7

<211> 164

<212> PRT

<213> Homo sapiens HER3 isoform 2

<400> 7

```
Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
1               5                  10                  15

Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
            20                  25                  30

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
        35                  40                  45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
    50                  55                  60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65                  70                  75                  80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
                85                  90                  95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
            100                 105                 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Gly Gln Phe Pro Met Val Pro
        115                 120                 125

Ser Gly Leu Thr Pro Gln Pro Ala Gln Asp Trp Tyr Leu Leu Asp Asp
    130                 135                 140

Asp Pro Arg Leu Leu Thr Leu Ser Ala Ser Ser Lys Val Pro Val Thr
145                 150                 155                 160

Leu Ala Ala Val
```

<210> 8

<211> 312

<212> PRT

<213> Homo sapiens HER3 isoform 3

<400> 8

```
Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
1               5                  10                  15

Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
            20                  25                  30

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
        35                  40                  45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
    50                  55                  60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65                  70                  75                  80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
                85                  90                  95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
            100                 105                 110
```

```
Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
        115                 120                 125

Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
    130                 135                 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
145                 150                 155                 160

Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp
                165                 170                 175

Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala
            180                 185                 190

Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys
        195                 200                 205

His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys
    210                 215                 220

Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val Pro Arg Cys
225                 230                 235                 240

Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn
                245                 250                 255

Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro
            260                 265                 270

His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro
        275                 280                 285

Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys
    290                 295                 300

Gly Gly Leu Cys Pro Lys Ala Phe

305                 310
```

<210> 9

<211> 624

<212> PRT

<213> Homo sapiens HER3 isoform 1 extracellular region

<400> 9

```
Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
1               5                   10                  15

Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
            20                  25                  30

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
        35                  40                  45

Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
    50                  55                  60
```

```
Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65                  70                  75                  80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
                85                  90                  95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
            100                 105                 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
        115                 120                 125

Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
    130                 135                 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
145                 150                 155                 160

Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp
                165                 170                 175

Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala
            180                 185                 190

Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys
        195                 200                 205

His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys

    210                 215                 220

Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val Pro Arg Cys
225                 230                 235                 240

Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn
                245                 250                 255

Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro
            260                 265                 270

His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro
        275                 280                 285

Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys
    290                 295                 300

Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser Gly Ser Arg
305                 310                 315                 320

Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val Asn Cys Thr
                325                 330                 335

Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu Asn Gly Asp
            340                 345                 350

Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu Asn Val Phe
        355                 360                 365

Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln Ser Trp Pro
    370                 375                 380
```

```
Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr Thr Ile Gly
385                 390                 395                 400

Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile Met Lys Asn
                405                 410                 415

Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu Ile Ser Ala
            420                 425                 430

Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr His His Ser
        435                 440                 445

Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu Arg Leu Asp
    450                 455                 460

Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu Gly Lys Val
465                 470                 475                 480

Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly Pro Gly
                485                 490                 495

Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys Val Thr
            500                 505                 510

His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala His Glu Ala
        515                 520                 525

Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu Gly Thr Ala
    530                 535                 540

Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala His Phe
545                 550                 555                 560

Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly Val Leu Gly
                565                 570                 575

Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg
            580                 585                 590

Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln
        595                 600                 605

Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr His Leu Thr
    610                 615                 620
```

<210> 10

<211> 21

<212> PRT

<213> Homo sapiens HER3 isoform 1 transmembrane domain

<400> 10

```
Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe Met Met Leu
1               5                   10                  15

Gly Gly Thr Phe Leu
            20
```

<210> 11

<211> 678

<212> PRT

<213> Homo sapiens Human HER3 isoform 1 cytoplasmic domain

<400> 11

```
Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr
1               5                   10                  15

Leu Glu Arg Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala
            20                  25                  30

Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr Glu Leu Arg Lys Leu
        35                  40                  45

Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val His Lys Gly Val Trp
    50                  55                  60

Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Val Ile
65                  70                  75                  80

Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala Val Thr Asp His Met
                85                  90                  95

Leu Ala Ile Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly
            100                 105                 110

Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu
        115                 120                 125

Gly Ser Leu Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro
    130                 135                 140

Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr
145                 150                 155                 160

Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val
                165                 170                 175

Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala
            180                 185                 190

Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr Ser Glu Ala Lys
        195                 200                 205

Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr
    210                 215                 220

Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu
225                 230                 235                 240

Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu Val
                245                 250                 255

Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile Cys
            260                 265                 270

Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp Glu
        275                 280                 285
```

```
Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu Phe Thr Arg Met
    290                 295                 300

Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser Gly Pro
305                 310                 315                 320

Gly Ile Ala Pro Gly Pro Glu Pro His Gly Leu Thr Asn Lys Lys Leu
                325                 330                 335

Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp Leu Glu
            340                 345                 350

Ala Glu Glu Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala Leu Ser
        355                 360                 365

Leu Pro Val Gly Thr Leu Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu
    370                 375                 380

Ser Pro Ser Ser Gly Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu
385                 390                 395                 400

Ser Cys Gln Glu Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg
                405                 410                 415

Pro Val Ser Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser
            420                 425                 430

Ser Glu Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val
        435                 440                 445

Ser Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly
    450                 455                 460

Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro Val Thr
465                 470                 475                 480

Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly Tyr Val
                485                 490                 495

Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg Glu Gly Thr
            500                 505                 510

Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr Glu Glu Glu Asp
        515                 520                 525

Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg Arg Arg His Ser Pro
    530                 535                 540

Pro His Pro Pro Arg Pro Ser Ser Leu Glu Glu Leu Gly Tyr Glu Tyr
545                 550                 555                 560

Met Asp Val Gly Ser Asp Leu Ser Ala Ser Leu Gly Ser Thr Gln Ser
                565                 570                 575

Cys Pro Leu His Pro Val Pro Ile Met Pro Thr Ala Gly Thr Thr Pro
            580                 585                 590

Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg Asp Gly Gly Gly Pro
        595                 600                 605

Glu Glu Asp Tyr Ala Ala Met Glu Ala Cys Pro Ala Ser Glu Gln Glu
```

```
Gly Gly Asp Tyr Ala Ala Met Gly Ala Cys Pro Ala Ser Glu Gln Gly
    610                 615                 620

Tyr Glu Glu Met Arg Ala Phe Gln Gly Pro Gly His Gln Ala Pro His
625                 630                 635                 640

Val His Tyr Ala Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp
                645                 650                 655

Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys
            660                 665                 670

Ala Asn Ala Gln Arg Thr
        675
```

<210> 12

<211> 44

<212> PRT

<213> Homo sapiens HER3 isoform 1 juxtamembrane segment

<400> 12

```
Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr
1               5                   10                  15

Leu Glu Arg Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala
            20                  25                  30

Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr Glu
        35                  40
```

<210> 13

<211> 258

<212> PRT

<213> Homo sapiensHER3 isoform 1 protein kinase domain

<400> 13

```
Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val His
1               5                   10                  15

Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val Cys
            20                  25                  30

Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala Val
        35                  40                  45

Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His Ala His Ile Val
    50                  55                  60

Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr Gln
65                  70                  75                  80

Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg Gln His Arg Gly
                85                  90                  95

Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala Lys
            100                 105                 110

Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala
        115                 120                 125
```

```
Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp
    130                 135                 140

Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr
145                 150                 155                 160

Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His
                165                 170                 175

Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
            180                 185                 190

Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg
        195                 200                 205

Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln
    210                 215                 220

Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp
225                 230                 235                 240

Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu
                245                 250                 255

Phe Thr
```

<210> 14

<211> 376

<212> PRT

<213> Homo sapiens HER3 isoform 1 C terminal segment

<400> 14

```
Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser
1               5                   10                  15

Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro His Gly Leu Thr Asn Lys
            20                  25                  30

Lys Leu Glu Glu Val Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp
        35                  40                  45

Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala
    50                  55                  60

Leu Ser Leu Pro Val Gly Thr Leu Asn Arg Pro Arg Gly Ser Gln Ser
65                  70                  75                  80

Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro Met Asn Gln Gly Asn Leu
                85                  90                  95

Gly Glu Ser Cys Gln Glu Ser Ala Val Ser Gly Ser Ser Glu Arg Cys
            100                 105                 110

Pro Arg Pro Val Ser Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser
        115                 120                 125

Glu Ser Ser Glu Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu
    130                 135                 140
```

```
Lys Val Ser Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro
145                 150                 155                 160

Arg Gly Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro
                165                 170                 175

Val Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly
            180                 185                 190

Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg Glu
        195                 200                 205

Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr Glu Glu
    210                 215                 220

Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg Arg Arg His
225                 230                 235                 240

Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu Glu Leu Gly Tyr
                245                 250                 255

Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala Ser Leu Gly Ser Thr
            260                 265                 270

Gln Ser Cys Pro Leu His Pro Val Pro Ile Met Pro Thr Ala Gly Thr
        275                 280                 285

Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg Asp Gly Gly
    290                 295                 300

Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly Ala Cys Pro Ala Ser Glu
305                 310                 315                 320

Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln Gly Pro Gly His Gln Ala
                325                 330                 335

Pro His Val His Tyr Ala Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala
            340                 345                 350

Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe
        355                 360                 365

Pro Lys Ala Asn Ala Gln Arg Thr
    370                 375
```

<210> 15

<211> 164

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain I

<400> 15

```
Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr Leu Asn Gly
1               5                   10                  15

Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr Leu Tyr Lys
            20                  25                  30

Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu Ile Val Leu
        35                  40                  45
```

```
Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg Glu Val
    50                  55                  60

Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr Leu Pro Leu
65                  70                  75                  80

Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp Gly Lys Phe
                85                  90                  95

Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser His Ala Leu
            100                 105                 110

Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser Gly Gly Val
        115                 120                 125

Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr Ile Asp Trp
    130                 135                 140

Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val Lys Asp Asn
145                 150                 155                 160

Gly Arg Ser Cys
```

<210> 16

<211> 146

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain II

<400> 16

```
Pro Pro Cys His Glu Val Cys Lys Gly Arg Cys Trp Gly Pro Gly Ser
1               5                   10                  15

Glu Asp Cys Gln Thr Leu Thr Lys Thr Ile Cys Ala Pro Gln Cys Asn
            20                  25                  30

Gly His Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys
        35                  40                  45

Ala Gly Gly Cys Ser Gly Pro Gln Asp Thr Asp Cys Phe Ala Cys Arg
    50                  55                  60

His Phe Asn Asp Ser Gly Ala Cys Val Pro Arg Cys Pro Gln Pro Leu
65                  70                  75                  80

Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn Pro His Thr Lys
                85                  90                  95

Tyr Gln Tyr Gly Gly Val Cys Val Ala Ser Cys Pro His Asn Phe Val
            100                 105                 110

Val Asp Gln Thr Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu
        115                 120                 125

Val Asp Lys Asn Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys
    130                 135                 140

Pro Lys
145
```

<210> 17

<211> 166

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain III

<400> 17

```
Ala Cys Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser
1               5                   10                  15

Ser Asn Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn Leu
            20                  25                  30

Asp Phe Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro
        35                  40                  45

Ala Leu Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile
    50                  55                  60

Thr Gly Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met His Asn Phe
65                  70                  75                  80

Ser Val Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Leu Tyr Asn
                85                  90                  95

Arg Gly Phe Ser Leu Leu Ile Met Lys Asn Leu Asn Val Thr Ser Leu
            100                 105                 110

Gly Phe Arg Ser Leu Lys Glu Ile Ser Ala Gly Arg Ile Tyr Ile Ser
        115                 120                 125

Ala Asn Arg Gln Leu Cys Tyr His His Ser Leu Asn Trp Thr Lys Val
    130                 135                 140

Leu Arg Gly Pro Thr Glu Glu Arg Leu Asp Ile Lys His Asn Arg Pro
145                 150                 155                 160

Arg Arg Asp Cys Val Ala
                165
```

<210> 18

<211> 148

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain IV

<400> 18

```
Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly
1               5                   10                  15

Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly
            20                  25                  30

Val Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe
        35                  40                  45

Ala His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met
    50                  55                  60
```

```
Glu Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln
65                  70                  75                  80

Cys Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His
                85                  90                  95

Gly Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln
            100                 105                 110

Asn Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly
        115                 120                 125

Pro Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys
    130                 135                 140

Thr His Leu Thr
145
```

<210> 19

<211> 17

<212> PRT

<213> Homo sapiens HER3 extracellular region subdomain II dimerisation loop

<400> 19

```
Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn Pro
1               5                   10                  15

His
```

<210> 20

<211> 1283

<212> PRT

<213> Homo macaque HER3

<400> 20

```
Met Gly Asn Leu Glu Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser
1               5                   10                  15

Phe Leu Gln Trp Ile Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met
            20                  25                  30

Asn Glu Phe Ser Thr Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly
        35                  40                  45

Thr Gln Val Tyr Asp Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr
    50                  55                  60

Asn Thr Asn Ser Ser His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu
65                  70                  75                  80

Thr Glu Ile Leu Ser Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu
                85                  90                  95

Cys His Met Asp Thr Ile Asp Trp Lys Asp Ile Val Arg Asp Gln Asp
            100                 105                 110

Ala Glu Ile Val Val Lys Asp Asn Gly Arg Ser Cys Pro Leu Cys His
        115                 120                 125
```

```
Glu Val Cys Lys Gly Arg Cys Trp Gly Pro Gly Pro Glu Asp Cys Gln
    130                 135                 140

Thr Leu Thr Lys Thr Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe
145                 150                 155                 160

Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys
                165                 170                 175

Ser Gly Pro Gln Asp Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp
            180                 185                 190

Ser Gly Ala Cys Val Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys
        195                 200                 205

Leu Thr Phe Gln Leu Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly
    210                 215                 220

Gly Val Cys Val Ala Ser Cys Pro His Asn Phe Val Val Asp Gln Thr
225                 230                 235                 240

Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn
                245                 250                 255

Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys
            260                 265                 270

Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn
        275                 280                 285

Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe
    290                 295                 300

Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu
305                 310                 315                 320

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
                325                 330                 335

Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met Tyr Asn Phe Ser Val
            340                 345                 350

Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly
        355                 360                 365

Phe Ser Leu Leu Ile Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe
    370                 375                 380

Arg Ser Leu Lys Glu Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn
385                 390                 395                 400

Arg Gln Leu Cys Tyr His His Ser Leu Asn Trp Thr Lys Val Leu Arg
                405                 410                 415

Gly Pro Thr Glu Glu Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg
            420                 425                 430

Asp Cys Val Ala Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly
        435                 440                 445

Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr
```

```
     450                 455                 460

Ser Arg Gly Gly Val Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu
465                 470                 475                 480

Pro Arg Glu Phe Ala His Glu Ala Glu Cys Phe Ser Cys His Pro Glu
                485                 490                 495

Cys Gln Pro Met Glu Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp
            500                 505                 510

Thr Cys Ala Gln Cys Ala His Phe Arg Asp Gly Pro His Cys Val Ser
        515                 520                 525

Ser Cys Pro His Gly Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr
    530                 535                 540

Pro Asp Val Gln Asn Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln
545                 550                 555                 560

Gly Cys Lys Gly Pro Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val
                565                 570                 575

Leu Ile Gly Lys Thr His Leu Thr Met Ala Leu Thr Val Ile Ala Gly
            580                 585                 590

Leu Val Val Ile Phe Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg
        595                 600                 605

Gly Arg Arg Ile Gln Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg
    610                 615                 620

Gly Glu Ser Ile Glu Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val
625                 630                 635                 640

Leu Ala Arg Ile Phe Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu
                645                 650                 655

Gly Ser Gly Val Phe Gly Thr Val His Lys Gly Val Trp Ile Pro Glu
            660                 665                 670

Gly Glu Ser Ile Lys Ile Pro Val Cys Ile Lys Ile Ile Glu Asp Lys
        675                 680                 685

Ser Gly Arg Gln Ser Phe Gln Ala Val Thr Asp His Met Leu Ala Ile
    690                 695                 700

Gly Ser Leu Asp His Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro
705                 710                 715                 720

Gly Ser Ser Leu Gln Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu
                725                 730                 735

Leu Asp His Val Arg Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu
            740                 745                 750

Leu Asn Trp Gly Val Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu
        755                 760                 765

His Gly Met Val His Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys
    770                 775                 780
```

```
Ser Pro Ser Gln Val Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu
785                 790                 795                 800

Pro Pro Asp Asp Lys Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile
                805                 810                 815

Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln
            820                 825                 830

Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe
        835                 840                 845

Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu
    850                 855                 860

Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp
865                 870                 875                 880

Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg
                885                 890                 895

Pro Thr Phe Lys Glu Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp
            900                 905                 910

Pro Pro Arg Tyr Leu Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala
        915                 920                 925

Pro Gly Pro Glu Pro His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val

    930                 935                 940

Glu Leu Glu Pro Glu Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu
945                 950                 955                 960

Asp Asn Leu Ala Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val
                965                 970                 975

Gly Thr Leu Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser
            980                 985                 990

Ser Gly Tyr Met Pro Met Asn Gln  Gly Asn Leu Gly Glu  Ala Phe Gln
        995                 1000                1005

Glu Ser  Ala Val Ser Gly Ser  Ser Glu Trp Cys Pro  Arg Pro Val
    1010                1015                1020

Ser Leu  His Pro Met Pro Arg  Gly Cys Leu Ala Ser  Glu Ser Ser
    1025                1030                1035

Glu Gly  His Val Thr Gly Ser  Glu Ala Glu Leu Gln  Glu Lys Val
    1040                1045                1050

Ser Thr  Cys Arg Ser Arg Ser  Arg Ser Arg Ser Pro  Arg Pro Arg
    1055                1060                1065

Gly Asp  Ser Ala Tyr His Ser  Gln Arg His Ser Leu  Leu Thr Pro
    1070                1075                1080

Val Thr  Pro Leu Ser Pro Pro  Gly Leu Glu Glu Glu  Asp Val Asn
    1085                1090                1095
```

1085 1090 1095

Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser
1100 1105 1110

Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly
1115 1120 1125

Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg
1130 1135 1140

Arg Arg Arg His Ser Pro Pro Arg Pro Pro Arg Pro Ser Ser Leu
1145 1150 1155

Glu Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser
1160 1165 1170

Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro
1175 1180 1185

Val Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr
1190 1195 1200

Met Asn Arg Gln Arg Gly Gly Ser Gly Pro Gly Gly Asp Tyr Ala
1205 1210 1215

Ala Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met
1220 1225 1230

Arg Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr
1235 1240 1245

Ala His Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala
1250 1255 1260

Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala
1265 1270 1275

Asn Ala Gln Arg Thr
1280

<210> 21

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Epitope recognised by anti-HER3 antibody clone 10A6

<400> 21

Tyr Asn Lys Leu Thr Phe Gln Leu Glu Pro Asn Pro His
1 5 10

<210> 22

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Epitope recognised by anti-HER3 antibody clone 4-35-B2 and 4-35-B4

<400> 22

```
Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe
1               5                   10
```

<210> 23

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Composite sequence of epitopes recognised by anti-HER3 antibody clones 4-35-B2, 4-35-B4 and 10A6

<400> 23

```
Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
1               5                   10                  15


Glu Pro Asn Pro His
            20
```

<210> 24

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 heavy chain variable region

<400> 24

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1               5                   10                  15


Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30


Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45


Met Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60


Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80


Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95


Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Leu Thr Val Ser Ser
        115                 120
```

<210> 25

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75 heavy chain variable region

<400> 25

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Thr Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 26

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76 heavy chain variable region

<400> 26

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95
```

```
Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 27

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c77 heavy chain variable region

<400> 27

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 28

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v1 heavy chain variable region

<400> 28

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60
```

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 29

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v2 heavy chain variable region

<400> 29

Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 30

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 1oD1_11B heavy chain variable region

<400> 30

Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

```
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 31

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1 heavy chain variable region

<400> 31

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 32

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v2 heavy chain variable region

<400> 32

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 33

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85o1 heavy chain variable region

<400> 33

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Glu Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110
```

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 34

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 1oD1_c85o2 heavy chain variable region

<400> 34

Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 35

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87 heavy chain variable region

<400> 35

Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser

65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 36
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89 heavy chain variable region

<400> 36
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Leu Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 37
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 heavy chain variable region

<400> 37
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Phe Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Leu Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 38

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 heavy chain variable region

<400> 38

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Tyr Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Leu Ala Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ala Val Thr Val Ser Ser
115 120

<210> 39

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c92 heavy chain variable region

<400> 39

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Thr Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 40

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c93 heavy chain variable region

<400> 40

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 41
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1, 10D1_c75, 0D1_c76, 0D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1 _c85v1, 10D1_c85v2, 10D1_c85o1, 0D1_c85o2, 10D1_c87, 10D1_c89, 0D1_c90, 10D1_c92, 10D1_c93 heavy chain CDR1

<400> 41
Gly Tyr Ser Ile Thr Ser Gly Tyr Ser
1 5

<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c91 heavy chain CDR1

<220>
<221> MISC_FEATURE
<222> (3) .. (3)
<223> X = S or Y

<400> 42
Gly Tyr Tyr Ile Thr Ser Gly Tyr Ser
1 5

<210> 43
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 derived consensus heavy chain CDR1

<220>
<221> MISC_FEATURE
<222> (3) .. (3)
<223> X = S or Y

<400> 43
Gly Tyr Xaa Ile Thr Ser Gly Tyr Ser
1 5

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain CDR2

<400> 44

```
Ile His Tyr Ser Gly Gly Thr
1               5
```

<210> 45

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c89, 10D1_c90, 10D1_c91 heavy chain CDR2

<400> 45

```
Ile Arg Tyr Ser Gly Gly Thr
1               5
```

<210> 46

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 derived consensus heavy chain CDR2

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X = H or R

<400> 46

```
Ile Xaa Tyr Ser Gly Gly Thr
1               5
```

<210> 47

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10 D1_c85v1, 10D1_c85v2, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain CDR3

<400> 47

```
Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr
1               5                   10
```

<210> 48

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89, 10D1_c90, 10D1_c91 heavy chain CDR3

<400> 48

```
Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr
1               5                   10
```

<210> 49

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85o1 heavy chain CDR3

<400> 49

```
Ala Arg Glu Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr
1               5                   10
```

<210> 50

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 1oD1_c85o2 heavy chain CDR3

<400> 50

```
Ala Arg Gly Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr
1               5                   10
```

<210> 51

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 derived consensus heavy chain CDR3

<220>

<221> MISC_FEATURE

<222> (3) .. (3)

<223> X = M, E or G

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> X = R or W

<400> 51

```
Ala Arg Xaa Thr Thr Ala Pro Xaa Tyr Pro Phe Asp Tyr
1               5                   10
```

<210> 52
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2,10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain FR1

<400> 52
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Thr
20 25

<210> 53
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 110D1_c89, 10D1_c91 heavy chain FR1

<400> 53
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 54
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 heavy chain FR1

<400> 54
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Phe Leu Thr Cys Thr Val Ser
20 25

<210> 55
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 heavy chain FR1

<400> 55
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln

1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr
20 25

<210> 56

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c85v1, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain FR2

<400> 56

Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp Ile Gly
1 5 10 15

Ser

<210> 57

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v2, 10D1_c85v2, 10D1_c85o1, 1oD1_c85o2 heavy chain FR2

<400> 57

Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10 15

Ser

<210> 58

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 heavy chain FR2

<400> 58

Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met Gly
1 5 10 15

Ser

<210> 59

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89, 10D1_c90, 10D1_c91 heavy chain FR2

<400> 59

Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10 15

Ser

<210> 60

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_11B heavy chain FR2

<400> 60

Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10 15

Ser

<210> 61

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75, 10D1_c92 heavy chain FR3

<400> 61

Asn Tyr Asn Pro Thr Leu Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
20 25 30

Thr Ala Val Tyr Phe Cys
35

<210> 62

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2 heavy chain FR3

<400> 62

Asn Tyr Asn Pro Ser Leu Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
20 25 30

Thr Ala Val Tyr Phe Cys
35

<210> 63

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_11B heavy chain FR3

<400> 63

```
Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Arg Asp Thr
1               5                   10                  15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
            20                  25                  30

Thr Ala Val Tyr Tyr Cys
        35
```

<210> 64

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 1oD1_c85o2 heavy chain FR3

<400> 64

```
Asn Tyr Asn Pro Ser Leu Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr
1               5                   10                  15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Gly Ser Val Thr Ala Ala Asp
            20                  25                  30

Thr Ala Val Tyr Phe Cys
        35
```

<210> 65

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87, 10D1_c93 heavy chain FR3

<400> 65

```
Asn Tyr Asn Pro Ser Leu Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr
1               5                   10                  15

Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp
            20                  25                  30

Thr Ala Val Tyr Phe Cys
        35
```

<210> 66

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89 heavy chain FR3

<400> 66

```
Asp Tyr Asn Pro Ser Leu Lys Ser Leu Val Thr Ile Ser Ala Asp Thr
1               5                   10                  15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
            20                  25                  30

Thr Ala Val Tyr Tyr Cys
        35
```

<210> 67

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c90 heavy chain FR3

<400> 67

```
Asp Tyr Asn Pro Ser Leu Lys Ser Leu Val Thr Ile Ser Val Asp Thr
1               5                   10                  15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
            20                  25                  30

Thr Ala Val Tyr Tyr Cys
        35
```

<210> 68

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 heavy chain FR3

<400> 68

```
Asp Tyr Asn Pro Ser Leu Lys Ser Leu Ala Thr Ile Ser Ala Asp Thr
1               5                   10                  15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
            20                  25                  30

Thr Ala Val Tyr Tyr Cys
        35
```

<210> 69

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 heavy chain FR3

<400> 69

```
Asn Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr
1               5                   10                  15

Ser Lys Asn Gln Phe Phe Leu Gln Leu Asn Ser Val Thr Thr Glu Asp
            20                  25                  30

Thr Ala Thr Tyr Phe Cys
        35
```

<210> 70

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c8 5v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c92, 10D1_c93 heavy chain FR4

<400> 70

```
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1               5                   10
```

<210> 71

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89, 10D1_c90 heavy chain FR4

<400> 71

```
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1               5                   10
```

<210> 72

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 heavy chain FR4

<400> 72

```
Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser

1               5                   10
```

<210> 73

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1, 4-35-B4, 10A6 heavy chain FR4

<400> 73

```
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1               5                   10
```

<210> 74

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 light chain variable region

<400> 74

```
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Ala
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105
```

<210> 75

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75 light chain variable region

<400> 75

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Leu Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Met Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Phe Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 76

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76 light chain variable region

<400> 76

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Gly Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Tyr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Ala
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 77

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c77 light chain variable region

<400> 77

Val Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Pro Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
35 40 45

```
Tyr Ser Ala Ser Tyr Gly Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Thr His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 78

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v1, 10D1_c78v2, 1oD1_11B light chain variable region

<400> 78

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Gly Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 79

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2 light chain variable region

<400> 79

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
```

35 40 45

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 80

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85o1 light chain variable region

<400> 80

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
35 40 45

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 81

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 1oD1_c85o2 light chain variable region

<400> 81

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
35 40 45

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 82

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87 light chain variable region

<400> 82

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
20 25 30

Val Ala Trp Tyr Gln Gln Met Pro Gly Lys Ser Pro Glu Pro Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Met Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 83

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89 light chain variable region

<400> 83

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Pro Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 84

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c90 light chain variable region

<400> 84

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Phe Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Pro Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Ser Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Met Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Thr Thr His Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 85

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 light chain variable region

<400> 85

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Met Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Gly Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 86

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c92 light chain variable region

<400> 86

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Leu Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Met Lys Leu Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Phe Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Glu Tyr Phe Cys Gln Gln Tyr Phe Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 87

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c93 light chain variable region

<400> 87

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Met Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 88

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1, 10D1_c75, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2,10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_ c92, 10D1_c93 light chain CDR1

<400> 88

```
Gln Ile Val Gly Ser Asn
1               5
```

<210> 89

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76 light chain CDR1

<400> 89

```
Gln Ile Val Gly Tyr Asn
1               5
```

<210> 90

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c77 light chain CDR1

<400> 90

```
Gln Ile Val Gly Pro Asn
1               5
```

<210> 91

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 derived consensus light chain CDR1

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> X = S, Y or P

<400> 91

```
Gln Ile Val Gly Xaa Asn
1               5
```

<210> 92

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1, 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 1oD1_11B, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 light chain CDR2

<400> 92

```
Ser Ala Ser
1
```

<210> 93

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 1oD1_c85o2 light chain CDR2

<400> 93

```
Ser Ala Arg
1
```

<210> 94

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 derived consensus light chain CDR2

<220>
<221> MISC_FEATURE
<222> (3) .. (3)
<223> X = S or R

<400> 94
Ser Ala Xaa
1

<210> 95
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1, 10D1_c75, 10D1_c76, 0D1_c78v1, 10D1_c78v2, 0D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 0D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c91, 10D1_c93 light chain CDR3

<400> 95
Gln Gln Tyr Ser Ser His Pro Leu Thr
1 5

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c77 light chain CDR3

<400> 96
Gln Gln Tyr Ser Thr His Pro Leu Thr
1 5

<210> 97
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 light chain CDR3

<400> 97
Gln Gln Tyr Thr Thr His Pro Leu Thr
1 5

<210> 98
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c92 light chain CDR3

<400> 98
Gln Gln Tyr Phe Ser His Pro Leu Thr
1 5

<210> 99
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1 derived consensus light chain CDR3

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X = S, T or F

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X = S or T

<400> 99
Gln Gln Tyr Xaa Xaa His Pro Leu Thr
1 5

<210> 100
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75, 10D1_c92 light chain FR1

<400> 100
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Leu Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 101
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c76 light chain FR1

<400> 101
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Gly Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 102
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c77 light chain FR1

<400> 102
Val Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 103
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c93 light chain FR1

<400> 103
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 104
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c89, 10D1_c91 light chain FR1

<400> 104
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 105
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c90 light chain FR1

<400> 105

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Phe Thr Cys Lys Ala Ser
20 25

<210> 106

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 light chain FR1

<400> 106

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser
20 25

<210> 107

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75 light chain FR2

<400> 107

Val Ala Trp Tyr Gln Met Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
1 5 10 15

Tyr

<210> 108

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 1oD1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c93 light chain FR2

<400> 108

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
1 5 10 15

Tyr

<210> 109

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87 light chain FR2

<400> 109

```
Val Ala Trp Tyr Gln Gln Met Pro Gly Lys Ser Pro Glu Pro Leu Ile
1               5                   10                  15

Tyr
```

<210> 110

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89, 10D1_c90 light chain FR2

<400> 110

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Pro Leu Ile
1               5                   10                  15

Tyr
```

<210> 111

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 light chain FR2

<400> 111

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Met Pro Leu Ile
1               5                   10                  15

Tyr
```

<210> 112

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c92 light chain FR2

<400> 112

```
Val Ala Trp Tyr Gln Met Lys Leu Gly Lys Ser Pro Lys Pro Leu Ile
1               5                   10                  15

Tyr
```

<210> 113

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 light chain FR2

<400> 113

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile
1               5                   10                  15

Tyr
```

<210> 114

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75, 10D1_c92 light chain FR3

<400> 114

```
Tyr Leu Tyr Phe Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1               5                   10                  15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala
            20                  25                  30

Glu Tyr Phe Cys
        35
```

<210> 115

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76 light chain FR3

<400> 115

```
Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Ala Ser Gly Ser Gly
1               5                   10                  15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala
            20                  25                  30

Glu Tyr Phe Cys
        35
```

<210> 116

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c77 light chain FR3

<400> 116

Tyr Gly Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala
20 25 30

Glu Tyr Phe Cys
35

<210> 117

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v1, 10D1_c78v2, 1oD1_11B light chain FR3

<400> 117

Tyr Gly Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro Glu Asp Val Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 118

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 1oD1_c85o2 light chain FR3

<400> 118

Tyr Gln Tyr Ser Gly Val Pro Phe Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 119

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87, 10D1_c93 light chain FR3

<400> 119

Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Met Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 120

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89 light chain FR3

<400> 120

Tyr Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 121

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c90 light chain FR3

<400> 121

Tyr Leu Tyr Ser Ser Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Glu Phe Thr Met Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 122

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 light chain FR3

<400> 122

Tyr Gly Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 123

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 light chain FR3

<400> 123

Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Ala Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Glu Asp Leu Ala
20 25 30

Glu Tyr Phe Cys
35

<210> 124

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 1oD1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c90, 10D1_c92, 10D1_c93 light chain FR4

<400> 124

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 125

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89, 10D1_c91 light chain FR4

<400> 125

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 126

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 light chain FR4

<400> 126

```
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
1               5                   10
```

<210> 127

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 heavy chain variable region

<400> 127

```
Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
            20                  25                  30

Asn Met Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45

Gly His Ile Asn Pro Tyr Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Phe
65                  70                  75                  80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Val Ser Leu Arg Trp Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
            100                 105                 110

Val Thr Val Ser Ser
        115
```

<210> 128

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 heavy chain CDR1

<400> 128

```
Gly Tyr Ser Phe Thr Asp Tyr Asn
1               5
```

<210> 129

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 heavy chain CDR2

<400> 129
Ile Asn Pro Tyr Asn Gly Gly Thr
1 5

<210> 130
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain CDR3

<400> 130
Val Ser Leu Arg Trp Gly Ala Met Asp Tyr
1 5 10

<210> 131
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain FR1

<400> 131
Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 132
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain FR2

<400> 132
Met Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly
1 5 10 15

His

<210> 133
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 heavy chain FR3

<400> 133
Thr Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys
1 5 10 15

Ser Ser Ser Thr Ala Phe Met His Leu Asn Ser Leu Thr Ser Glu Asp
20 25 30

Ser Ala Val Tyr Phe Cys
35

<210> 134

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 heavy chain FR4

<400> 134

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1 5 10

<210> 135

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 light chain variable region

<400> 135

Gln Ile Val Leu Thr Gln Ser Pro Ala Leu Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Tyr Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 136

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 light chain CDR1

<400> 136
Ser Ser Val Ser Tyr
1 5

<210> 137
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain CDR2

<400> 137
Leu Thr Ser
1

<210> 138
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain CDR3

<400> 138
Gln Gln Trp Asn Ser Asn Pro Tyr Thr
1 5

<210> 139
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain FR1

<400> 139
Gln Ile Val Leu Thr Gln Ser Pro Ala Leu Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser
20 25

<210> 140
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain FR2

<400> 140
Met Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile
1 5 10 15

Tyr

<210> 141
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2 light chain FR3

<400> 141

```
Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1               5                   10                  15

Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala
            20                  25                  30

Thr Tyr Tyr Cys
        35
```

<210> 142
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B2, 4-35-B4, 10A6 light chain FR4

<400> 142

```
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1               5                   10
```

<210> 143
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 heavy chain variable region

<400> 143

```
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
            20                  25                  30

Tyr Ile His Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Lys Ile Ile Asp Pro Ala Asn Gly Asn Thr Asn Tyr Asp Pro Lys
    50                  55                  60

Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala
65                  70                  75                  80

Tyr Leu Gln Leu Ser Ser Leu Ser Ser Glu Asp Thr Ala Val Tyr Phe
```

85 90 95

Cys Ala Arg Gly Leu His Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

Ser

<210> 144

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain CDR1

<400> 144

Gly Phe Asn Ile Lys Asp Thr Tyr
1 5

<210> 145

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain CDR2

<400> 145

Ile Asp Pro Ala Asn Gly Asn Thr
1 5

<210> 146

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain CDR3

<400> 146

Ala Arg Gly Leu His
1 5

<210> 147

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 heavy chain FR1

<400> 147

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser

20 25

<210> 148
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 heavy chain FR2

<400> 148
Ile His Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly
1 5 10 15

Lys

<210> 149
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 heavy chain FR3

<400> 149
Asn Tyr Asp Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr
1 5 10 15

Ser Ser Asn Thr Ala Tyr Leu Gln Leu Ser Ser Leu Ser Ser Glu Asp
20 25 30

Thr Ala Val Tyr Phe Cys
35

<210> 150
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 light chain variable region

<400> 150
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 151

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 light chain CDR1

<400> 151
Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr

1 5 10

<210> 152

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 light chain CDR2

<400> 152
Leu Ala Ser
1

<210> 153

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 light chain CDR3

<400> 153
Gln His Ser Arg Glu Leu Pro Tyr Thr
1 5

<210> 154

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 light chain FR1

<400> 154
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser
20 25

<210> 155

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 light chain FR2

<400> 155

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 156

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 light chain FR3

<400> 156

Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 157

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain variable region

<400> 157

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Asn Phe Ile Thr Ser Gly
20 25 30

Tyr Phe Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Phe Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Lys Pro Ser Leu
50 55 60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Glu Asn Tyr Gly Phe Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 158

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain CDR1

<400> 158

Gly Asn Phe Ile Thr Ser Gly Tyr Phe
1 5

<210> 159

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain CDR2

<400> 159

Ile Ser Tyr Asp Gly Ser Asn
1 5

<210> 160

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain CDR3

<400> 160

Ala Arg Glu Asn Tyr Gly Phe Gly Phe Asp Tyr
1 5 10

<210> 161

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain FR1

<400> 161

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr
20 25

<210> 162

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain FR2

<400> 162

Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met Gly
1 5 10 15

Phe

<210> 163

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain FR3

<400> 163

Asn Tyr Lys Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Phe Leu Lys Leu Asn Ser Val Thr Thr Glu Asp
20 25 30

Thr Ala Thr Tyr Tyr Cys
35

<210> 164

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 light chain variable region

<400> 164

Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Pro Val Ser Ile Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asp Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Trp Lys Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Phe Thr Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 165

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 light chain CDR1

<400> 165

Gln Ser Leu Leu Tyr Ser Asp Asn Gln Lys Asn Tyr
1 5 10

<210> 166

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 light chain CDR2

<400> 166

Trp Ala Ser
1

<210> 167

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 light chain CDR3

<400> 167

Gln Gln Tyr Phe Thr Phe Pro Trp Thr
1 5

<210> 168

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 light chain FR1

<400> 168

```
Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Pro Val Ser Ile Gly
1               5                   10                  15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser
            20                  25
```

<210> 169

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 light chain FR2

<400> 169

```
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
1               5                   10                  15

Tyr
```

<210> 170

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 light chain FR3

<400> 170

```
Thr Trp Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
1               5                   10                  15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu Ala
            20                  25                  30

Val Tyr Tyr Cys
        35
```

<210> 171

<211> 330

<212> PRT

<213> Homo sapiens IgG1 consant region (IGHG1; UniProt:P01857-1, v1)

<400> 171

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
```

50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 172

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> CH1 IgG1 (positions 1-98 of P01857-1, v1)

<400> 172

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                  10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val
```

<210> 173

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Hinge IgG1 (positions 99-110 of P01857-1, v1)

<400> 173

```
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
1               5                  10
```

<210> 174

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> CH2 IgG1 (positions 111-223 of P01857-1, v1)

<400> 174

```
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
1               5                  10                  15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            20                  25                  30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
        35                  40                  45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    50                  55                  60
```

```
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65                  70                  75                  80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                85                  90                  95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            100                 105                 110

Lys
```

<210> 175

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> CH3 IgG1 (positions 224-330 of P01857-1, v1)

<400> 175

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1               5                   10                  15

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                  90                  95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105
```

<210> 176

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> CH3 (D356E, L358M; positions numbered according to EU numbering)

<400> 176

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1               5                   10                  15

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45
```

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 177

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Ckappa CL (IGCK; UniProt: P01834-1, v2)

<400> 177

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 178

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 heavy chain SignalP

<400> 178

Met Lys Val Leu Ser Leu Leu Tyr Leu Leu Thr Ala Ile Pro Gly Ile
1 5 10 15

Leu Ser

<210> 179

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 heavy chain SignalP

<400> 179

```
Met Arg Val Leu Ile Leu Leu Cys Leu Phe Thr Ala Phe Pro Gly Ile
1               5                  10                  15

Leu Ser
```

<210> 180

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 light chain SignalP

<400> 180

```
Met Glu Ser Gln Thr Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser
1               5                  10                  15

Gly Val Asp Gly
            20
```

<210> 181

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 heavy chain SignalP

<400> 181

```
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Thr Gly
1               5                  10                  15

Val His Ser
```

<210> 182

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 light chain SignalP

<400> 182

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Met Ser Ala Ser
1               5                  10                  15

Val Met Met Ser Arg Gly
            20
```

<210> 183
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 heavy chain SignalP

<400> 183
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
1 5 10 15

Val Asn Ser

<210> 184
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-35-B4 light chain SignalP

<400> 184
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly
20

<210> 185
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92, 10D1_c93 heavy chain SignalP

<400> 185
Met Glu Leu Gly Leu Arg Trp Val Phe Leu Ile Ala Thr Leu Ala Gly
1 5 10 15

Ala Arg Cys

<210> 186
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c75, 10D1_c76, 10D1_c77, 10D1_c78v1, 10D1_c78v2, 10D1_11B, 10D1_c85v1, 10D1_c85v2, 10D1_c85o1, 10D1_c85o2, 10D1_c87, 10D1_c89, 10D1_c90, 10D1_c91, 10D1_c92,

10D1_c93 light chain SignalP

<400> 186

```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                  10                  15

Leu Arg Gly Ala Arg Cys
            20
```

<210> 187

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75 VH-CH1-CH2-CH3

<400> 187

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Thr Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 188

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c75 VL-Ckappa

<400> 188

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Leu Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30
```

```
Val Ala Trp Tyr Gln Met Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Phe Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 189

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76 VH-CH1-CH2-CH3

<400> 189

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80
```

65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

```
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 190

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c76 VL-Ckappa

<400> 190

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Gly Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Tyr Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Ala
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
```

```
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 191

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c77 VH-CH1-CH2-CH3

<400> 191

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu

        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 192

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c77 VL-Ckappa

<400> 192

```
Val Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Pro Asn
```

```
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Pro Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Gly Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Thr His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 193

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v1 VH-CH1-CH2-CH3

<400> 193

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60
```

```
Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
```

385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 194

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c78v2 VH-CH1-CH2-CH3

<400> 194

Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

- - - - - - - - - - - - - - -

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 195
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 10D1_c78v1, 10D1_c78v2, 10D1_11B VL-Ckappa

<400> 195

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Gly Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 196

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_11B VH-CH1-CH2-CH3

<400> 196

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45
```

```
Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Glu Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
```

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 197

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1 VH-CH1-CH2-CH3

<400> 197

Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

```
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 198

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v2 VH-CH1-CH2-CH3

<400> 198

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Glu Lys
```

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 199

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85v1, 10D1_c85v2 VL-Ckappa

<400> 199

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
35 40 45

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 200

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85o1 VH-CH1-CH2-CH3

<400> 200

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser

65                  70                  75                  80

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Glu Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
```

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 201

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85o1 VL-Ckappa

<400> 201

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 202

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85o2 VH-CH1-CH2-CH3

<400> 202

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Gly Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Gly Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
```

```
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 203

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c85o2 VL-Ckappa

<400> 203

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Arg Tyr Gln Tyr Ser Gly Val Pro Phe Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
```

```
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 204

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87 VH-CH1-CH2-CH3

<400> 204

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
```

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 205

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c87 VL-Ckappa

<400> 205

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Met Pro Gly Lys Ser Pro Glu Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Met Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 206

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89 VH-CH1-CH2-CH3

<400> 206

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Leu Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
```

```
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 207

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c89 VL-Ckappa

<400> 207

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
```

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 208

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c90 VH-CH1-CH2-CH3

<400> 208

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Phe Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Leu Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

```
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 209

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c90 VL-Ckappa

<400> 209

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Phe Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Ser Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Met Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Thr Thr His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 210

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 VH-CH1-CH2-CH3

<400> 210

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Tyr Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Leu Ala Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ala Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

```
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 211

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c91 VL-Ckappa

<400> 211

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Met Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Gly Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
```

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 212

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c92 VH-CH1-CH2-CH3

<400> 212

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Thr Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
```

```
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 213

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c92 VL-Ckappa

<400> 213

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Leu Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Met Lys Leu Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Phe Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Glu Tyr Phe Cys Gln Gln Tyr Phe Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 214

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c93 VH-CH1-CH2-CH3

<400> 214

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
```

```
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 215

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_c93 VL-Ckappa

<400> 215

```
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Leu Tyr Ser Asp Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Met Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
```

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 216

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 VH-CH1-CH2-CH3

<400> 216

Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

```
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 217

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 VL-Ckappa

<400> 217

```
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Ile Val Gly Ser Asn
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Ala
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Ser Ser His Pro Leu
                85                  90                  95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 218

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 VH-CH1-CH2-CH3

<400> 218

```
Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
            20                  25                  30

Asn Met Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45

Gly His Ile Asn Pro Tyr Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Phe
65                  70                  75                  80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Val Ser Leu Arg Trp Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His

    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
```

305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 219

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B2 VL-Ckappa

<400> 219

Gln Ile Val Leu Thr Gln Ser Pro Ala Leu Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Asn Ser Asn Pro Tyr Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

```
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210
```

<210> 220

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 VH-CH1-CH2-CH3

<400> 220

```
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
            20                  25                  30

Tyr Ile His Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Lys Ile Ile Asp Pro Ala Asn Gly Asn Thr Asn Tyr Asp Pro Lys
    50                  55                  60

Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala
65                  70                  75                  80

Tyr Leu Gln Leu Ser Ser Leu Ser Ser Glu Asp Thr Ala Val Tyr Phe
                85                  90                  95

Cys Ala Arg Gly Leu His Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
            100                 105                 110

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
        115                 120                 125

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
    130                 135                 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145                 150                 155                 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
                165                 170                 175
```

```
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
            180                 185                 190

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
        195                 200                 205

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
    210                 215                 220

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
            340                 345                 350

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 221

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-35-B4 VL-Ckappa

<400> 221

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95

Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 222

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 VH-CH1-CH2-CH3

<400> 222

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Asn Phe Ile Thr Ser Gly
            20                  25                  30
```

```
Tyr Phe Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Phe Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Lys Pro Ser Leu
    50                  55                  60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asn Tyr Gly Phe Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350
```

```
                 ---                 ---                 ---

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 223

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> 10A6 VL-Ckappa

<400> 223

```
Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Pro Val Ser Ile Gly
1               5                   10                  15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
            20                  25                  30

Asp Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Trp Lys Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

Tyr Phe Thr Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160
```

```
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 224

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1_11B heavy chain FR1

<400> 224

```
Asp Val Gln Leu Gln Glu Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Tyr
            20                  25
```

<210> 225

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1F.FcA VH-CH1-CH2-CH3 (GASDALIE; LCKC) (10D1F.FcB)

<400> 225

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Leu Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
```

```
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Ala Gly
225                 230                 235                 240

Pro Asp Val Phe Cys Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Leu Pro Glu Glu
                325                 330                 335

Cys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
```

```
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 226

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1F.FcA VH-CH1-CH2-CH3 (N297Q)

<400> 226

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Ser Ile Arg Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Leu Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Trp Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
```

```
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 227

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 VH-CH1-CH2-CH3 (GASDALIE; LCKC)

<400> 227

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Glu Asn Lys Leu Glu Trp
```

```
Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Ala Gly
225                 230                 235                 240

Pro Asp Val Phe Cys Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Leu Pro Glu Glu
                325                 330                 335

Cys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
```

```
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 228

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 VH-CH1-CH2-CH3 (GASD)

<400> 228

```
Asp Val Gln Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Ser Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95

Ala Arg Met Thr Thr Ala Pro Arg Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
```

145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Ala Gly
225 230 235 240

Pro Asp Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 229

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> HER3 binding site for 10D1-derived clones

<400> 229

```
Cys Phe Gly Pro Asn Pro Asn Gln Cys Cys His Asp Glu Cys Ala Gly
1               5                  10                  15

Gly Cys
```

<210> 230

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 binding site motif 1

<400> 230

```
Pro Asn Pro Asn Gln
1               5
```

<210> 231

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 10D1 binding site motif 2

<400> 231

```
Asp Glu Cys Ala Gly
1               5
```

REFERENCES CITED IN THE DESCRIPTION

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Patentkrav

1. Isoleret antigenbindende molekyle, som kan binde til HER3, hvor det antigenbindende molekyle omfatter:
(i) en tungkæde-variabel (VH) region, der indbefatter følgende CDR'er:
HC-CDR1 med aminosyresekvensen SEQ ID NO:41
HC-CDR2 med aminosyresekvensen SEQ ID NO:45
HC-CDR3 med aminosyresekvensen SEQ ID NO:48; og
(ii) en letkæde-variabel (VL) region, der indbefatter følgende CDR'er:
LC-CDR1 med aminosyresekvensen SEQ ID NO:88
LC-CDR2 med aminosyresekvensen SEQ ID NO:92
LC-CDR3 med aminosyresekvensen SEQ ID NO:95.

2. Antigenbindende molekyle ifølge krav 1, hvor det antigenbindende molekyle omfatter:
en VH-region, der omfatter en aminosyresekvens, der har mindst 70 % sekvensidentitet med aminosyresekvensen SEQ ID NO:36; og
en VL-region, der omfatter en aminosyresekvens, der har mindst 70 % sekvensidentitet med aminosyresekvensen SEQ ID NO:83.

3. Antigenbindende molekyle ifølge krav 1 eller krav 2, hvor det antigenbindende molekyle omfatter:
en VH-region, der indbefatter følgende framework-regioner (FR'er):
HC-FR1 med aminosyresekvensen SEQ ID NO:53
HC-FR2 med aminosyresekvensen SEQ ID NO:59
HC-FR3 med aminosyresekvensen SEQ ID NO:66
HC-FR4 med aminosyresekvensen SEQ ID NO:71.

4. Antigenbindende molekyle ifølge et hvilket som helst af kravene 1 til 3, hvor det antigenbindende molekyle omfatter:
en VL-region, der indbefatter følgende framework-regioner (FR'er):
LC-FR1 med aminosyresekvensen SEQ ID NO:104
LC-FR2 med aminosyresekvensen SEQ ID NO:110
LC-FR3 med aminosyresekvensen SEQ ID NO:120
LC-FR4 med aminosyresekvensen SEQ ID NO:125.

5. Antigenbindende molekyle ifølge et hvilket som helst af kravene 1 til 4, hvor det antigenbindende molekyle omfatter den konstante tungkæde-sekvens med SEQ ID NO:171.

6. Antigenbindende molekyle ifølge et hvilket som helst af kravene 1 til 5, hvor det antigenbindende molekyle omfatter den konstante letkæde-sekvens med SEQ ID NO:177.

7. Isoleret nukleinsyre eller en flerhed af isolerede nukleinsyrer, der koder for et antigenbindende molekyle ifølge et hvilket som helst af kravene 1 til 6.

8. Ekspressionsvektor eller en flerhed af ekspressionsvektorer, der omfatter en nukleinsyre eller en flerhed af nukleinsyrer ifølge krav 7.

9. Celle omfattende et antigenbindende molekyle ifølge et hvilket som helst af kravene 1 til 6, en nukleinsyre eller en flerhed af nukleinsyrer ifølge krav 7 eller en ekspressionsvektor eller en flerhed af ekspressionsvektorer ifølge krav 8.

10. Fremgangsmåde, der omfatter dyrkning af en celle, der omfatter en nukleinsyre eller en flerhed af nukleinsyrer ifølge krav 7 eller en ekspressionsvektor eller en flerhed af ekspressionsvektorer ifølge krav 8, under betingelser, der er egnede til ekspression af det antigenbindende molekyle fra nukleinsyren (nukleinsyrerne) eller ekspressionsvektoren (ekspressionsvektorerne).

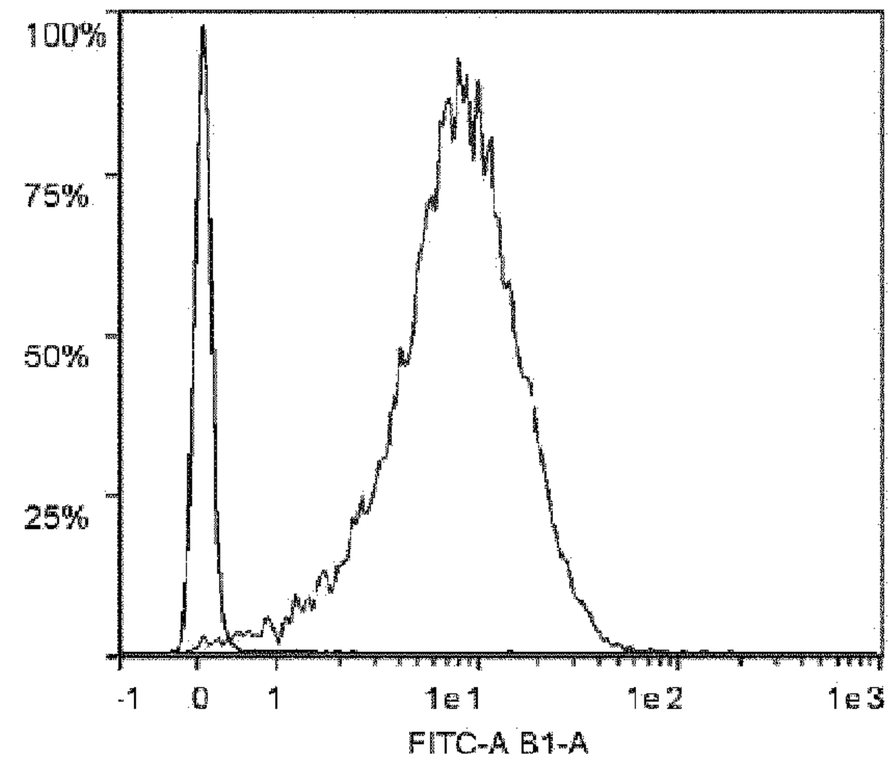
11. Antigenbindende molekyle ifølge et hvilket som helst af kravene 1 til 6, nukleinsyre eller en flerhed af nukleinsyrer ifølge krav 7, ekspressionsvektor eller en flerhed af ekspressionsvektorer ifølge krav 8 eller celle ifølge krav 9 til anvendelse i en fremgangsmåde til behandling eller forebyggelse af en cancer.

12. Antigenbindende molekyle, nukleinsyre eller flerhed af nukleinsyrer, ekspressionsvektor eller flerhed af ekspressionsvektorer, eller celle til anvendelse ifølge krav 11, hvor canceren er udvalgt blandt: en HER3-eksprimerende cancer, gastrisk cancer, hoved- og halscancer, brystcancer, ovariecancer, lungecancer, melanom, prostatacancer, cancer i mundhulen, nyrecancer,

kolorektal cancer, øsofaguscancer, pancreascancer, en fast cancer og en hæmatologisk cancer.

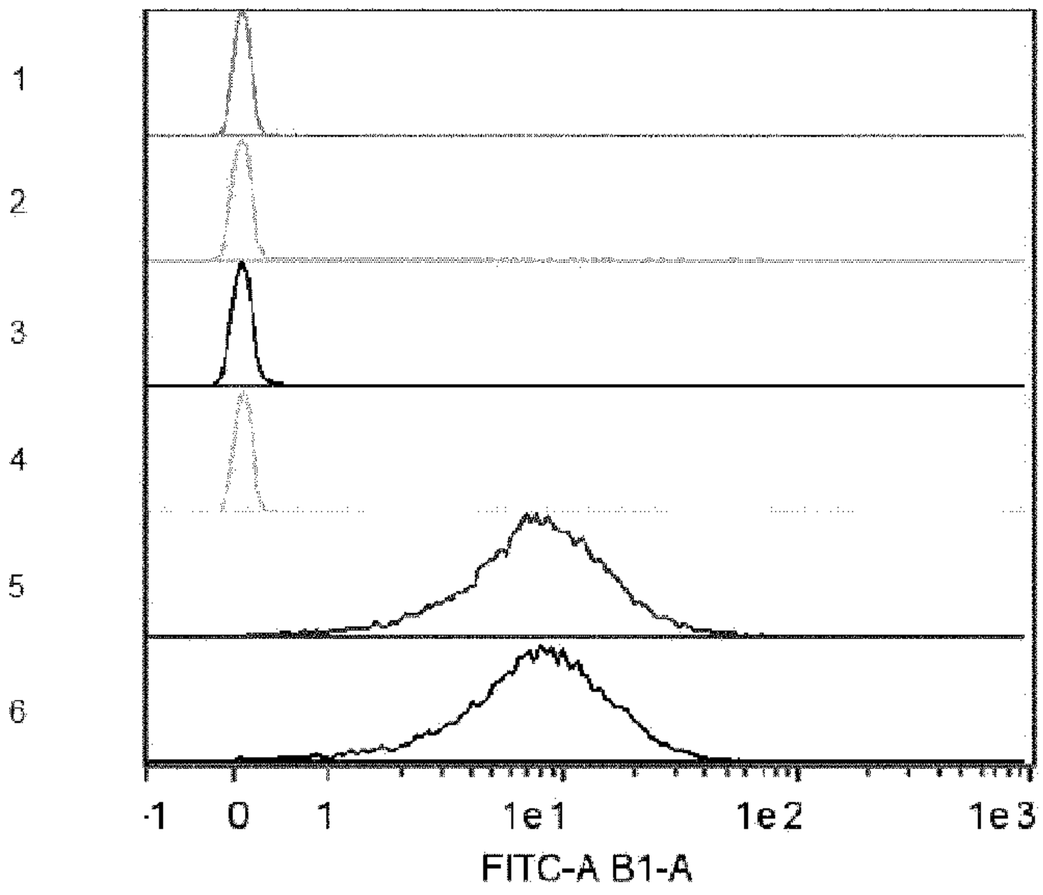
13. Fremgangsmåde til detektering af HER3, omfattende at bringe en prøve, der indeholder, eller mistænkes for at indeholde, HER3, i kontakt med et antigenbindende molekyle ifølge et hvilket som helst af kravene 1 til 6 *in vitro,* og at detektere dannelsen af et kompleks af det antigenbindende molekyle med HER3.

DRAWINGS



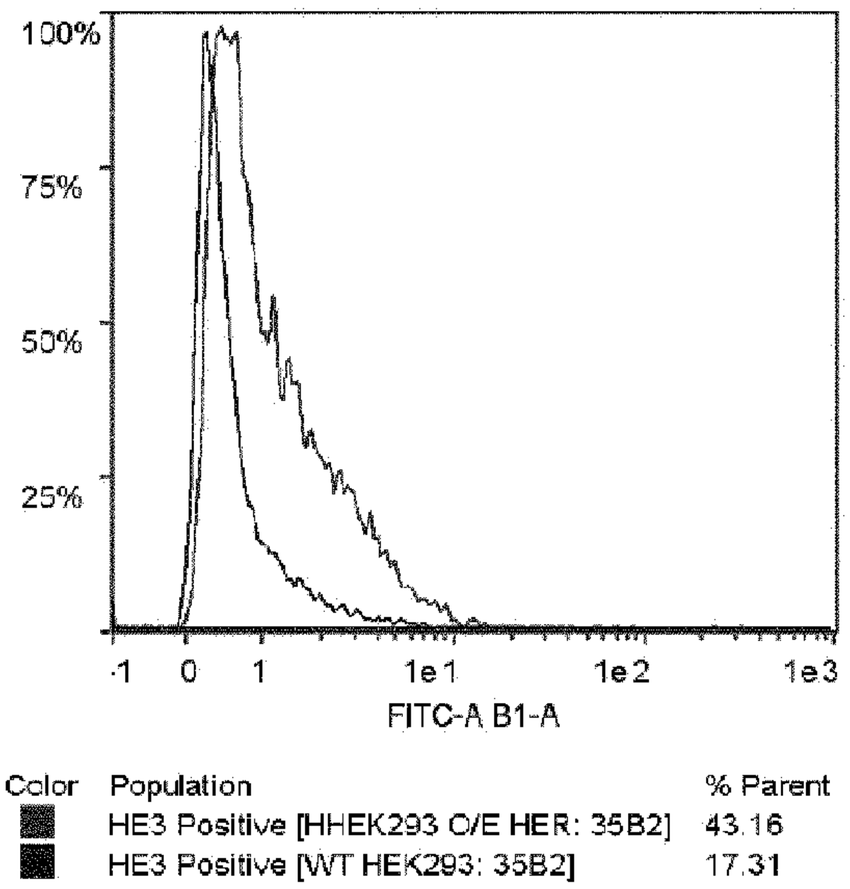
Color	Population	% Parent
■	HER 3 positive [HEK293 O/E H3: 10D1]	98.98
■	HER 3 positive [WT HEK293 :10D1]	0.60

Figure 1A



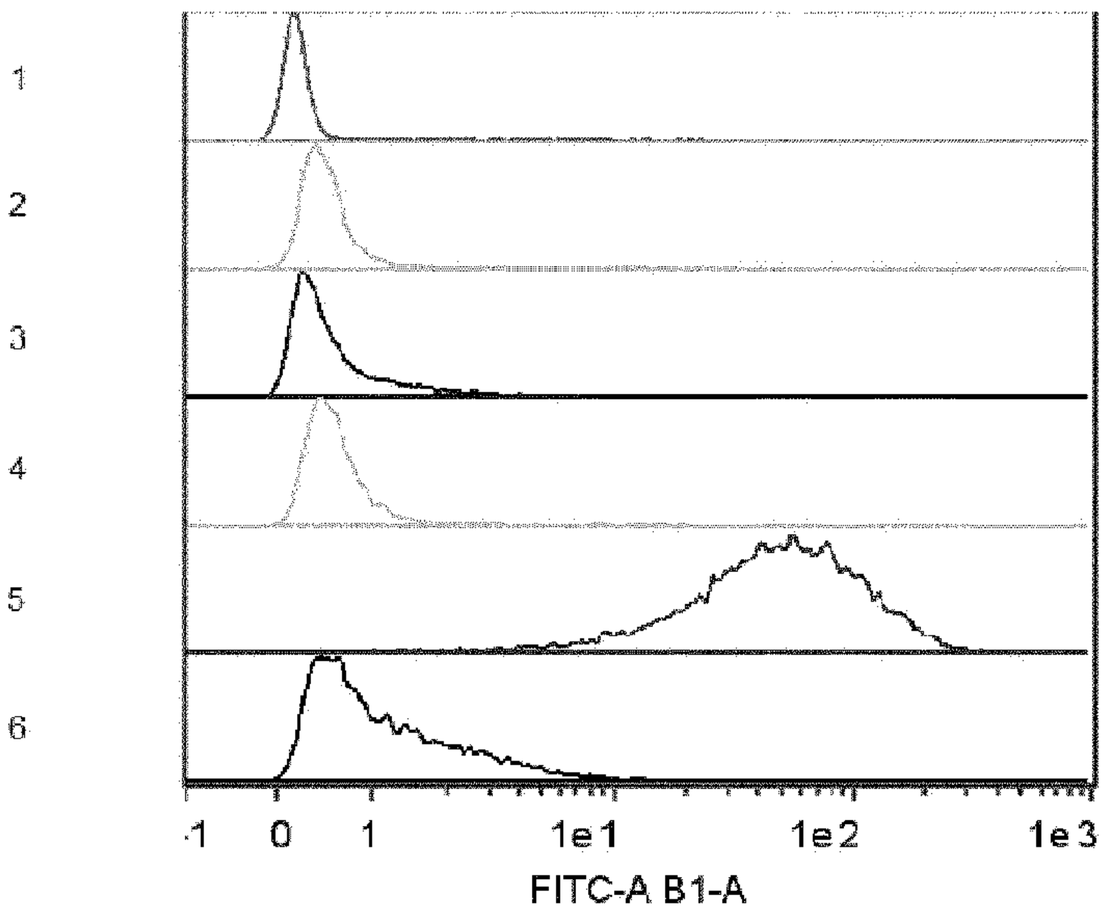
	Color	Population	% Parent
1	■	HER3 positive [WT HEK293: Isotype]	0.07
2	■	HER3 positive [WT HEK293: LJM716]	1.91
3	■	HER3 positive [WT HEK293: 10D1]	0.60
4	■	HER3 positive [HEK293 O/E H3: Isotyppe]	0.12
5	■	HER3 positive [HEK293 O/E H3: LJM716]	99.46
6	■	HER3 positive [HEK293 O/E H3: 10D1]	98.98

Figure 1B



Color	Population	% Parent
	HE3 Positive [HHEK293 O/E HER: 35B2]	43.16
	HE3 Positive [WT HEK293: 35B2]	17.31

Figure 2A



	Color	Population	% Parent
1		HE3 Positive [WT HEK293: Isotype]	1.68
2		HE3 Positive [WT HEK293: LJM716]	8.15
3		HE3 Positive [WT HEK293: 35B2]	17.31
4		HE3 Positive [HEK293 O/E HER: Isotype]	13.90
5		HE3 Positive [HEK293 O/E HER: LJM716]	98.65
6		HE3 Positive [HHEK293 O/E HER: 35B2]	43.16

Figure 2B

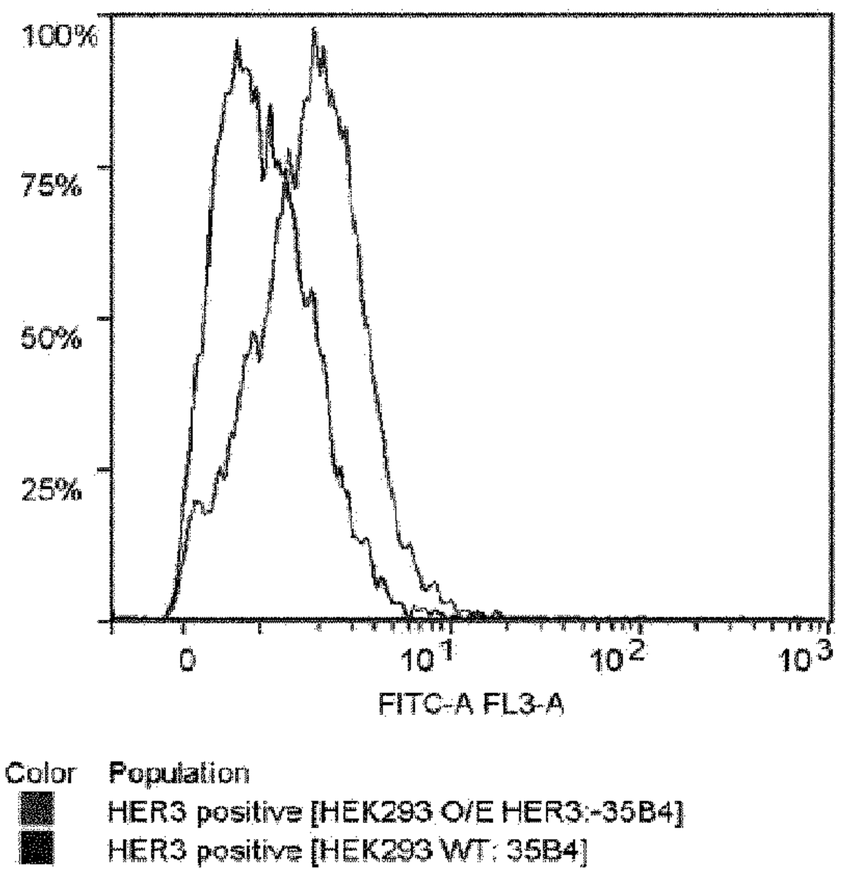
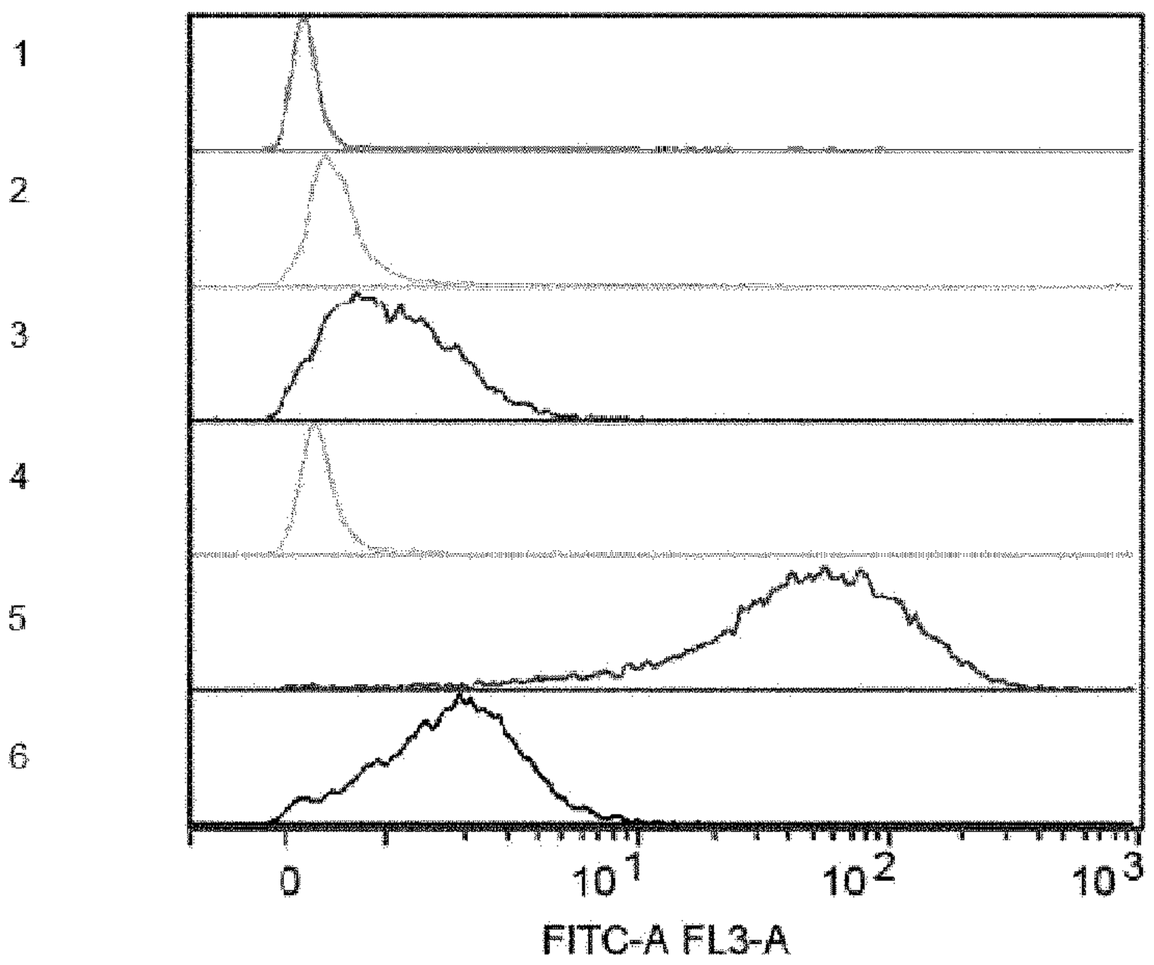


Figure 3A



	Color	Population
1		HEK293 WT: Isotype
2		HEK293 WT: LJM716
3		HEK293 WT: 35B4
4		HEK293 O/E HER3: Isotype
5		HEK293 O/E HER3: LJM716
6		HEK293 O/E HER3:-35B4

Figure 3B

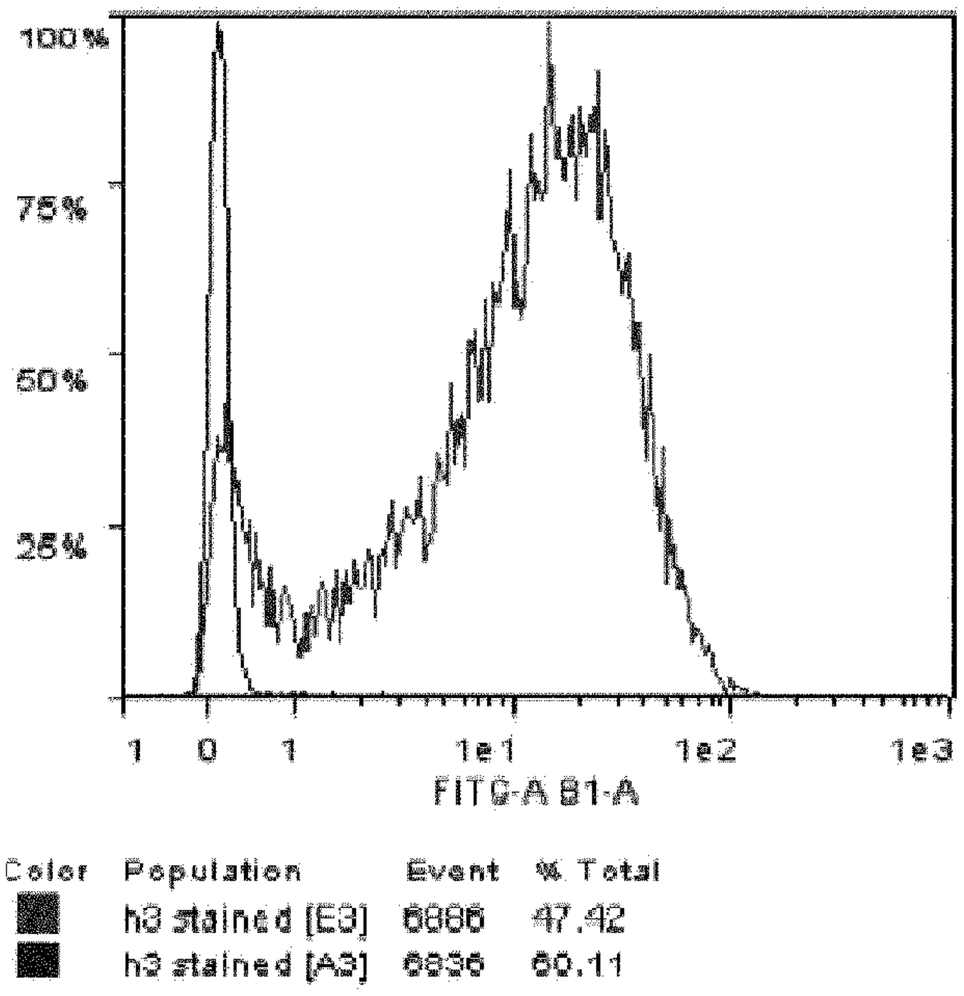
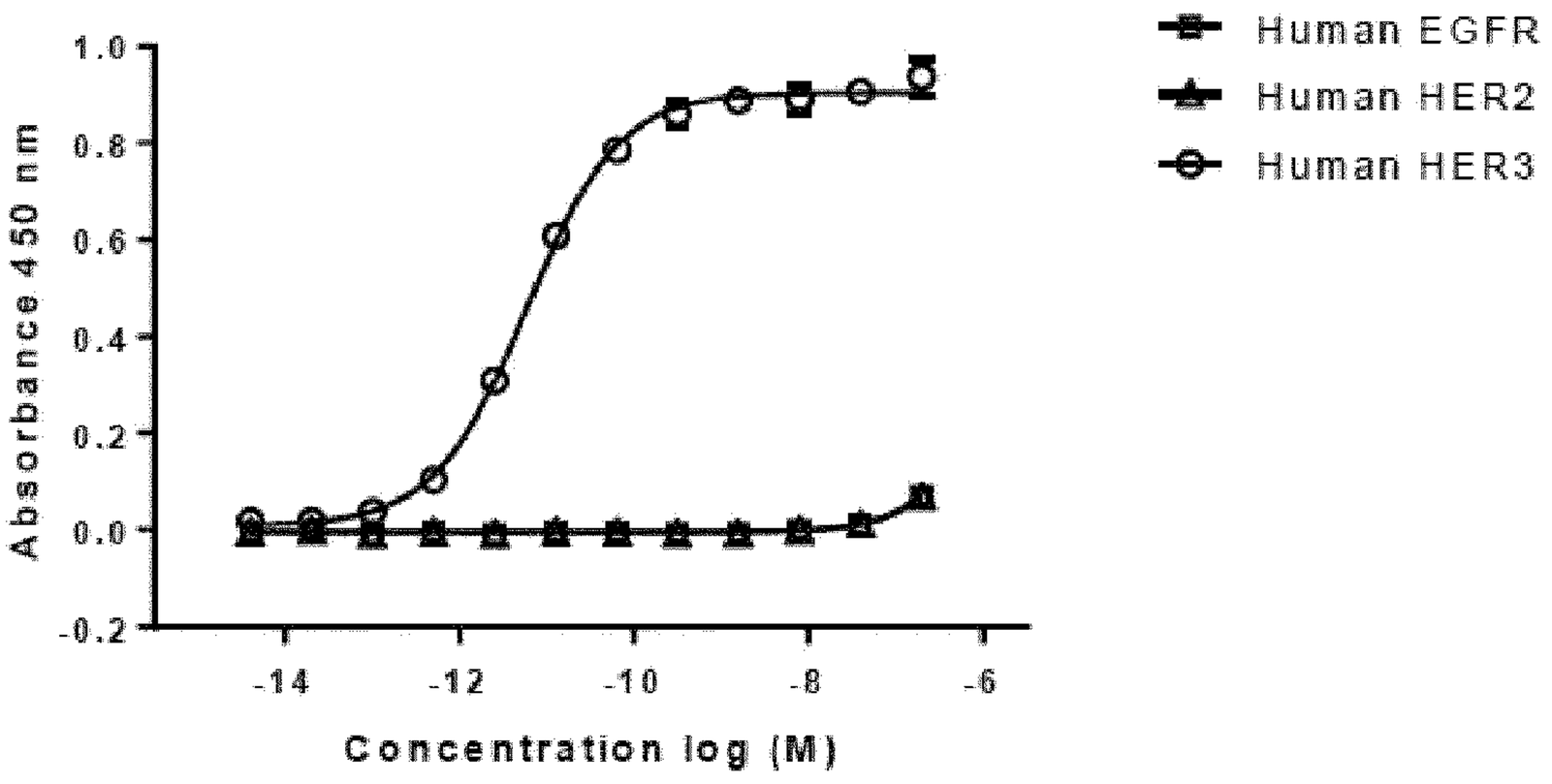
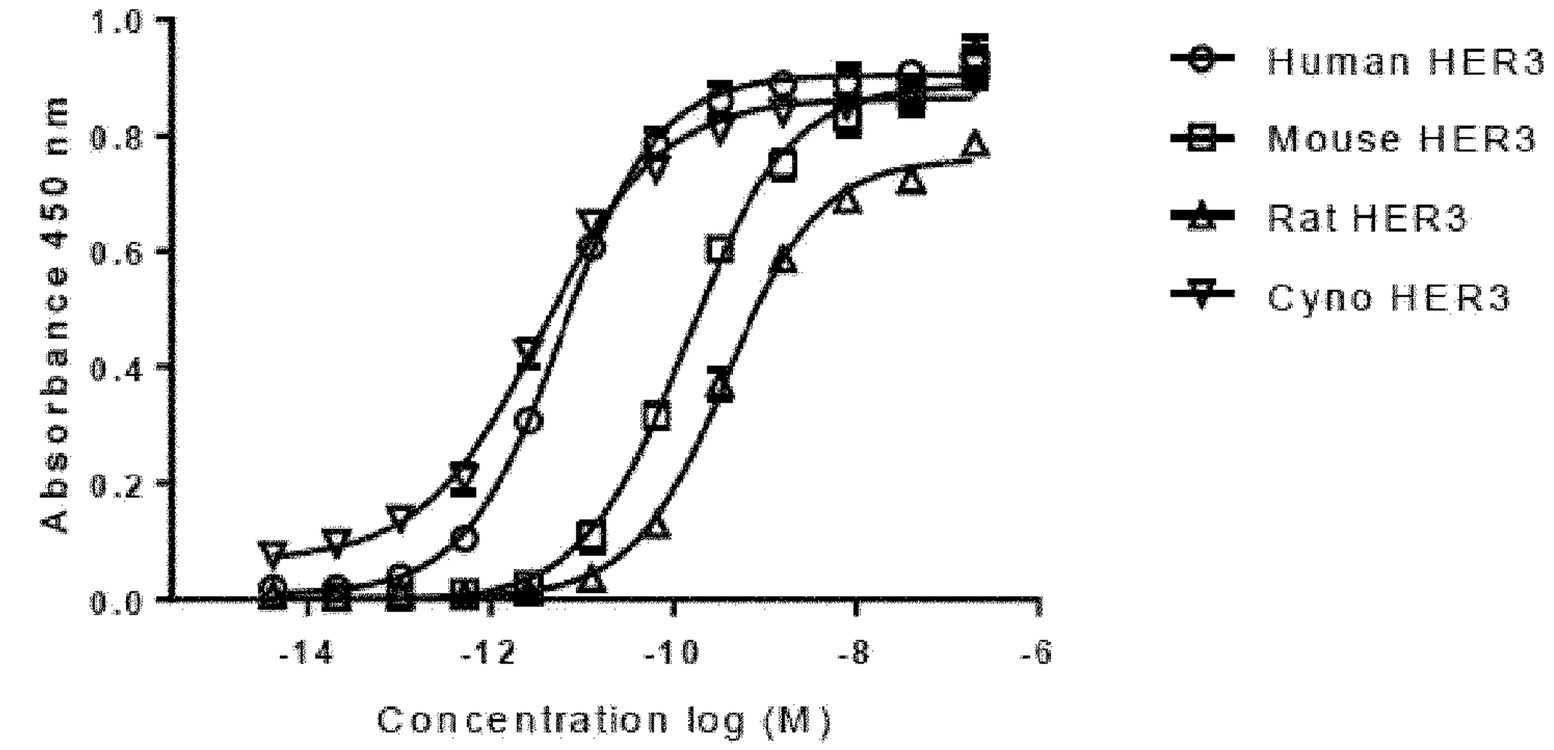


Figure 4



	Human EGFR	Human HER2	Human HER3
EC_{50} (M)	NA	NA	5.88E-12

Figure 5A



	Human HER3	Mouse HER3	Rat HER3	Cyno HER3
EC_{50} (M)	5.88E-12	1.37E-10	3.72E-10	3.68E-12

Figure 5B

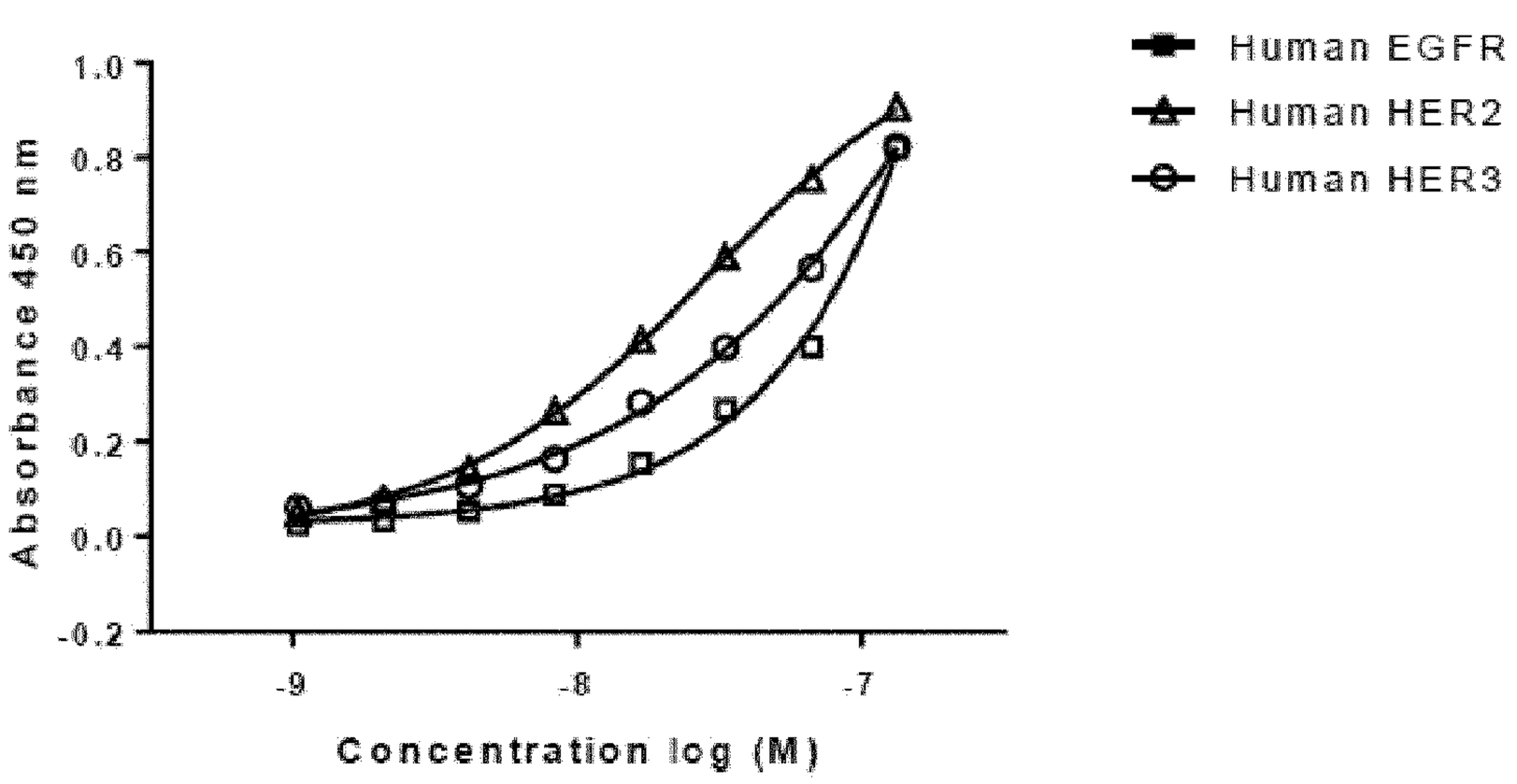


Figure 6A

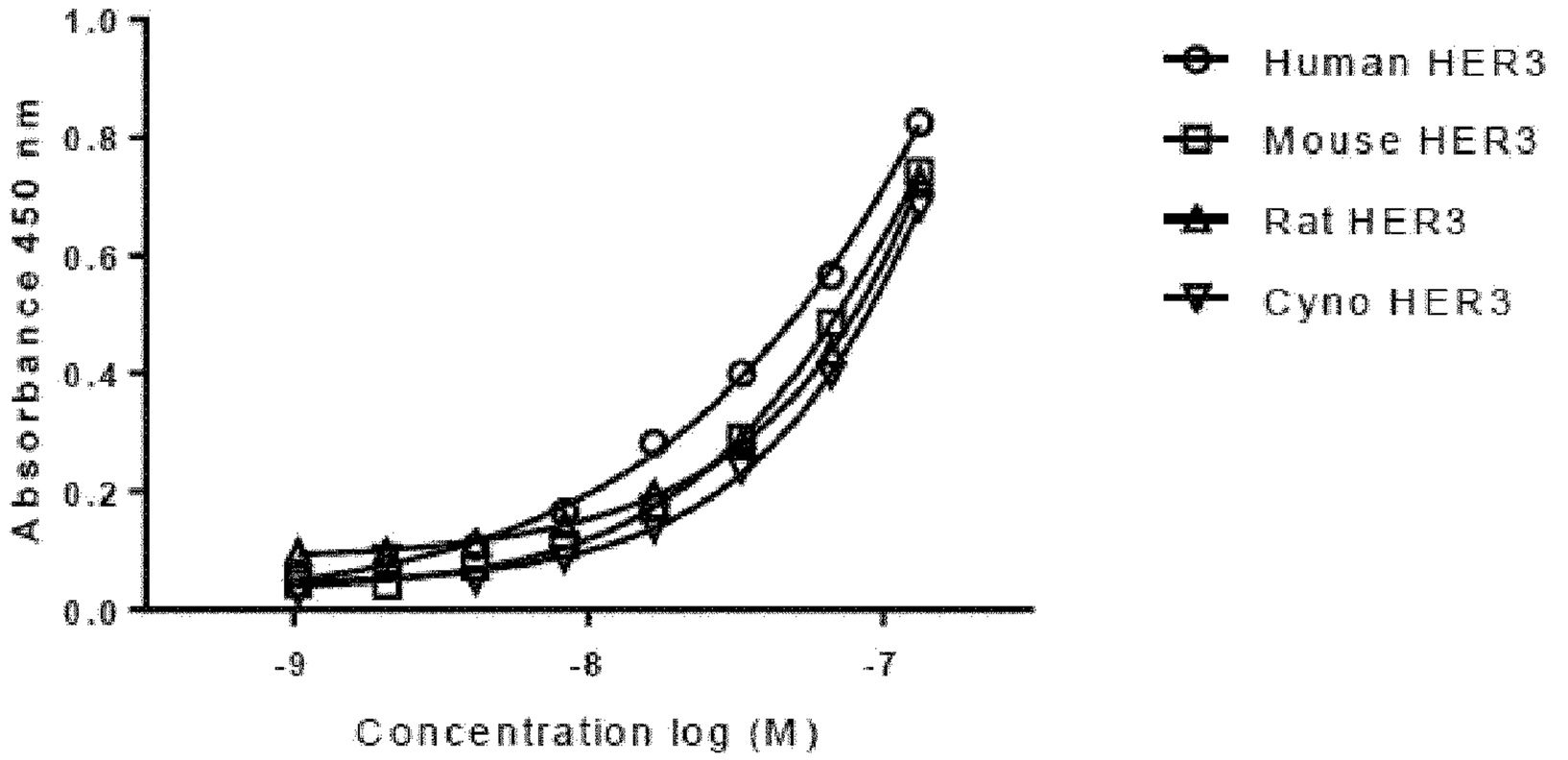


Figure 6B

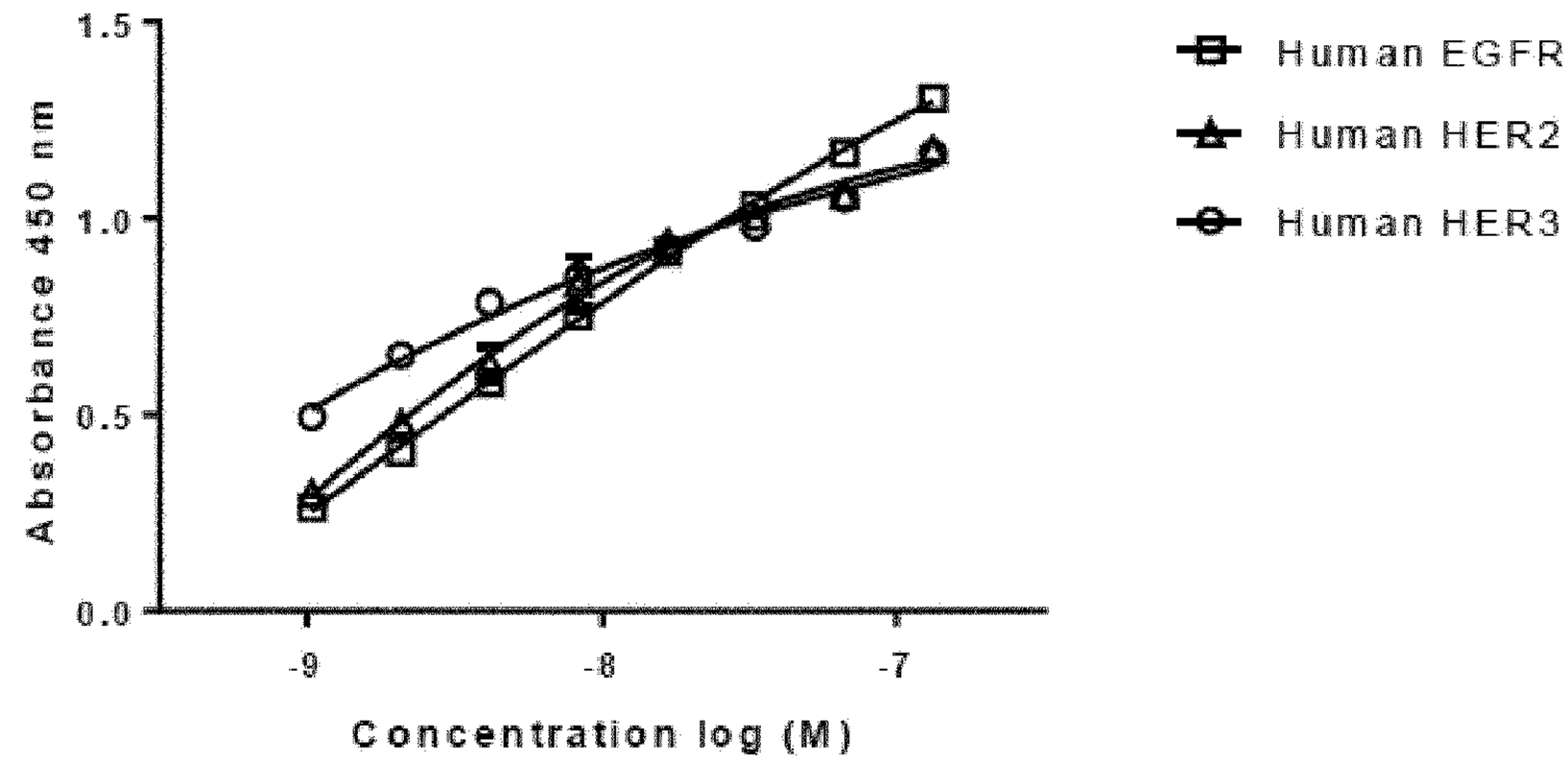


Figure 7A

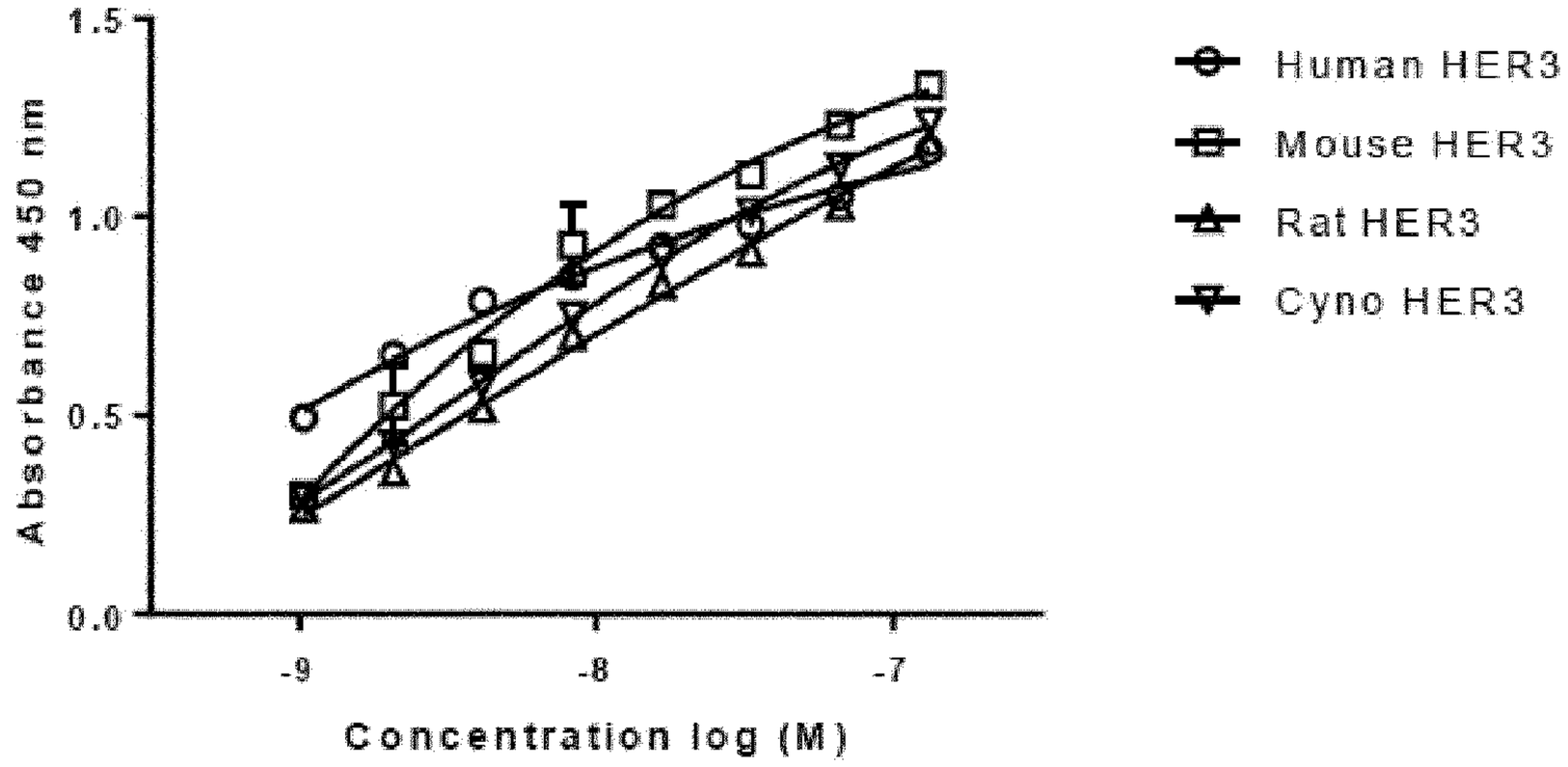
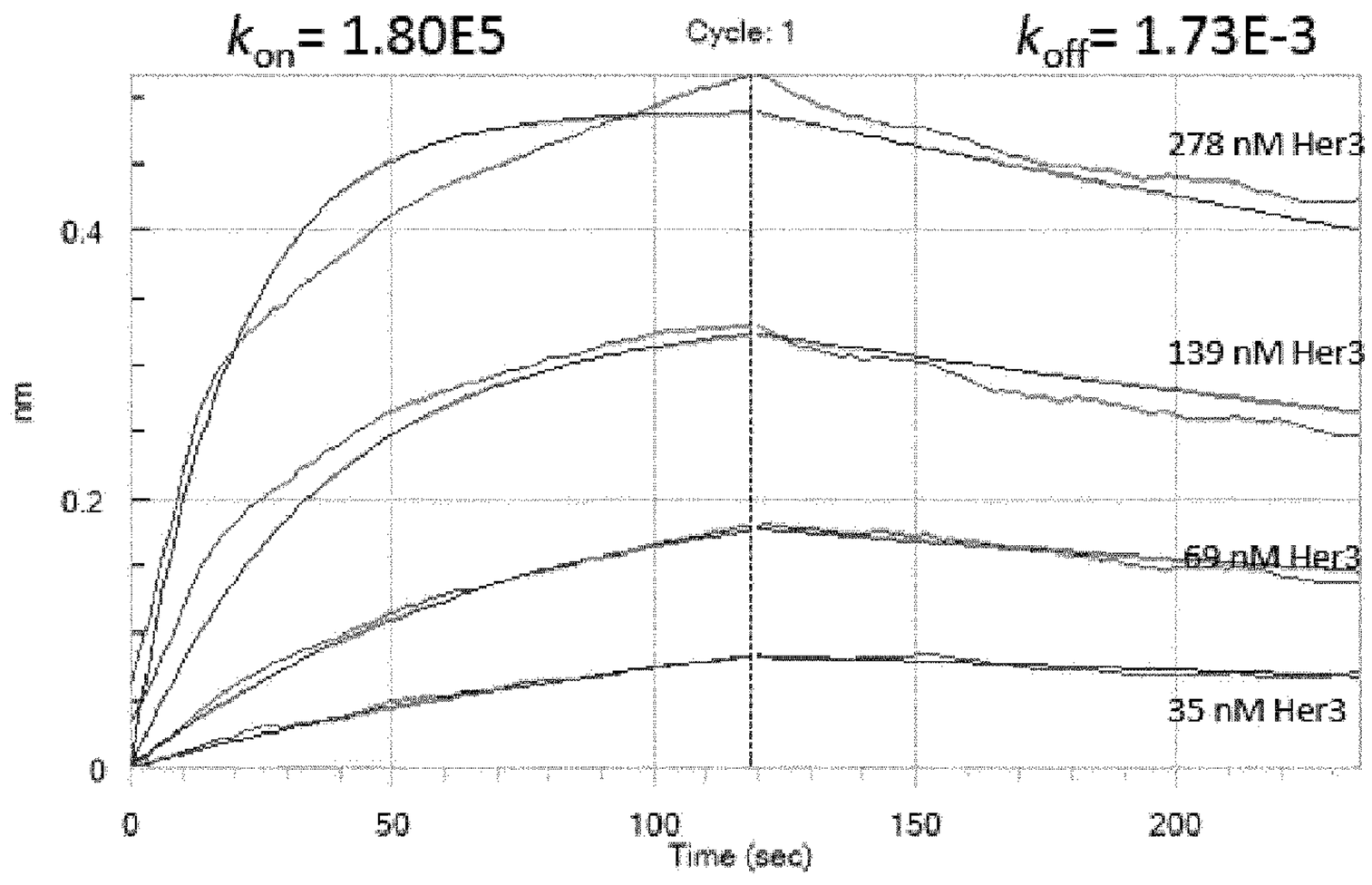

Absorbance 450 nm
1.5
1.0
0.5
0.0
-9
-8
-7
Concentration log (M)
Human HER3
Mouse HER3
Rat HER3
Cyno HER3

Figure 7B



k_d= 9.58 nM

R^2 = 0.9898

Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
10D1p	1	278	0.5079	9.58E-09	9.70E-10	1.80E+05	8.22E+03	1.73E-03	1.56E-04	0.5055	0.0063	5.18E-02	0.4886	96.7	0.0301	0.9898
10D1p	1	35	0.0794	9.58E-09	9.70E-10	1.80E+05	8.22E+03	1.73E-03	1.56E-04	0.1718	0.01	8.03E-03	0.1348	78.5	0.0301	0.9898
10D1p	1	139	0.3278	9.58E-09	9.70E-10	1.80E+05	8.22E+03	1.73E-03	1.56E-04	0.359	0.0076	2.68E-02	0.3359	93.5	0.0301	0.9898
10D1p	1	69	0.1744	9.58E-09	9.70E-10	1.80E+05	8.22E+03	1.73E-03	1.56E-04	0.2471	0.0089	1.42E-02	0.2169	87.8	0.0301	0.9898

Figure 8

DK/EP 3645571 T3

Kd = 8.09E-08

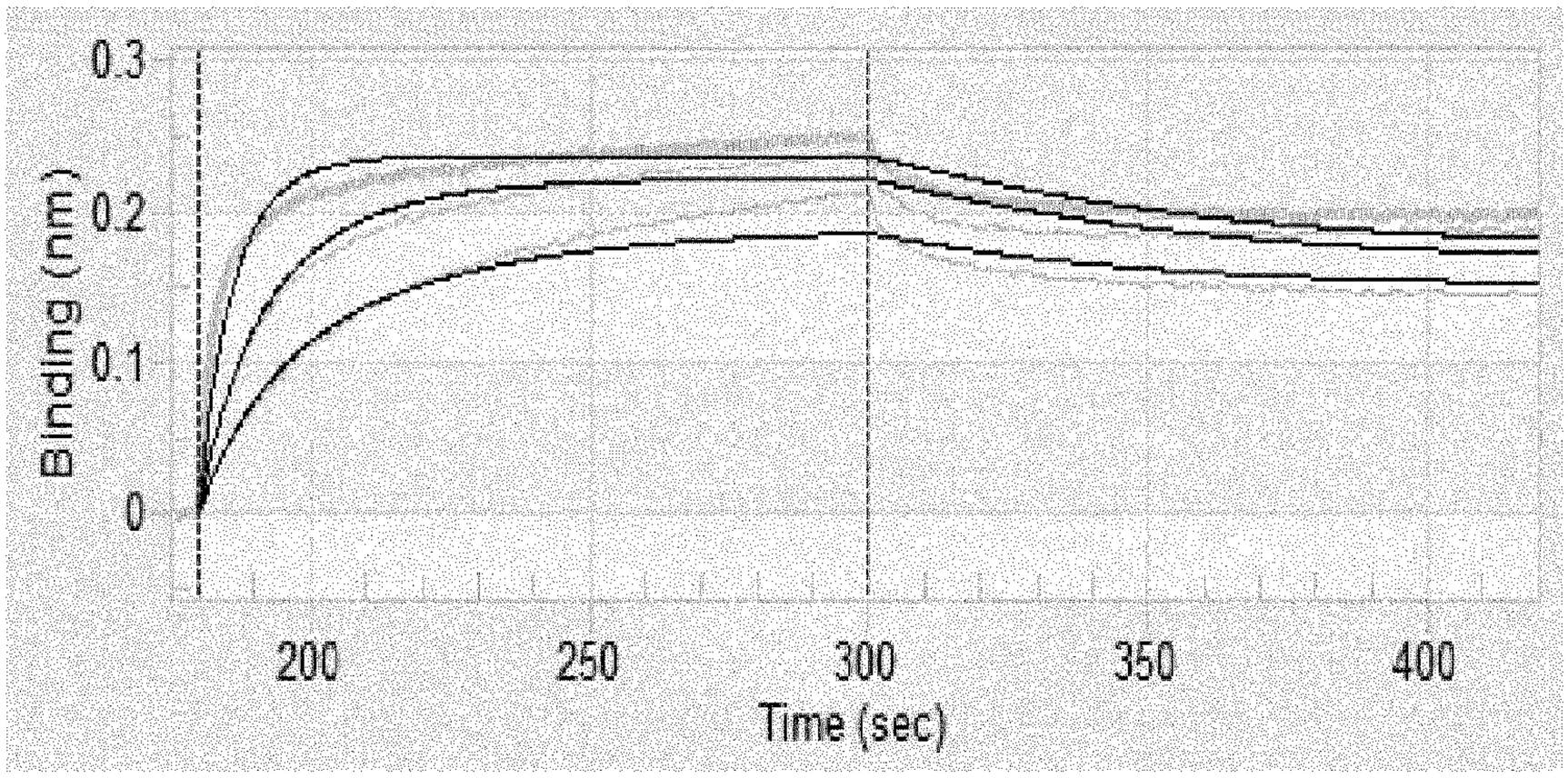


Figure 9

Kd = 5.03E-08

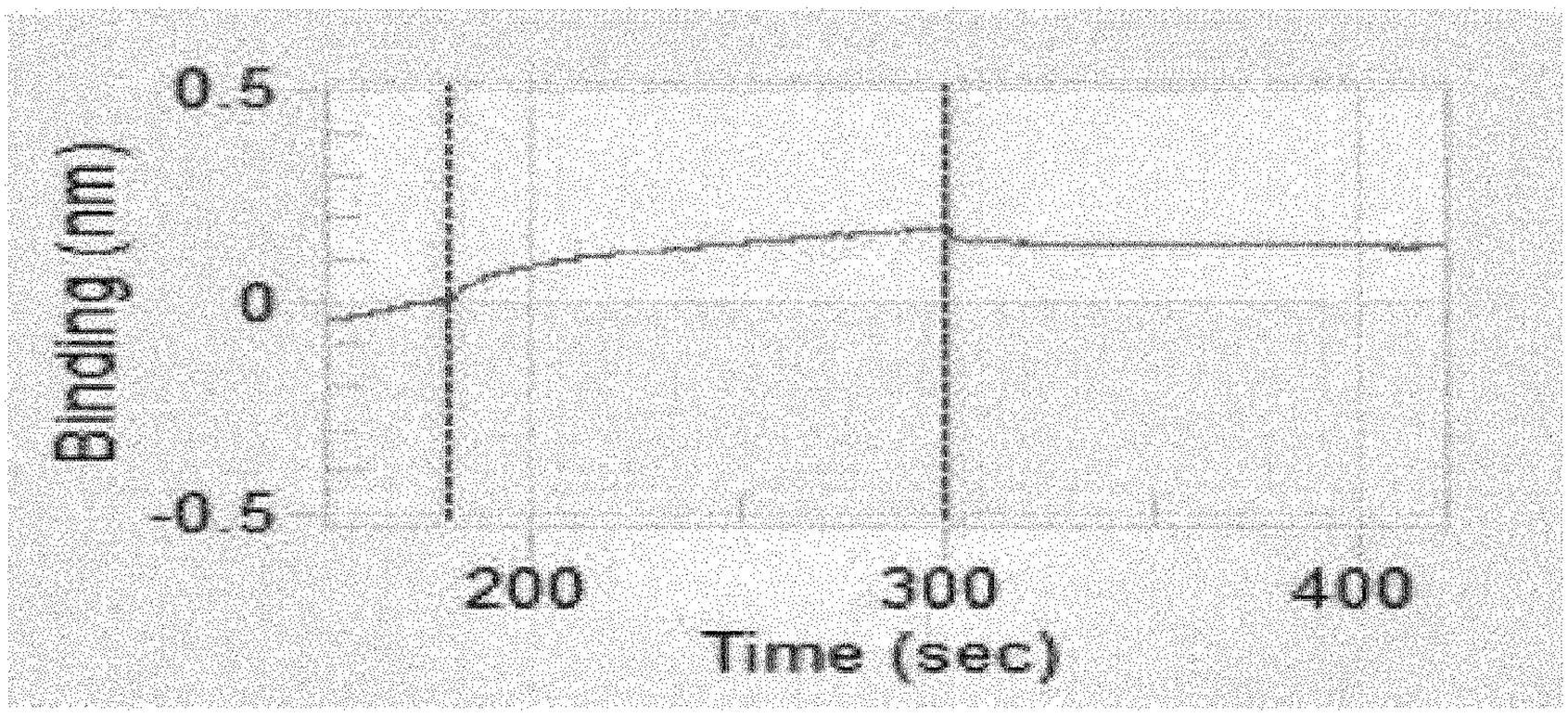


Figure 10

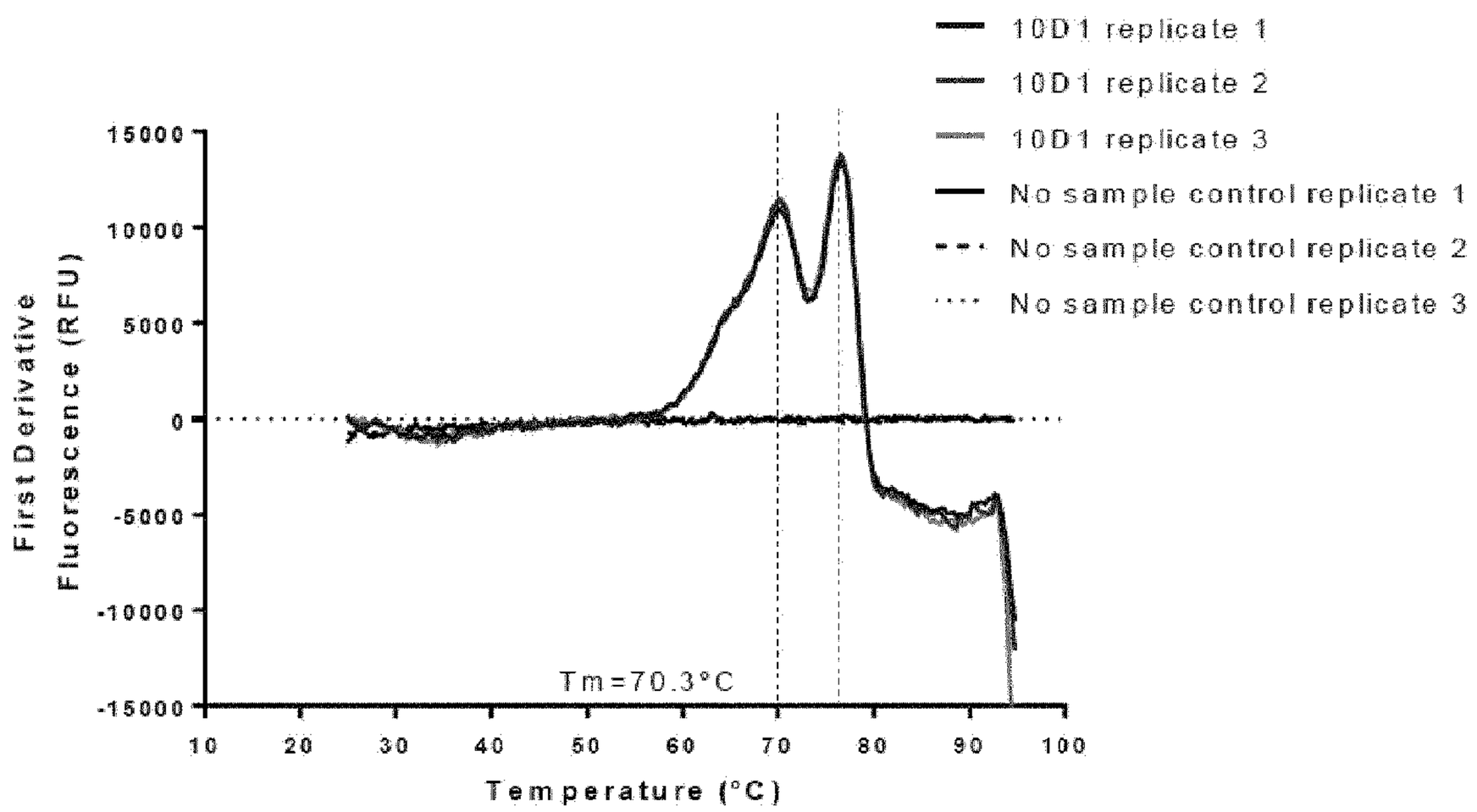


Figure 11

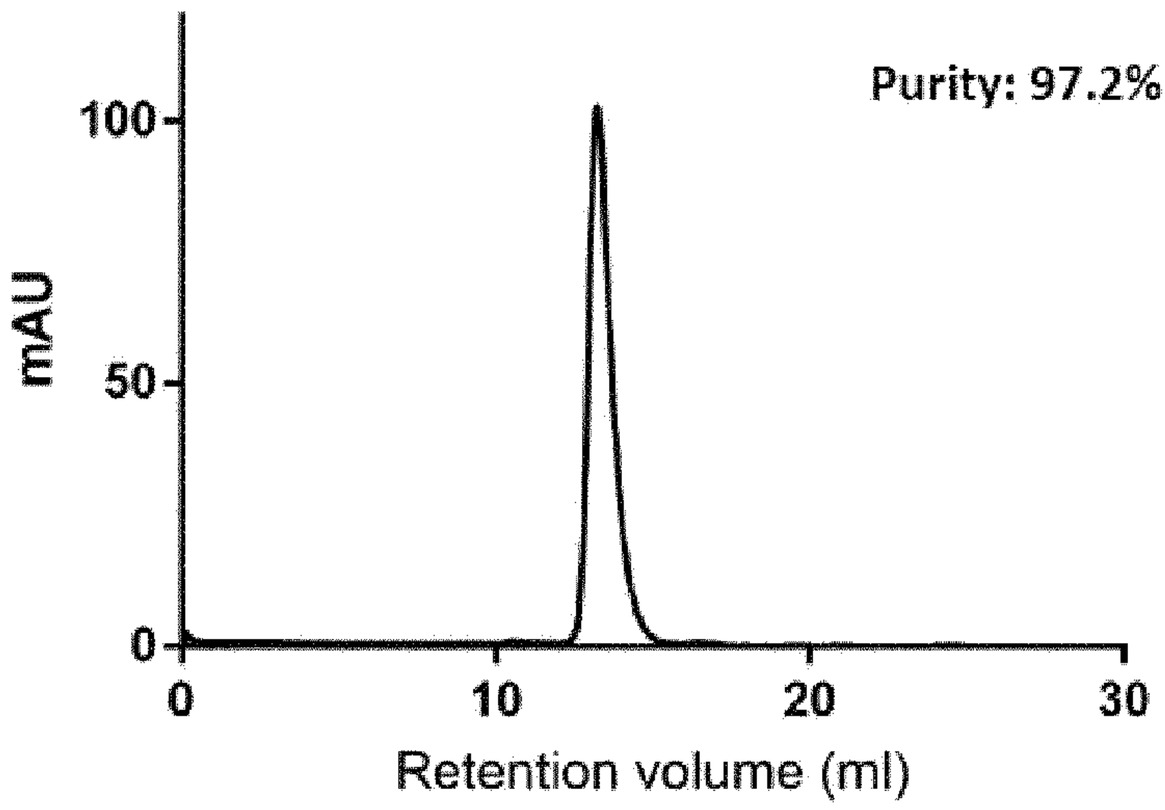


Figure 12

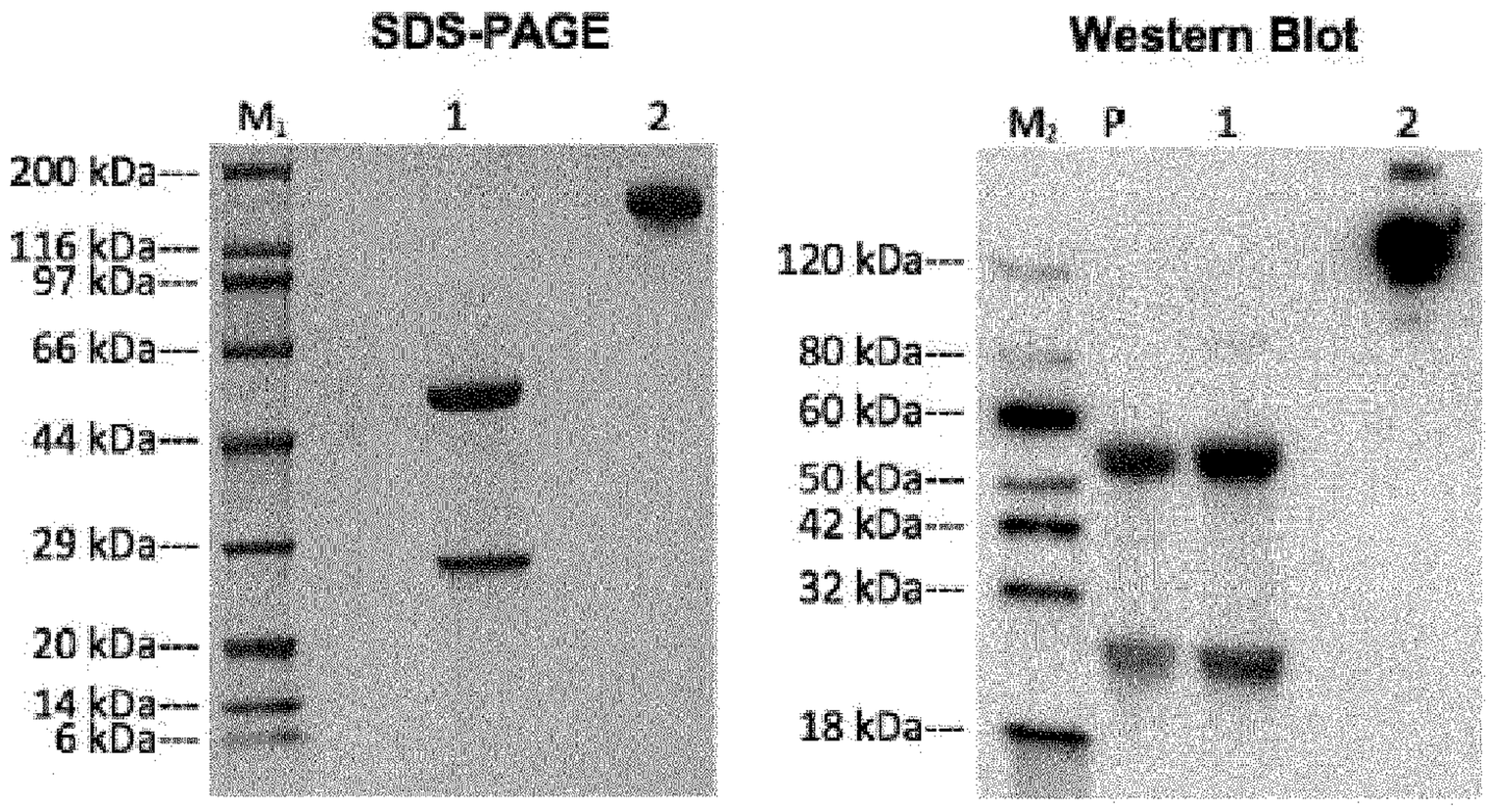

SDS-PAGE
M1
1
2
200 kDa
116 kDa
97 kDa
66 kDa
44 kDa
29 kDa
20 kDa
14 kDa
6 kDa
Western Blot
M2
P
1
2
120 kDa
80 kDa
60 kDa
50 kDa
42 kDa
32 kDa
18 kDa

Figure 13

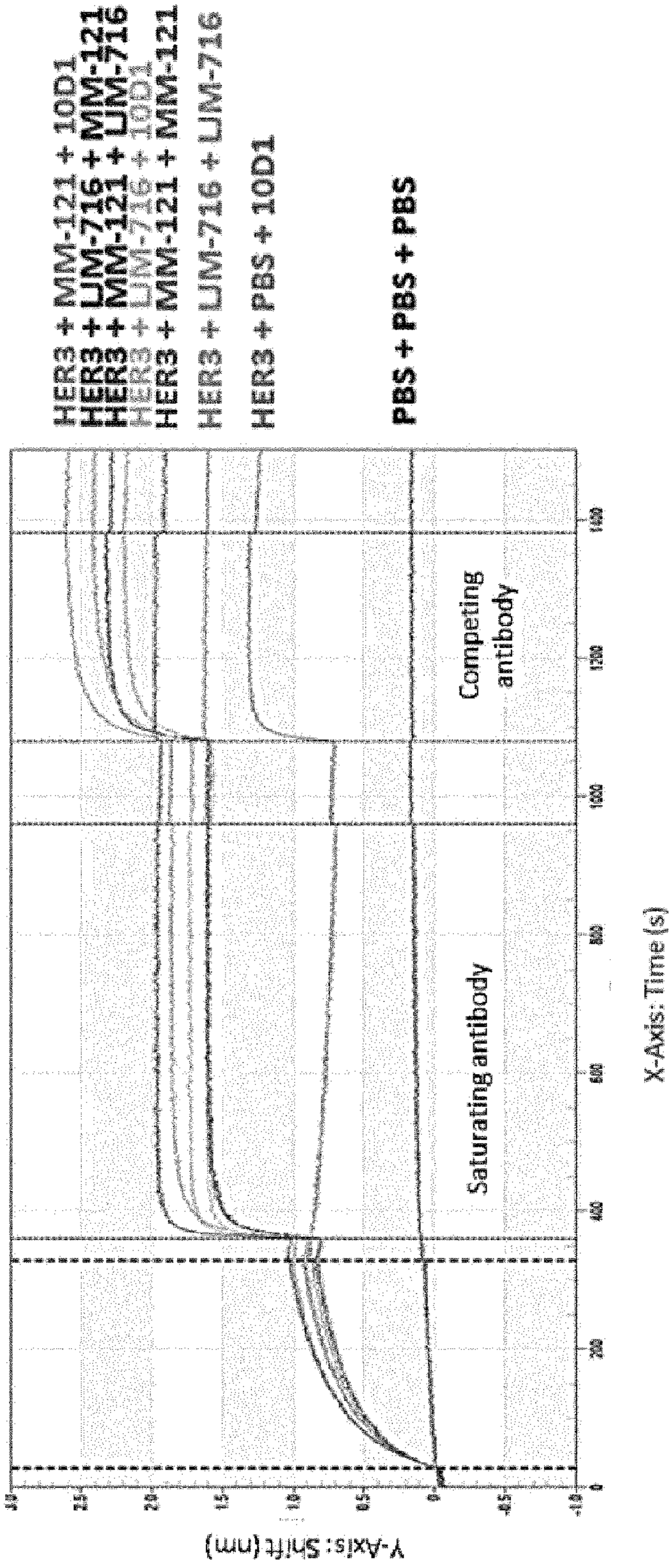

HER3 + MM-121 + 10D1
HER3 + + UM-716 + + MM-121
HER3 + + MM-121 + + UM-716
HER3 + + UM-716 + + 10D1
HER3 + + MM-121 + MM-121
HER3 + + UM-716 + UM-716
HER3 + + PBS + 10D1
PBS + PBS + PBS
Competing antibody
Saturating antibody
1400
1200
1000
800
600
400
200
0
3.0
2.5
2.0
1.5
1.0
0.5
0
-0.5
-1.0
X-Axis: Time (s)
Y-Axis: Shift (nm)

Figure 14A

		Competing Antibody		
		10D1	MM-121	UM-716
Saturating Antibody	10D1	x	x	x
	MM-121	0.757	x	0.729
	UM-716	0.638	0.693	x

Figure 14B

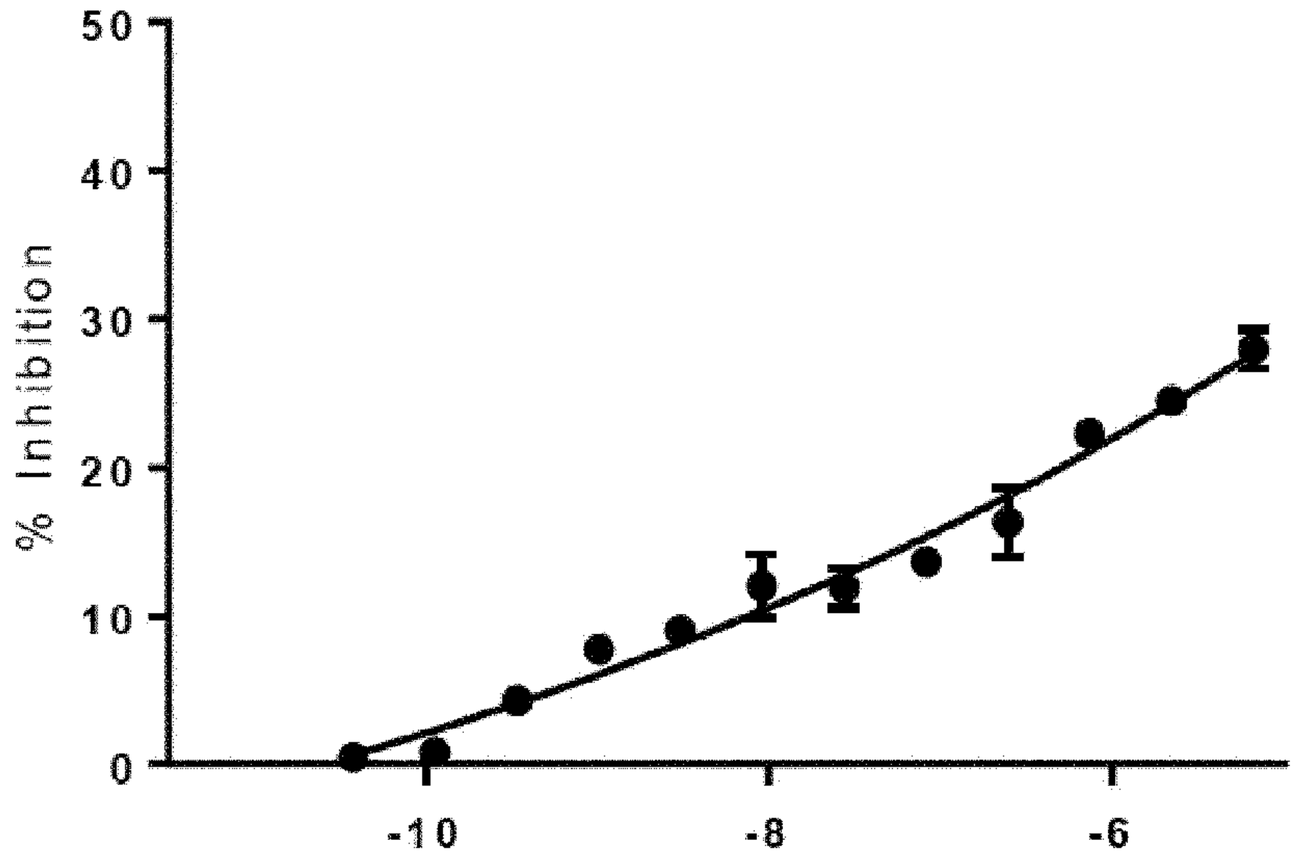


Figure 15

Solid Tumor	Cell Line	mRNA Expression (Data from CCLE*)						Protein expression (Data based on FACS**)		
		EGFR	HER2	HER3	HER4	EGF	NRG1	EGFR	HER2	HER3
Gastric	N87	7.08	13.18	9.67	3.83	4.08	4.22	358	618	5.6
	SNU16	6.88	7.8	11.06	4.04	3.78	4.26	13.6	28.3	1.87
Colorectal	HT29	6.54	8.11	10.8	3.81	3.83	4.53	27.5	20.3	4.2
Head and Neck	FaDu	7.99	7.36	8.35	4.01	3.89	4.96	65.1	11.6	1.5
Lung	A549	7.29	6.79	5.18	3.85	4.2	8.81	19	17.7	7.4
	HCC95	7.33	7.06	7.31	3.85	4.19	11.24	100.8	44.5	8.2
Ovarian	OvCAR8	6.19	6.72	8.24	3.86	4.72	6.65	44.5	130.5	4.7
Kidney	ACHN	7.81	6.78	6.32	3.8	4.66	8.04	93.6	67.5	4

*CCLE gene expression data is log2-transformed robust multi-array (RMA)-normalized data generated from Affymetrix gene chips. The expression values in rather are relative

** Median fluorescence intensity normalized to isotype calculated by FlowLogic.

Figure 16A

DK/EP 3645571 T3

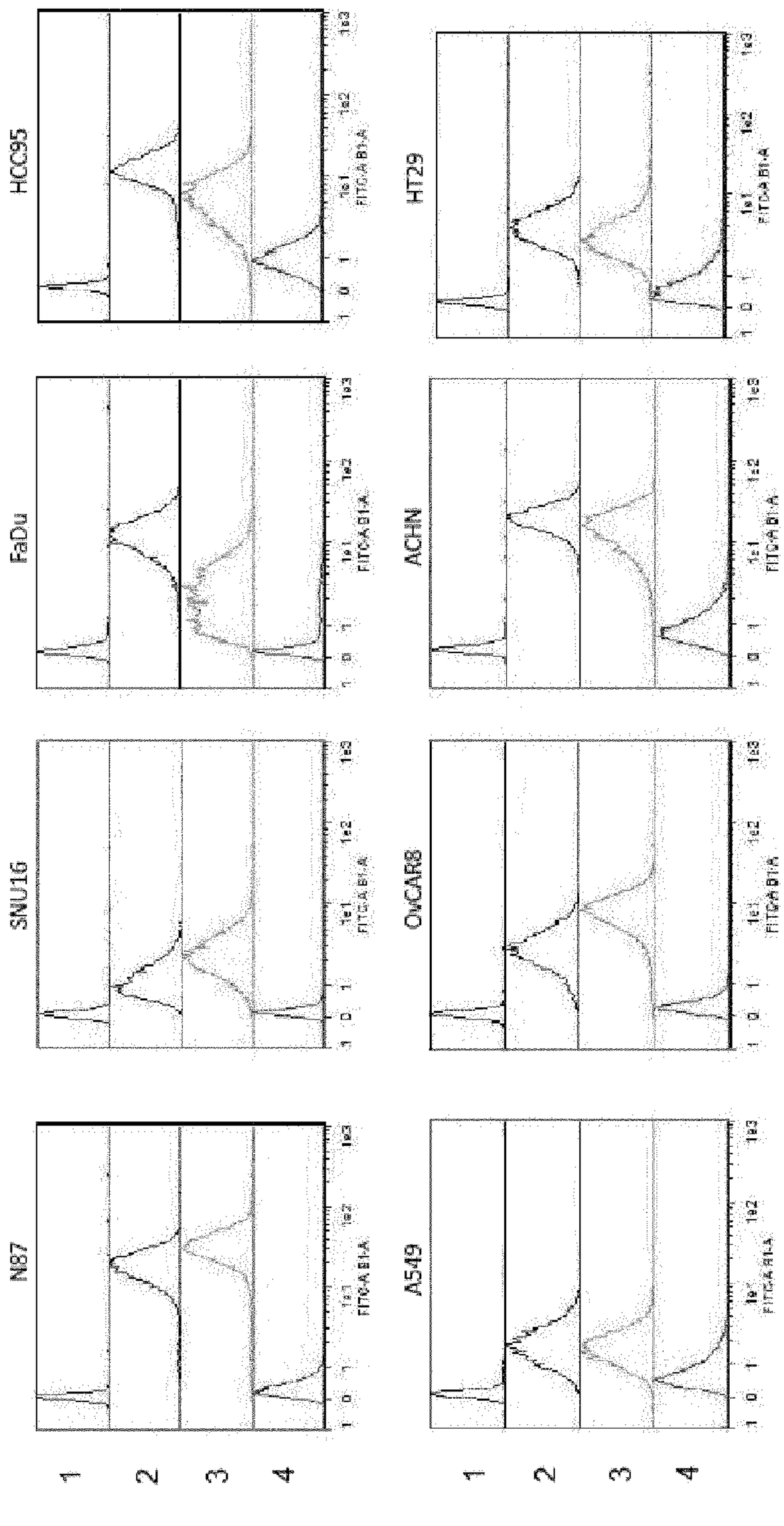

1 Isotype
2 EGFR
3 HER2
4 HER3
HCC95
HT29
FaDu
ACHN
SNU16
OvCAR8
N87
A549
FITC-A B1-A

Figure 16B

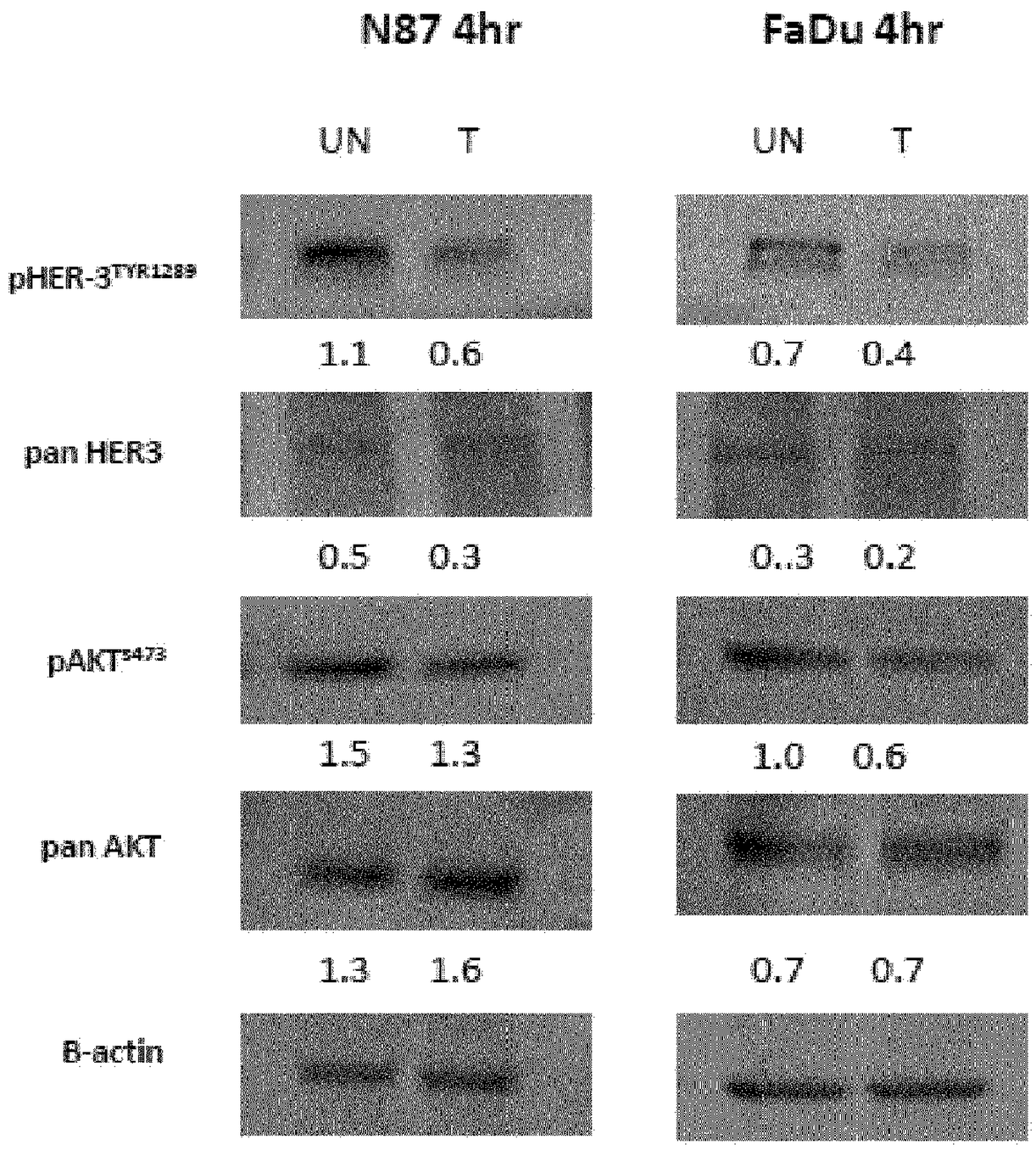

N87 4hr
FaDu 4hr
UN = Untreated
T = Treated
UN
T
UN
T
pHER-3TYR1289
1.1
0.6
0.7
0.4
pan HER3
0.5
0.3
0..3
0.2
pAKT5473
1.5
1.3
1.0
0.6
pan AKT
1.3
1.6
0.7
0.7
B-actin

Figure 17

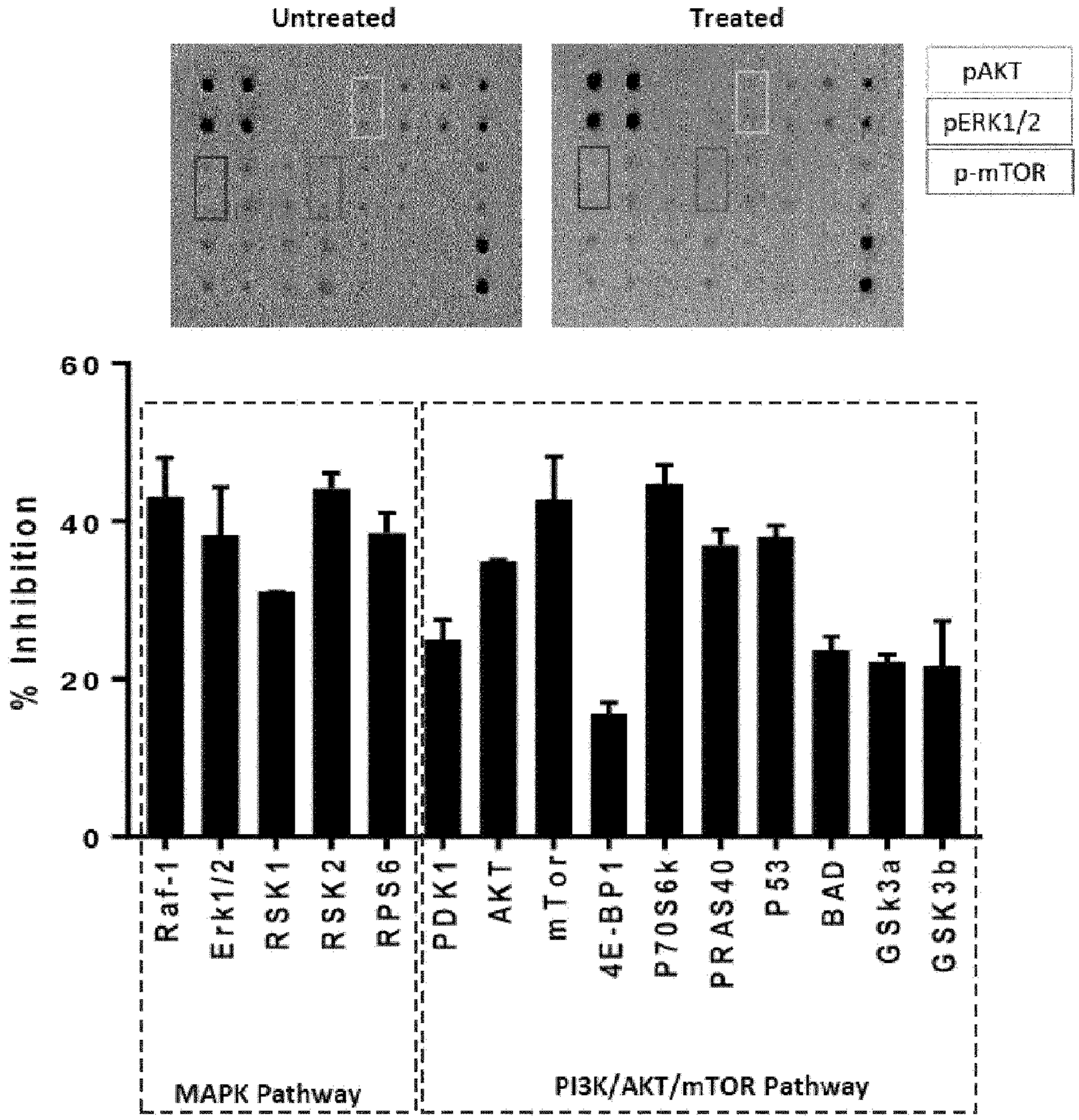

Untreated
Treated
pAKT
pERK1/2
p-mTOR
% Inhibition
60
40
20
0
Raf-1
Erk1/2
RSK1
RSK2
RPS6
PDK1
AKT
mTor
4E-BP1
P70S6k
PRAS40
P53
BAD
GSk3a
GSK3b
MAPK Pathway
PI3K/AKT/mTOR Pathway

Figure 18

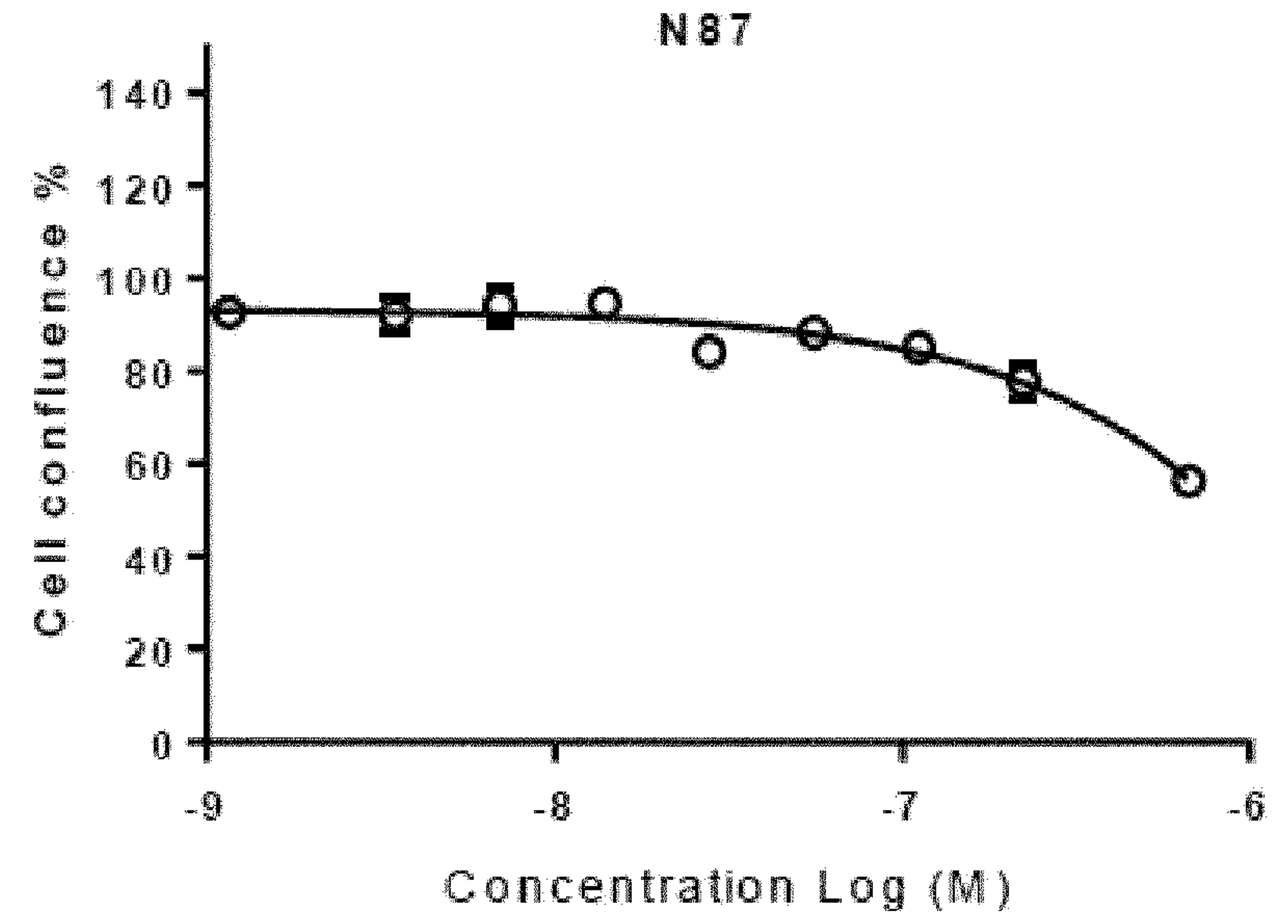


Figure 19A

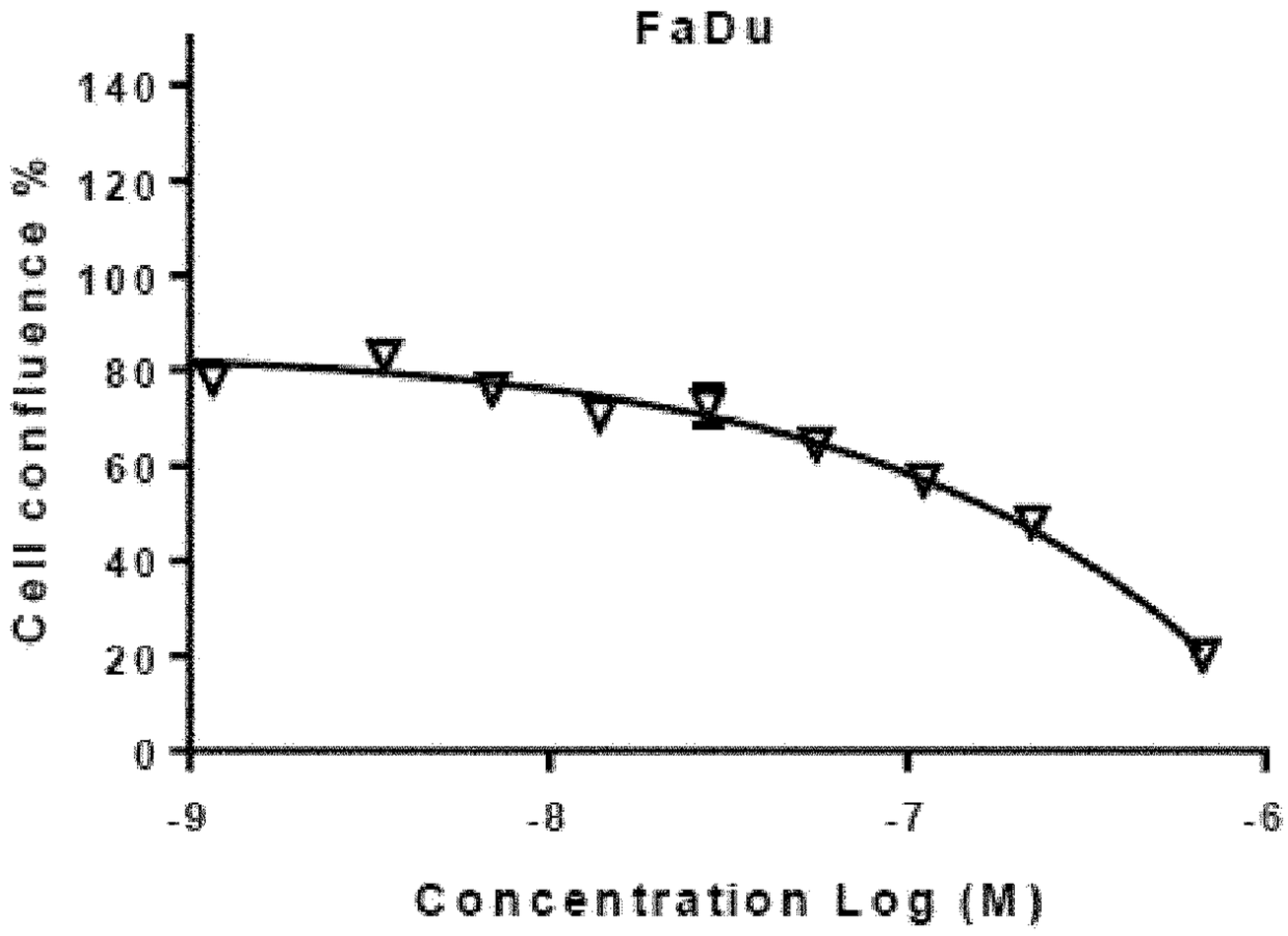


Figure 19B

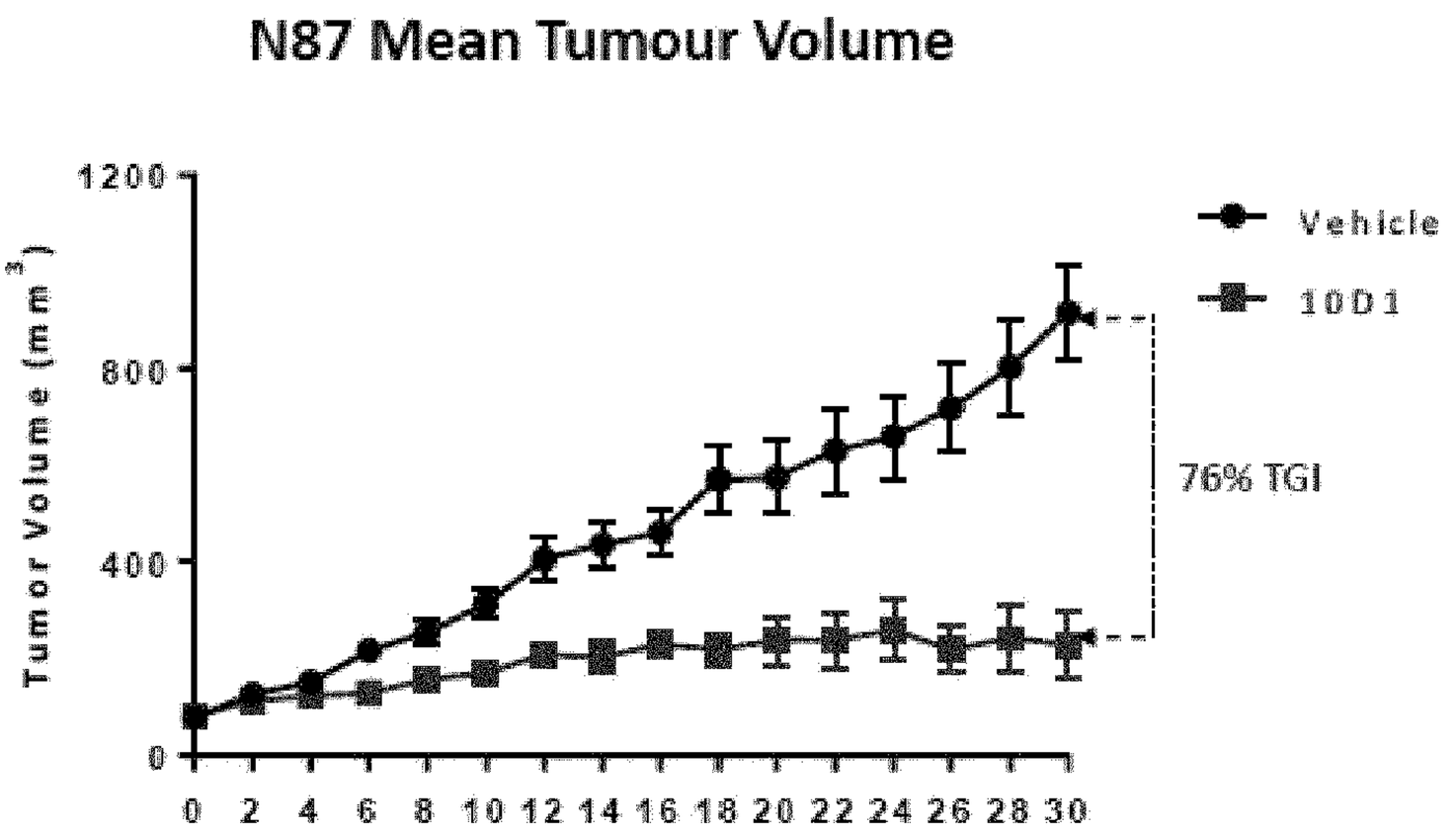


Figure 20

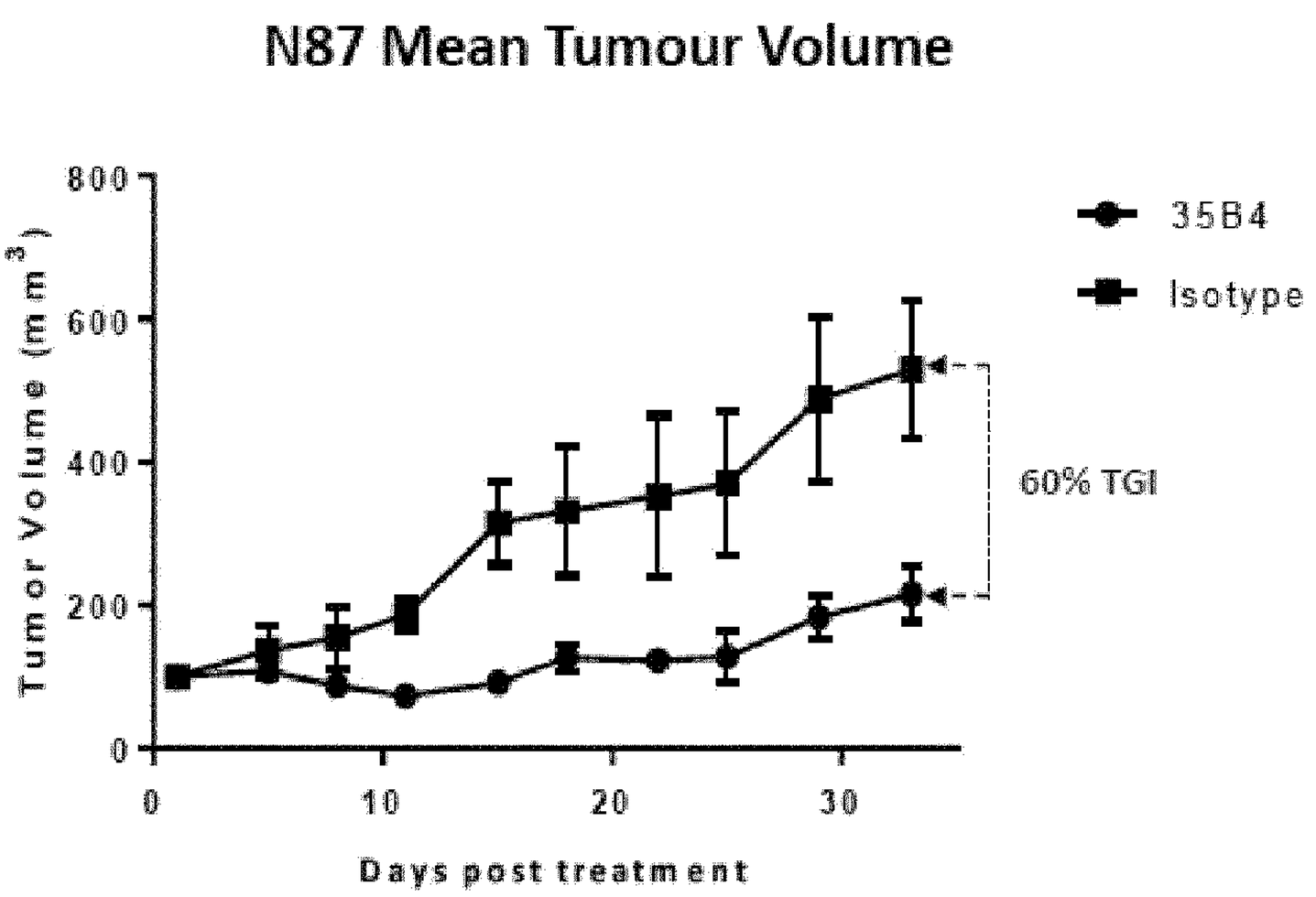


Figure 21

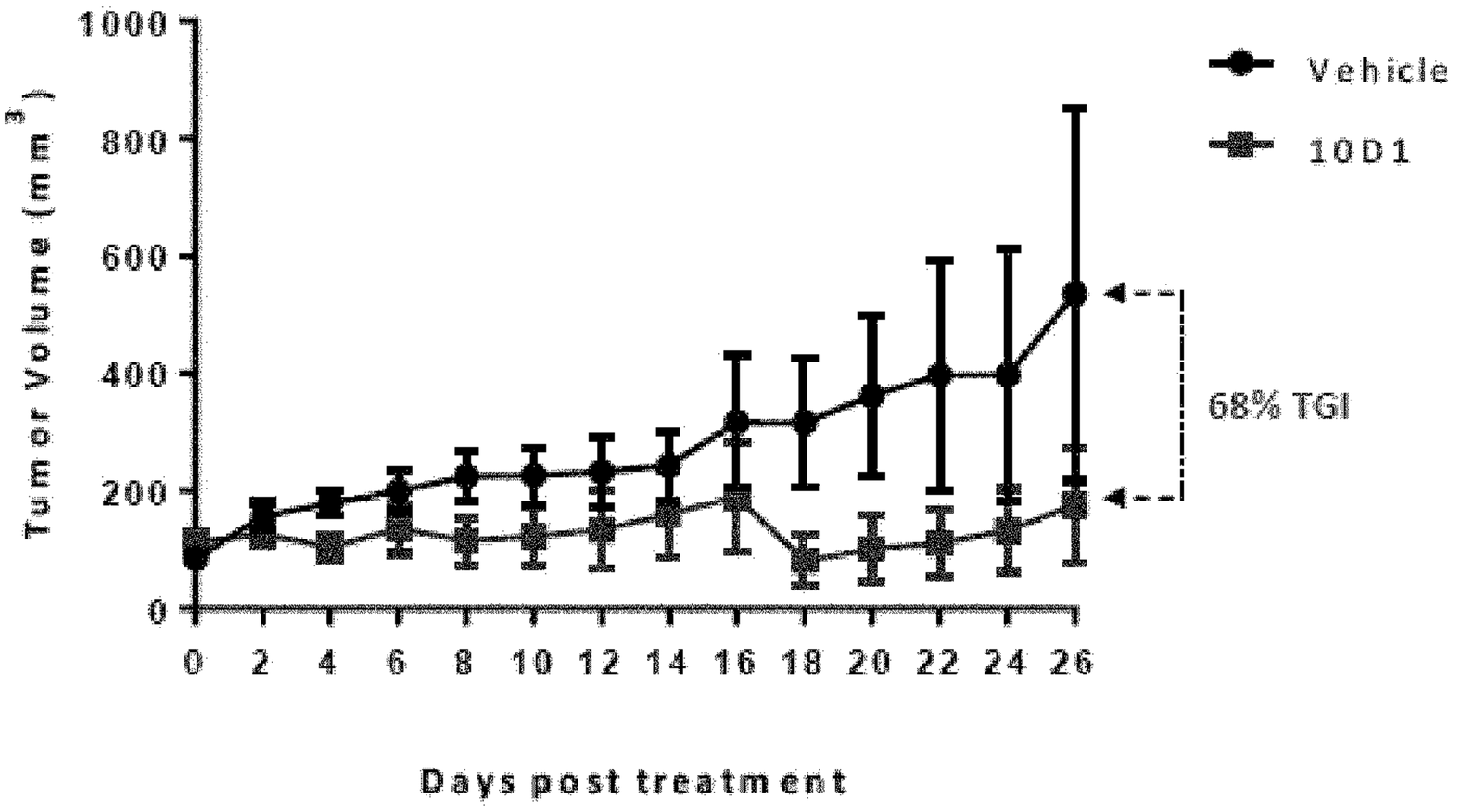


Figure 22

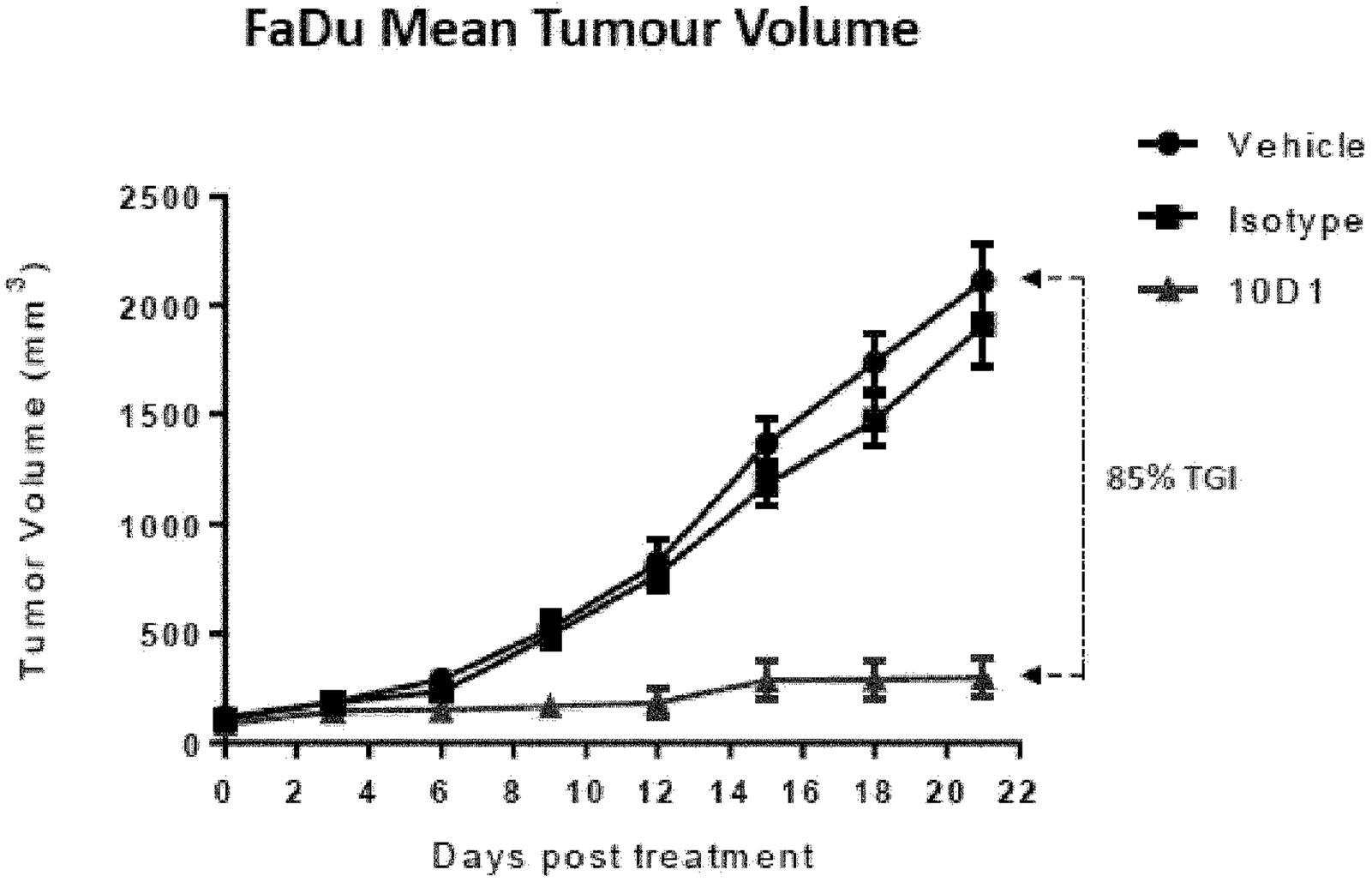


Figure 23

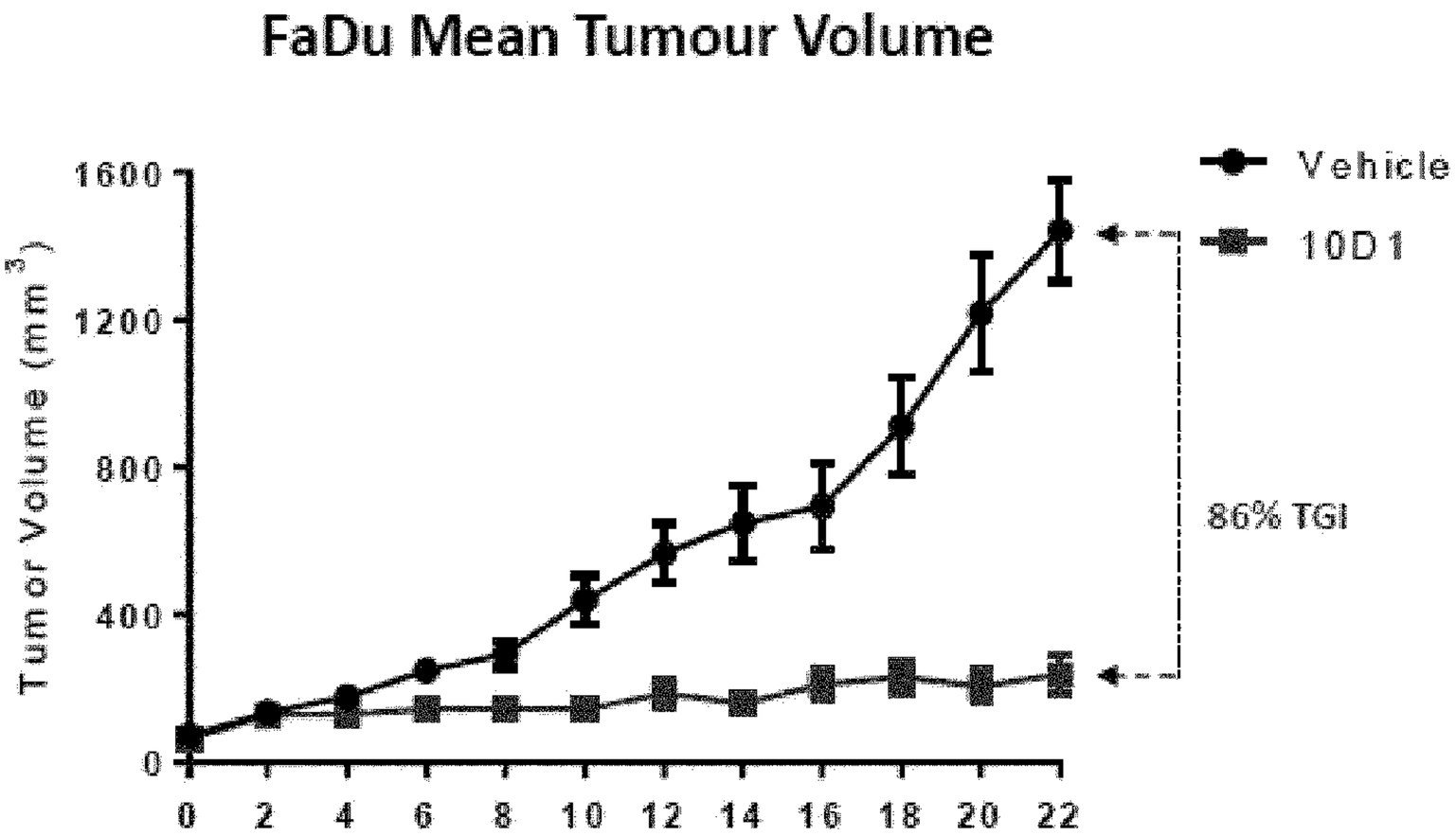


Figure 24

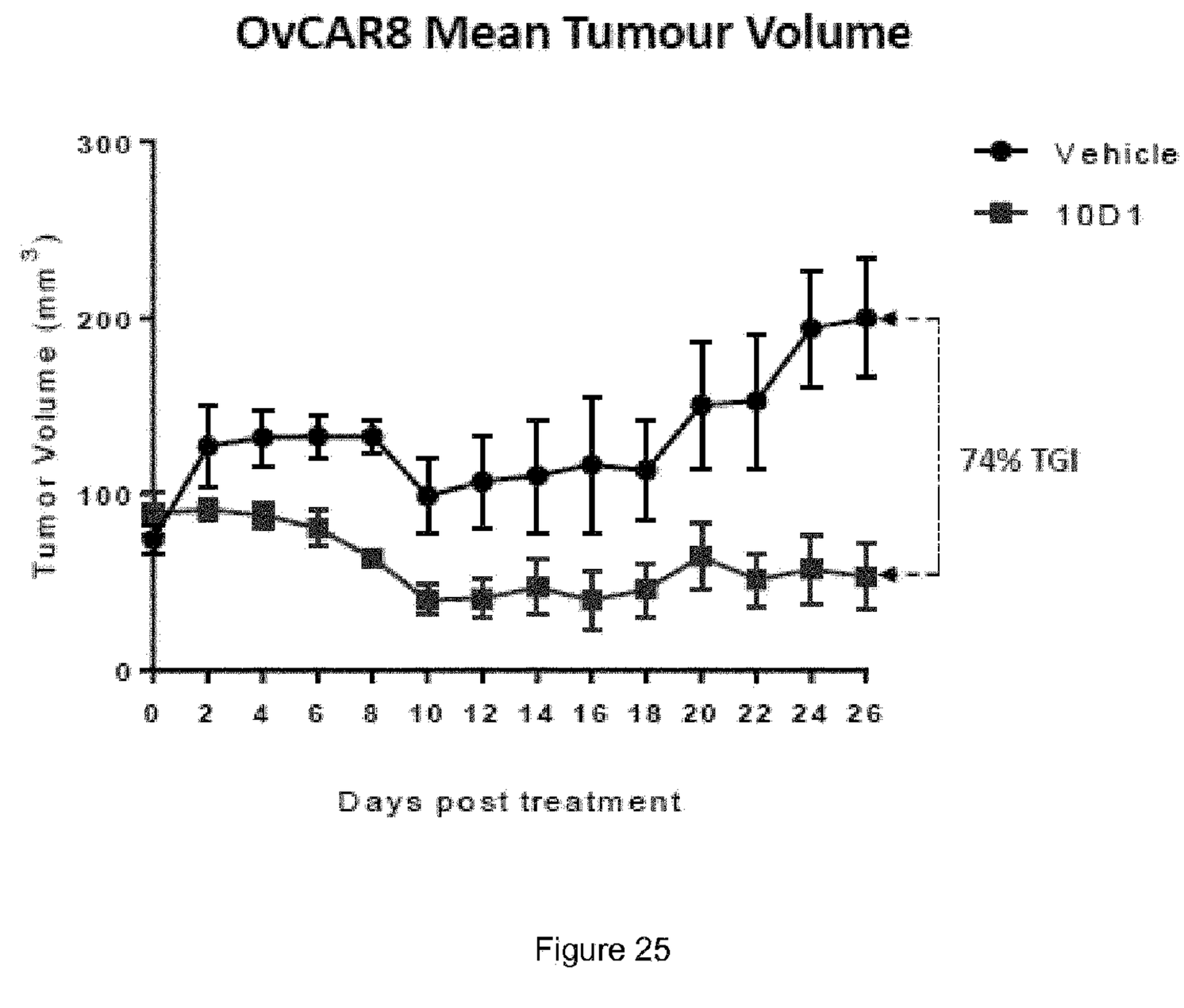


Figure 25

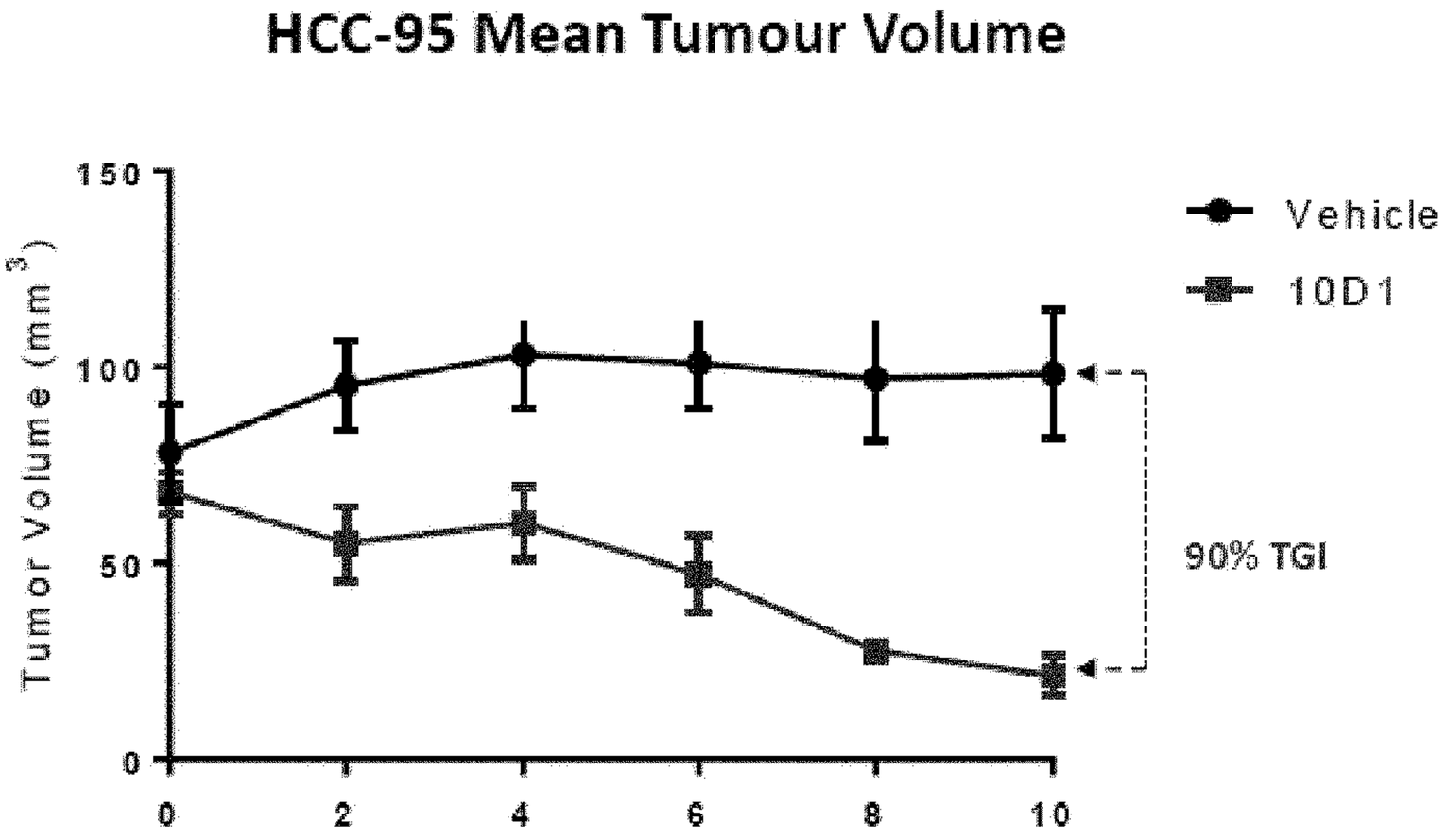


Figure 26

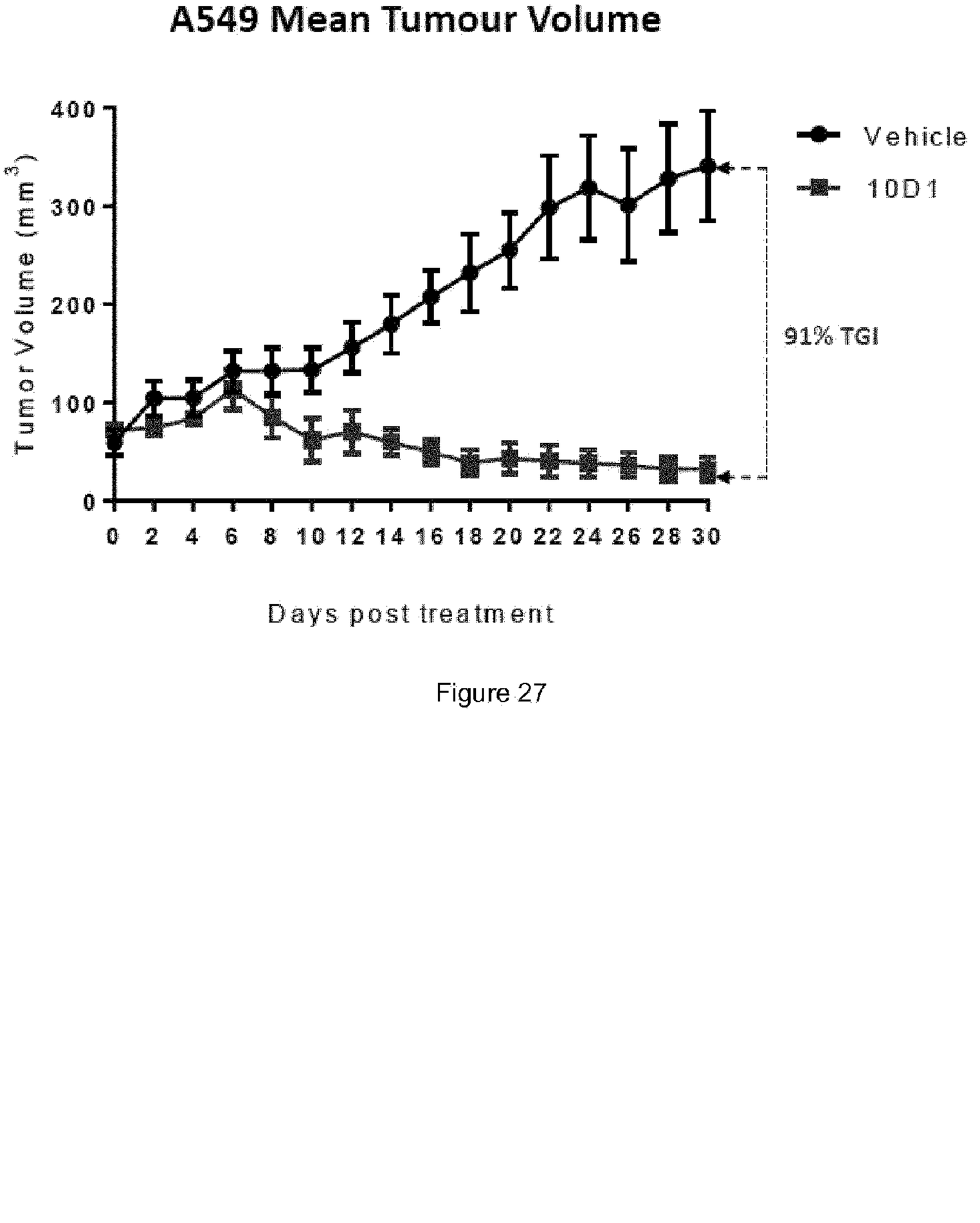


Figure 27

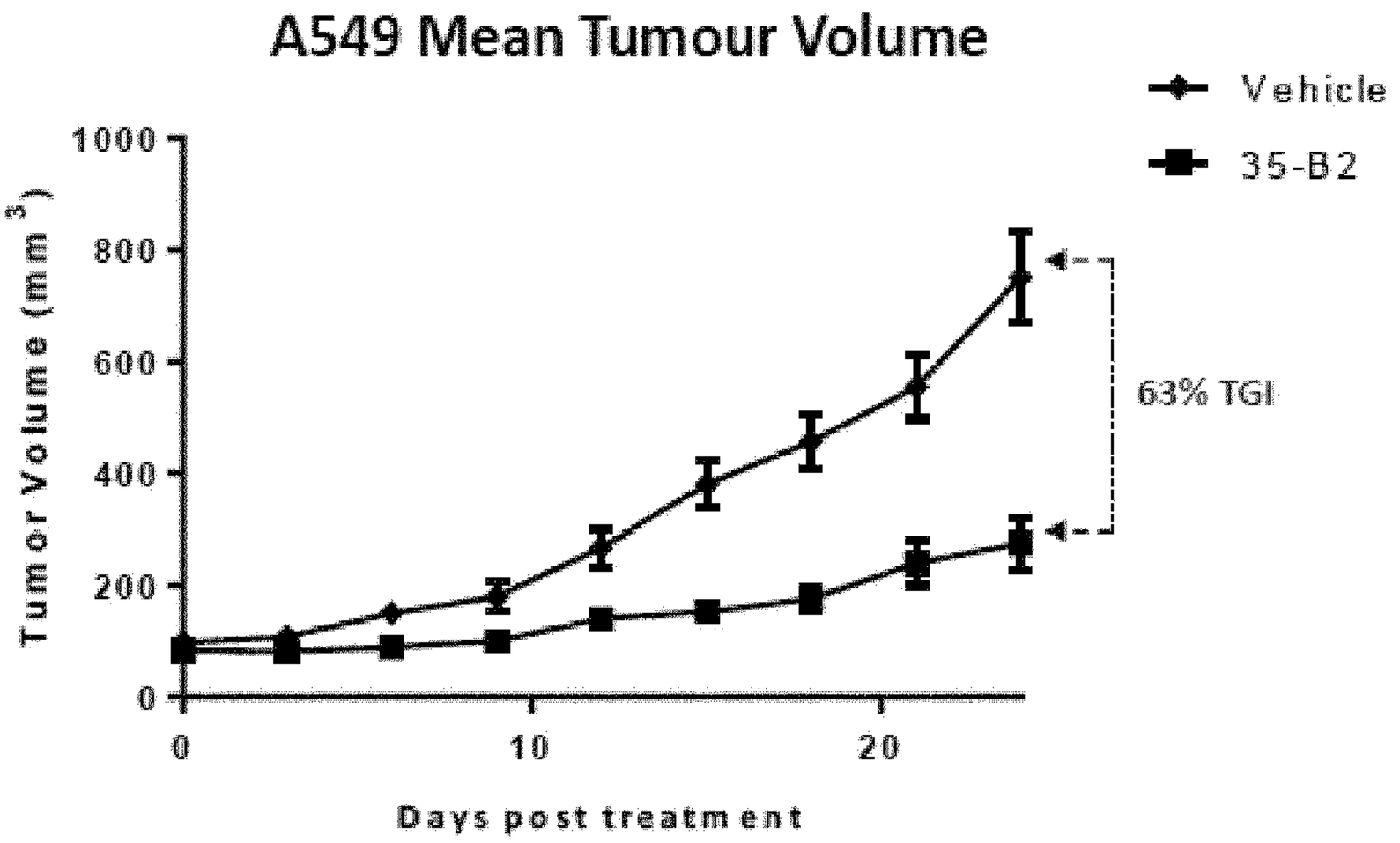


Figure 28

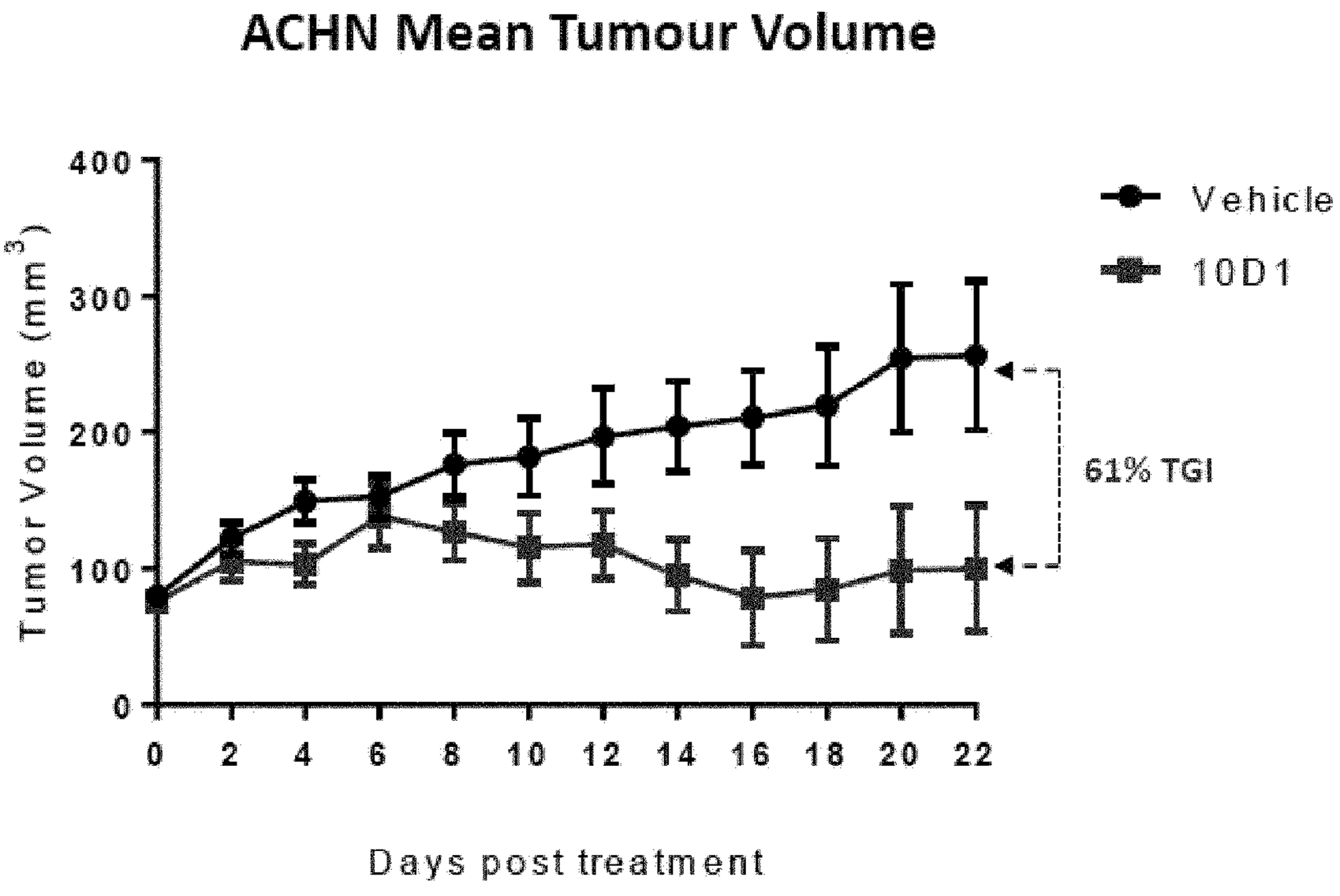
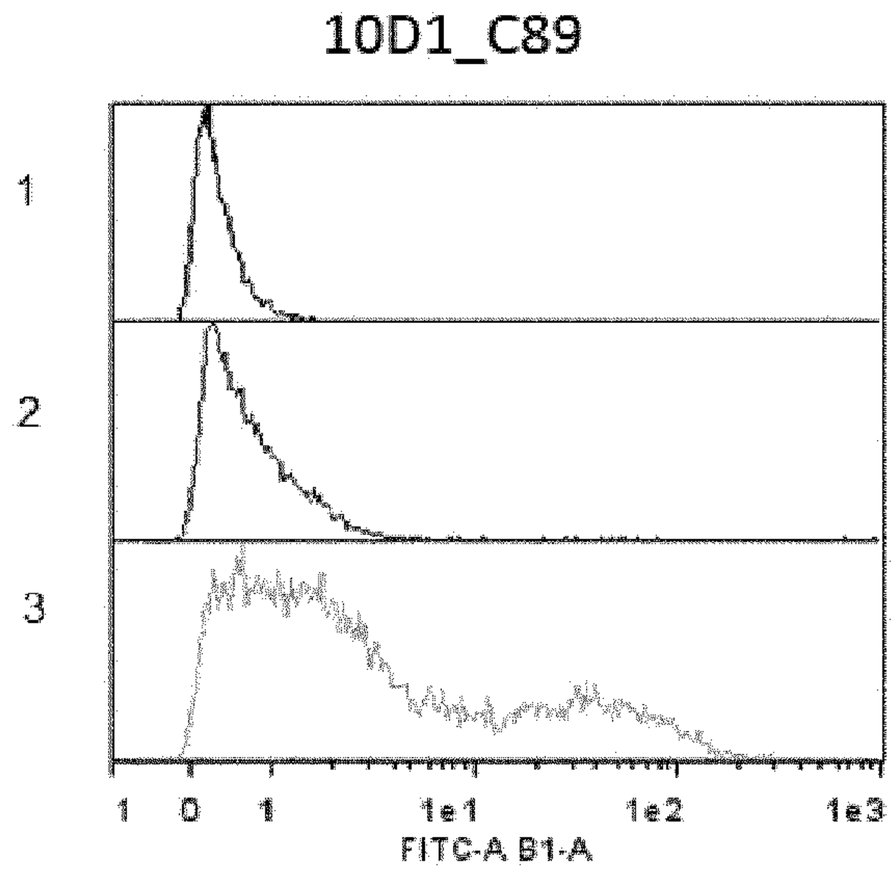
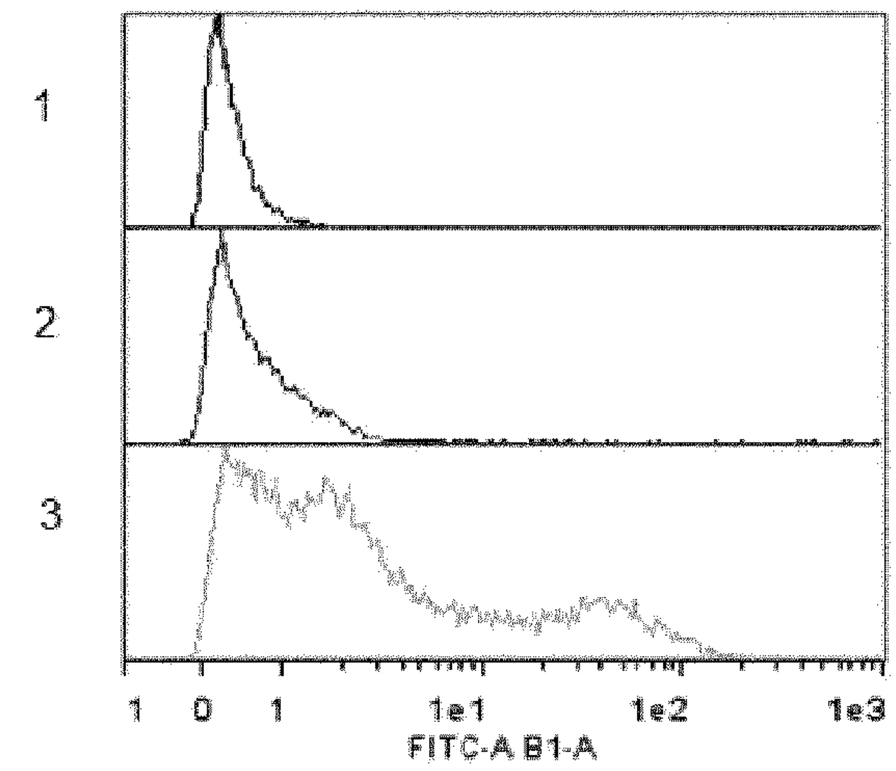


Figure 29



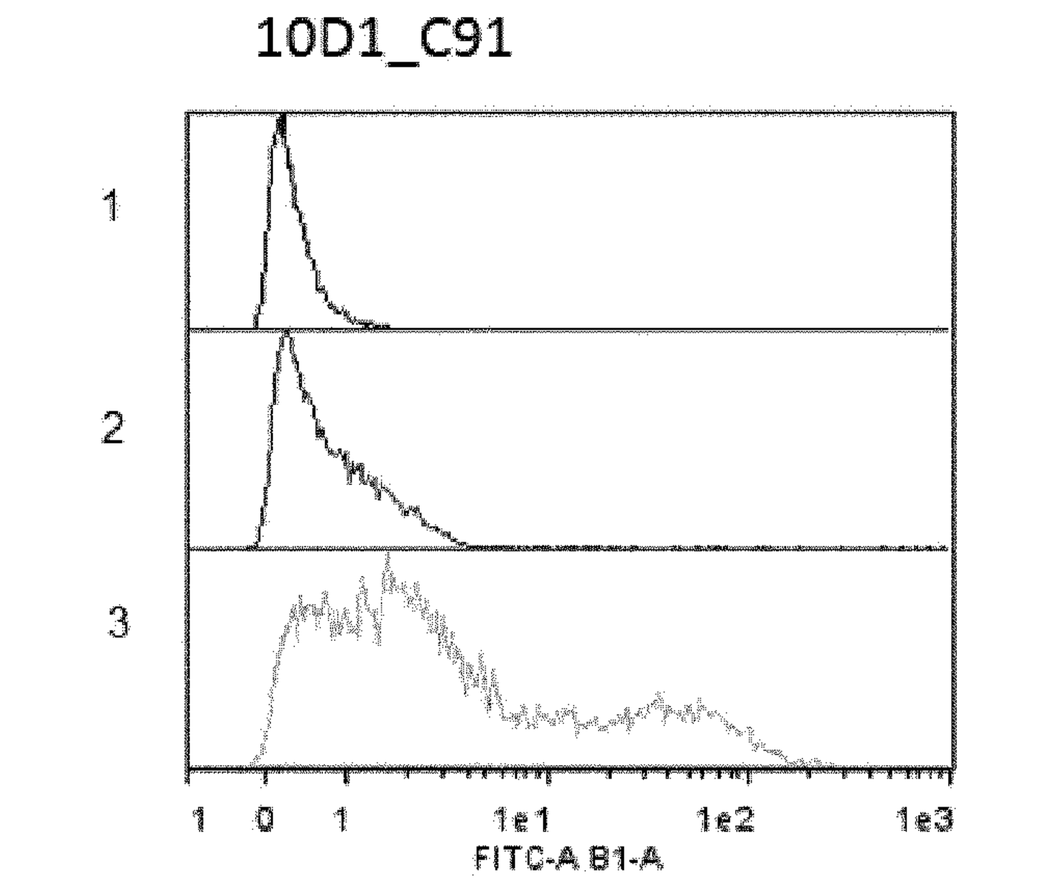
	Color	Population	% Parent
1		HER3 Positive [293_Unstained]	0.14
2		HER3 Positive [293_10D1_C-89Sc]	2.79
3		HER3 Positive [293_OE HER3_10D1_C-89Sc]	44.57

Figure 30



	Color	Population	% Parent
1		HER3 Positive [293_Unstained]	0.14
2		HER3 Positive [293_10D1_C-90Sc]	2.48
3		HER3 Positive [293_OE HER3_10D1_C-90Sc]	41.81

Figure 31



	Color	Population	% Parent
1		HER3 Positive [293_Unstained]	0.14
2		HER3 Positive [293_10D1_C-91Sc]	5.38
3		HER3 Positive [293_OE HER3_10D1_C-91Sc]	48.05

Figure 32

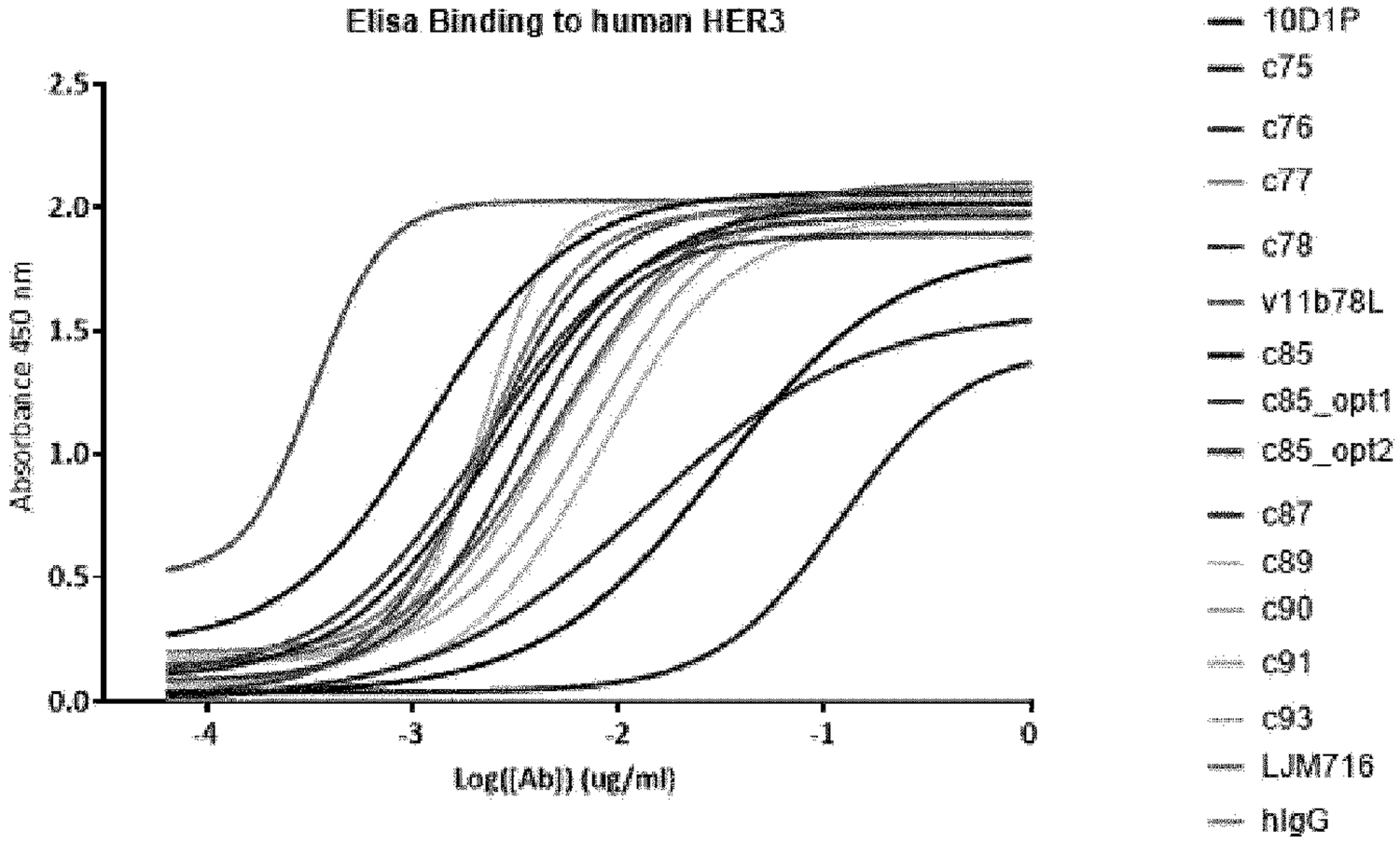


Figure 33A

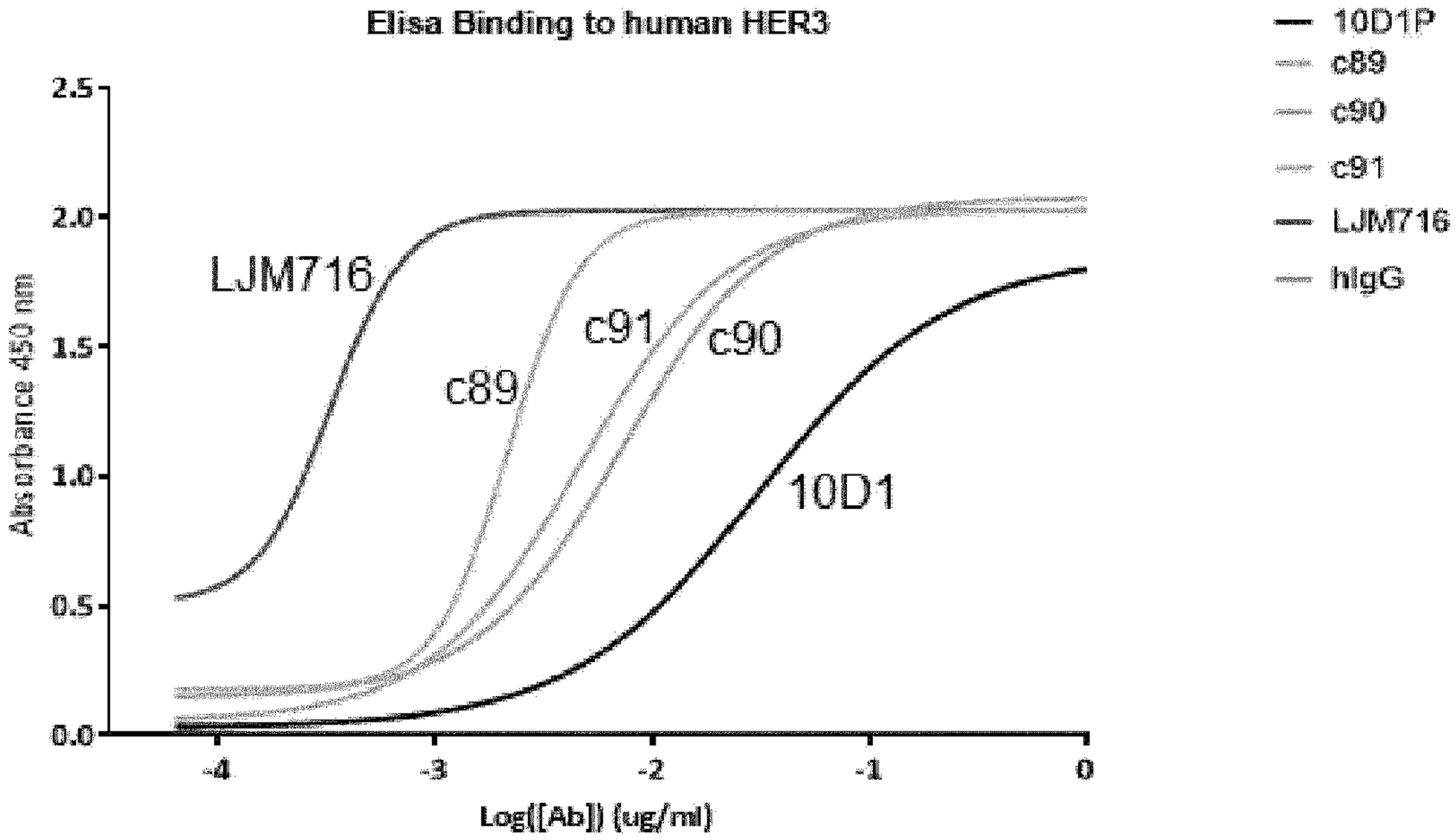


Figure 33B

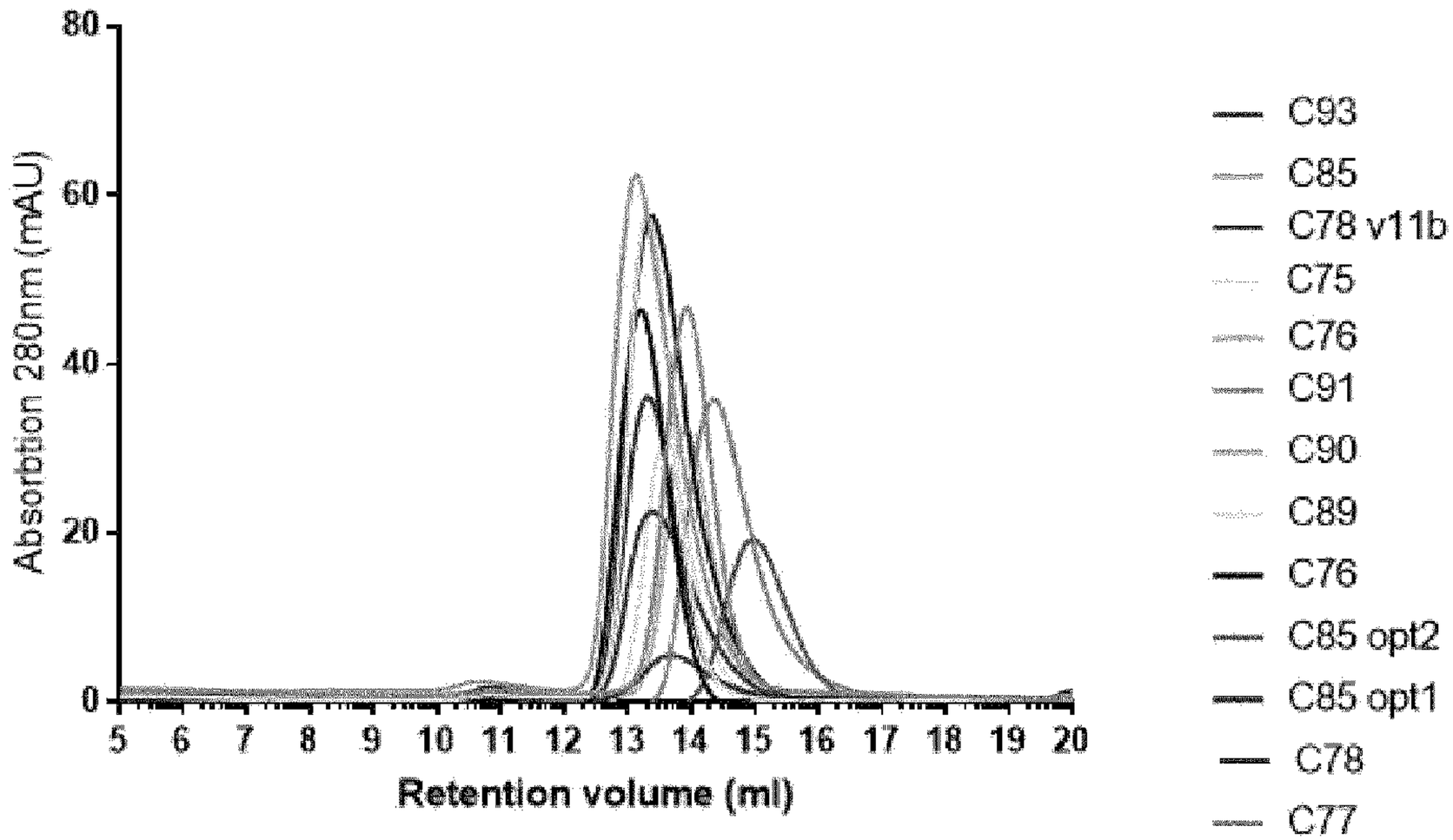


Figure 34A

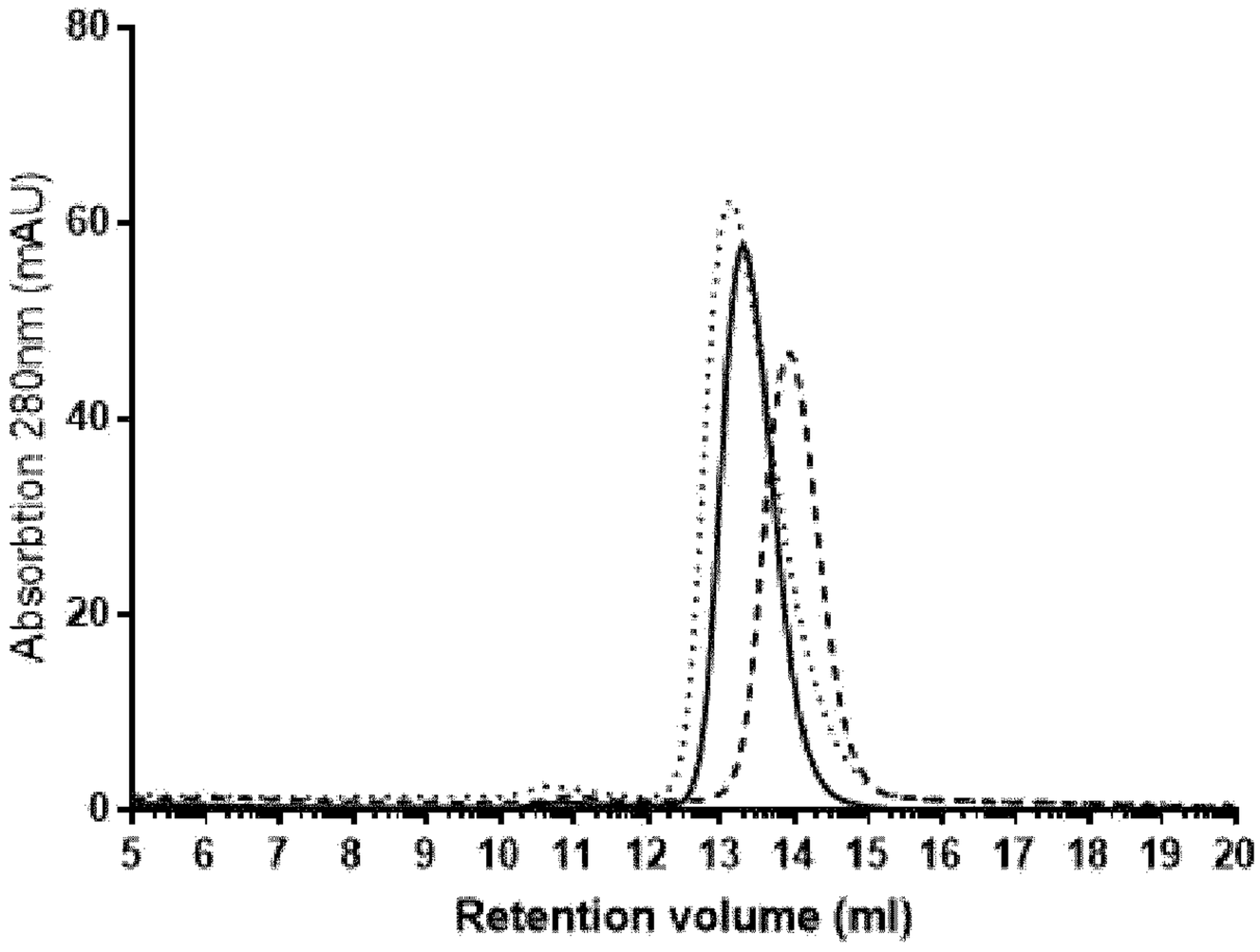
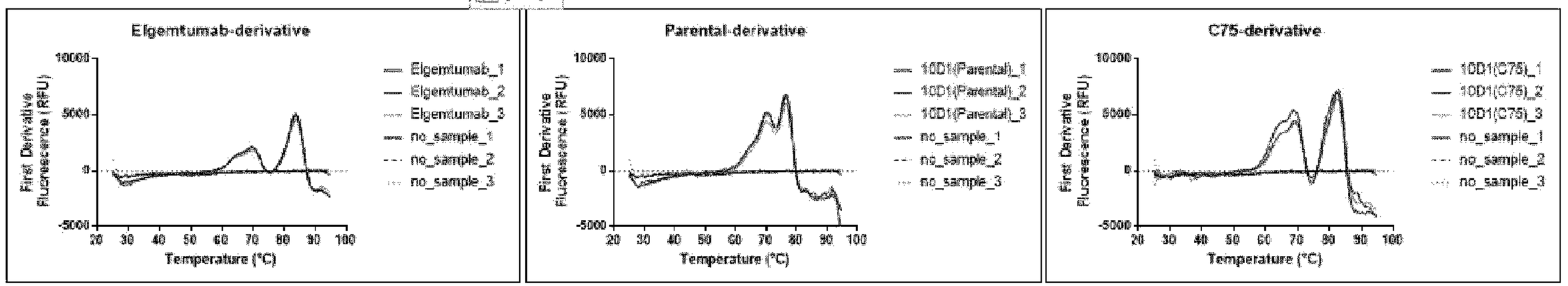

Absorbtion 280nm (mAU)
80
60
40
20
0
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
Retention volume (ml)
C91
C90
C89

Figure 34B

	Tm1 (°C)	Tm2 (°C)
UM716	70.8	83.8

	Tm1 (°C)	Tm2 (°C)
10D1 (Parental)	69.9	77.2

	Tm1 (°C)	Tm2 (°C)
10D1 (C75)	69.5	82.6



	Tm1 (°C)	Tm2 (°C)
10D1 (C76)	69.6	80.9

	Tm1 (°C)	Tm2 (°C)
10D1 (C77)	64.1	80.9

	Tm1 (°C)	Tm2 (°C)
10D1 (C78)	70.2	83.3

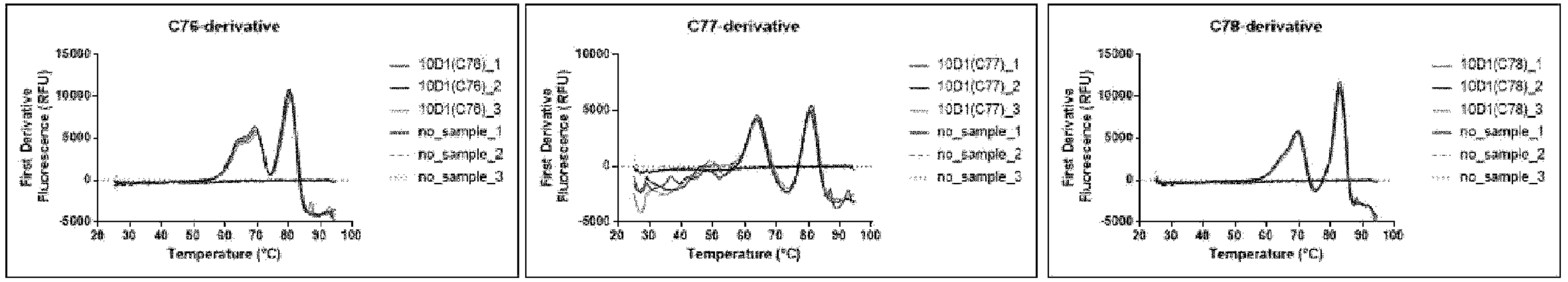
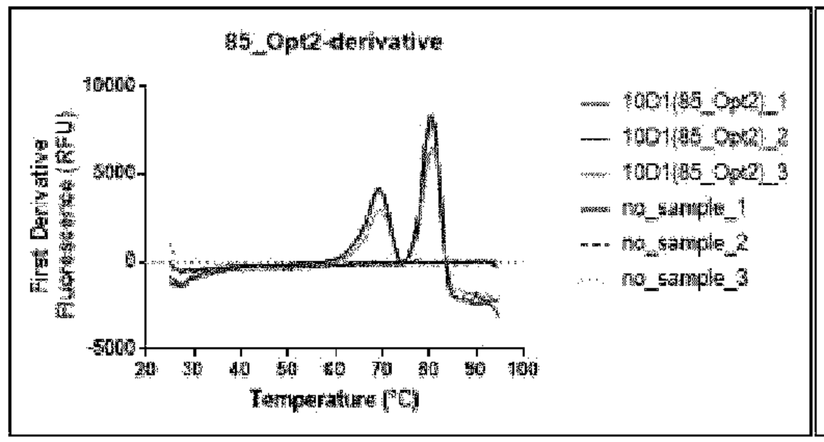
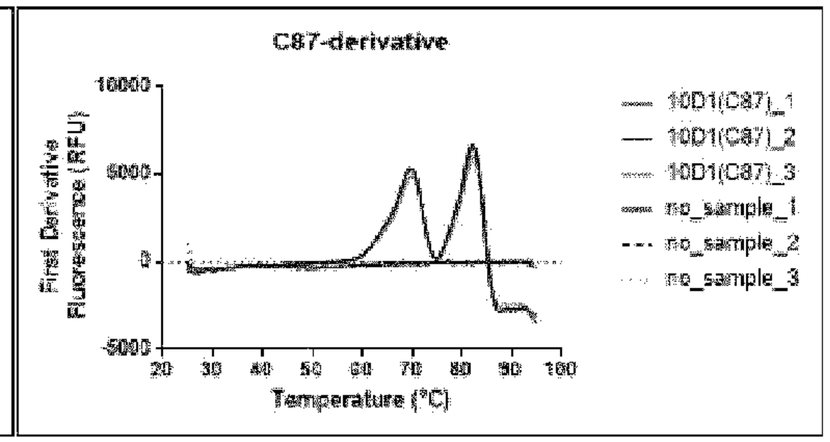


Figure 35A

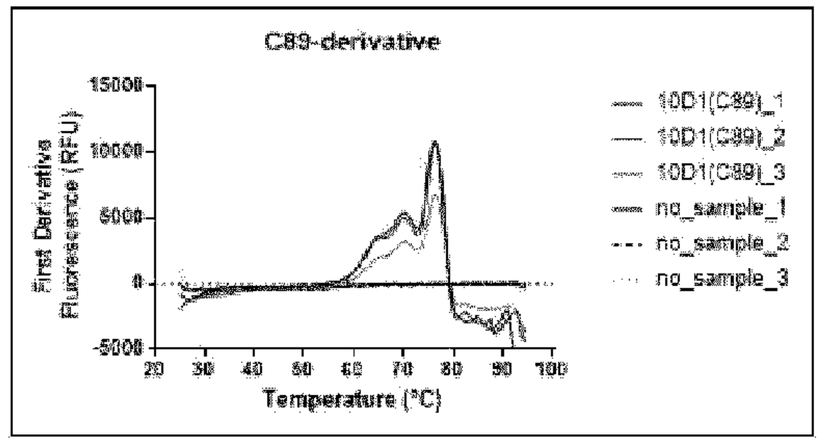
	Tm1 (°C)	Tm2 (°C)
10D1 (85 Opt2)	69.8	80.7



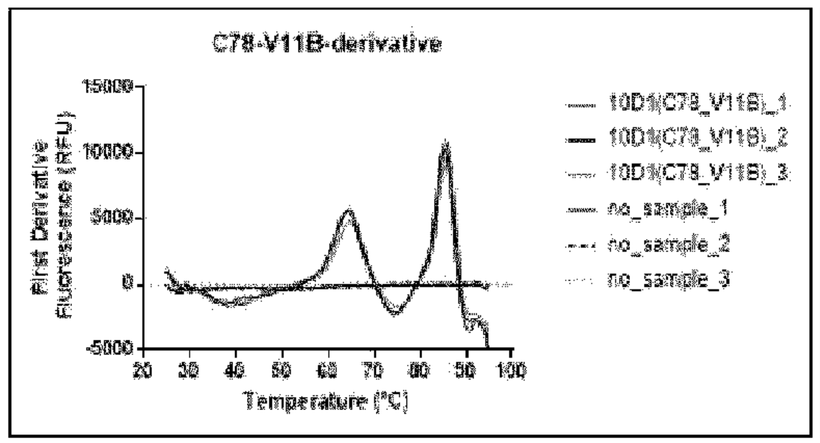
	Tm1 (°C)	Tm2 (°C)
10D1 (C87)	69.9	82.6



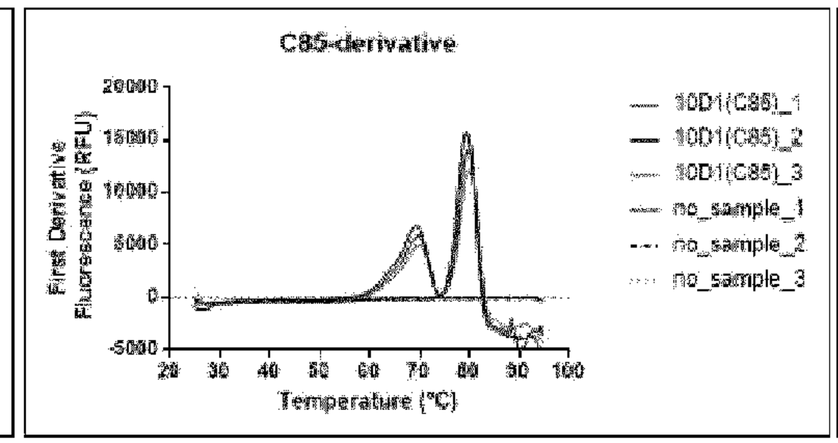
	Tm1 (°C)	Tm2 (°C)
10D1 (C89)	70.0	76.8



	Tm1 (°C)	Tm2 (°C)
10D1 (C78_V11B)	64.5	85.7



	Tm1 (°C)	Tm2 (°C)
10D1 (C85)	69.9	80.0



	Tm1 (°C)	Tm2 (°C)
10D1 (85 Opt1)	69.5	78.6

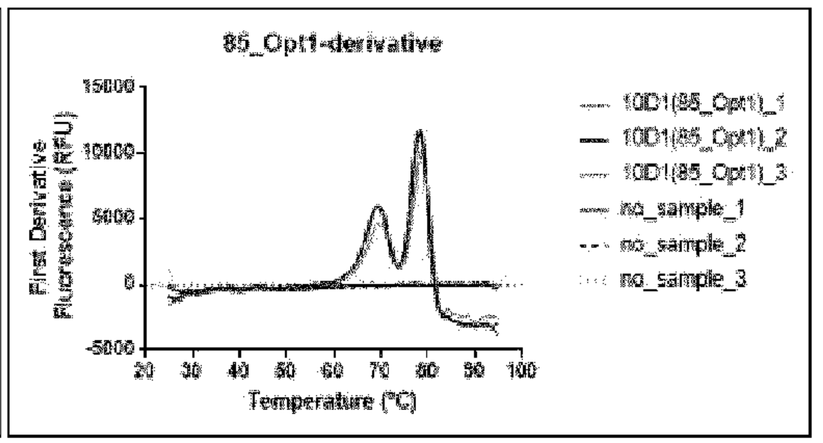


Figure 35B

	Tm1 (°C)	Tm2 (°C)
10D1 (C90)	70.5	73.6

	Tm1 (°C)	Tm2 (°C)
10D1 (C91)	74.3	

	Tm1 (°C)	Tm2 (°C)
10D1 (C93)	70.0	87.7

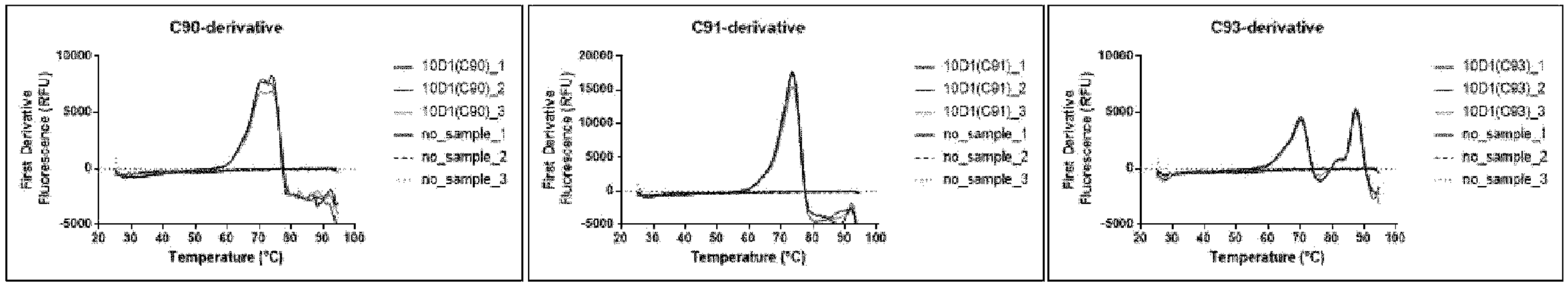
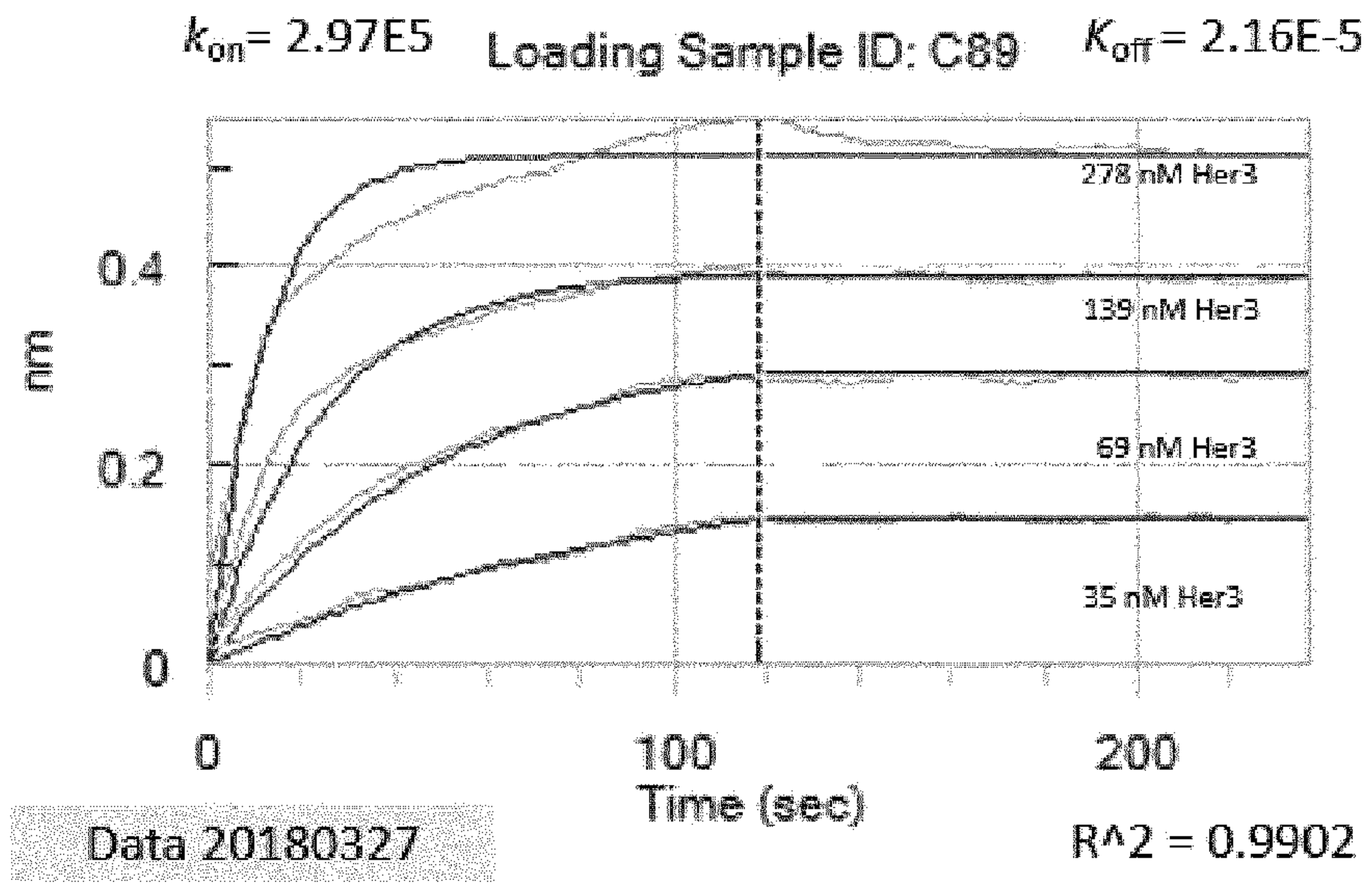
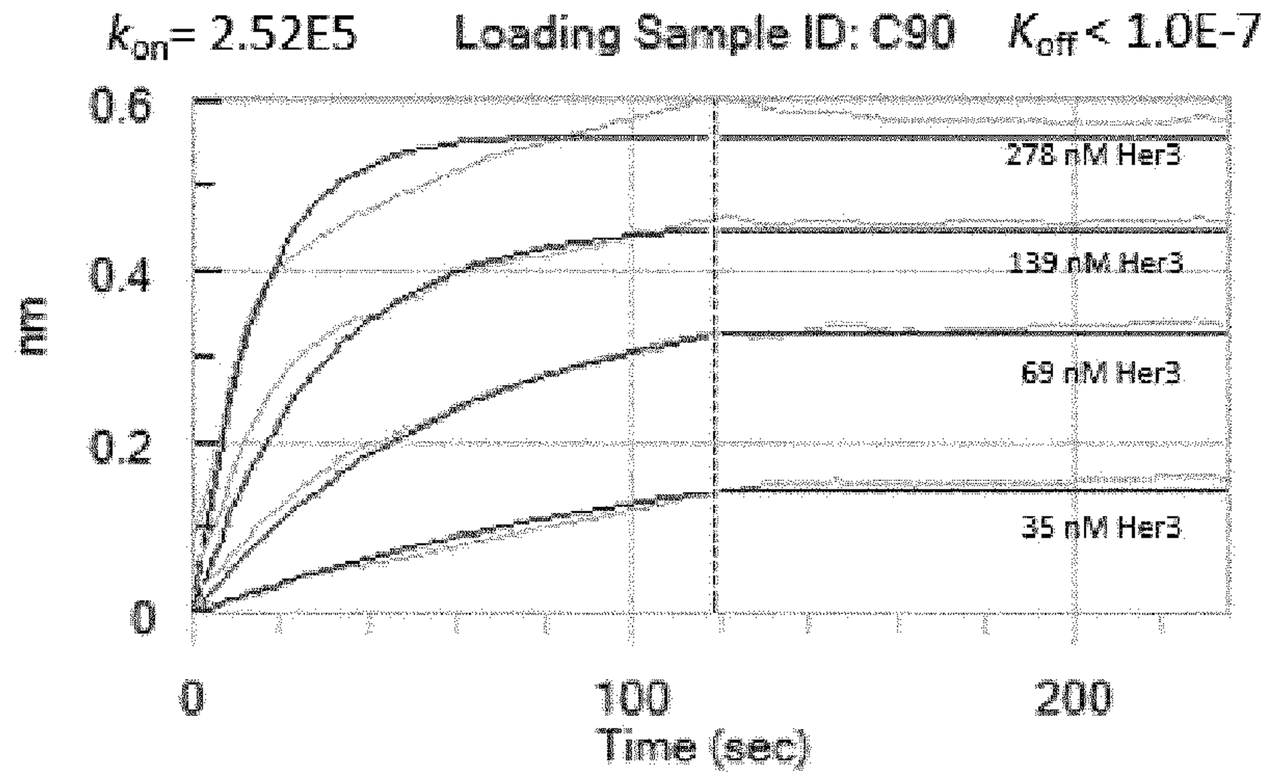


Figure 35C



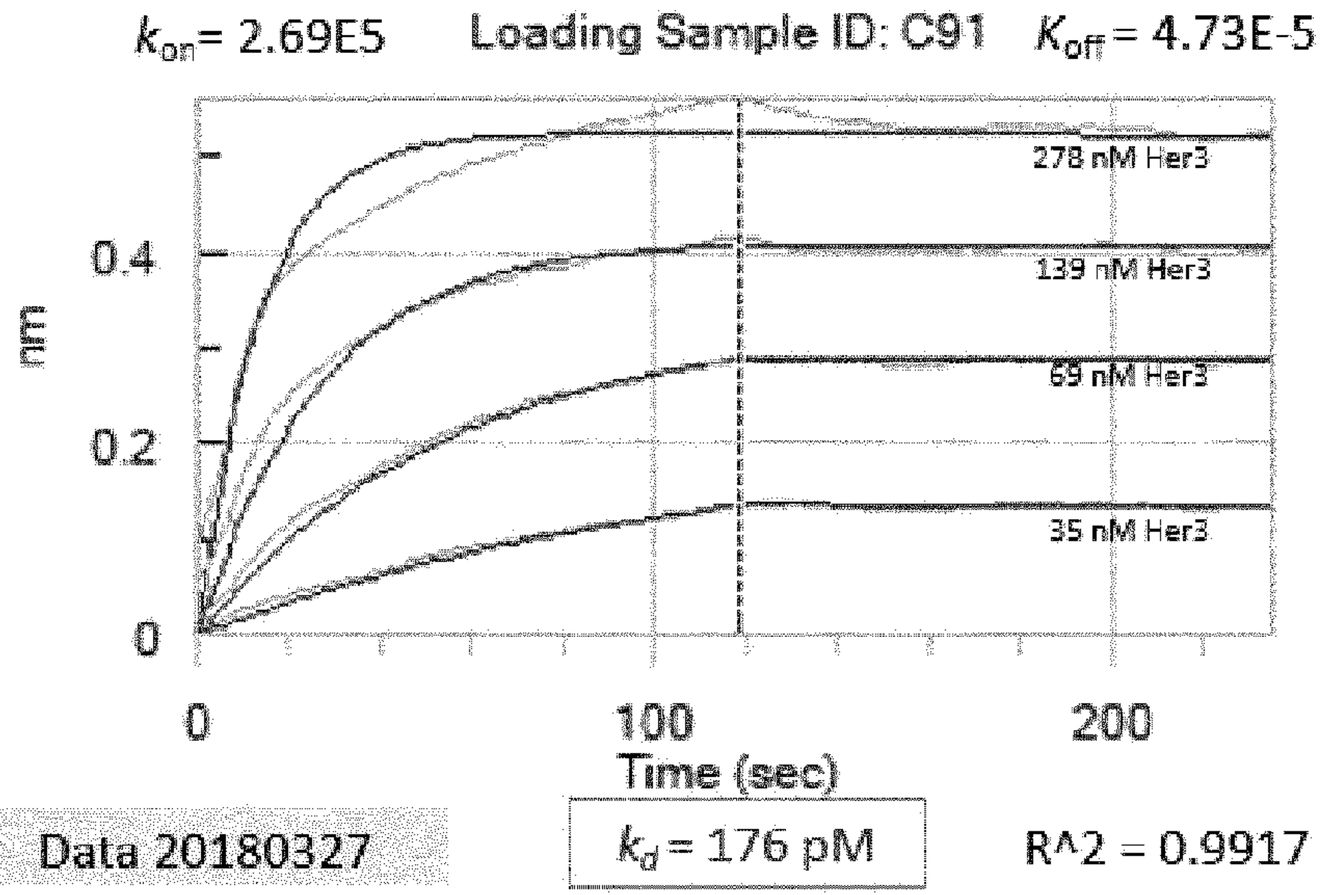
Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C89		2	69	0.2882	7.26E-11	3.68E-10	2.97E+05	1.12E+04	2.16E-05	1.15E-04	0.3206	0.0063	2.05E-02	0.3202	99.9	0.0341	0.9902
C89		2	35	0.1471	7.26E-11	3.68E-10	2.97E+05	1.12E+04	2.16E-05	1.15E-04	0.2066	0.0071	1.04E-02	0.2064	99.8	0.0341	0.9902
C89		2	278	0.5458	7.26E-11	3.68E-10	2.97E+05	1.12E+04	2.16E-05	1.15E-04	0.513	0.0041	8.26E-02	0.5129	100	0.0341	0.9902
C89		2	139	0.3968	7.26E-11	3.68E-10	2.97E+05	1.12E+04	2.16E-05	1.15E-04	0.3943	0.0046	4.13E-02	0.3941	99.9	0.0341	0.9902

Figure 36A



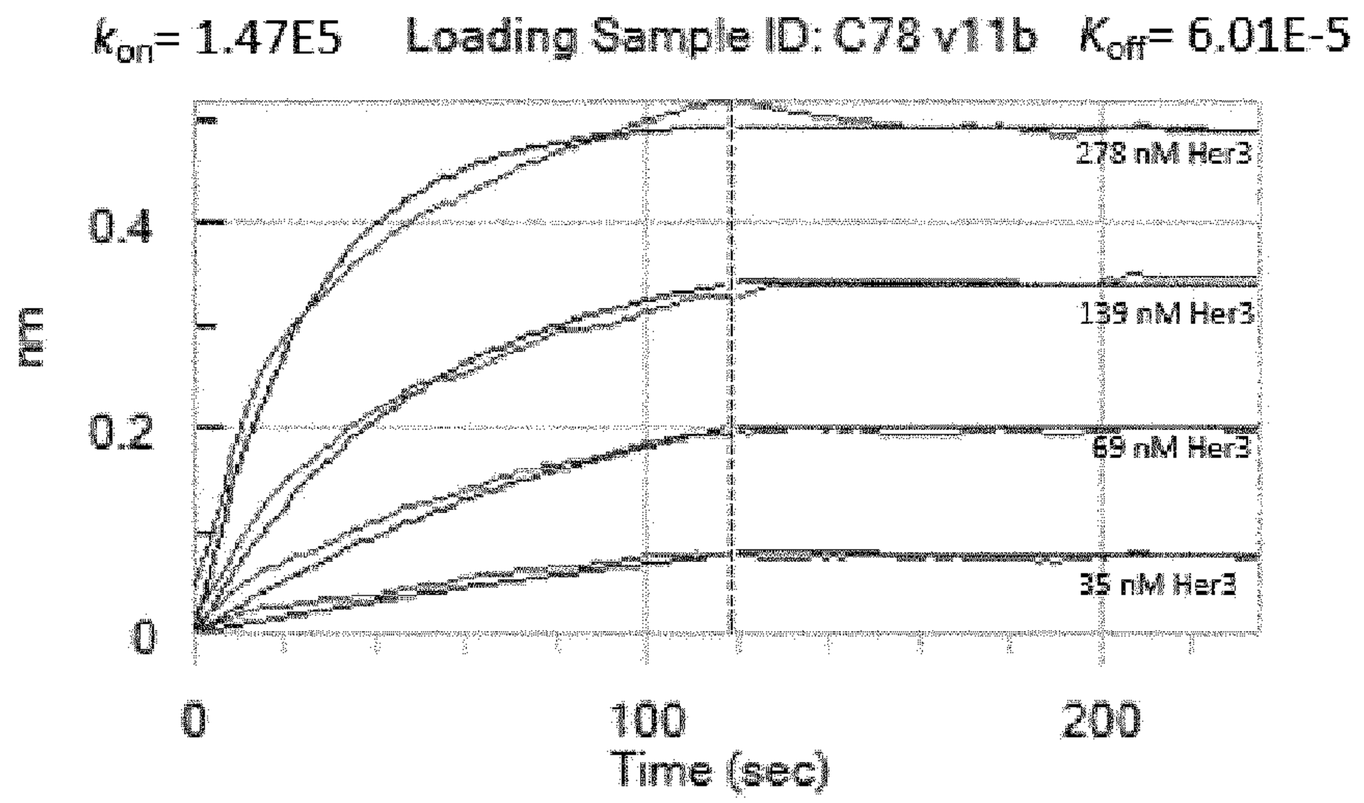
Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C90	6	35	0.1355	<1.0E-12	5.13E-10	2.52E+05	1.04E+04	<1.0E-07		0.2209	0.0092	8.80E-03	0.2209	100	0.0457	0.9891
C90	6	278	0.5944	<1.0E-12	5.13E-10	2.52E+05	1.04E+04	<1.0E-07		0.5578	0.0053	6.99E-02	0.5578	100	0.0457	0.9891
C90	6	139	0.4533	<1.0E-12	5.13E-10	2.52E+05	1.04E+04	<1.0E-07		0.4543	0.0064	3.50E-02	0.4543	100	0.0457	0.9891
C90	6	69	0.3221	<1.0E-12	5.13E-10	2.52E+05	1.04E+04	<1.0E-07		0.3709	0.009	1.74E-02	0.3709	100	0.0457	0.9891

Figure 36B



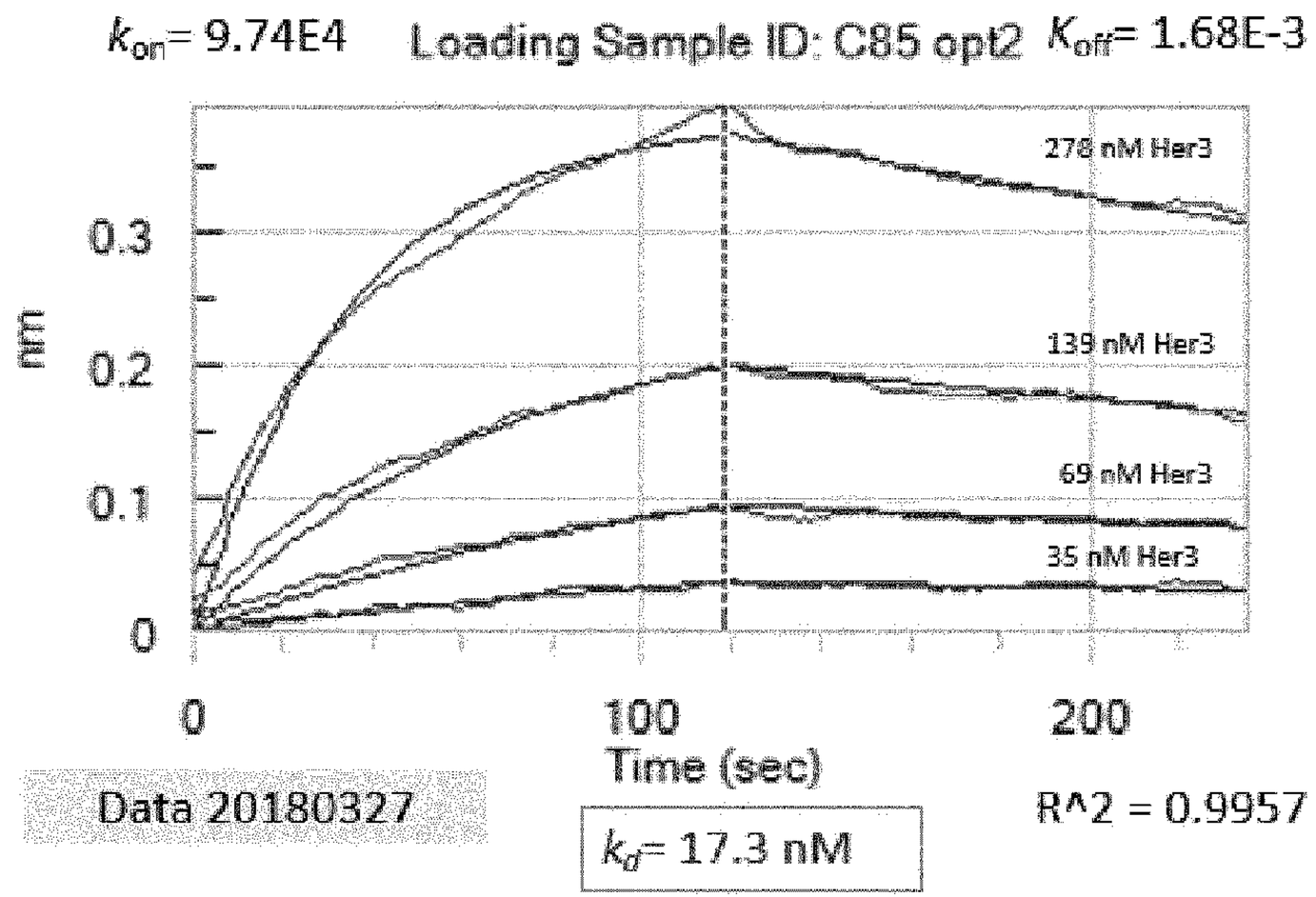
Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C91		3	35	0.1298	1.76E-10	4.12E-10	2.89E+05	9.57E+03	4.73E-05	1.11E-04	0.202	0.0071	9.46E-03	0.201	99.5	0.033	0.9917
C91		3	139	0.4098	1.76E-10	4.12E-10	2.89E+05	9.57E+03	4.73E-05	1.11E-04	0.4132	0.0048	3.74E-02	0.4127	99.9	0.033	0.9917
C91		3	278	0.5575	1.76E-10	4.12E-10	2.89E+05	9.57E+03	4.73E-05	1.11E-04	0.5256	0.0041	7.48E-02	0.5252	99.9	0.033	0.9917
C91		3	69	0.2851	1.76E-10	4.12E-10	2.89E+05	9.57E+03	4.73E-05	1.11E-04	0.3242	0.0065	1.86E-02	0.3234	99.7	0.033	0.9917

Figure 36C



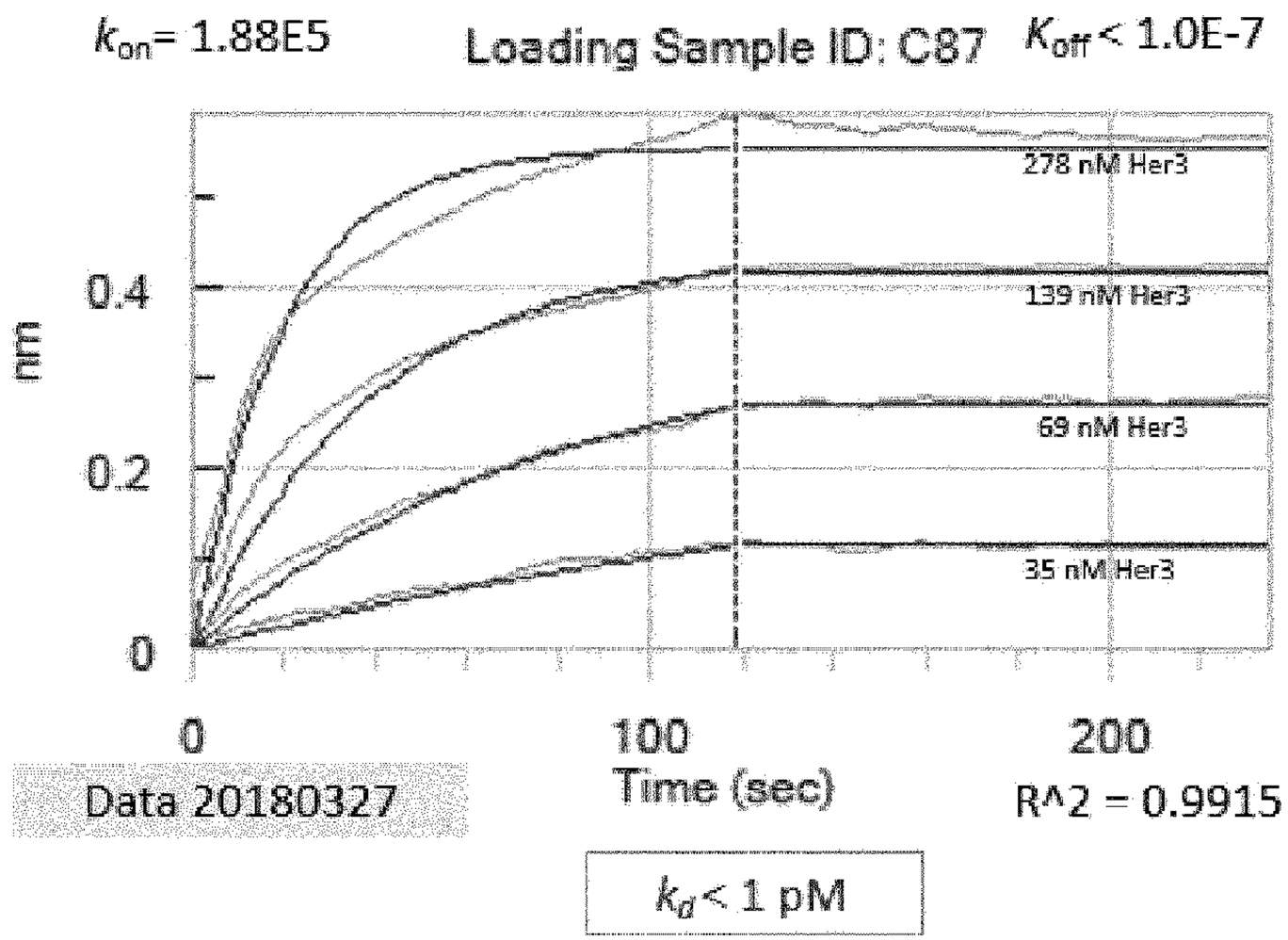
Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C78 v11b	7	69	0.1929	4.10E-10	6.84E-10	1.47E+05	4.57E+03	6.01E-05	1.00E-04	0.288	0.0074	1.02E-02	0.2863	99.4	0.0157	0.9954
C78 v11b	7	35	0.0786	4.10E-10	6.84E-10	1.47E+05	4.57E+03	6.01E-05	1.00E-04	0.1714	0.0072	5.19E-03	0.1695	98.8	0.0157	0.9954
C78 v11b	7	139	0.3283	4.10E-10	6.84E-10	1.47E+05	4.57E+03	6.01E-05	1.00E-04	0.3745	0.006	2.04E-02	0.3734	99.7	0.0157	0.9954
C78 v11b	7	278	0.5147	4.10E-10	6.84E-10	1.47E+05	4.57E+03	6.01E-05	1.00E-04	0.4982	0.0045	4.08E-02	0.4975	99.9	0.0157	0.9954

Figure 36D



Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C85 opt2	5	139	0.1967	1.73E-08	1.35E-09	9.74E+04	3.54E+03	1.68E-03	1.16E-04	0.2688	0.0066	1.52E-02	0.2389	88.9	0.0086	0.9957
C85 opt2	5	35	0.0338	1.73E-08	1.35E-09	9.74E+04	3.54E+03	1.68E-03	1.16E-04	0.1225	0.0074	5.09E-03	0.082	66.9	0.0086	0.9957
C85 opt2	5	278	0.3885	1.73E-08	1.35E-09	9.74E+04	3.54E+03	1.68E-03	1.16E-04	0.4109	0.006	2.88E-02	0.3868	94.1	0.0086	0.9957
C85 opt2	5	69	0.0911	1.73E-08	1.35E-09	9.74E+04	3.54E+03	1.68E-03	1.16E-04	0.1681	0.0069	8.40E-03	0.1504	80	0.0086	0.9957

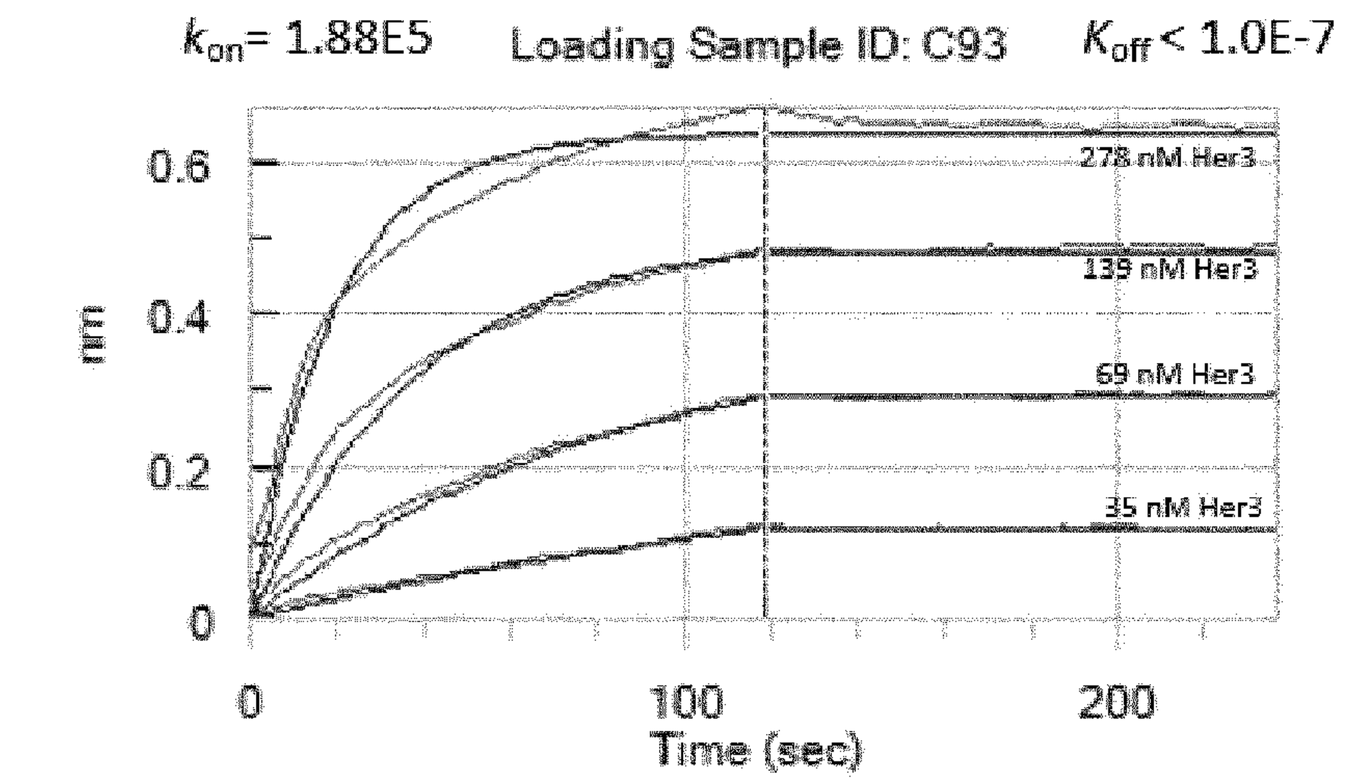
Figure 36E



Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C87	4	278	0.5768	<1.0E-12	6.64E-10	1.88E+05	7.36E+03	<1.0E-07		0.5516	0.0055	5.23E-02	0.5516	100	0.0357	0.9915
C87	4	69	0.2569	<1.0E-12	6.64E-10	1.88E+05	7.36E+03	<1.0E-07		0.3401	0.0095	1.30E-02	0.3401	100	0.0357	0.9915
C87	4	139	0.4134	<1.0E-12	6.64E-10	1.88E+05	7.36E+03	<1.0E-07		0.4359	0.0072	2.62E-02	0.4359	100	0.0357	0.9915
C87	4	35	0.114	<1.0E-12	6.64E-10	1.88E+05	7.36E+03	<1.0E-07		0.2098	0.0096	6.59E-03	0.2098	100	0.0357	0.9915

Figure 36F

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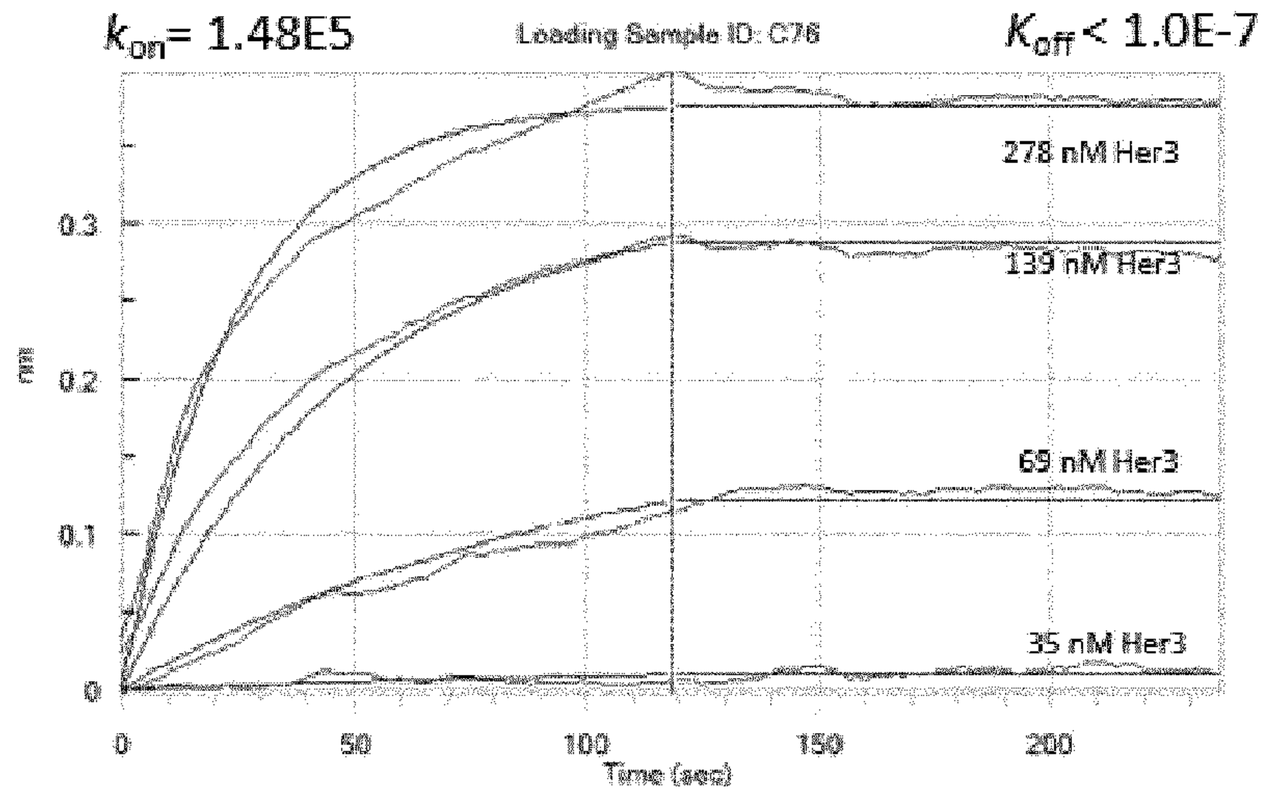
Data 20180327

k_d < 1 pM

R^2 = 0.9946

Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C93	1	69	0.2877	<1.0E-12	5.46E-10	1.88E+05	5.99E+03	<1.0E-07		0.37	0.0088	1.30E-02	0.37	100	0.0335	0.9946
C93	1	278	0.6639	<1.0E-12	5.46E-10	1.88E+05	5.99E+03	<1.0E-07		0.6372	0.0052	5.22E-02	0.6372	100	0.0335	0.9946
C93	1	139	0.4777	<1.0E-12	5.46E-10	1.88E+05	5.99E+03	<1.0E-07		0.5032	0.0088	2.61E-02	0.5032	100	0.0335	0.9946
C93	1	35	0.119	<1.0E-12	5.46E-10	1.88E+05	5.99E+03	<1.0E-07		0.2179	0.0088	6.58E-03	0.2179	100	0.0335	0.9946

Figure 36G



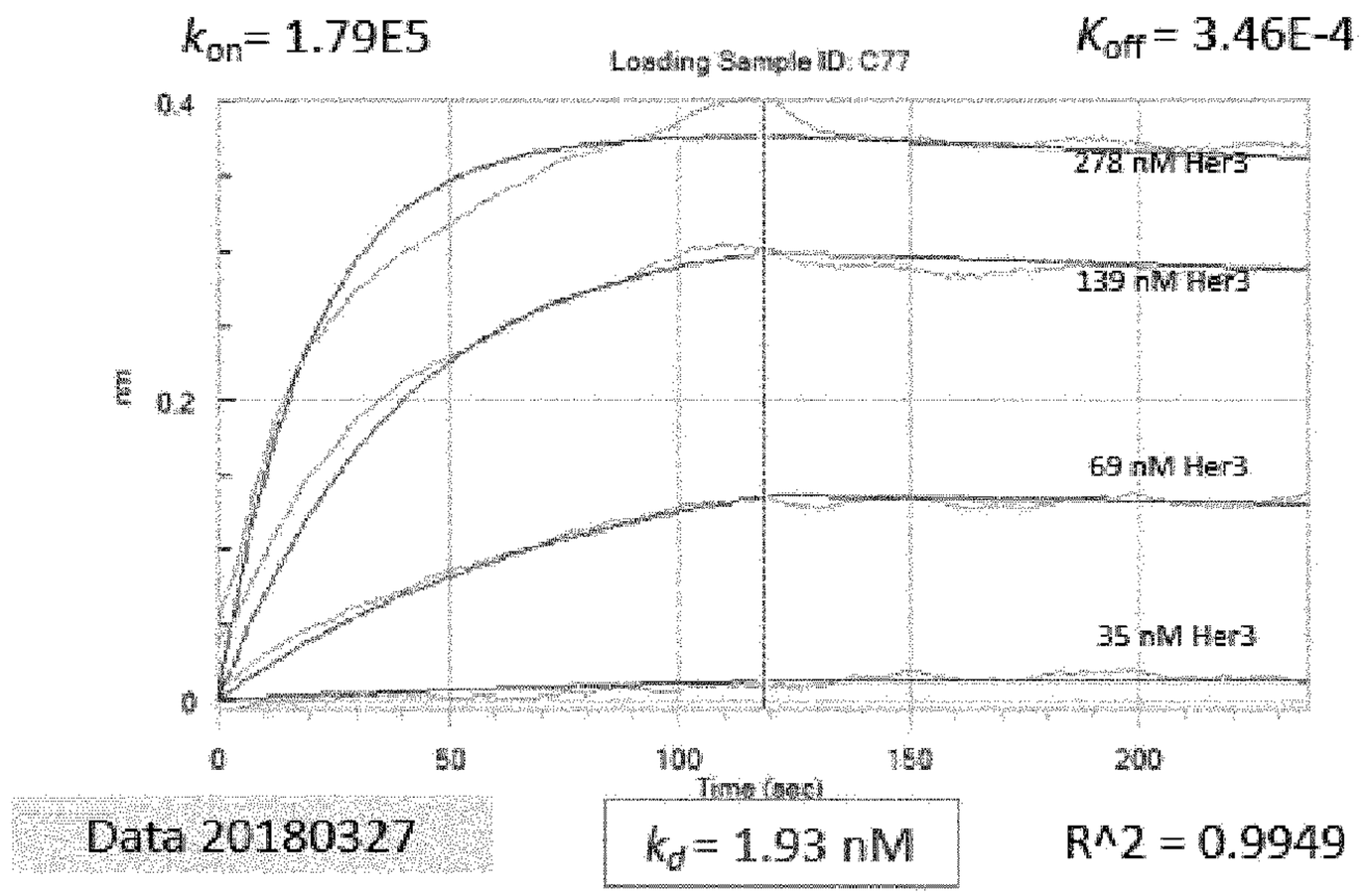
Data 20180327

k_d < 1 pM

R^2 = 0.9951

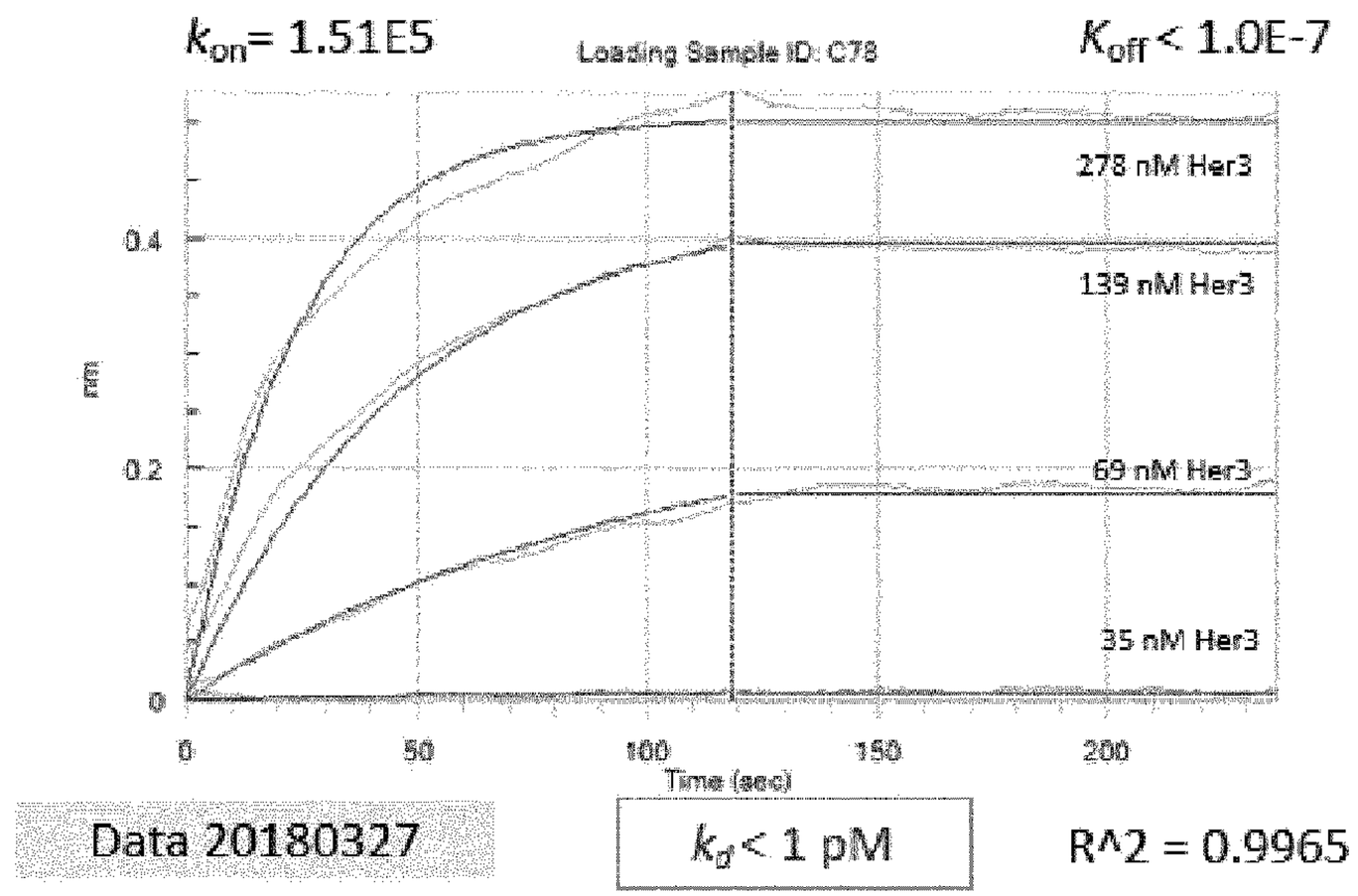
Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C76	3	278	0.3903	<1.0E-12	7.94E-10	1.48E+05	5.36E+03	<1.0E-07		0.3772	0.004	4.13E-02	0.3772	100	0.0122	0.9951
C76	3	139	0.2889	<1.0E-12	7.94E-10	1.48E+05	5.36E+03	<1.0E-07		0.3143	0.0057	2.06E-02	0.3143	100	0.0122	0.9951
C76	3	69	0.1082	<1.0E-12	7.94E-10	1.48E+05	5.36E+03	<1.0E-07		0.172	0.0054	1.02E-02	0.172	100	0.0122	0.9951
C76	3	35	0.0037	<1.0E-12	7.94E-10	1.48E+05	5.36E+03	<1.0E-07		0.0208	0.0047	5.19E-03	0.0208	100	0.0122	0.9951

Figure 36H



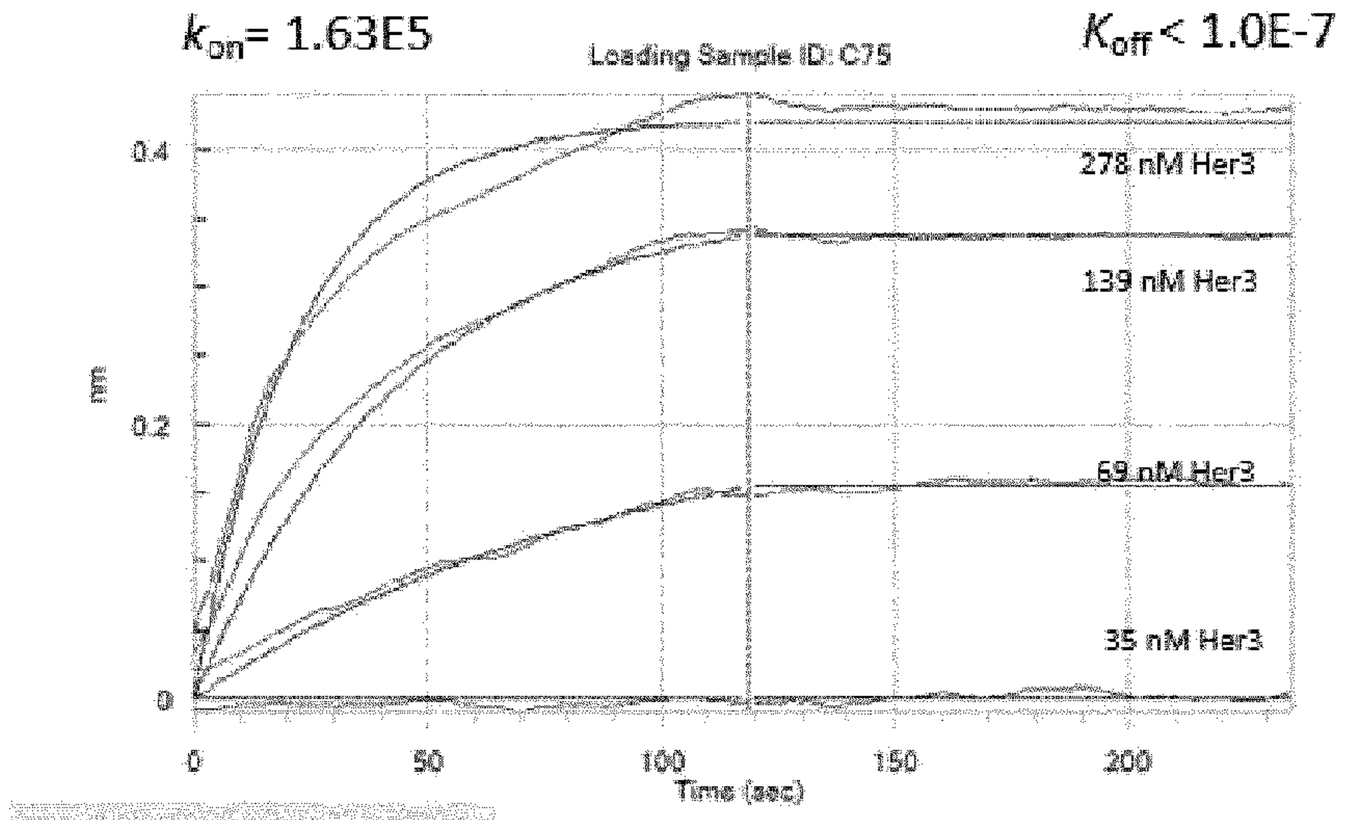
Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C77	2	35	0.0096	1.93E-09	6.58E-10	1.79E+05	6.34E+03	3.46E-04	1.17E-04	0.0236	0.0043	6.82E-03	0.0224	94.8	0.0142	0.9949
C77	2	69	0.1318	1.93E-09	6.58E-10	1.79E+05	6.34E+03	3.46E-04	1.17E-04	0.1794	0.0051	1.27E-02	0.1745	97.3	0.0142	0.9949
C77	2	139	0.3036	1.93E-09	6.58E-10	1.79E+05	6.34E+03	3.46E-04	1.17E-04	0.3187	0.005	2.53E-02	0.3143	98.6	0.0142	0.9949
C77	2	278	0.3995	1.93E-09	6.58E-10	1.79E+05	6.34E+03	3.46E-04	1.17E-04	0.3804	0.0038	5.02E-02	0.3778	99.3	0.0142	0.9949

Figure 36I



Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C78	4	278	0.5153	<1.0E-12	6.54E-10	1.51E+05	4.60E+03	<1.0E-07		0.5037	0.0044	4.21E-02	0.5037	100	0.0176	0.9965
C78	4	35	0.0036	<1.0E-12	6.54E-10	1.51E+05	4.60E+03	<1.0E-07		0.0136	0.0052	5.30E-03	0.0136	100	0.0176	0.9965
C78	4	69	0.1598	<1.0E-12	6.54E-10	1.51E+05	4.60E+03	<1.0E-07		0.2495	0.0064	1.04E-02	0.2495	100	0.0176	0.9965
C78	4	139	0.3891	<1.0E-12	6.54E-10	1.51E+05	4.60E+03	<1.0E-07		0.429	0.0064	2.10E-02	0.429	100	0.0176	0.9965

Figure 36J



Data 20180327

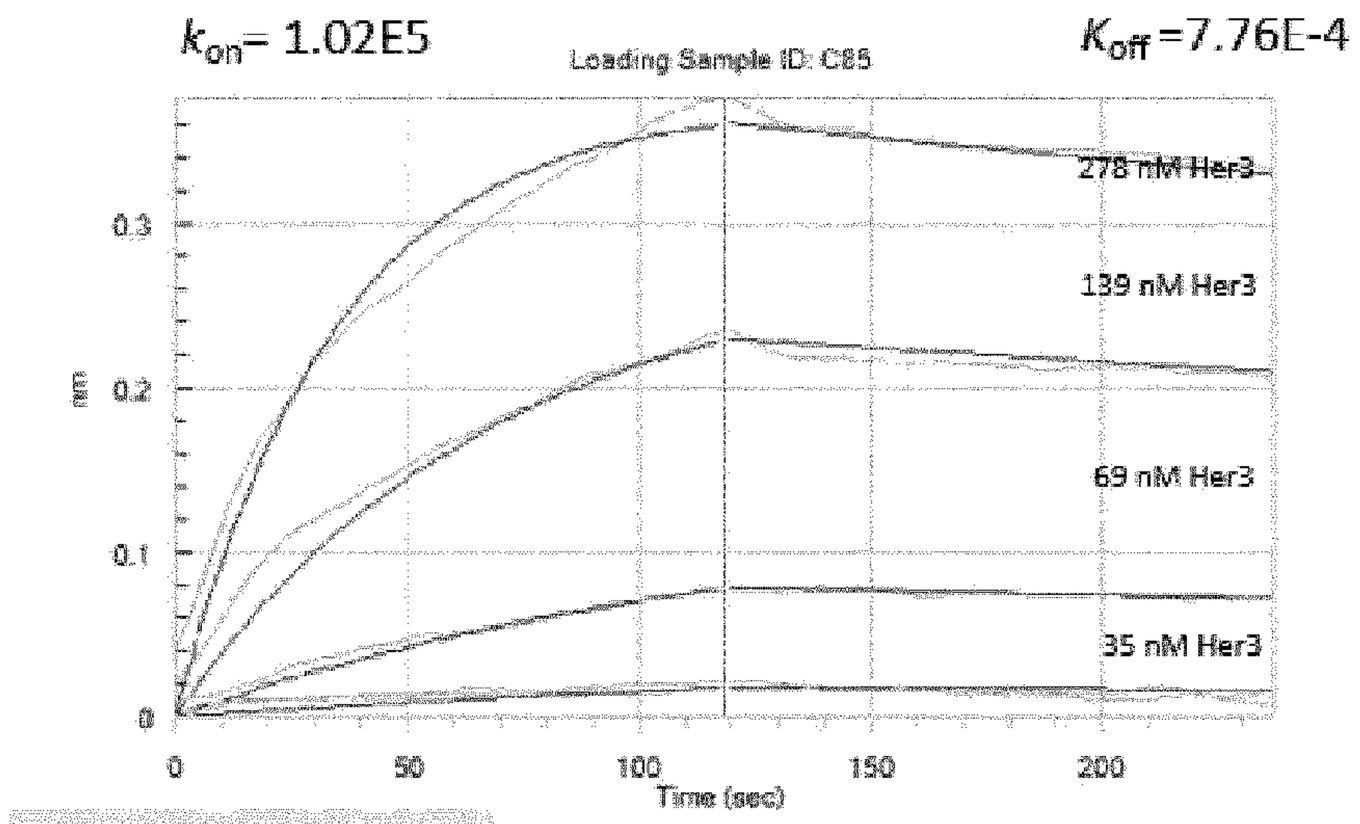
R^2 = 0.9955

k_d< 1 pM

Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C75		5	69	0.1507	<1.0E-12	8.91E-10	1.83E+05	5.62E+03	<1.0E-07	0.2092	0.0059	1.12E-02	0.2092	100	0.0161	0.9955
C75		5	139	0.3396	<1.0E-12	8.91E-10	1.83E+05	5.62E+03	<1.0E-07	0.3832	0.0059	2.27E-02	0.3832	100	0.0161	0.9955
C75		5	278	0.4384	<1.0E-12	8.91E-10	1.83E+05	5.62E+03	<1.0E-07	0.4216	0.004	4.53E-02	0.4216	100	0.0161	0.9955
C75		5	35	-0.0012	<1.0E-12	8.91E-10	1.83E+05	5.62E+03	<1.0E-07	0		5.70E-03	0	100	0.0161	0.9955

Figure 36K

DK/EP 3645571 T3



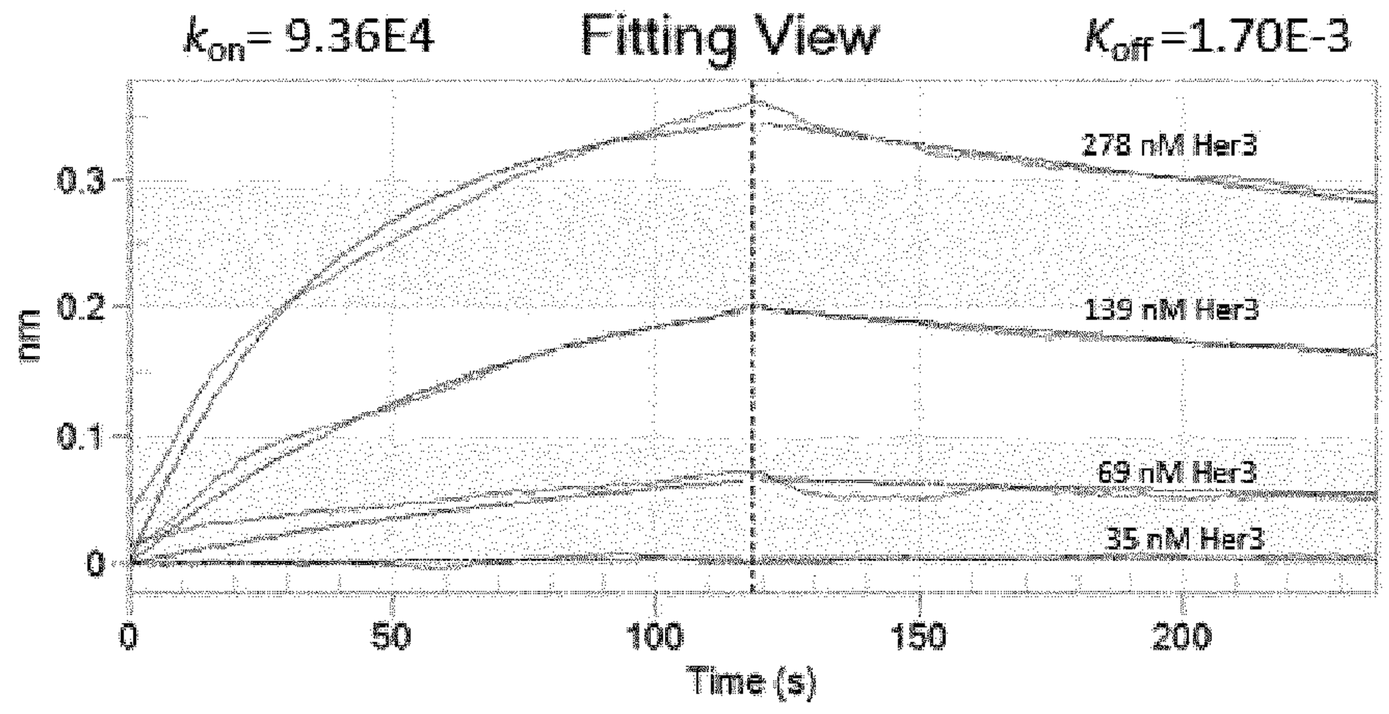
Data 20180327

R^2 = 0.9957

k_d = 7.58 nM

Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C85	1	278	0.3712	7.58E-09	1.19E-09	1.02E+05	3.85E+03	7.76E-04	1.19E-04	0.3816	0.0054	2.92E-02	0.3715	97.3	0.0091	0.9957
C85	1	69	0.0753	7.58E-09	1.19E-09	1.02E+05	3.85E+03	7.76E-04	1.19E-04	0.1436	0.0057	7.83E-03	0.1294	90.1	0.0091	0.9957
C85	1	139	0.2264	7.58E-09	1.19E-09	1.02E+05	3.85E+03	7.76E-04	1.19E-04	0.2898	0.007	1.50E-02	0.2748	94.8	0.0091	0.9957
C85	1	35	0.017	7.58E-09	1.19E-09	1.02E+05	3.85E+03	7.76E-04	1.19E-04	0.053	0.0050	4.36E-03	0.0435	82.2	0.0091	0.9957

Figure 36L



Data 20180327 | k_d= 18.2 nM | R^2 = 0.9957

Loading Sample ID	Cycle	Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
C85 opt1		1	278	0.3524	1.82E-08	1.54E-09	9.36E+04	3.75E+03	1.70E-03	1.27E-04	0.3807	0.0063	2.77E-02	0.3573	93.9	0.008	0.9957
C85 opt1		1	139	0.1929	1.82E-08	1.54E-09	9.36E+04	3.75E+03	1.70E-03	1.27E-04	0.2709	0.0074	1.47E-02	0.2396	88.4	0.008	0.9957
C85 opt1		1	69	0.0687	1.82E-08	1.54E-09	9.36E+04	3.75E+03	1.70E-03	1.27E-04	0.1329	0.0059	8.16E-03	0.1052	79.2	0.008	0.9957
C85 opt1		1	35	0.0006	1.82E-08	1.54E-09	9.36E+04	3.75E+03	1.70E-03	1.27E-04	0.0131	0.0061	4.97E-03	0.0086	65.8	0.008	0.9957

Figure 36M

Clones	Heavy Chain	Light Chain	Developability								
	Homology	Homology	Deamidation (NS, NG, NH, NN)	Isomerization (DS, DG)	Protease Cleavage (DP)	Free Cys	Exposed M	Glycosylation	Immunogenicity (HC+LC)	pI_HC	pI_LC
10D1_c75	82.5%(Hu)	80.0%(Ma)	NG,	None	None	None	YES (CDR3)	NPT	3+6	8.102	6.615
10D1_c76	83.5%(Hu)	77.9%(Ma)	NG,	None	None	None	YES (CDR3)	NPS	3+5	8.121	6.614
10D1_c77	83.5%(Hu)	78.5%(Hu)	NG,	None	None	None	YES (CDR3)	NPS	4+3	8.121	7.618
10D1_c78	83.5%(Hu)	81.1%(Ma)	None	None	None	None	YES (CDR3)	NPS	3+3	8.591	8.128
V11b78L	88.7%(Hu)	81.1%(Ma)	None	None	None	None	YES (CDR3)	NPS	3+3	8.453	8.128
10D1_c85	82.5% (Hu)	81.1%(Ma)	None	None	None	None	YES (CDR3)	NPS	1+3	8.952	8.578
10D1_c85_opt1	83.5% (Hu)	81.1%(Ma)	None	None	None	None	NO	NPS	0+3	8.6	8.578
10D1_c85_opt2	83.5% (Hu)	81.1%(Ma)	None	None	None	None	NO	NPS	0+3	8.952	8.578
10D1_c87	82.5% (Hu)	80.0%(Ma)	NG,	None	None	None	YES (CDR3)	NPS	3+5	8.13	4.646
10D1_c89	89.9% (Hu)	85.3% (Hu/Ma)	None	None	None	None	YES (CDR3)	None	3+4	7.965	6.545
10D1_c90	89.9% (Hu)	80.0% (Ma)	None	None	None	None	YES (CDR3)	None	3+4	7.965	5.388
10D1_c91	87.9% (Hu)	84.2 (Hu/Ma)	None	None	None	None	YES (CDR3)	None	3+3	7.935	7.468
10D1_c92	82.5% (Hu)	78.9% (Ma)	None	None	None	None	YES (CDR3)	N.A.	4+6	8.07	6.46
10D1_c93	82.5% (Hu)	82.1%(Ma)	NG	None	None	None	YES (CDR3)	NPS	3+5	8.13	7.535

Figure 37

k_{on} = 1.8e^5 M^{-1} s^{-1} K_D = 34 nM k_{dis} = 0.61e^{-2} s^{-1}

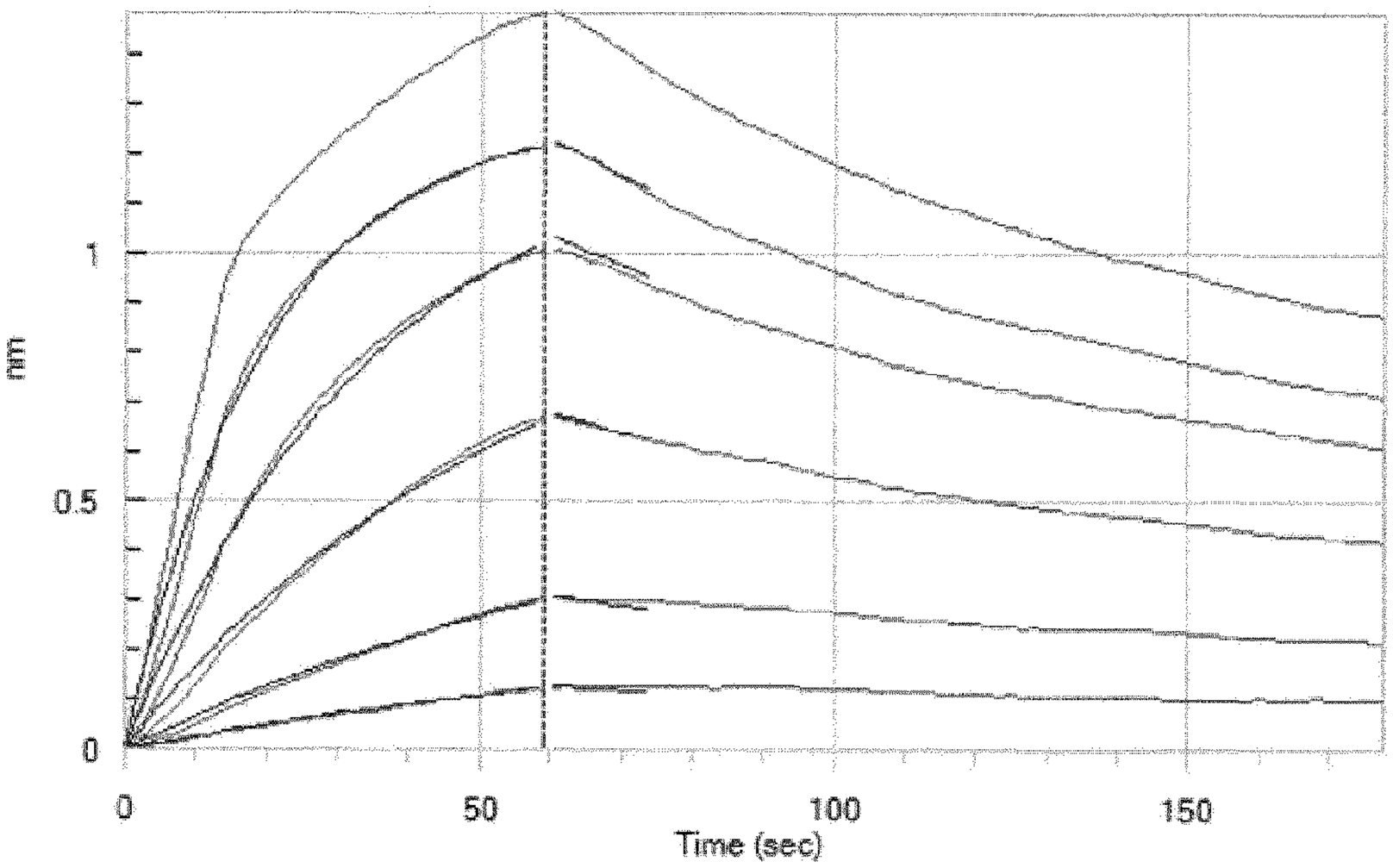


Figure 38A

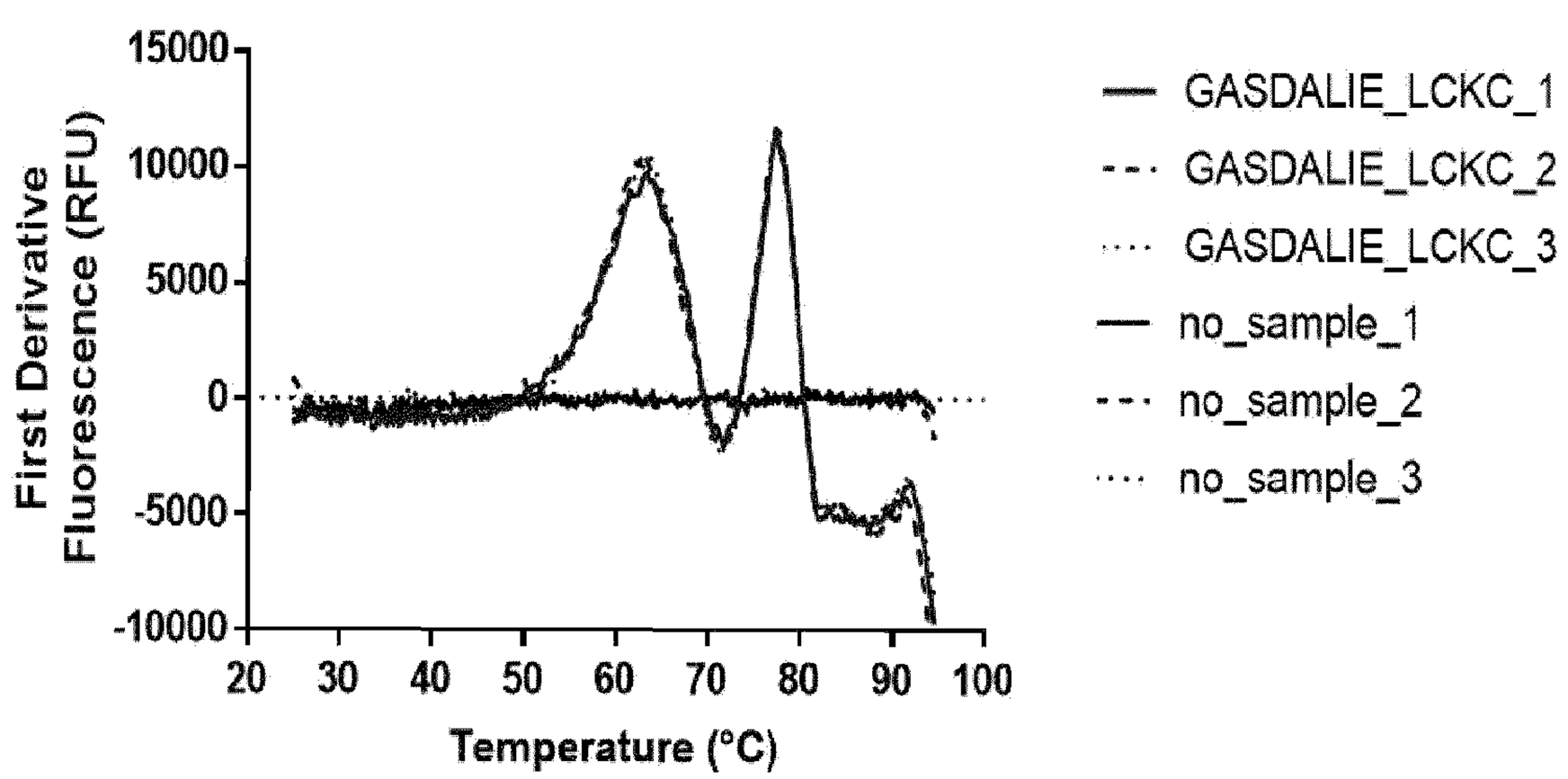


Figure 38B

$K_{on} = 1.3e^{5}\ M^{-1}\ s^{-1}$ $K_d = 298\ nM$ $K_{dis} = 4.0e^{-2}\ s^{-1}$

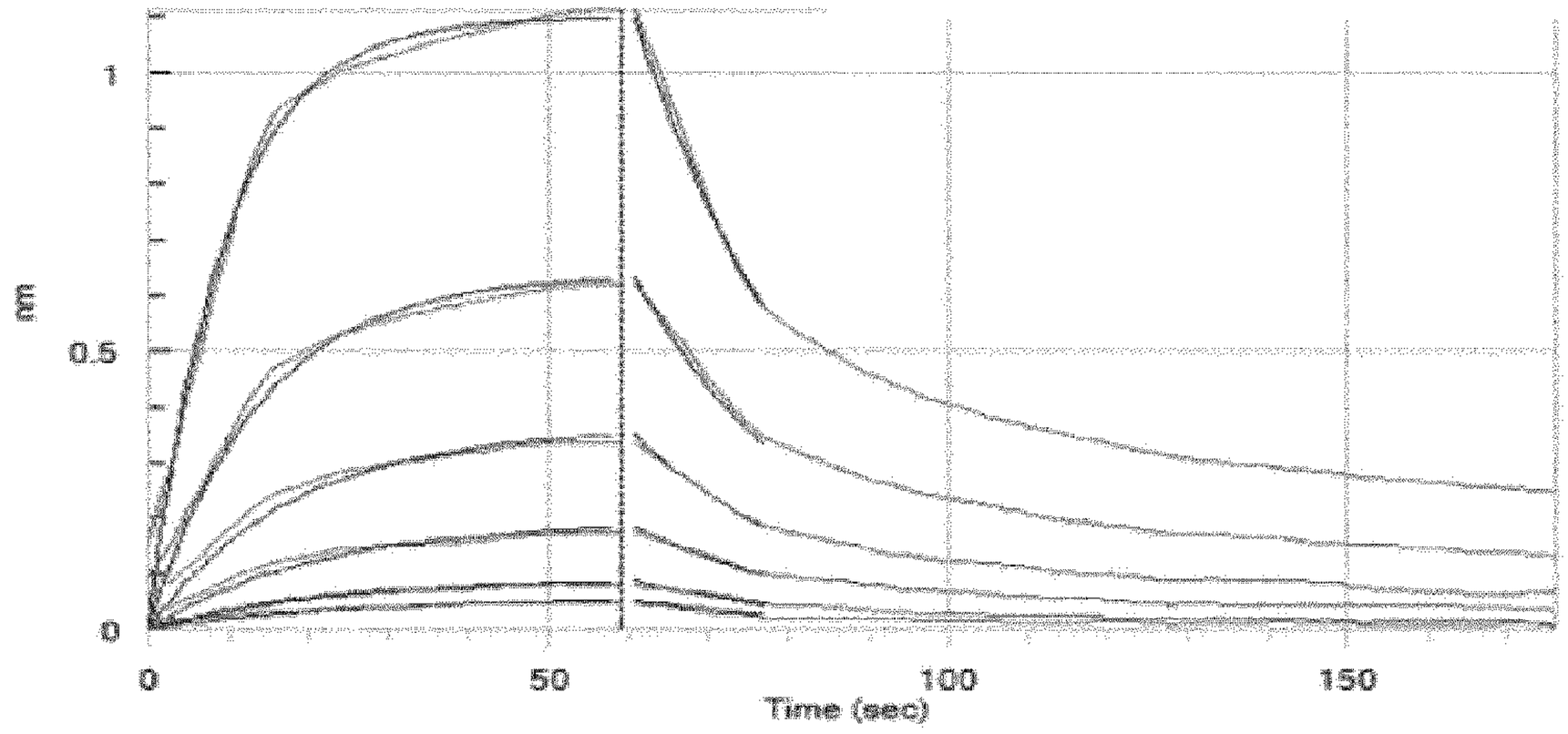


Figure 39A

$K_{on} = 1.6e^{5}\ M^{-1}\ s^{-1}$ $K_d = 58\ nM$ $K_{dis} = 0.90e^{-2}\ s^{-1}$

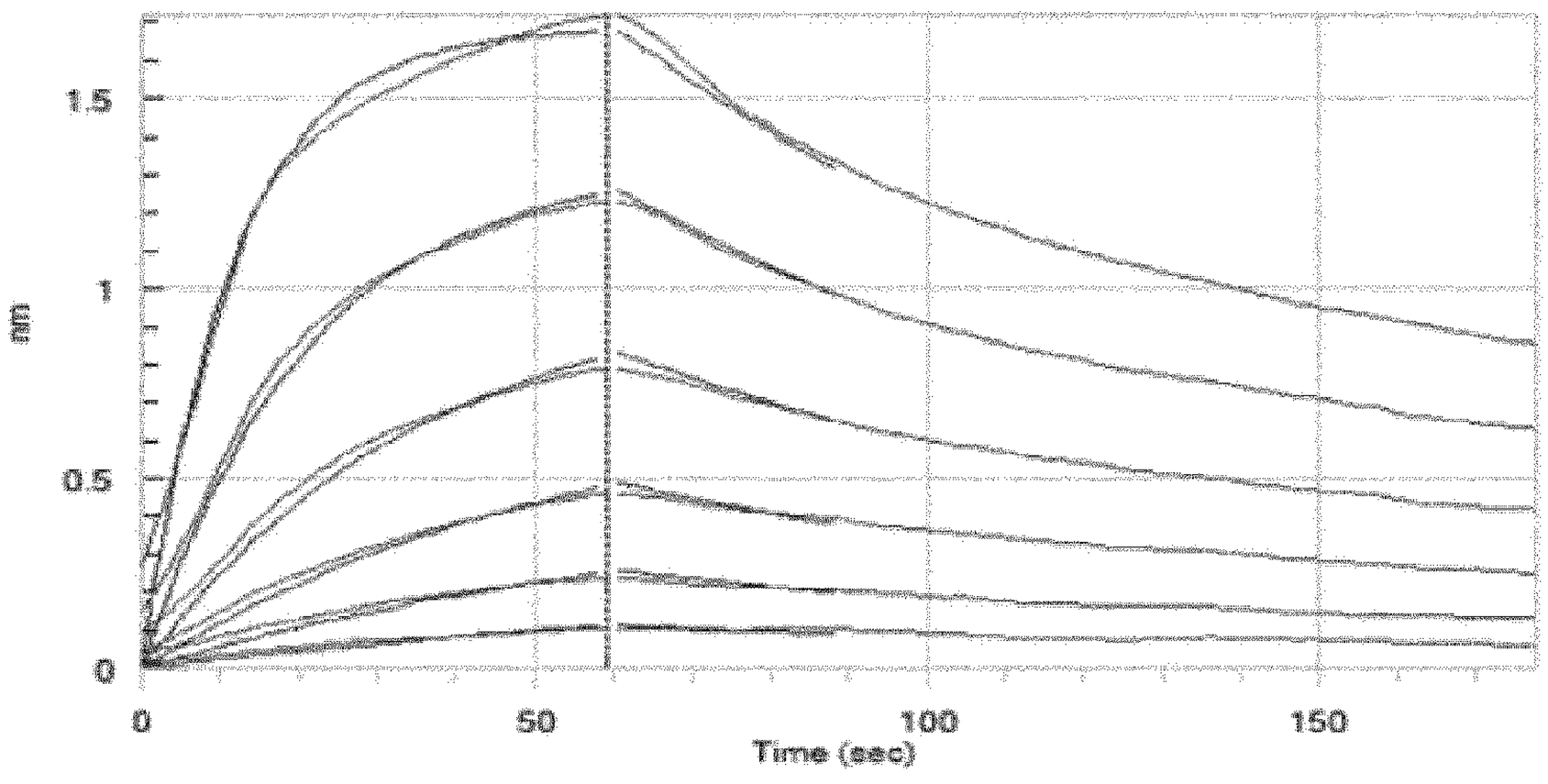


Figure 39B

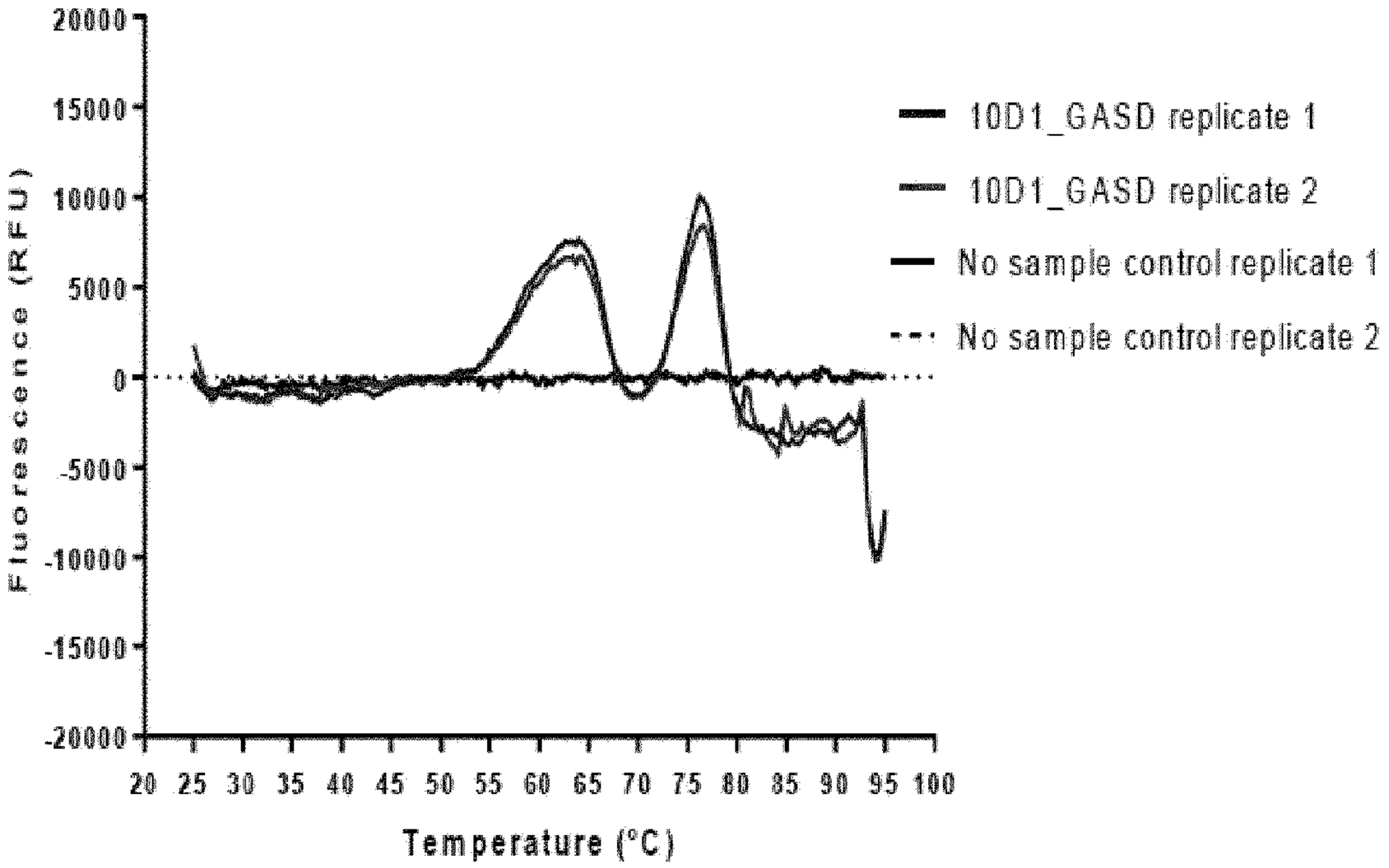

20000
15000
10000
5000
0
-5000
-10000
-15000
-20000
First Derivative Fluorescence (RFU)
20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
Temperature (°C)
10D1_GASD replicate 1
10D1_GASD replicate 2
No sample control replicate 1
No sample control replicate 2

Figure 40

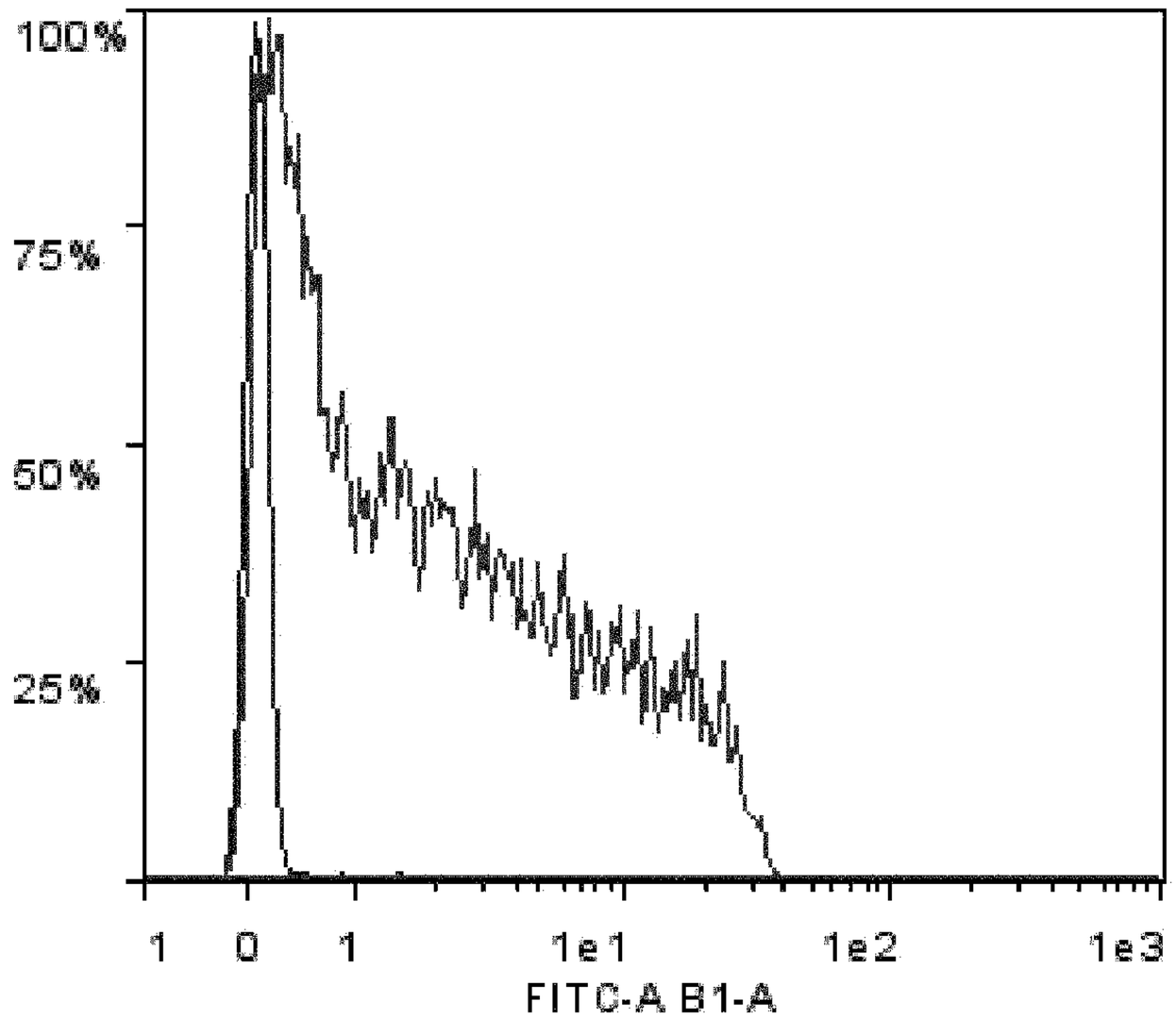
Receptor	Gene	Function	Binding Affinity	Reported K_D (nM)	10D1F.FcA: 10D1F hIgG1 K_D (nM)	10D1F.FcB: 10D1F hIgG1 GASDALIE.LCKC K_D (nM)	10D1F hIgG1 N297Q K_D (nM)	10D1F hIgG2 K_D (nM)	10D1F hIgG4 K_D (nM)	LJM716 hIgG1 K_D (nM)	Seribantumab hIgG2 K_D (nM)
FcRn	FCGRT	Recycling (Increased affinity → Increased half life)	Medium	hIgG1: 737 hIgG2: 540 hIgG3: 585 hIgG4: 717	47.6	37.4	54.6	6.43	10.3	16.5	11.5
FcgRIIIA (V158)	CD16A	Cell activation	Medium	hIgG1: 252-500 hIgG2: 14286 hIgG3: 102 hIgG4: 4000	986	82.1	ND	ND	ND	705	7050
FcgRIIIA (F158)	CD16A	Cell activation	Low	hIgG1: 855-4454 hIgG2: 33333 hIgG3: 130 hIgG4: 5000	ND	162	ND	ND	ND	5380	ND
FcgRIIA (H167)	CD32A	Cell activation	Low	hIgG1: 192-4486 hIgG2: 2222 hIgG3: 1124 hIgG4: 5882	1800	561	ND	670	ND	1480	222
FcgRIIA (R167)	CD32A	Cell activation	Low	hIgG1: 286-1550 hIgG2: 10000 hIgG3: 1099 hIgG4: 4762	976	400	ND	ND	ND	1500	243
FcgRIIB	CD32B	Cell inhibition	Low	hIgG1: 500-9275 hIgG2: 50000 hIgG3: 5882 hIgG4: 5000	ND	580	ND	ND	ND	ND	1440

Figure 41A

DK/EP 3645571 T3

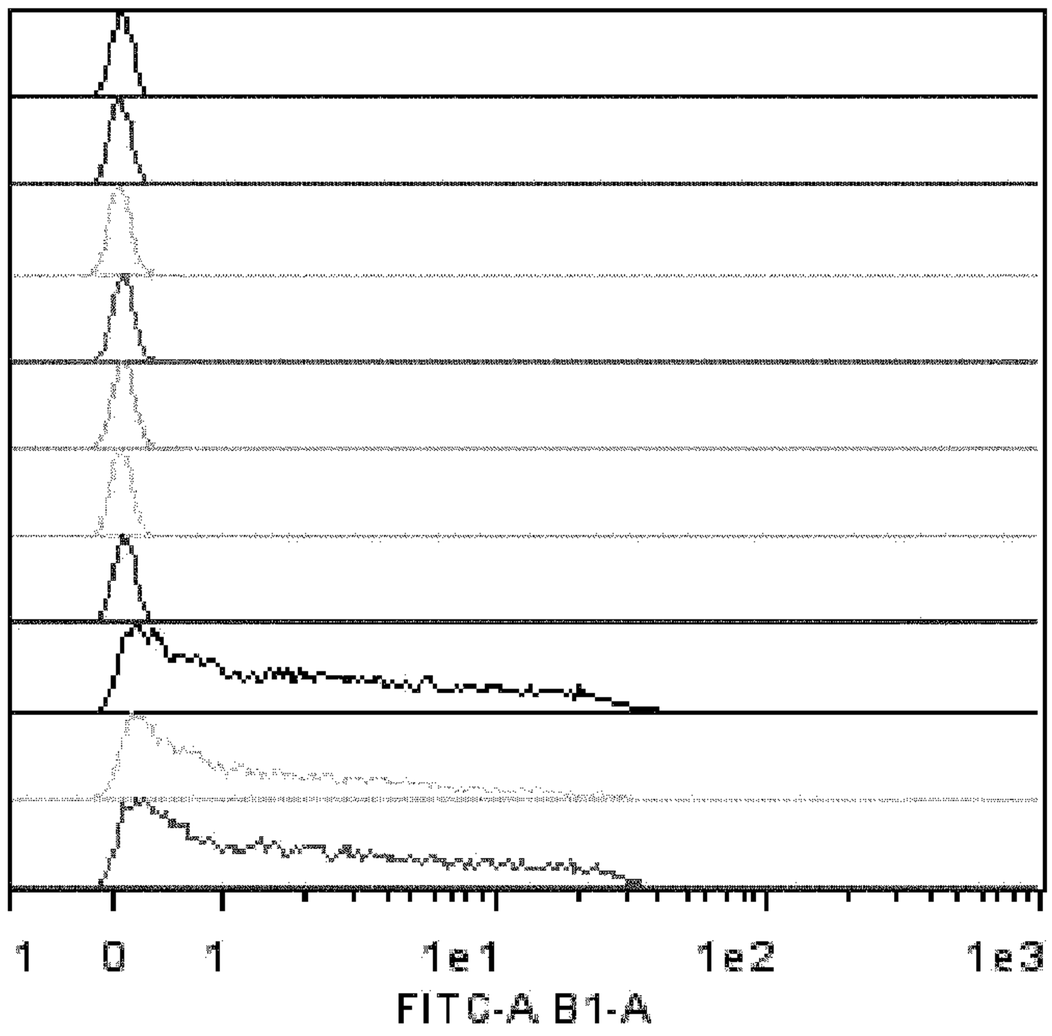
Receptor	Gene	Function	Binding affinity	Reported K_D (nM)		10D1F FcA 10D1F hIgG1 K_D (nM)	10D1F FcB 10D1F hIgG1 GASDALIE LCKC K_D (nM)	10D1F hIgG1 N297Q K_D (nM)	10D1F hIgG2 K_D (nM)	10D1F hIgG4 K_D (nM)	LJM716 hIgG1 K_D (nM)	Seribantumab hIgG2 K_D (nM)
moFcRn	FCGRT	Recycling (Increased affinity → Increased half life)	Medium	mIgG1: 1157 mIgG2a: 490 mIgG2b: 545 mIgG3: 140	hIgG1: 72 hIgG2: 63 hIgG3: 230 hIgG4: 116	14.6	15.2	13.7	7.33	13	12.8	6.69
moFcgRIV	CD16-2	Cell activation	High	mIgG1: ND mIgG2a: 34.5 mIgG2b: 59 mIgG3: ND	hIgG1: 280 hIgG2: ND hIgG3: 170 hIgG4: 26000	1,810	55.4	ND	ND	ND	701	ND
moFcgRIII	CD16	Cell activation	Low	mIgG1: 3200 mIgG2a: 1460 mIgG2b: 1555 mIgG3: ND	hIgG1: 9300 hIgG2: 9700 hIgG3: 1300 hIgG4: 21000	ND	ND	ND	ND	ND	ND	ND
moFcgRIIb	CD32	Cell inhibition	Low	mIgG1: 301 mIgG2a: 2390 mIgG2b: 448 mIgG3: ND	hIgG1: 1100 hIgG2: 7900 hIgG3: 700 hIgG4: 11000	ND	ND	ND	ND	ND	ND	ND

Figure 41B



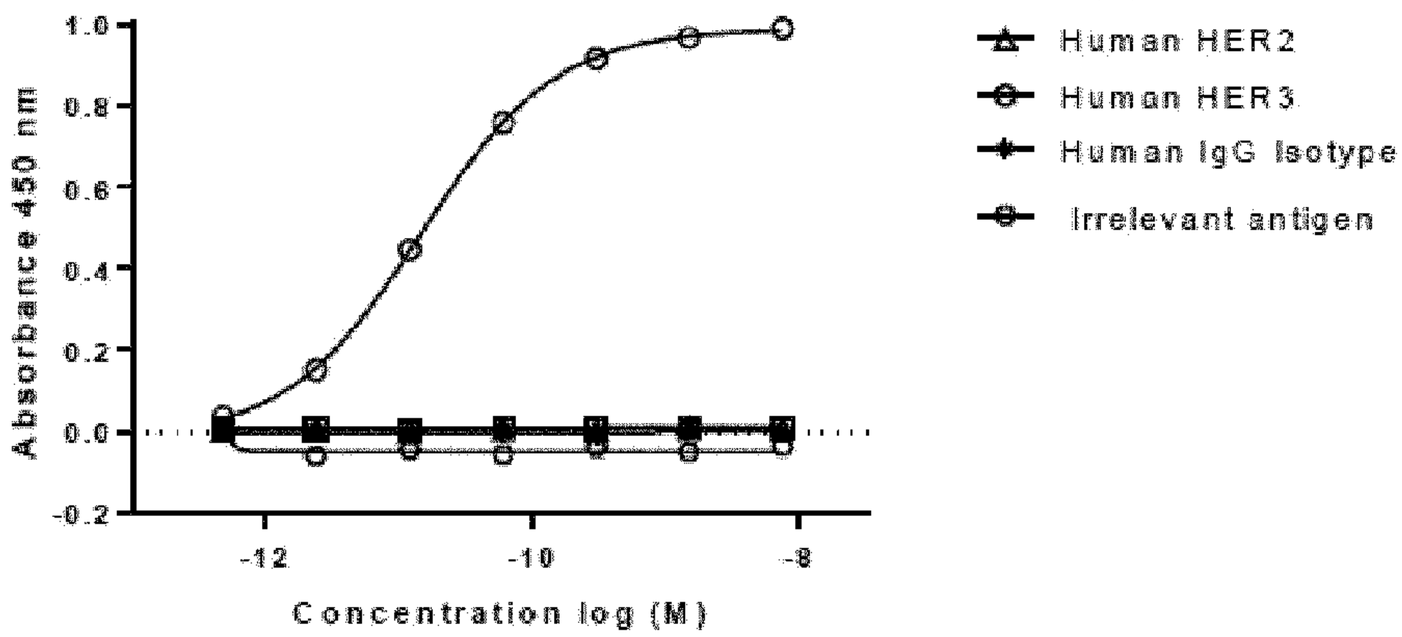
Color	Population	% Parent
	HER3 positive [HEK293T WT: 10 ug 10D1F]	0.07
	HER3 positive [HEK293T HER3 O/E: 10 ug 10D1F]	73.32

Figure 42A



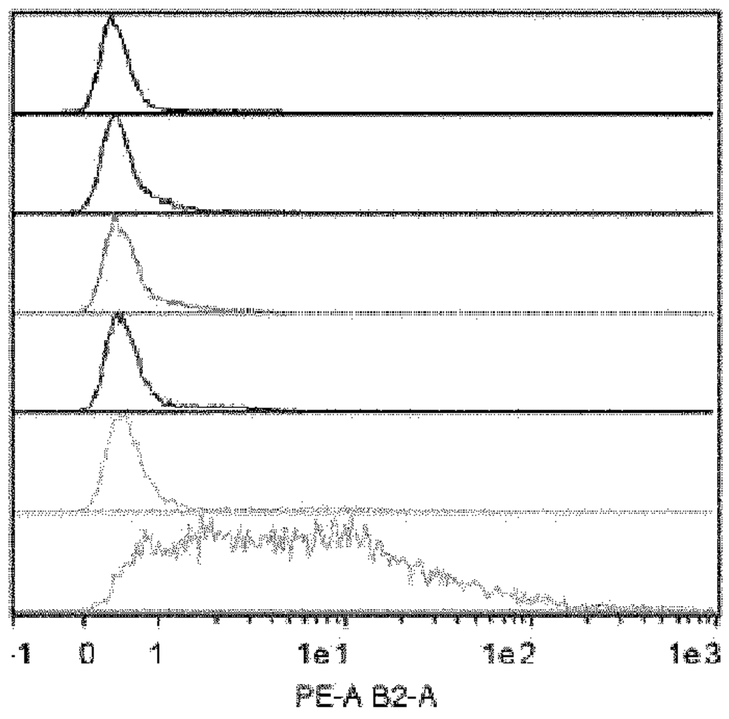
Color	Population	% Parent
	HER3 positive [HEK293T: unstained]	0.00
	HER3 positive [HEK293T WT: 10 ug hIgG1 Isotype]	0.07
	HER3 positive [HEK293T WT: 10 ug LJM716]	0.13
	HER3 positive [HEK293T WT: 10 ug 10D1P]	0.11
	HER3 positive [HEK293T WT: 10 ug 10D1F]	0.07
	HER3 positive [HEK293T HER3 O/E : unstained]	0.05
	HER3 positive [HEK293T HER3 O/E: 10 ug hIgG1 Isotype]	0.18
	HER3 positive [HEK293T HER3 O/E: 10 ug LJM716]	74.36
	HER3 positive [HEK293T HER3 O/E: 10 ug 10D1P]	65.74
	HER3 positive [HEK293T HER3 O/E: 10 ug 10D1F]	73.32

Figure 42B



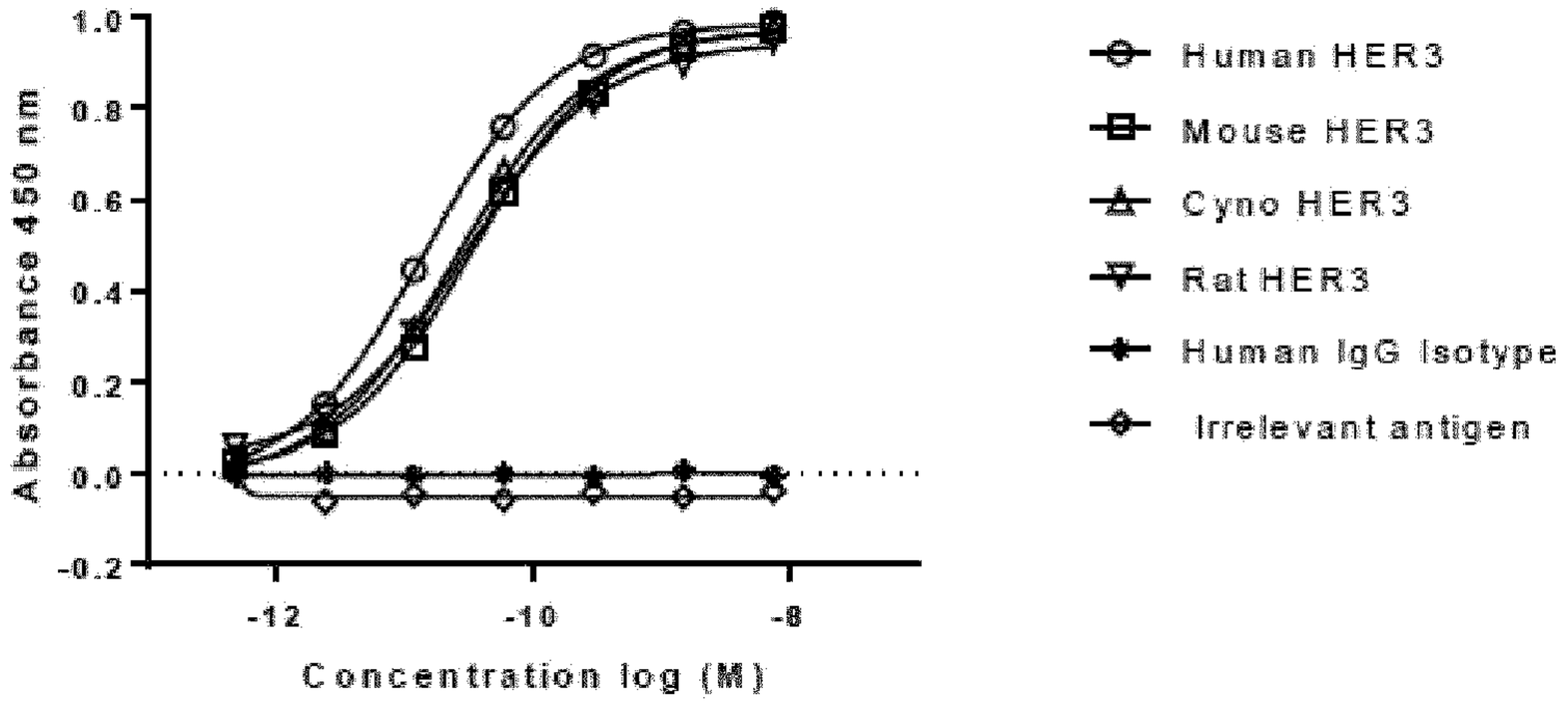
	Human EGFR	Human HER2	Human HER3
EC_{50} (M)	NA	NA	1.437e-011

Figure 43



Antibody	% Positive for HER4
Unstained	0
Isotype	0.07
10D1F.FcA	0.11
LJM-716	0.27
MM-121	8.73
Commercial anti-HER4	50.86

Figure 44



	Human HER3	Mouse HER3	Rat HER3	Cyno HER3
EC_{50} (M)	1.437e-011	3.322e-011	3.032e-011	2.581e-011

Figure 45

Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
69	0.2882	7.26E-11	3.88E-10	2.97E+05	1.12E+04	2.16E-05	1.15E-04	0.3206	0.0063	2.05E-02	0.3202	99.9	0.0341	0.9902
35	0.1471	7.26E-11	3.88E-10	2.97E+05	1.12E+04	2.16E-05	1.15E-04	0.2068	0.0071	1.04E-02	0.2064	99.8	0.0341	0.9902
278	0.5458	7.26E-11	3.88E-10	2.97E+05	1.12E+04	2.16E-05	1.15E-04	0.513	0.0041	8.26E-02	0.5129	100	0.0341	0.9902
139	0.3968	7.26E-11	3.88E-10	2.97E+05	1.12E+04	2.16E-05	1.15E-04	0.3943	0.0046	4.13E-02	0.3941	99.9	0.0341	0.9902

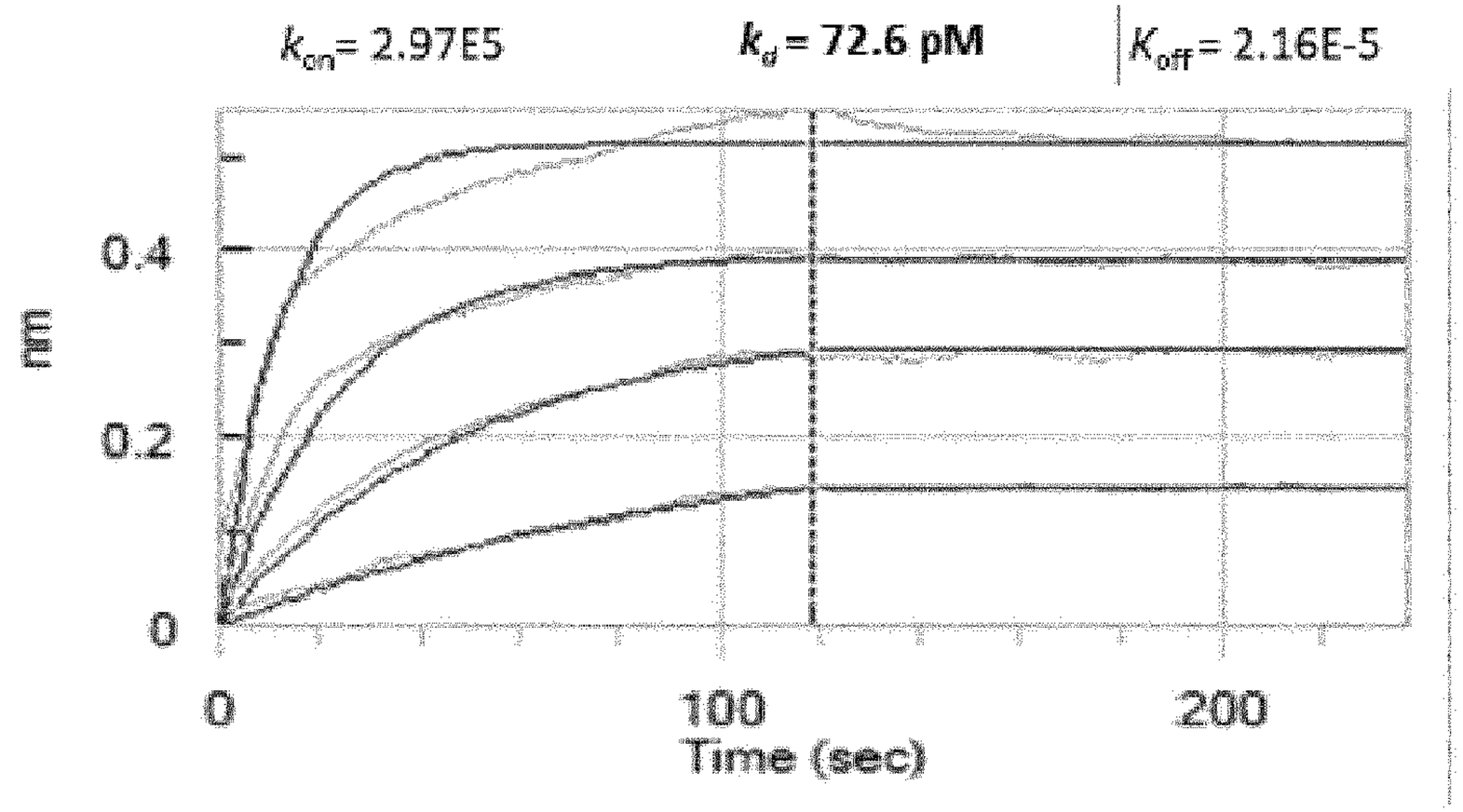


Figure 46A

Conc. (nM)	Response	KD (M)	KD Error	kon(1/Ms)	kon Error	kdis(1/s)	kdis Error	RMax	RMax Error	kobs(1/s)	Req	Req/Rmax(%)	Full X^2	Full R^2
242	0.4624	2.22E-11	2.70E-11	2.23E+05	3.28E+03	4.96E-06	6.03E-06	0.4468	0.001	5.40E-02	0.4467	100	0.0108	0.999
121	0.2437	2.22E-11	2.70E-11	2.23E+05	3.28E+03	4.96E-06	6.03E-06	0.2478	0.001	2.70E-02	0.2478	100	0.0108	0.999
60.5	0.0679	2.22E-11	2.70E-11	2.23E+05	3.28E+03	4.96E-06	6.03E-06	0.0869	0.0009	1.35E-02	0.0868	100	0.0108	0.999
30.3	0.0208	2.22E-11	2.70E-11	2.23E+05	3.28E+03	4.96E-06	6.03E-06	0.0469	0.0011	6.77E-03	0.0468	99.9	0.0108	0.999

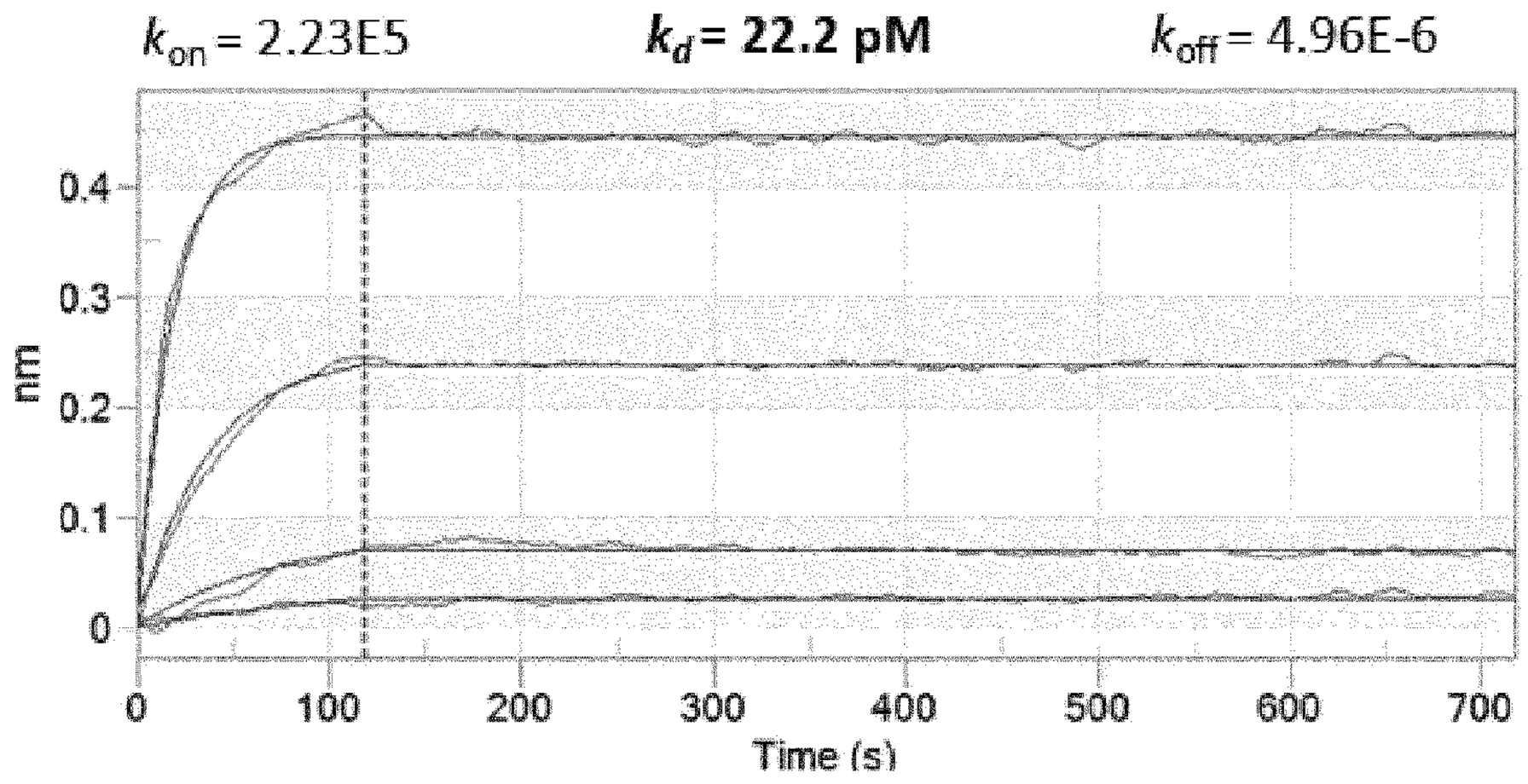
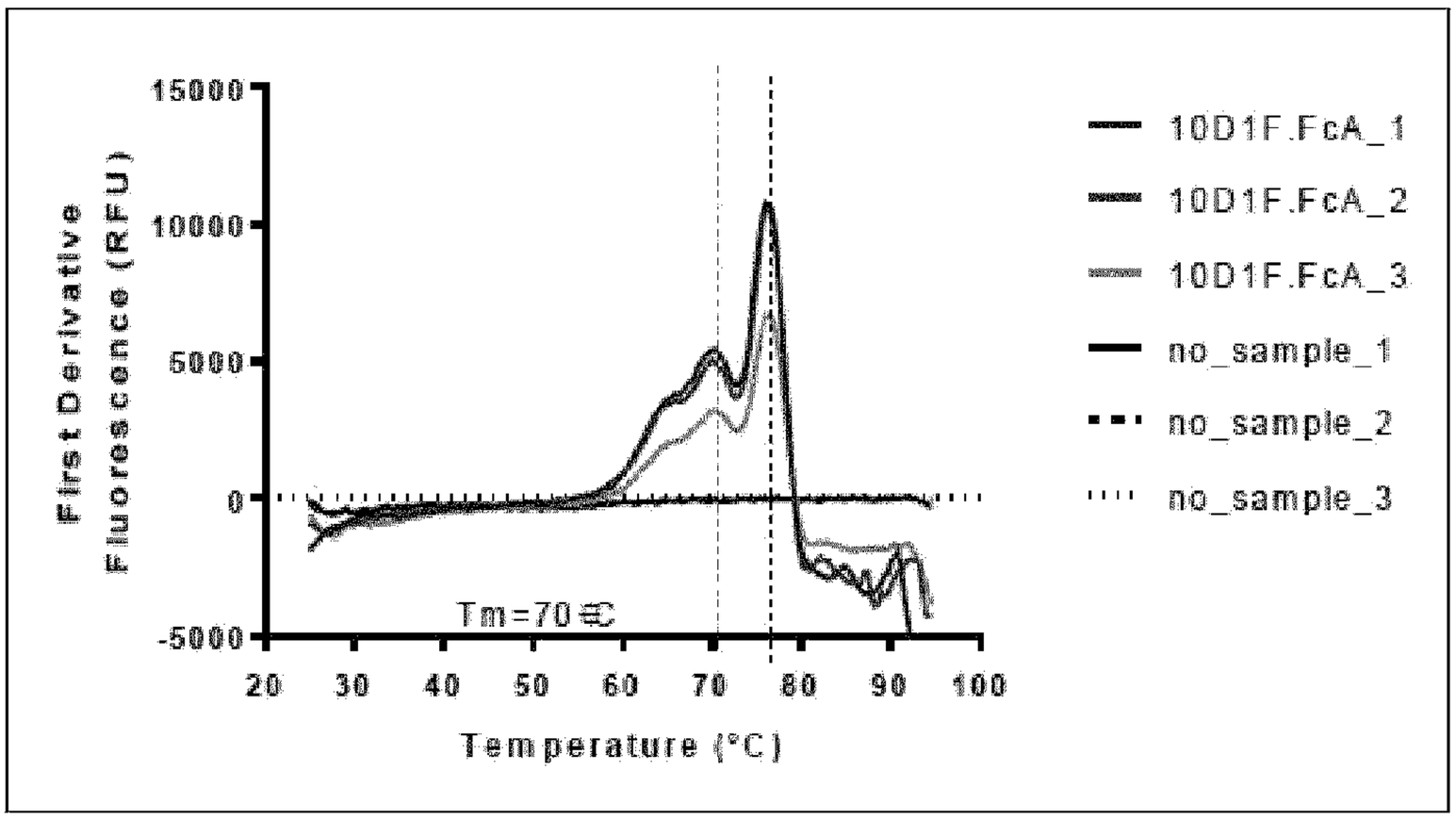
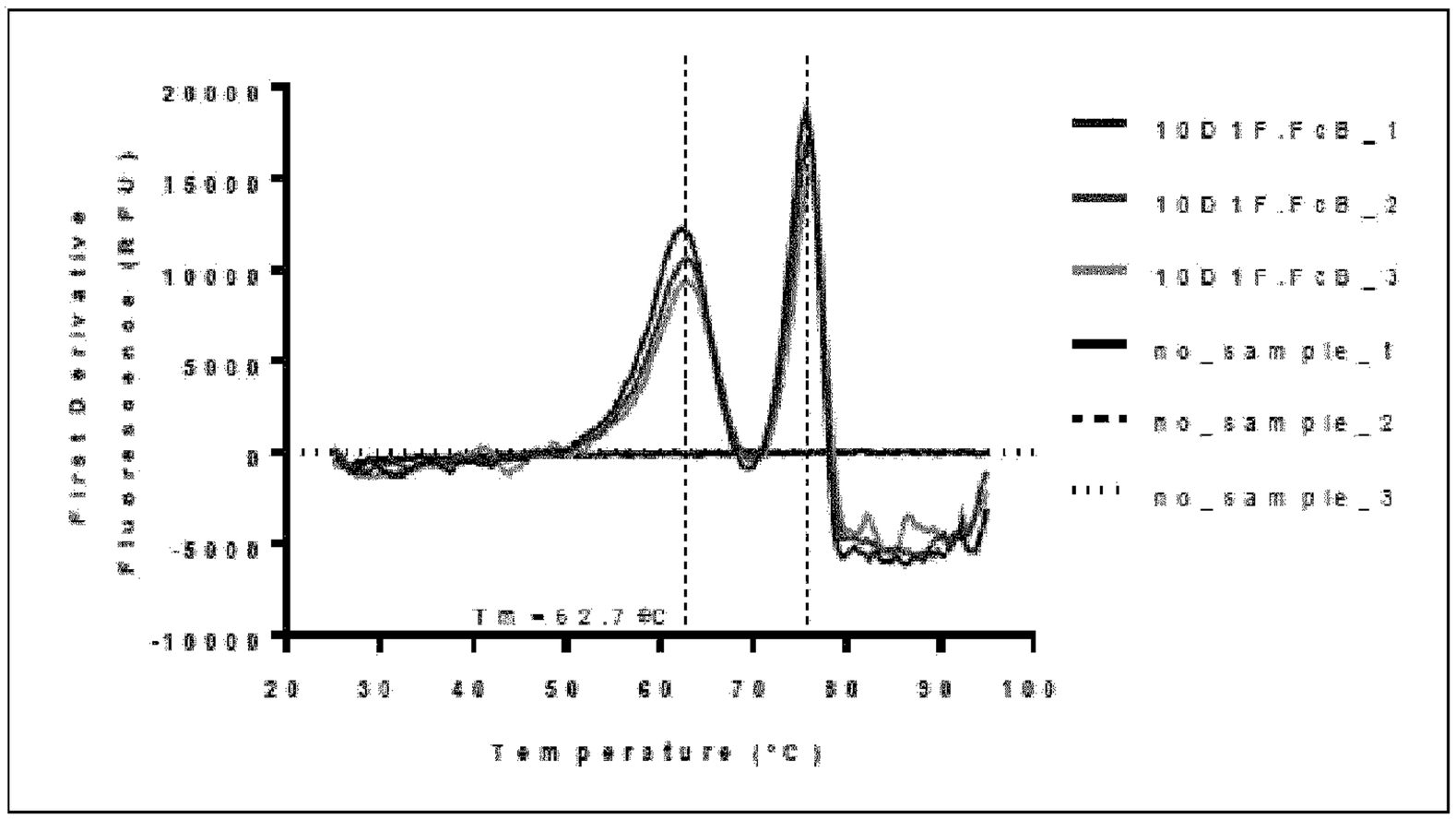


Figure 46B



	Tm1 (℃)	Tm2 (℃)
HMBD-001-10D1F.FcA	70.0	76.8

Figure 47A



	Tm1 (℃)	Tm2 (℃)
HMBD-001-10D1F.FcB	62.7	76.0

Figure 47B

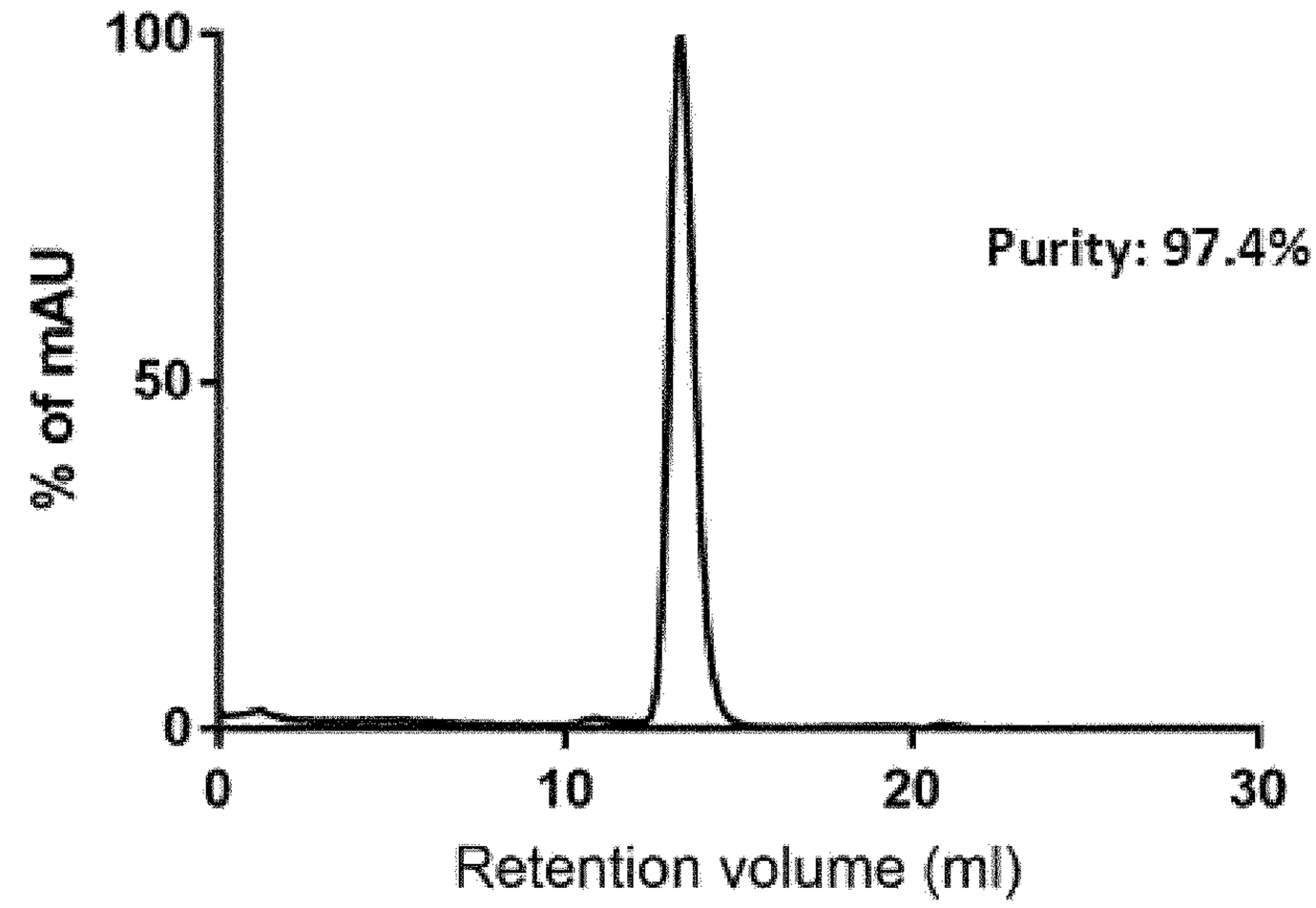


Figure 48A

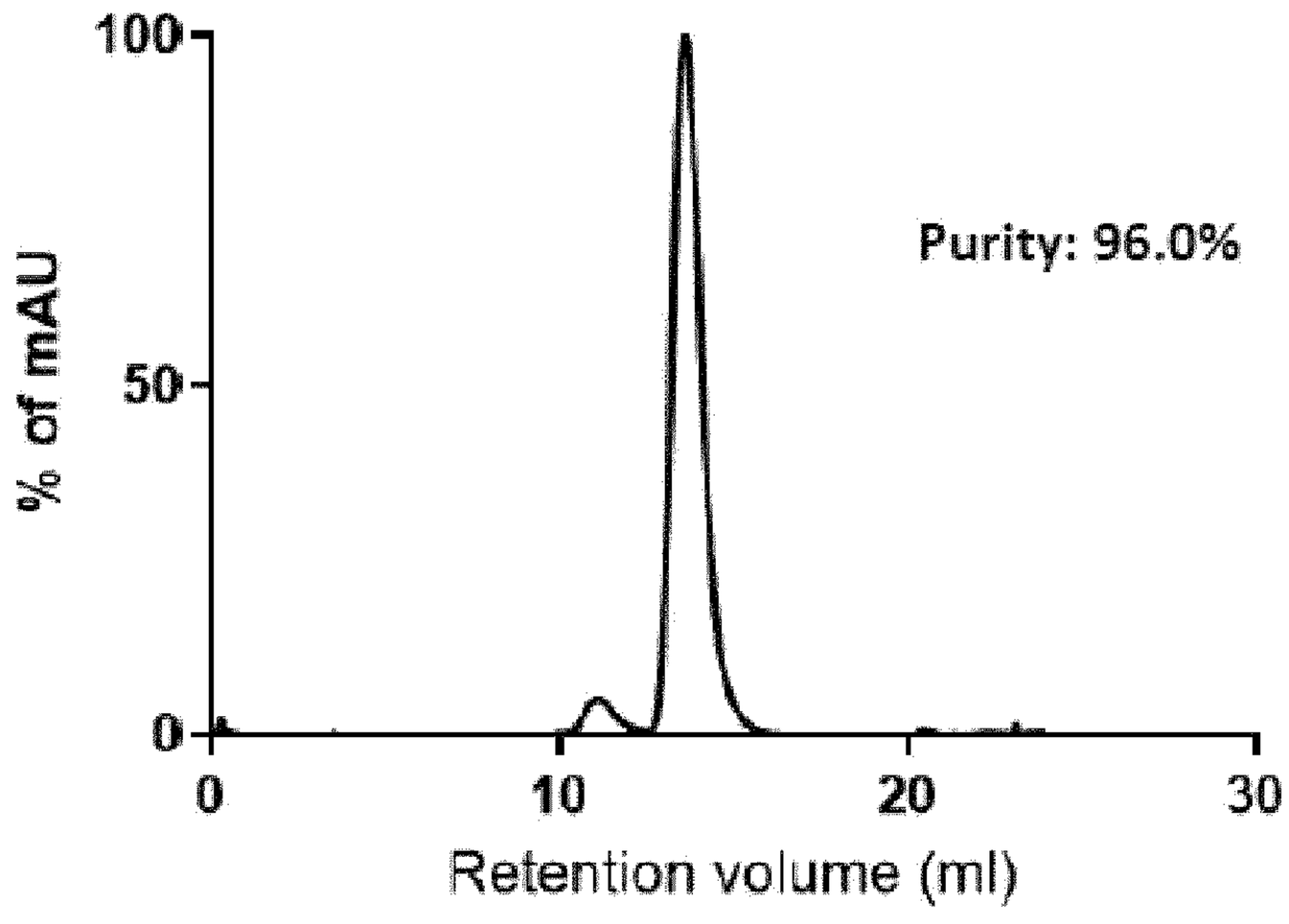


Figure 48B

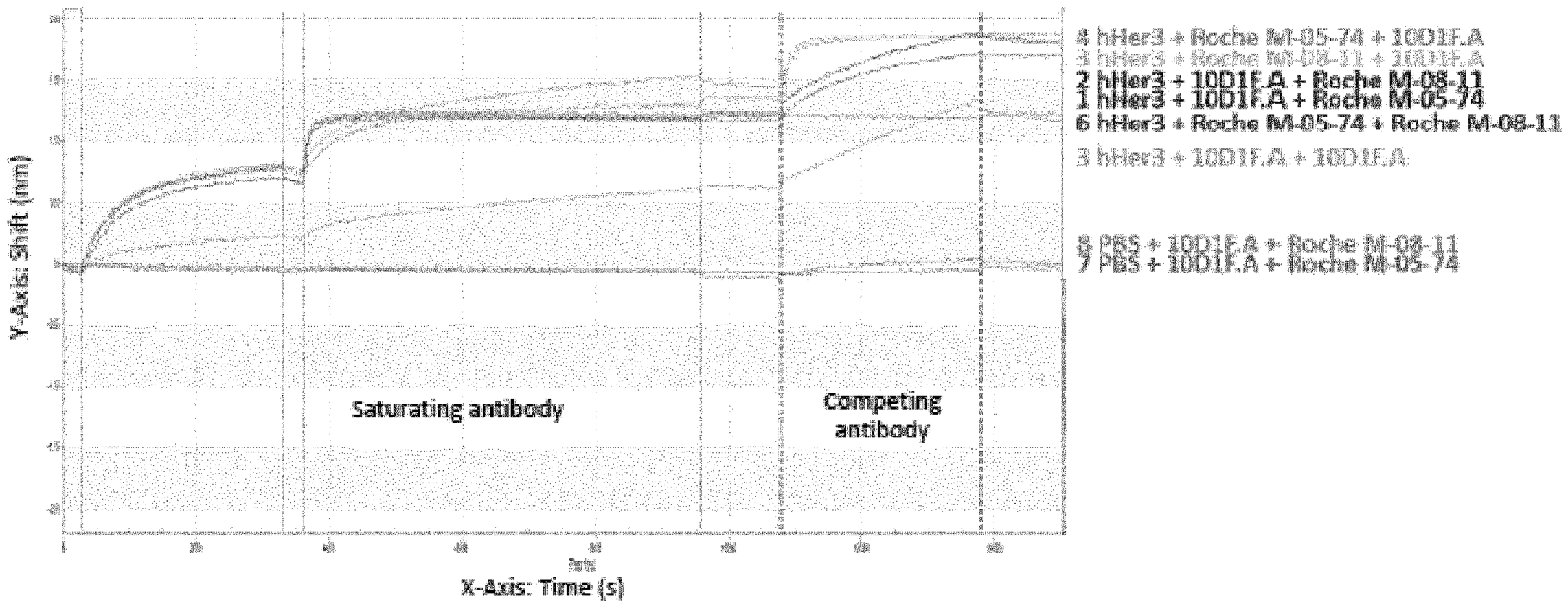

Y-Axis: Shift (nm)
X-Axis: Time (s)
Saturating antibody
Competing antibody
4 hHer3 + Roche M-05-74 + 10D1F.A
3 hHer3 + Roche M-08-11 + 10D1F.A
2 hHer3 + 10D1F.A + Roche M-08-11
1 hHer3 + 10D1F.A + Roche M-05-74
6 hHer3 + Roche M-05-74 + Roche M-08-11
3 hHer3 + 10D1F.A + 10D1F.A
8 PBS + 10D1F.A + Roche M-08-11
7 PBS + 10D1F.A + Roche M-05-74

Figure 49A

		Competing Antibody		
Saturating Antibody		10D1	Roche M-05-74	Roche M-08-11
	10D1	X	0.5084	0.5614
	Roche M-05-74	0.5023	X	0.6424
	Roche M-08-11	0.4114	x	x

Figure 49B

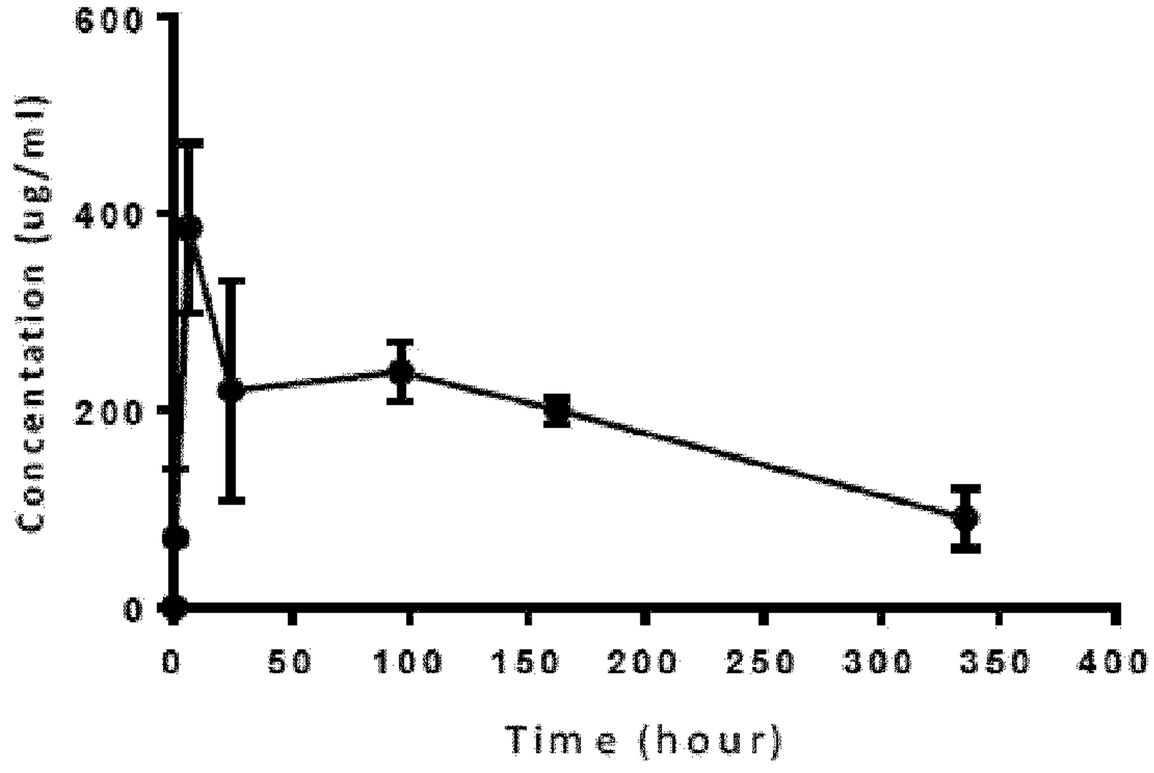


Figure 50

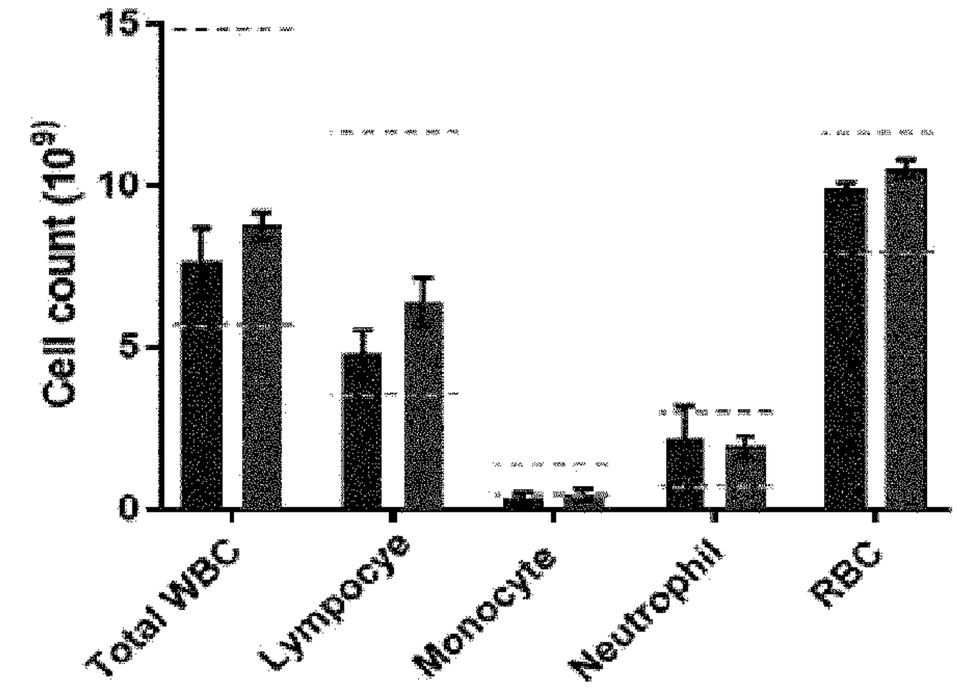


Figure 51A

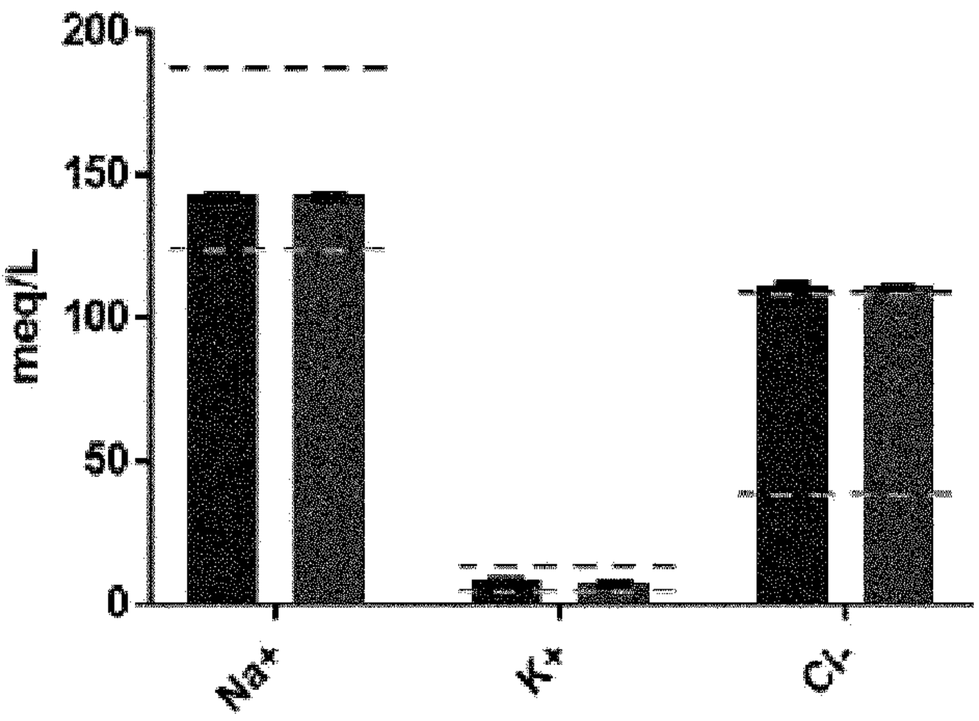


Figure 51B

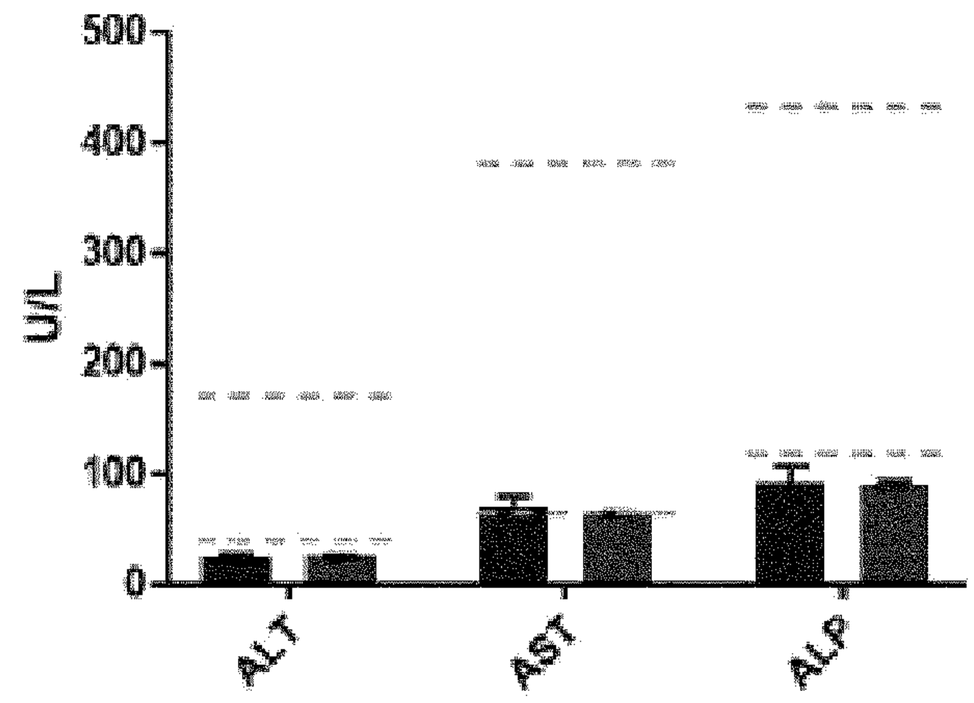


Figure 51C

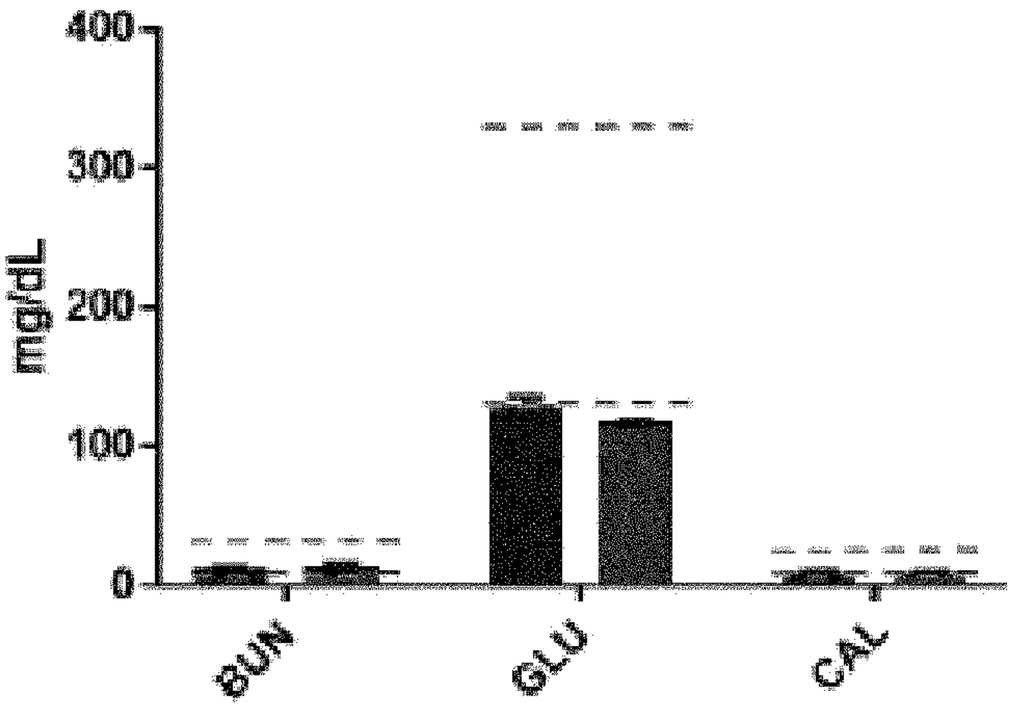


Figure 51D

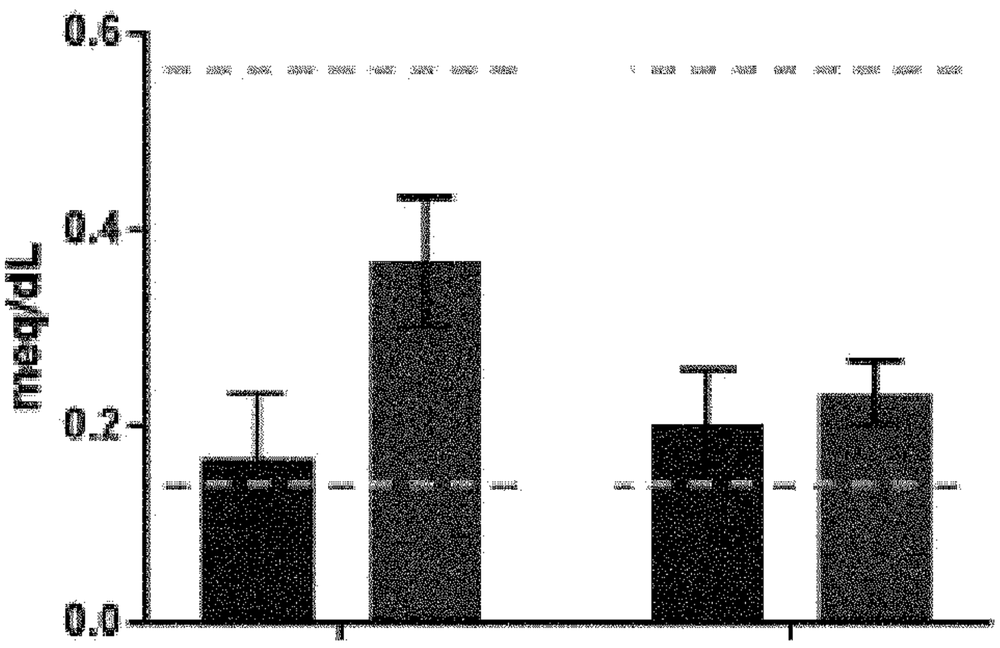


Figure 51E

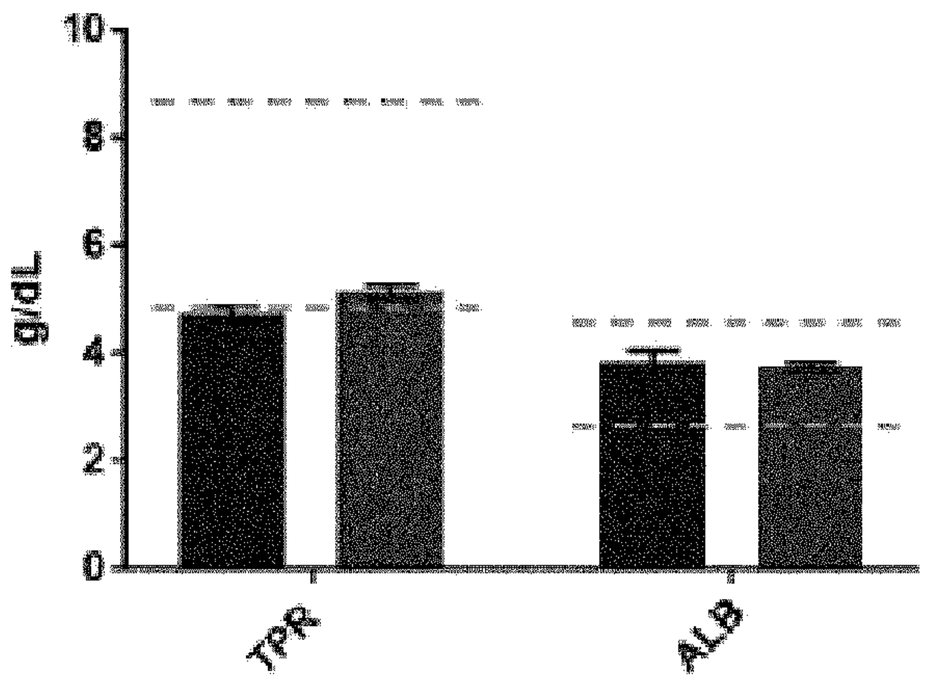
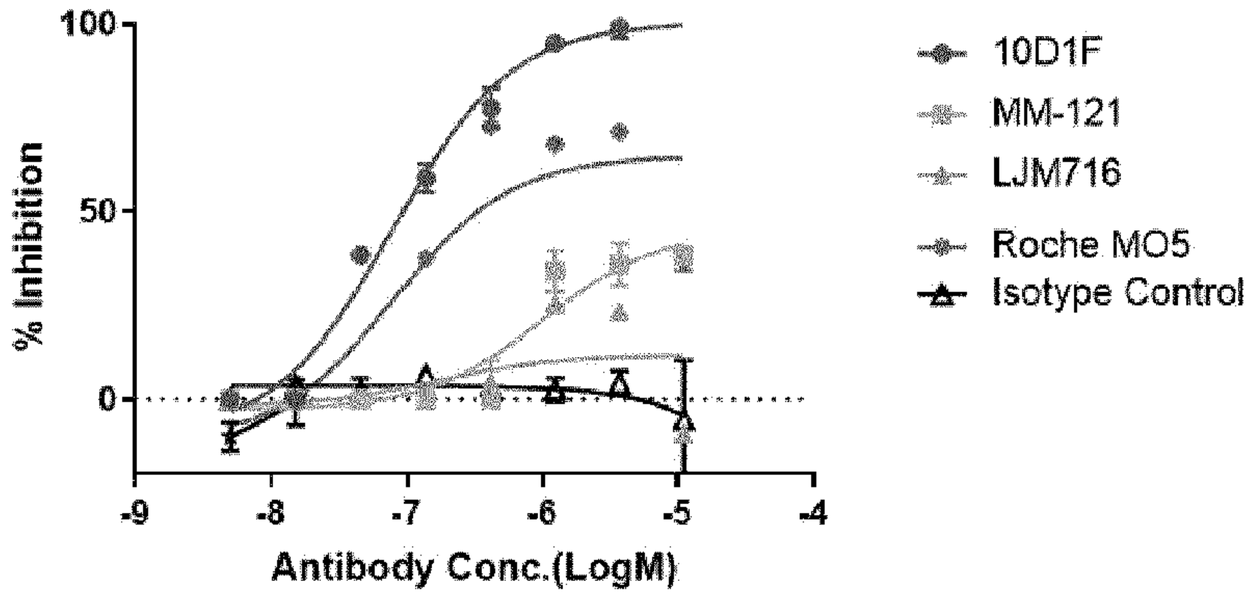
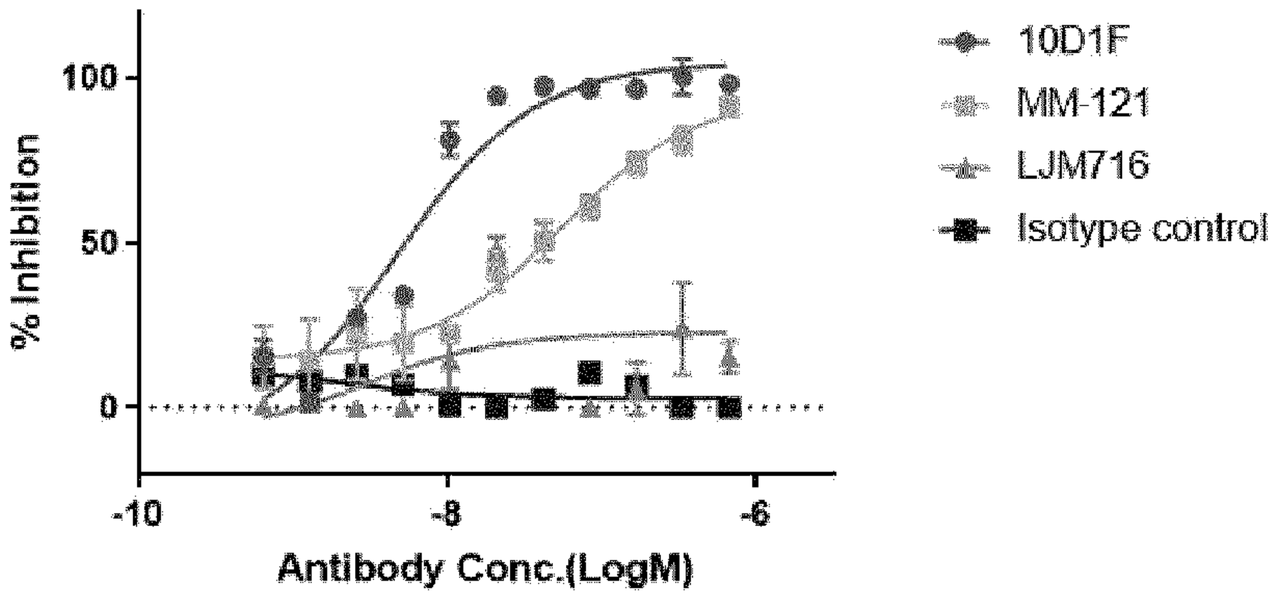


Figure 51F



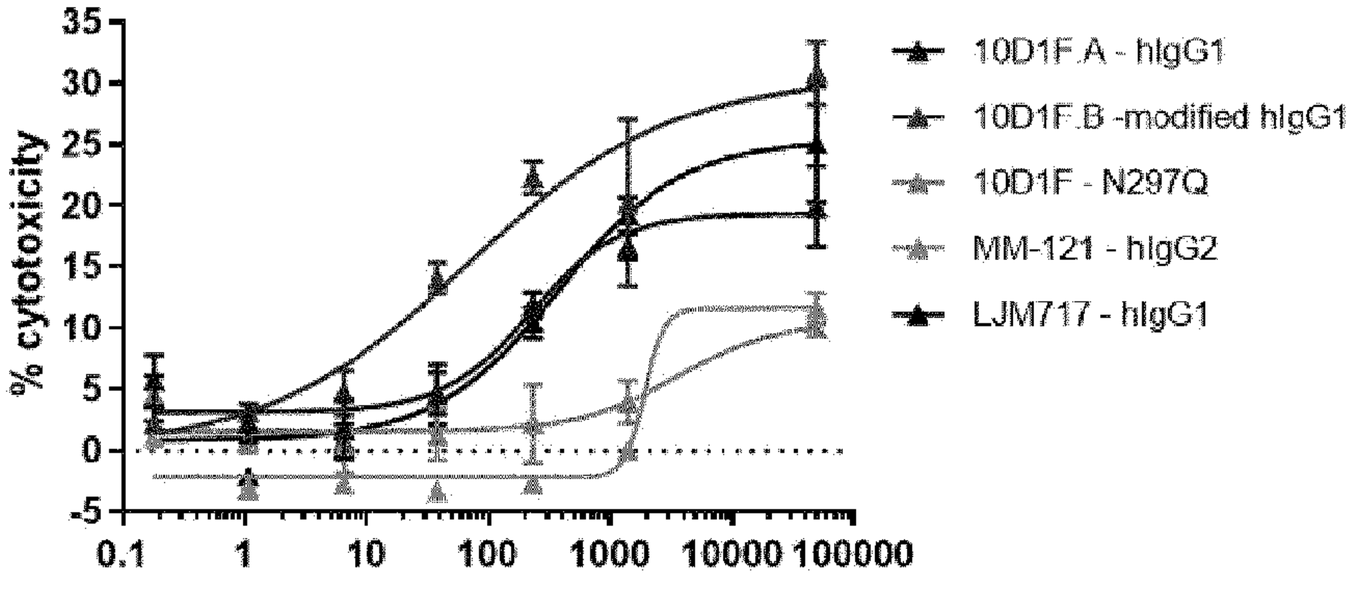
	10D1F	MM-121	LJM-716	Roche M05	Isotype Control
HER2:HER3 IC_{50} (M)	7.88e-008	N.A.	N.A.	8.025e-008	N.A.

Figure 52



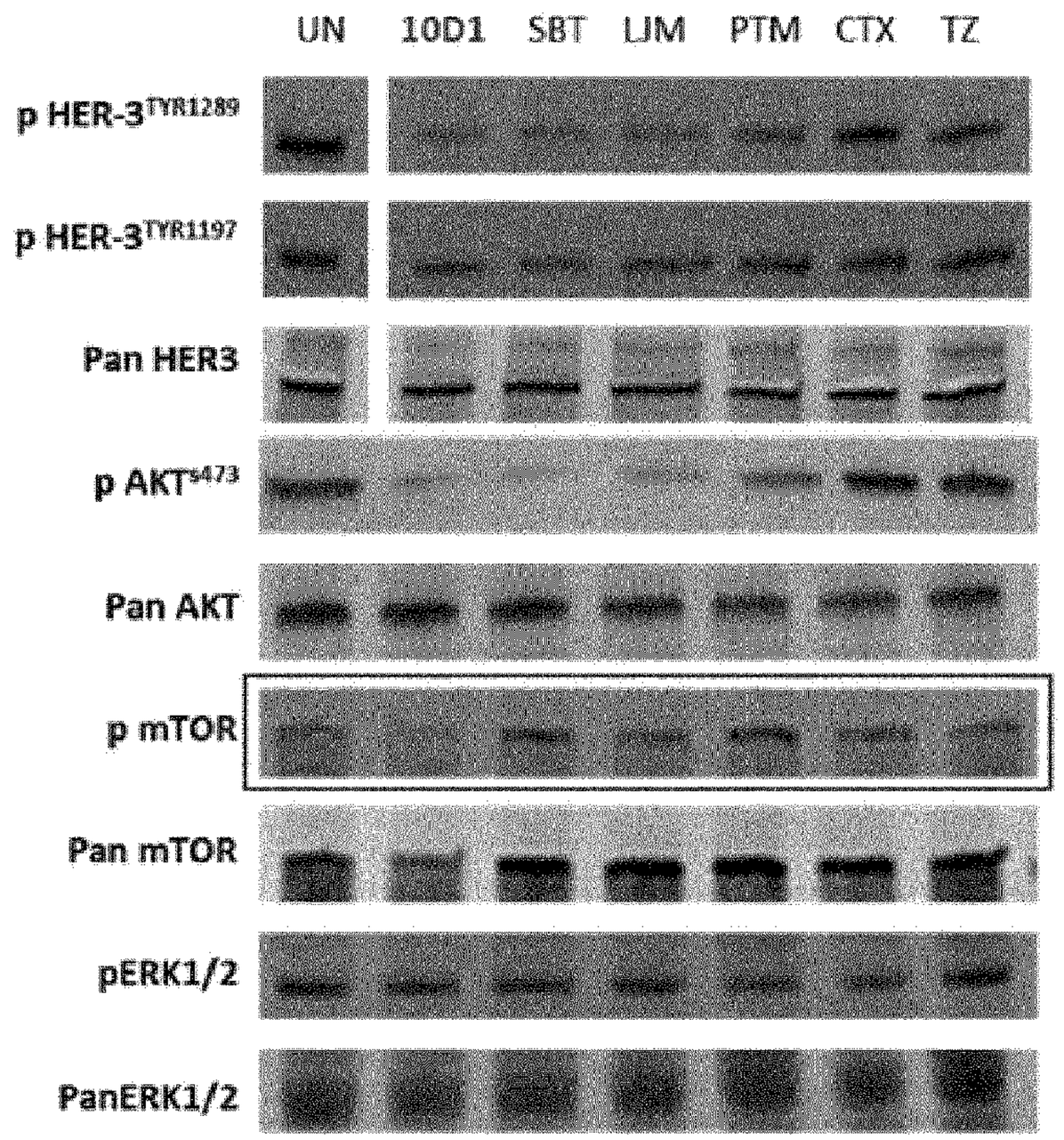
	10D1F	MM-121	LJM-716	Isotype Control
EGFR:HER3 IC_{50} (M)	4.781e-009	5.419e-008	N.A.	N.A.

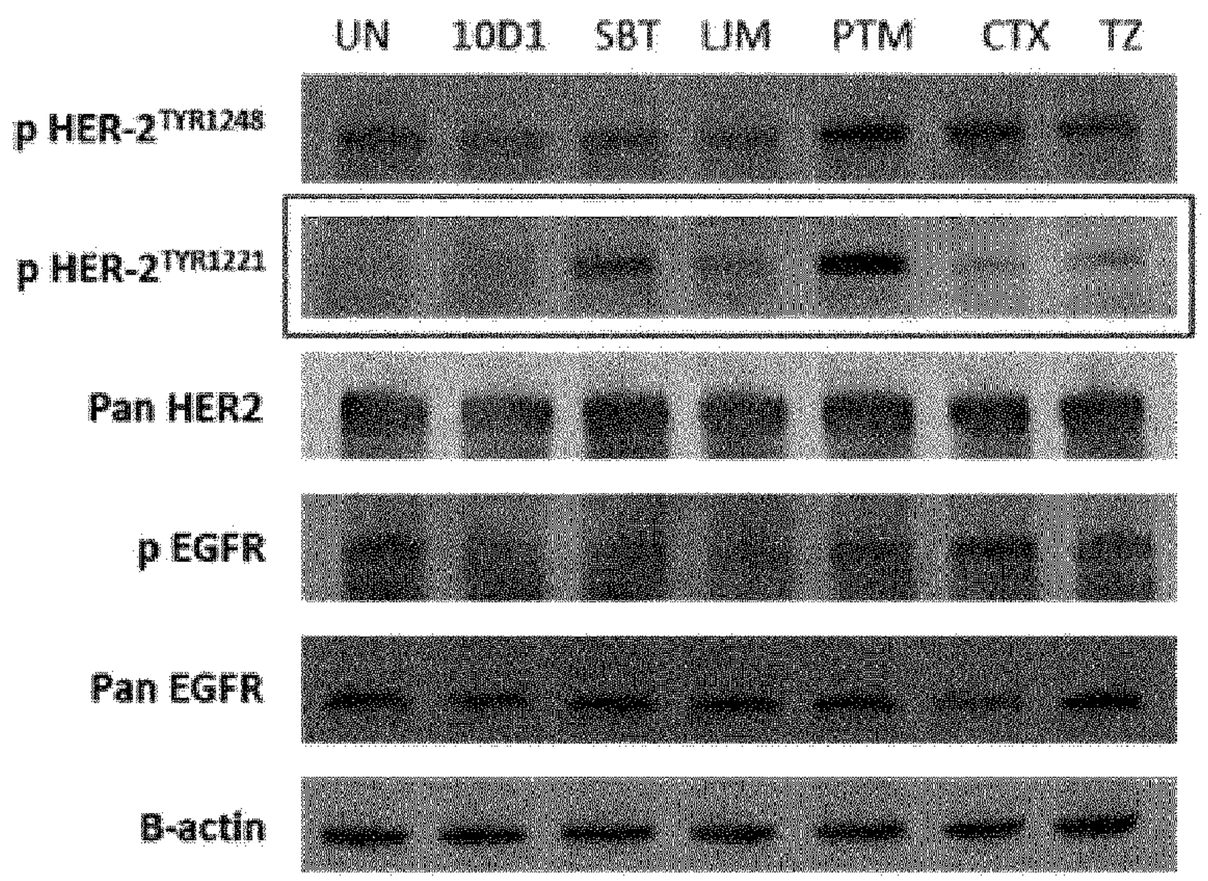
Figure 53



	10D1F.FcA 10D1F hIgG1	10D1F.FcB 10D1F hIgG1 GASDALIE-LCKC	10D1F hIgG1 N297Q	SBT hIgG2	LJM716 hIgG1
EC_{50} (ng/ml)	224.4	68.96	NA	NA	377.3

Figure 54





Legend:
UN = Untreated
10D1 = 10D1F.A
SBT = Seribantumab (MM-121)
LJM = Elgemtumab (LJM-716)
PTM = Pertuzumab
CTX = Cetuximab
TZ = Trastuzumab

Figure 55A

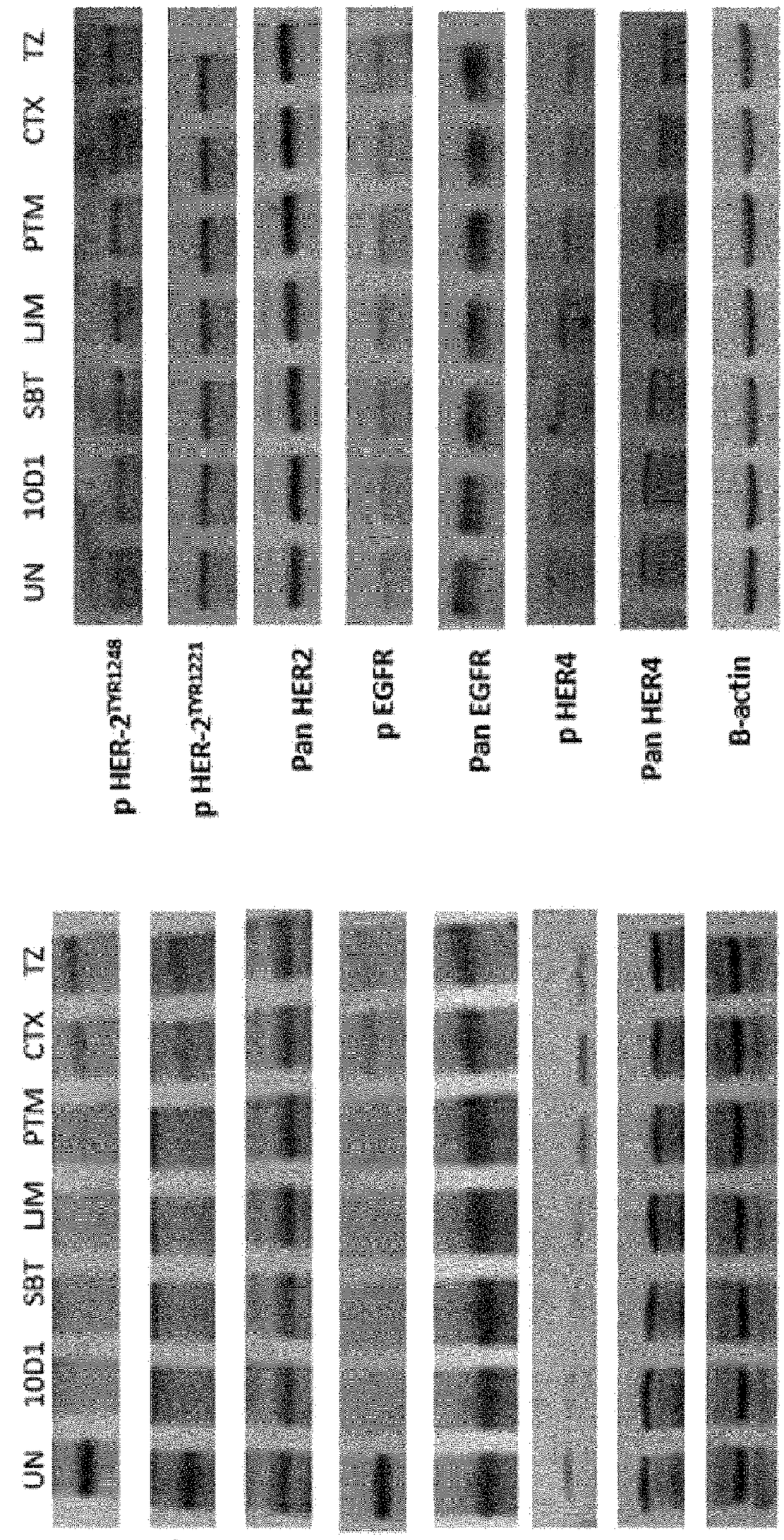
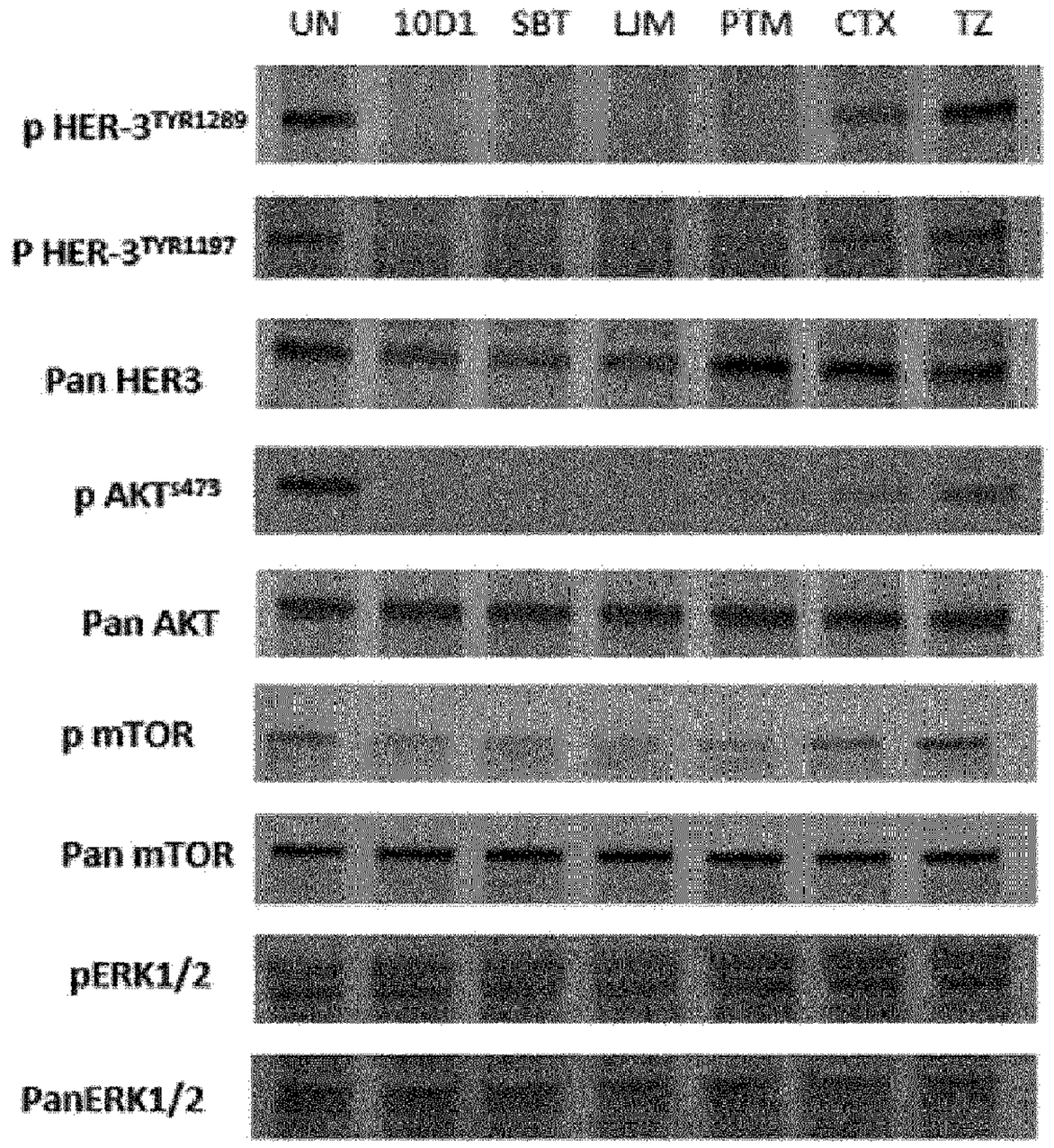
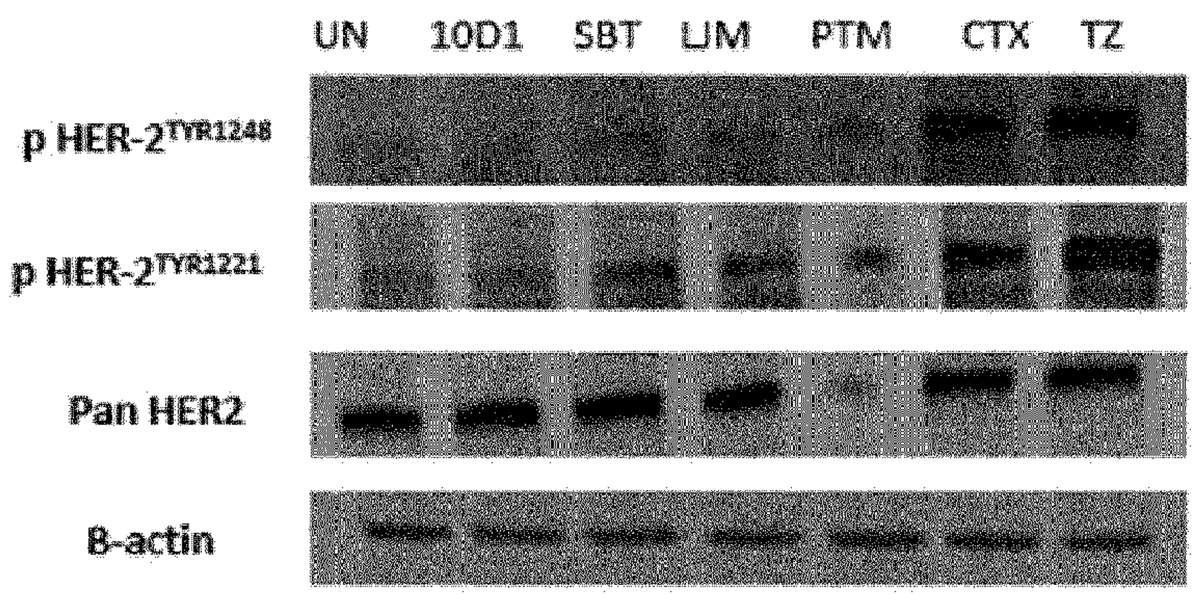

UN
10D1
SBT
LIM
PTM
CTX
TZ
p HER-2TYR1248
p HER-2TYR1221
Pan HER2
p EGFR
Pan EGFR
p HER4
Pan HER4
β-actin
Legend:
UN = Untreated
10D1 = 10D1F.FcA
SBT = MM-121
LIM = LIM-716
PTM = Pertuzumab
CTX = Cetuximab
TZ = Trastuzumab
p HER-3TYR1289
p HER-3TYR1197
Pan HER3
p AKTS473
Pan AKT
p mTOR
Pan mTOR
pERK1/2
PanERK1/2

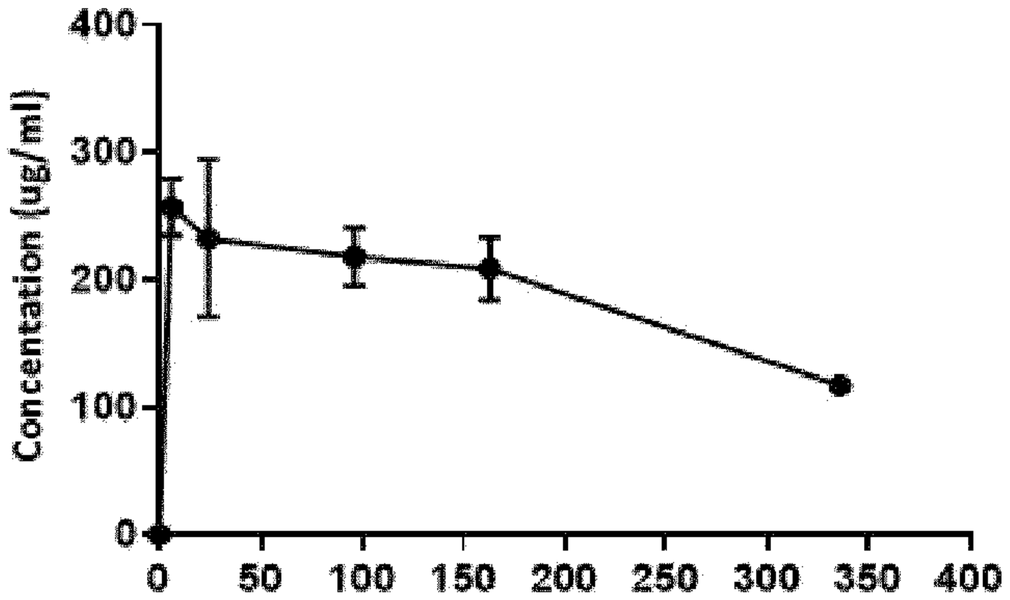
Figure 55B





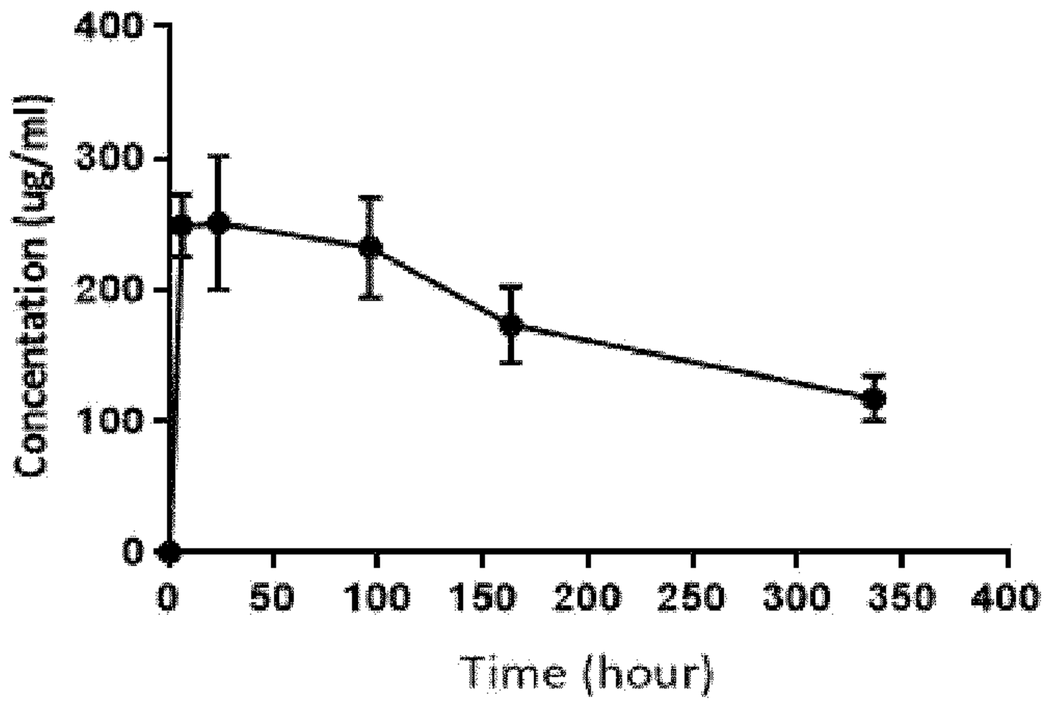
Legend:
UN = Untreated
10D1 = 10D1F.FcA
SBT = MM-121
LJM = LJM-716
PTM = Pertuzumab
CTX = Cetuximab
TZ = Trastuzumab

Figure 55C



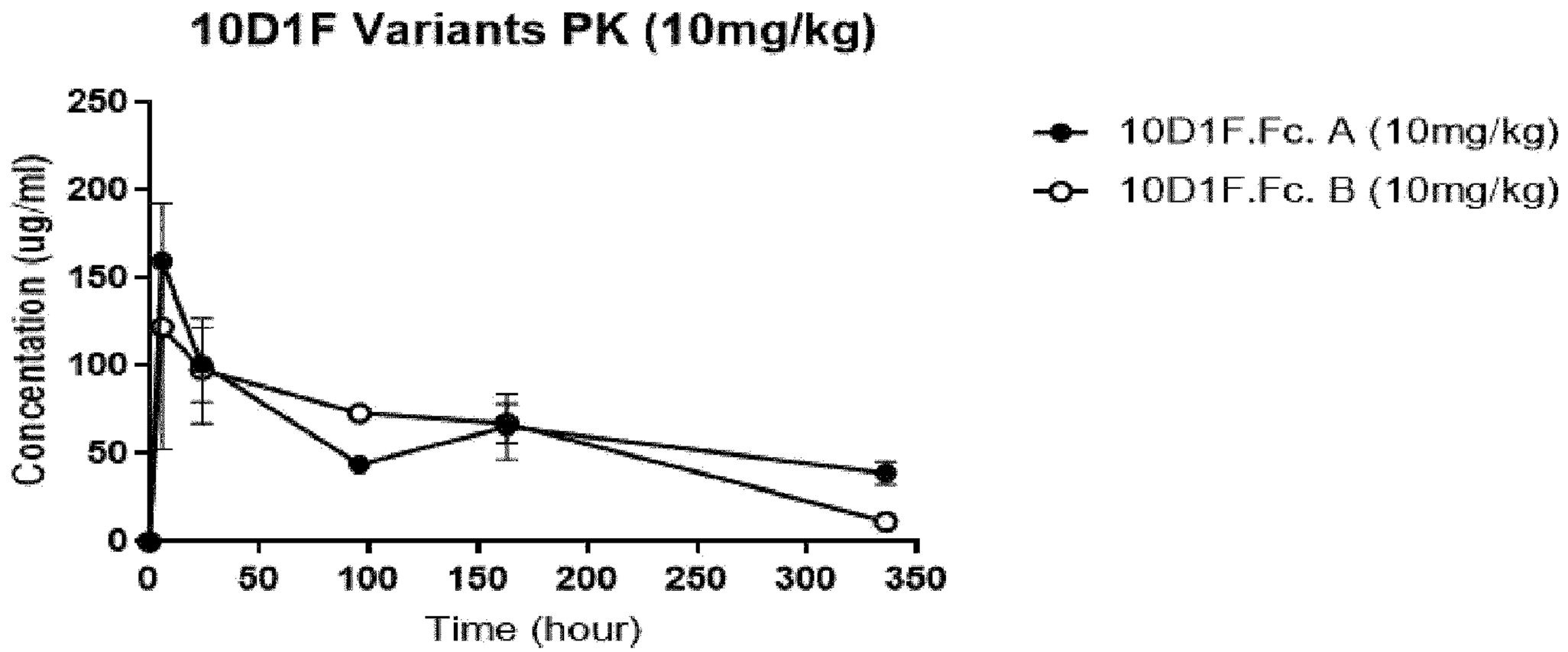
Cmax (ug/ml)	Tmax (hr)	AUC0-336 (ug*h/ml)	AUC0-Infinity (ug*h/ml)	Elimination Rate KEL(h-1)	T1/2 (hr)	CL (ml/h)	Vd (mL/kg)
257.297	6.000	64677.050	107359.970	0.003	252.753	0.005	1.697

Figure 56A



Cmax (ug/ml)	Tmax (hr)	AUC0-336 (ug*h/ml)	AUC0-Infinity (ug*h/ml)	Elimination Rate KEL(h-1)	T1/2 (hr)	CL (ml/h)	Vd (mL/kg)
250.673	24.000	62163.226	108529.704	0.003	273.167	0.005	1.804

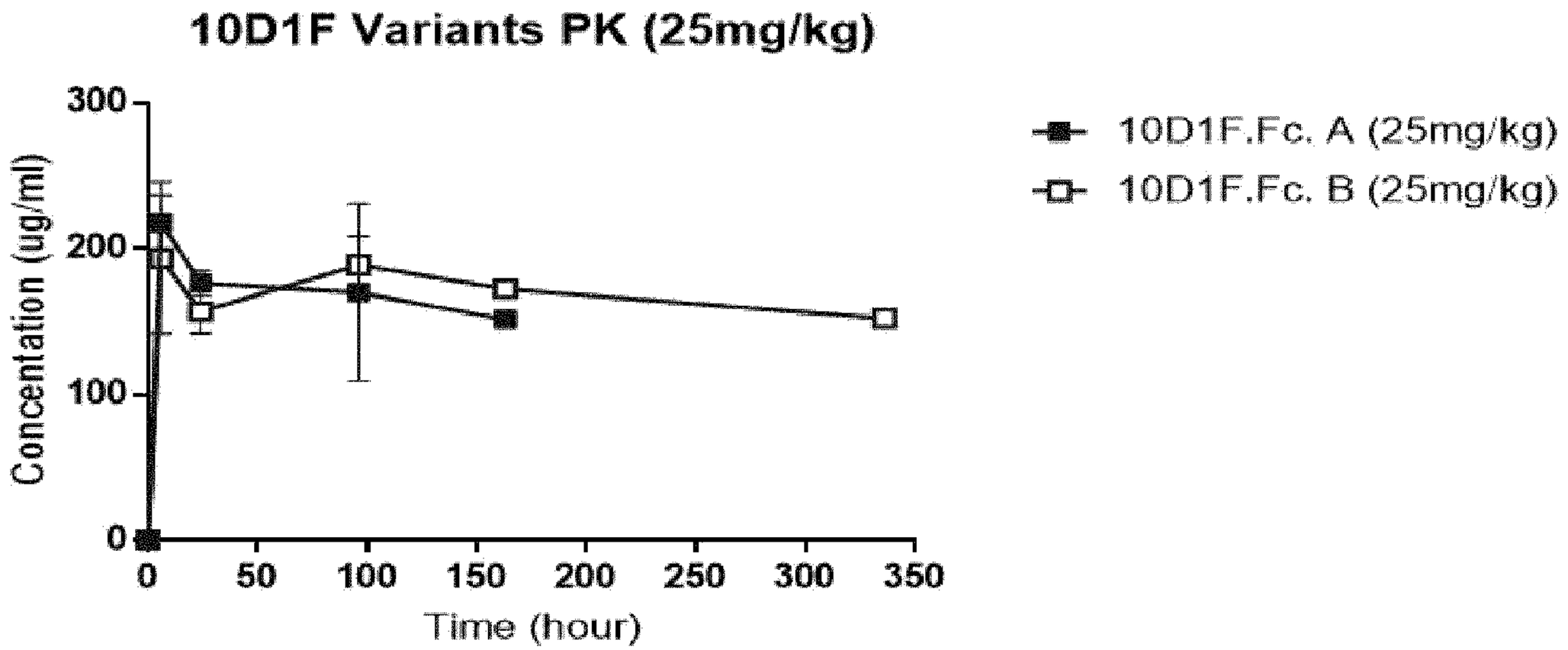
Figure 56B



Arms	Dose	Cmax (ug/ml)	Tmax (hr)	AUC0-336 (ug*h/ml)	AUC0-Infinity (ug*h/ml)	T1/2 (hr)	CL (ml/h)	Vd (mL/kg)
10D1F.Fc.A	10 mg/kg	159.851	6.000	21286.213	32543.407	199.434	0.077	23.273
10D1F.Fc.B	10 mg/kg	122.573	6.000	20585.915	22289.688	102.642	0.112	15.741

Figure 57A

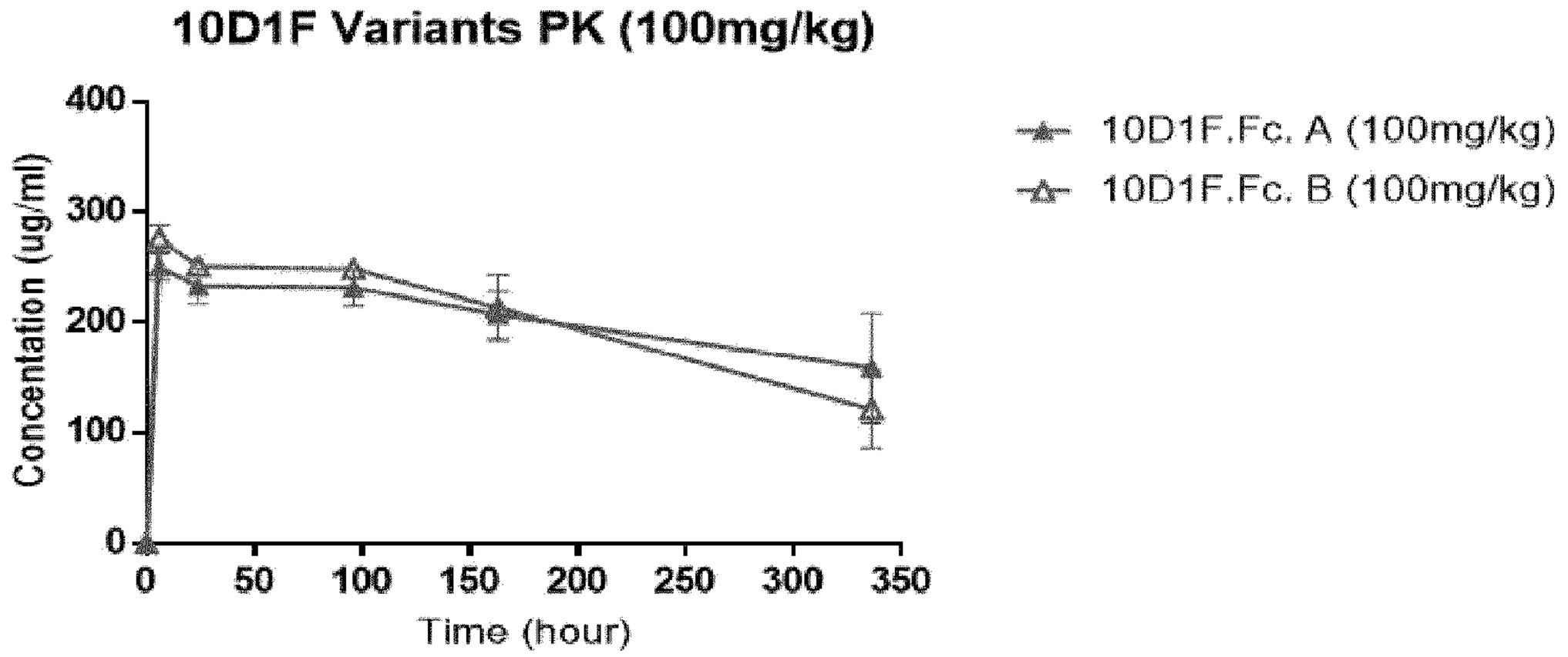
DK/EP 3645571 T3



Arms	Dose	Cmax (ug/ml)	Tmax (hr)	AUC0-336 (ug*h/ml)	AUC0-Infinity (ug*h/ml)	T1/2 (hr)	CL (ml/h)	Vd (mL/kg)
10D1F.Fc.A	25 mg/kg	217.686	6.000	28911.974	168078.210	639.672	0.037	34.093
10D1F.Fc.B	25 mg/kg	193.450	6.000	57007.087	228551.339	783.712	0.027	31.210

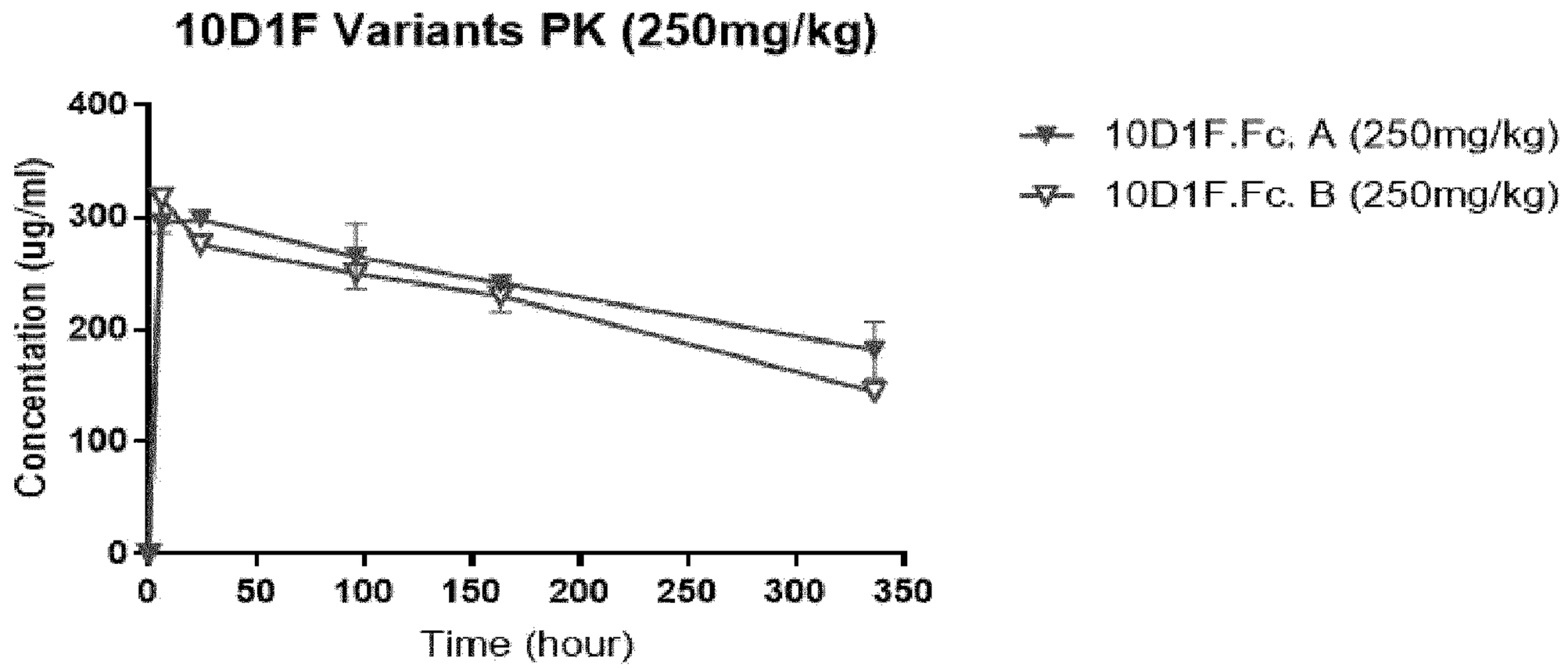
Figure 57B

DK/EP 3645571 T3



Arms	Dose	Cmax (ug/ml)	Tmax (hr)	AUC0-336 (ug*h/ml)	AUC0-Infinity (ug*h/ml)	T1/2 (hr)	CL (ml/h)	Vd (mL/kg)
10D1F.Fc.A	100 mg/kg	250.516	6.000	69078.168	169396.299	438.789	0.148	93.857
10D1F.FcB	100 mg/kg	276.288	6.000	69125.006	108489.826	225.714	0.230	75.978

Figure 57C



Arms	Dose	Cmax (ug/ml)	Tmax (hr)	AUC0-336 (ug*h/ml)	AUC0-Infinity (ug*h/ml)	T1/2 (hr)	CL (ml/h)	Vd (mL/kg)
10D1F.Fc.A	250 mg/kg	297.919	6.000	81208.032	196765.343	440.240	0.318	200.826
10D1F.FcB	250 mg/kg	317.402	6.000	75091.243	141663.523	317.629	0.441	198.287

Figure 57D

DK/EP 3645571 T3

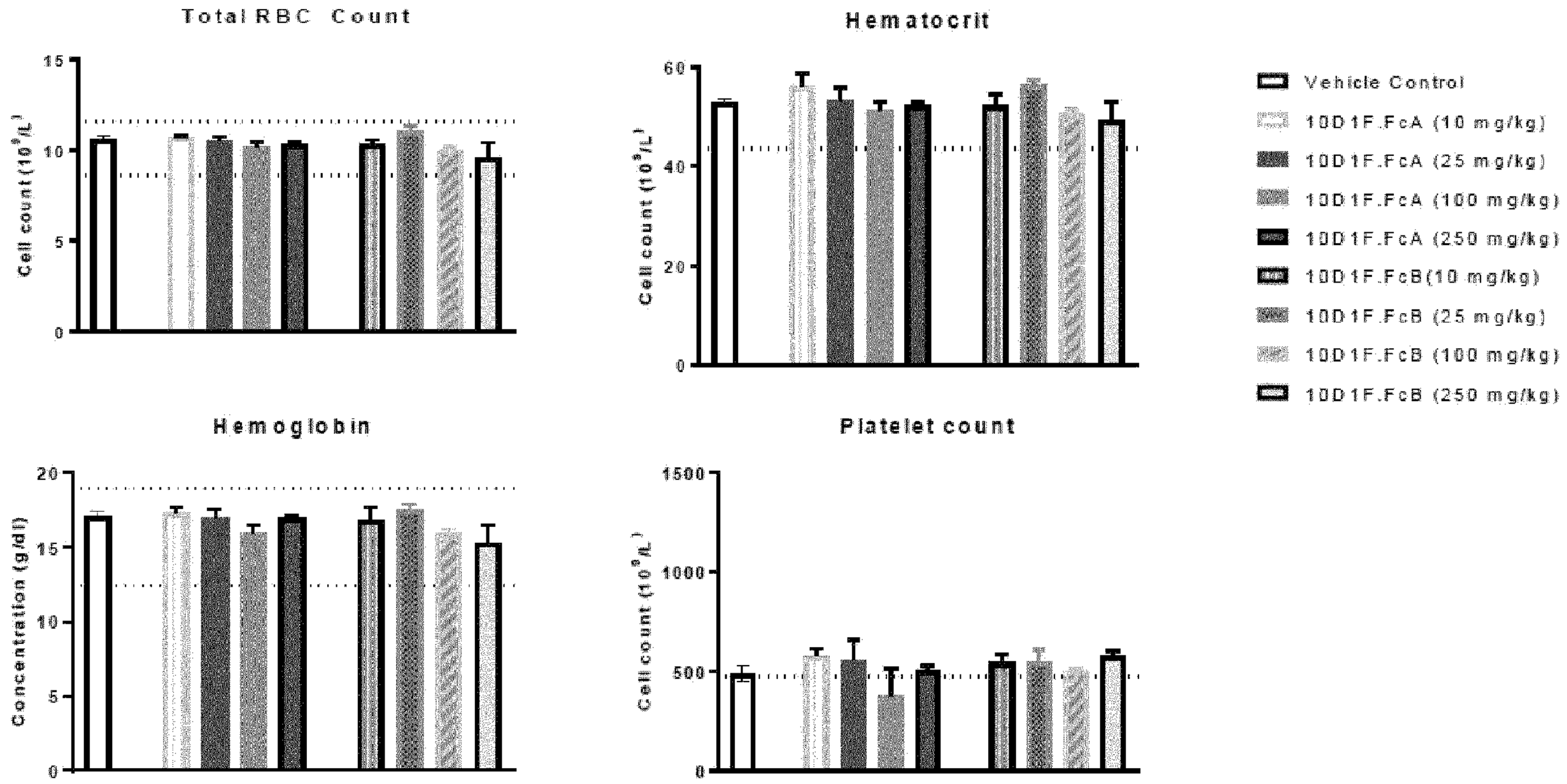


Figure 58A

DK/EP 3645571 T3

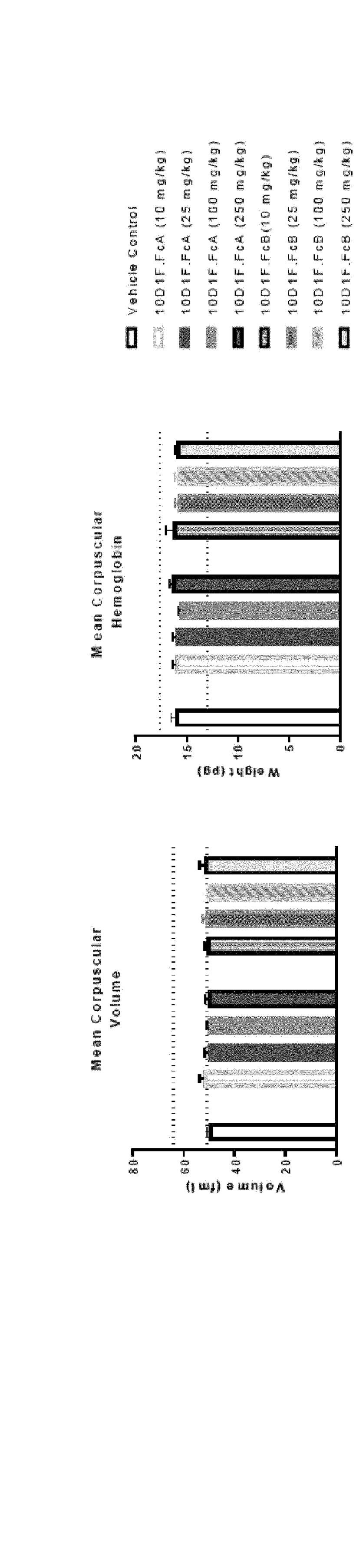

Vehicle Control
10D1F.FcA (10 mg/kg)
10D1F.FcA (25 mg/kg)
10D1F.FcA (100 mg/kg)
10D1F.FcA (250 mg/kg)
10D1F.FcB(10 mg/kg)
10D1F.FcB (25 mg/kg)
10D1F.FcB (100 mg/kg)
10D1F.FcB (250 mg/kg)
Mean Corpuscular Hemoglobin
Weight (pg)
0
5
10
15
20
Mean Corpuscular Volume
Volume (fm l)
0
20
40
60
80
Mean Corpuscular Hemoglobin Concentration
Concentration (g/dl)
0
10
20
30
40

Figure 58B

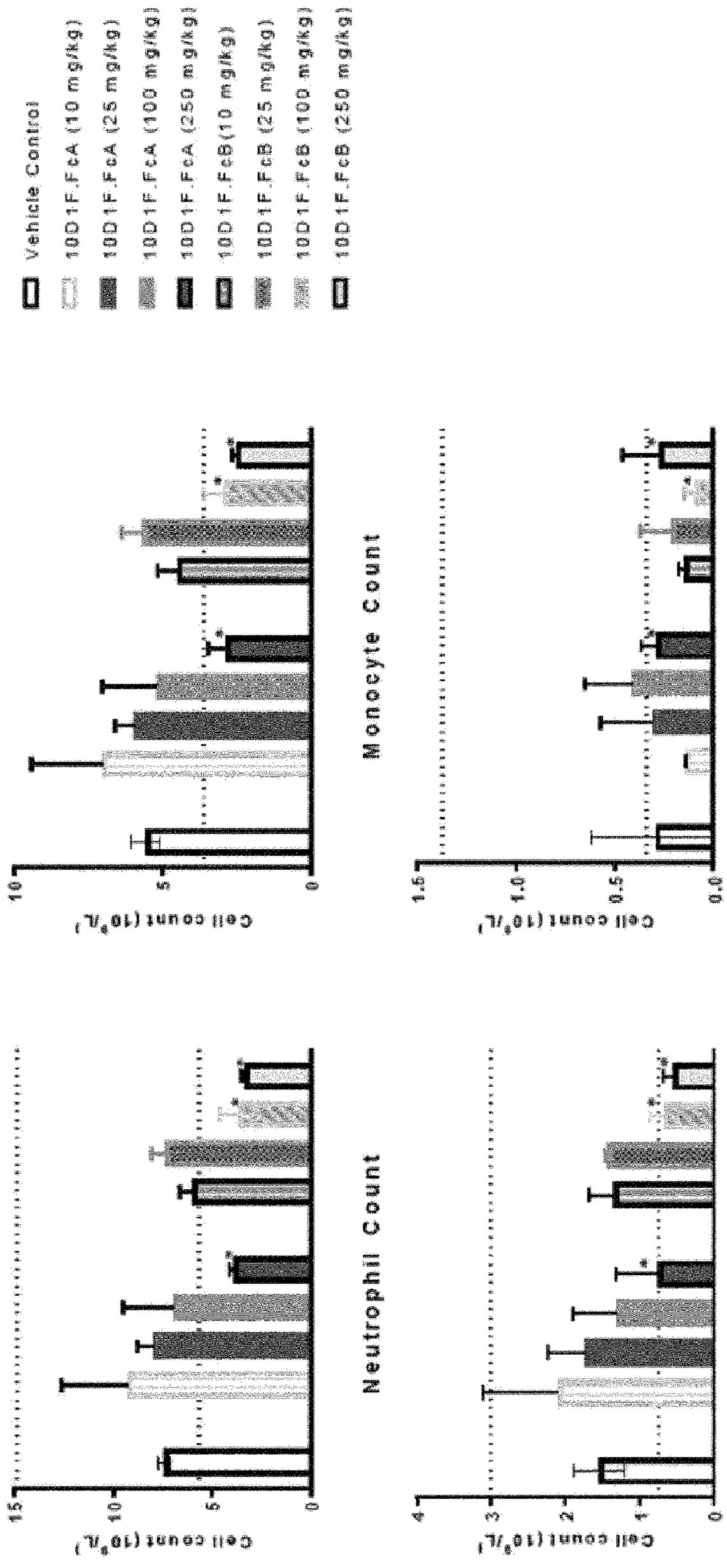

Vehicle Control
10D1F.FcA (10 mg/kg)
10D1F.FcA (25 mg/kg)
10D1F.FcA (100 mg/kg)
10D1F.FcA (250 mg/kg)
10D1F.FcB(10 mg/kg)
10D1F.FcB (25 mg/kg)
10D1F.FcB (100 mg/kg)
10D1F.FcB (250 mg/kg)
Lymphocyte Count
Cell count (10^3/L)
Monocyte Count
Cell count (10^3/L)
Total WBC Count
Cell count (10^3/L)
Neutrophil Count
Cell count (10^3/L)

Figure 58C

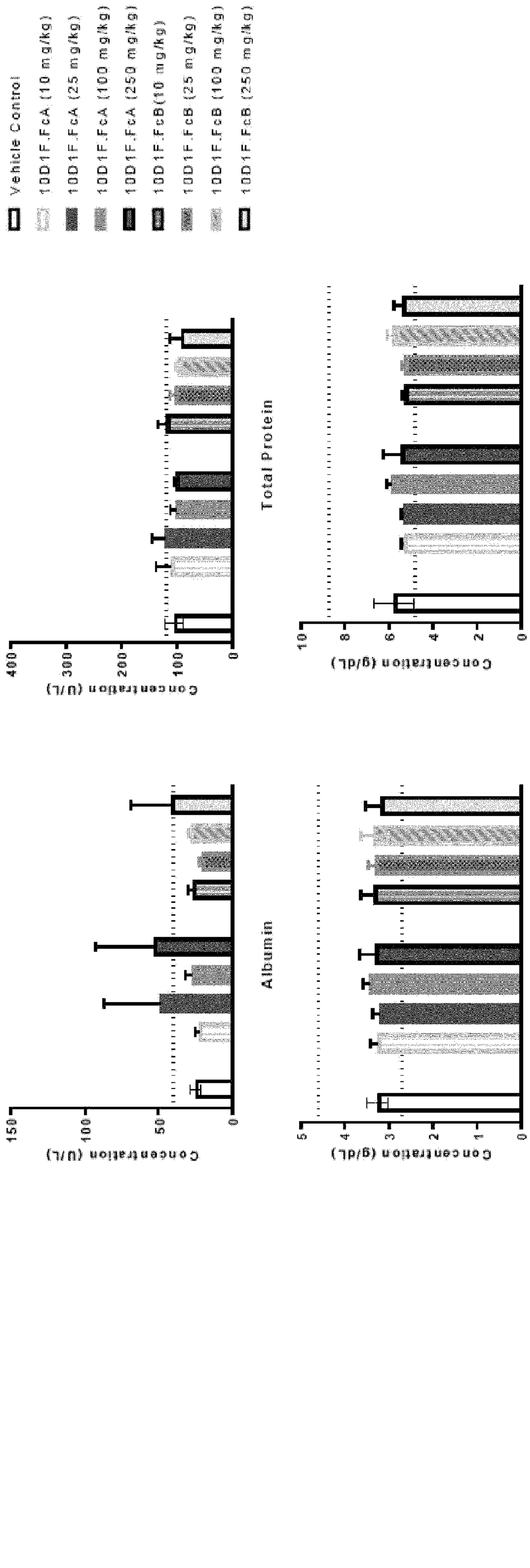

Vehicle Control
10D1F.FcA (10 mg/kg)
10D1F.FcA (25 mg/kg)
10D1F.FcA (100 mg/kg)
10D1F.FcA (250 mg/kg)
10D1F.FcB(10 mg/kg)
10D1F.FcB (25 mg/kg)
10D1F.FcB (100 mg/kg)
10D1F.FcB (250 mg/kg)
Alkaline Phosphatase
Concentration (U/L)
400
300
200
100
0
Total Protein
Concentration (g/dL)
10
8
6
4
2
0
Alanine Aminotransferase
Concentration (U/L)
150
100
50
0
Albumin
Concentration (g/dL)
5
4
3
2
1
0

Figure 58D

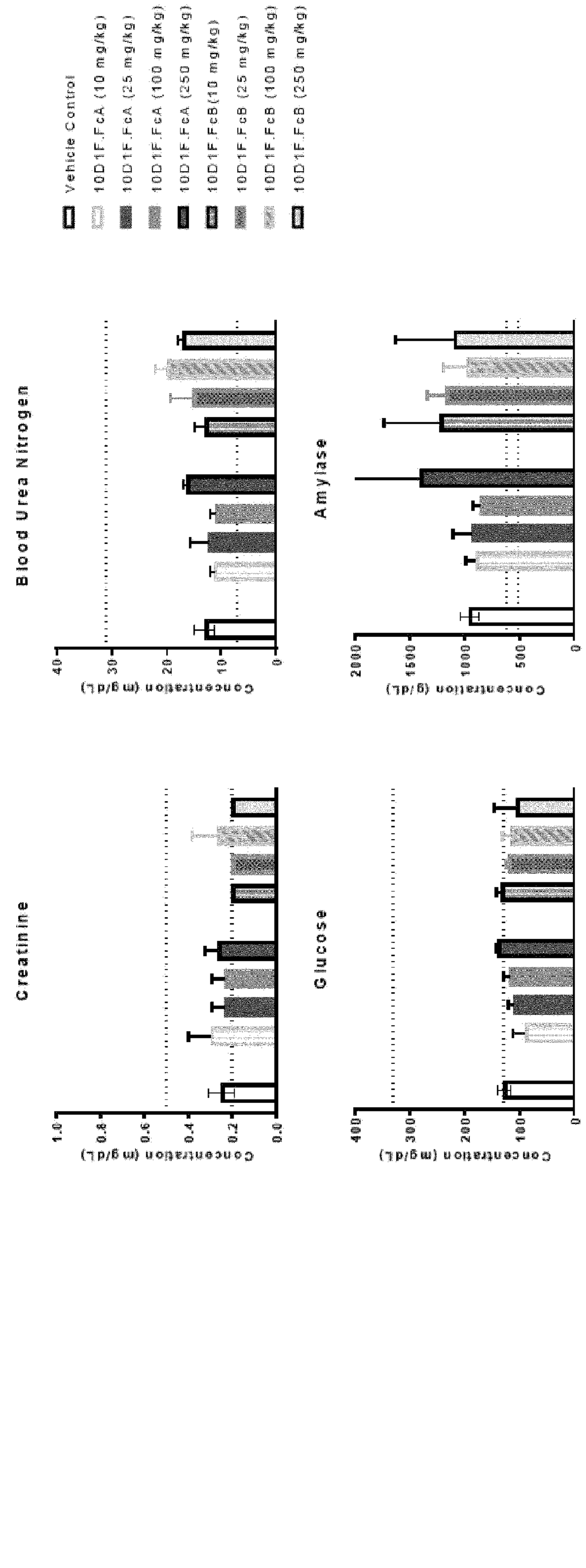

Vehicle Control
10D1F.FcA (10 mg/kg)
10D1F.FcA (25 mg/kg)
10D1F.FcA (100 mg/kg)
10D1F.FcA (250 mg/kg)
10D1F.FcB(10 mg/kg)
10D1F.FcB (25 mg/kg)
10D1F.FcB (100 mg/kg)
10D1F.FcB (250 mg/kg)
Blood Urea Nitrogen
Concentration (mg/dL)
40
30
20
10
0
Amylase
Concentration (g/dL)
2000
1500
1000
500
0
Creatinine
Concentration (mg/dL)
1.0
0.8
0.6
0.4
0.2
0.0
Glucose
Concentration (mg/dL)
400
300
200
100
0

Figure 58E

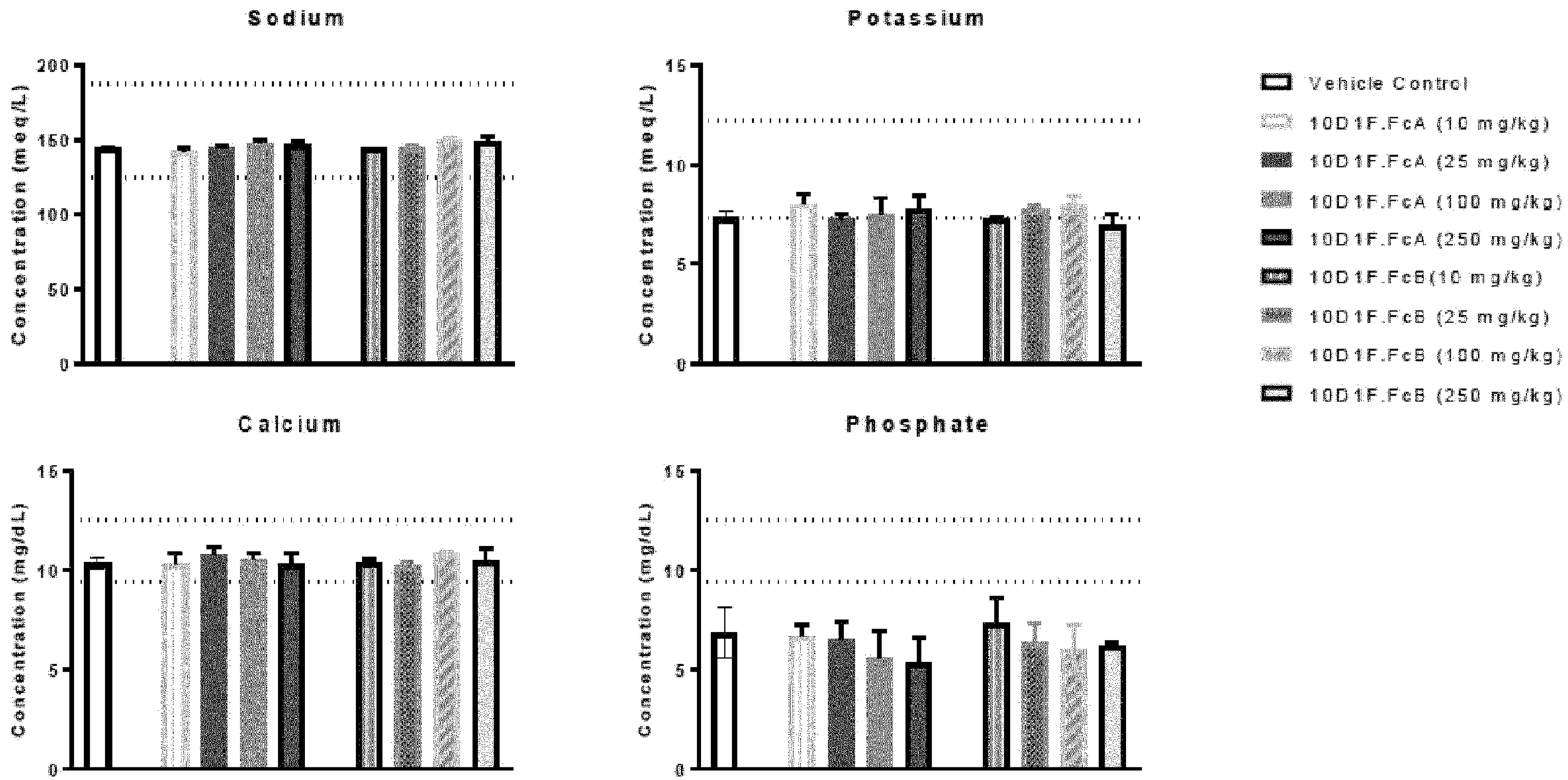


Figure 58F

DK/EP 3645571 T3

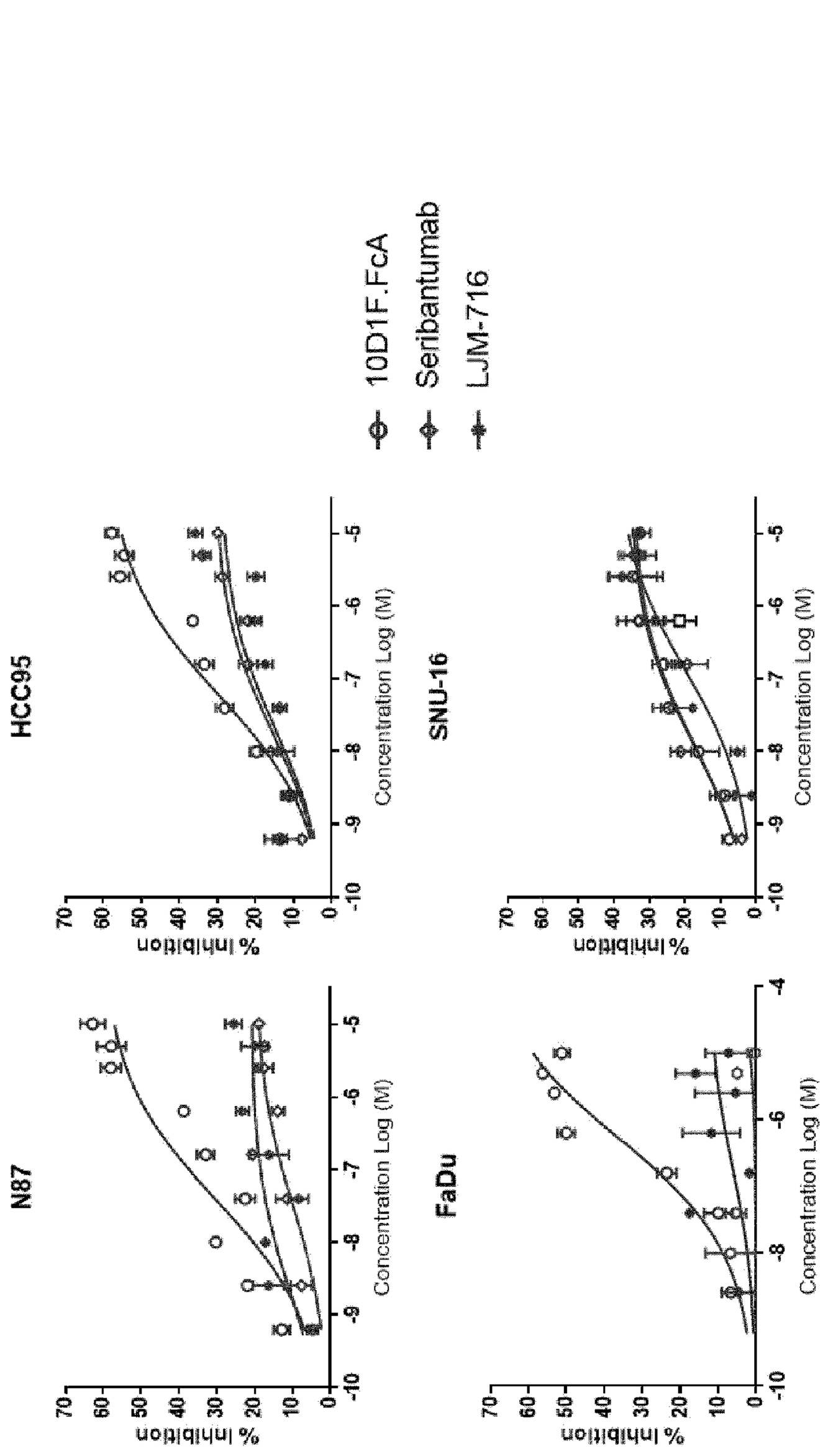

10D1F.FcA
Seribantumab
LJM-716
HCC95
SNU-16
N87
FaDu
% Inhibition
Concentration Log (M)

Figure 59A

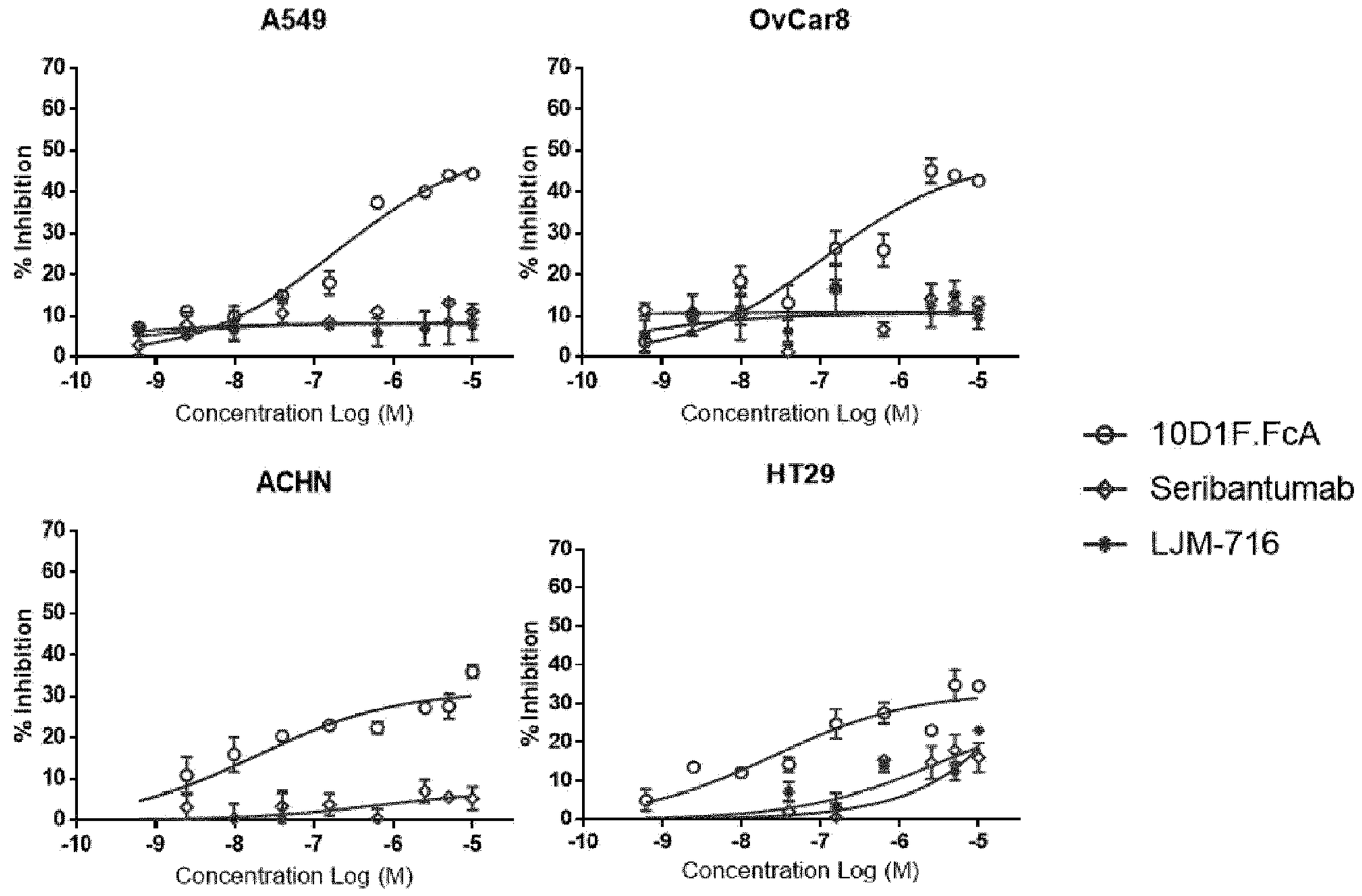


Figure 59B

DK/EP 3645571 T3

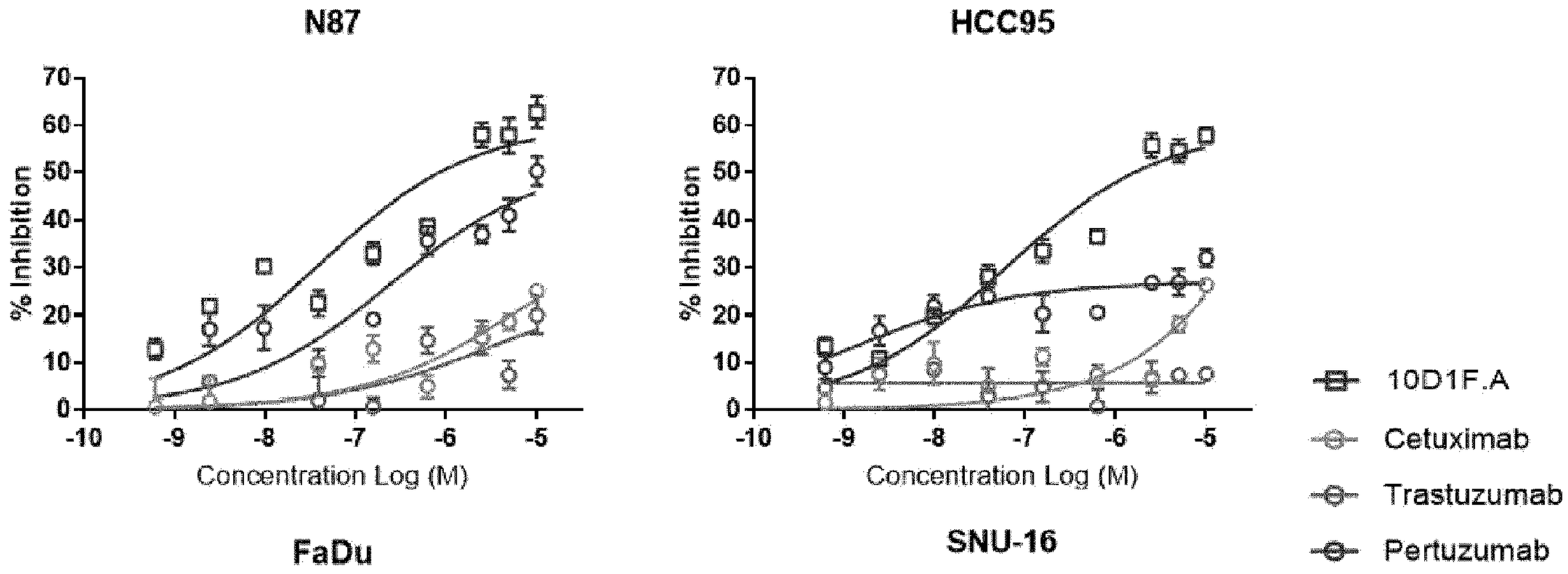


Figure 59C

DK/EP 3645571 T3

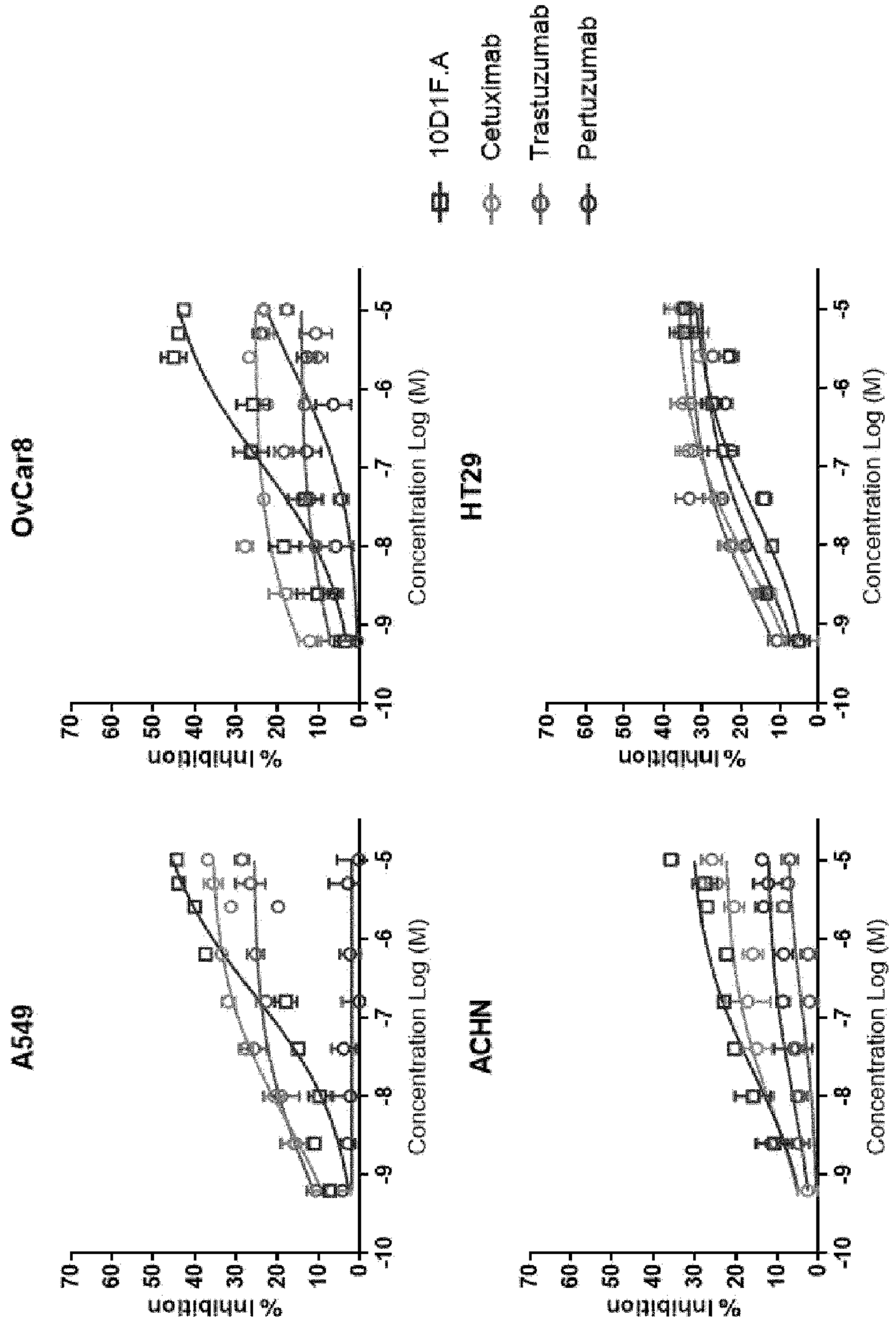

10D1F.A
Cetuximab
Trastuzumab
Pertuzumab
OvCar8
HT29
A549
ACHN
% Inhibition
Concentration Log (M)
0
10
20
30
40
50
60
70
-10
-9
-8
-7
-6
-5

Figure 59D

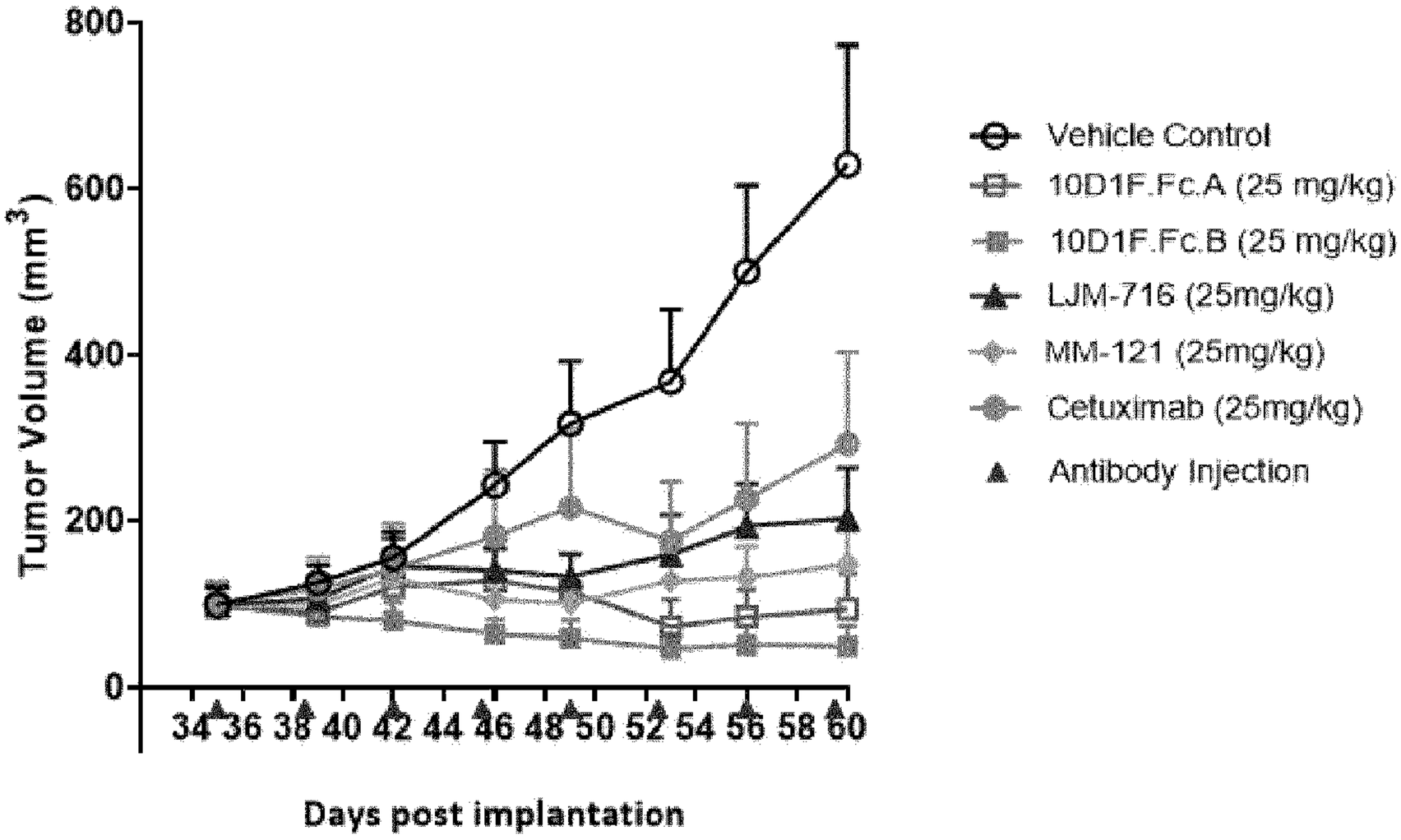


Figure 60

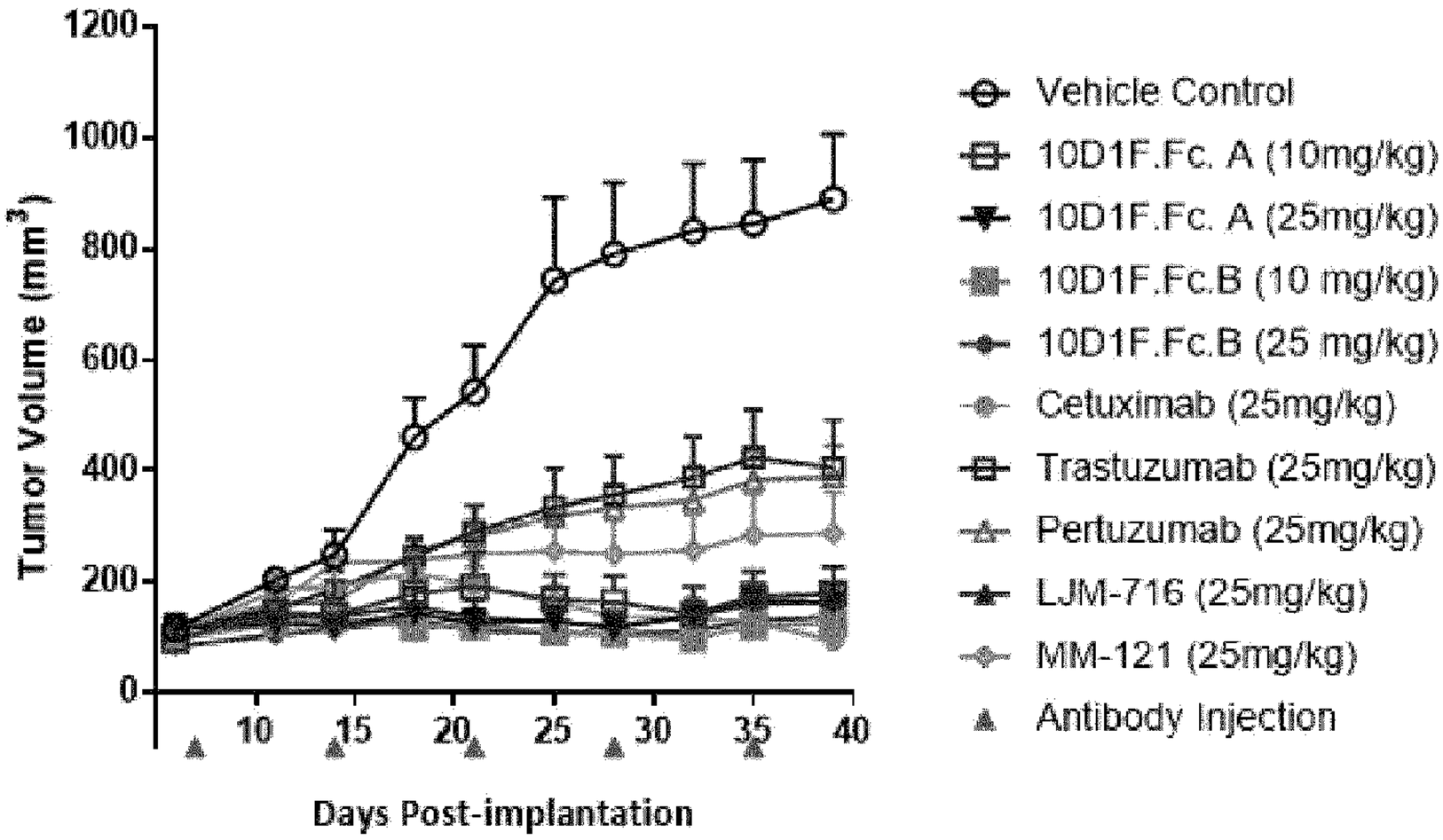


Figure 61

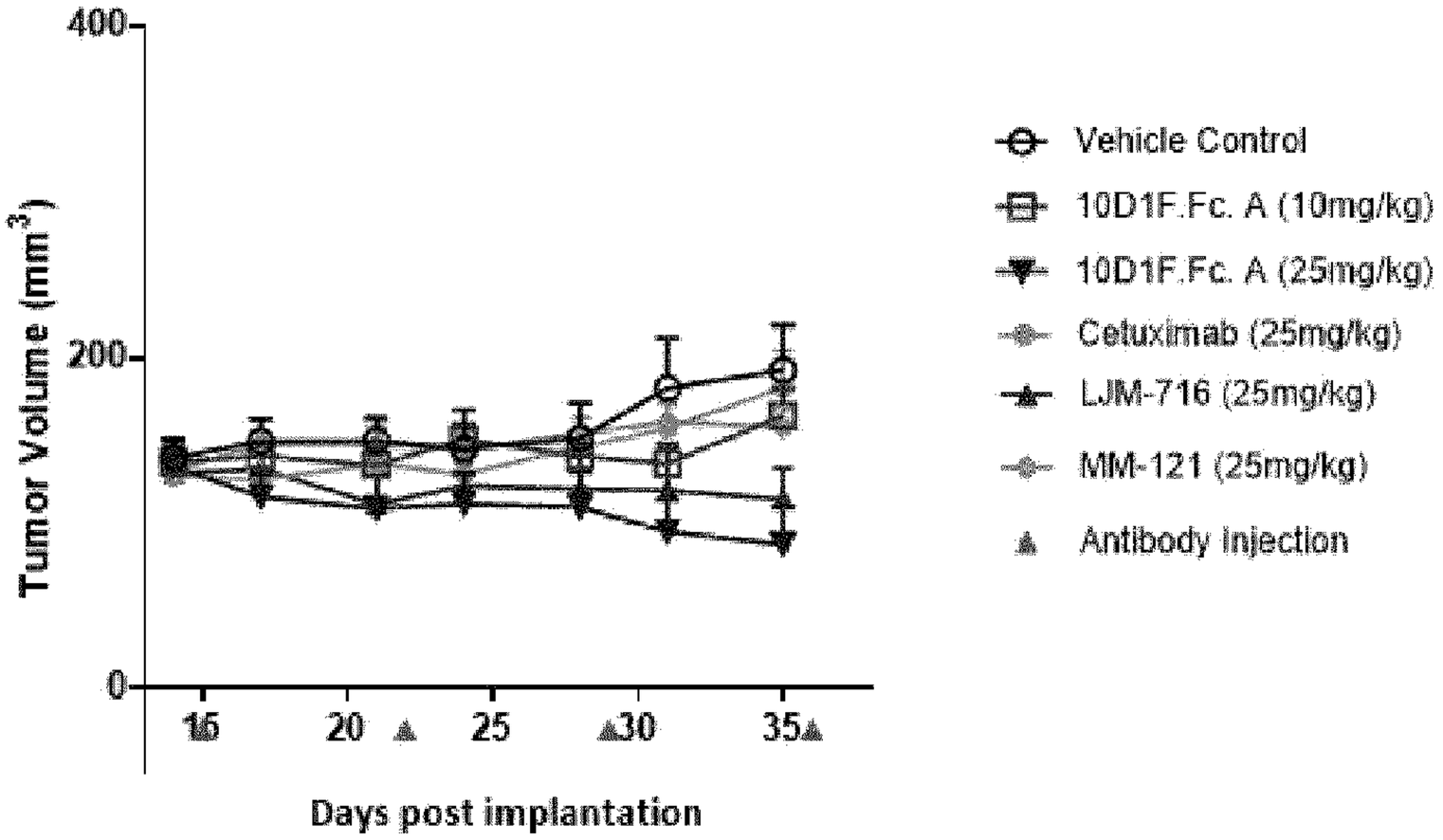


Figure 62

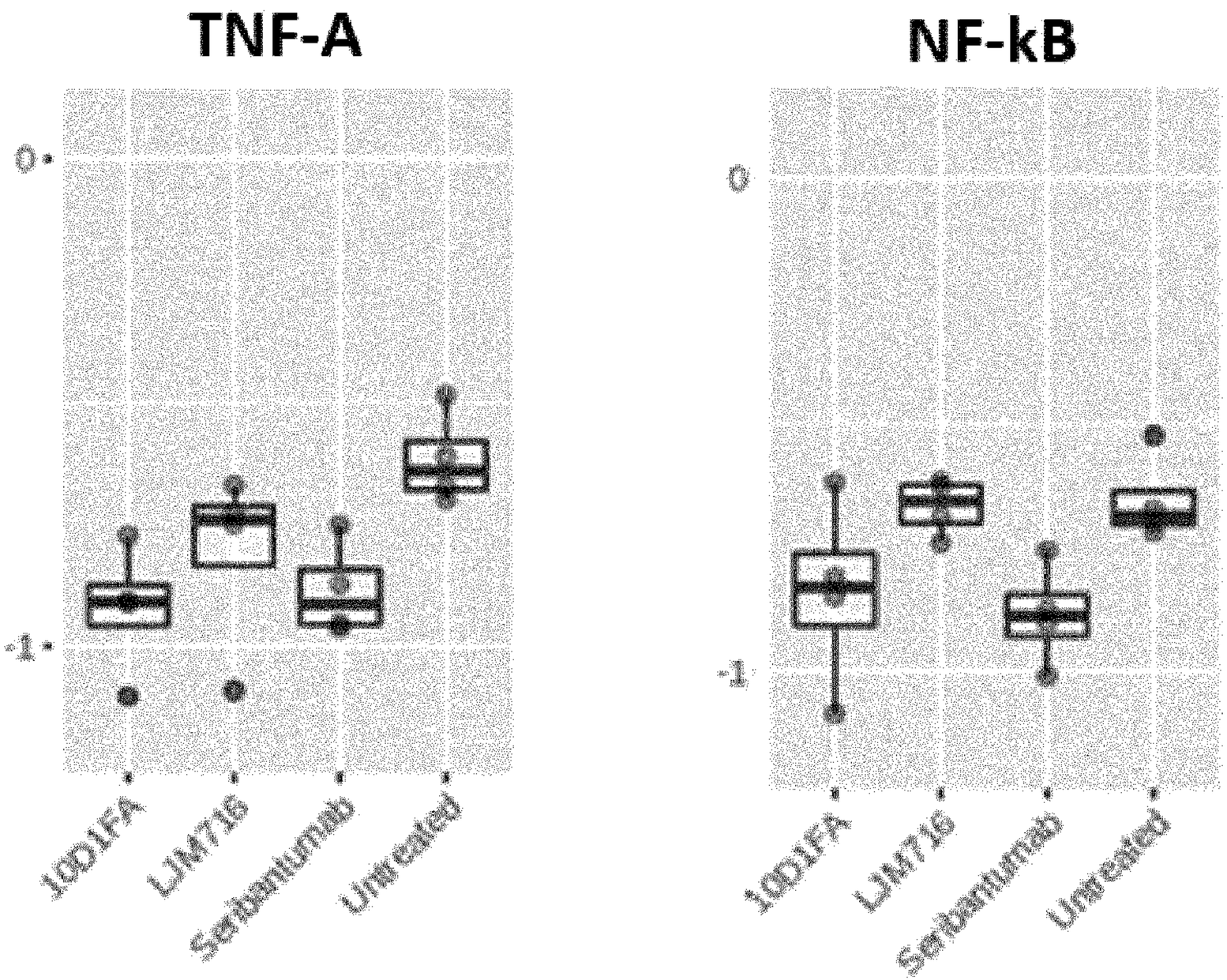
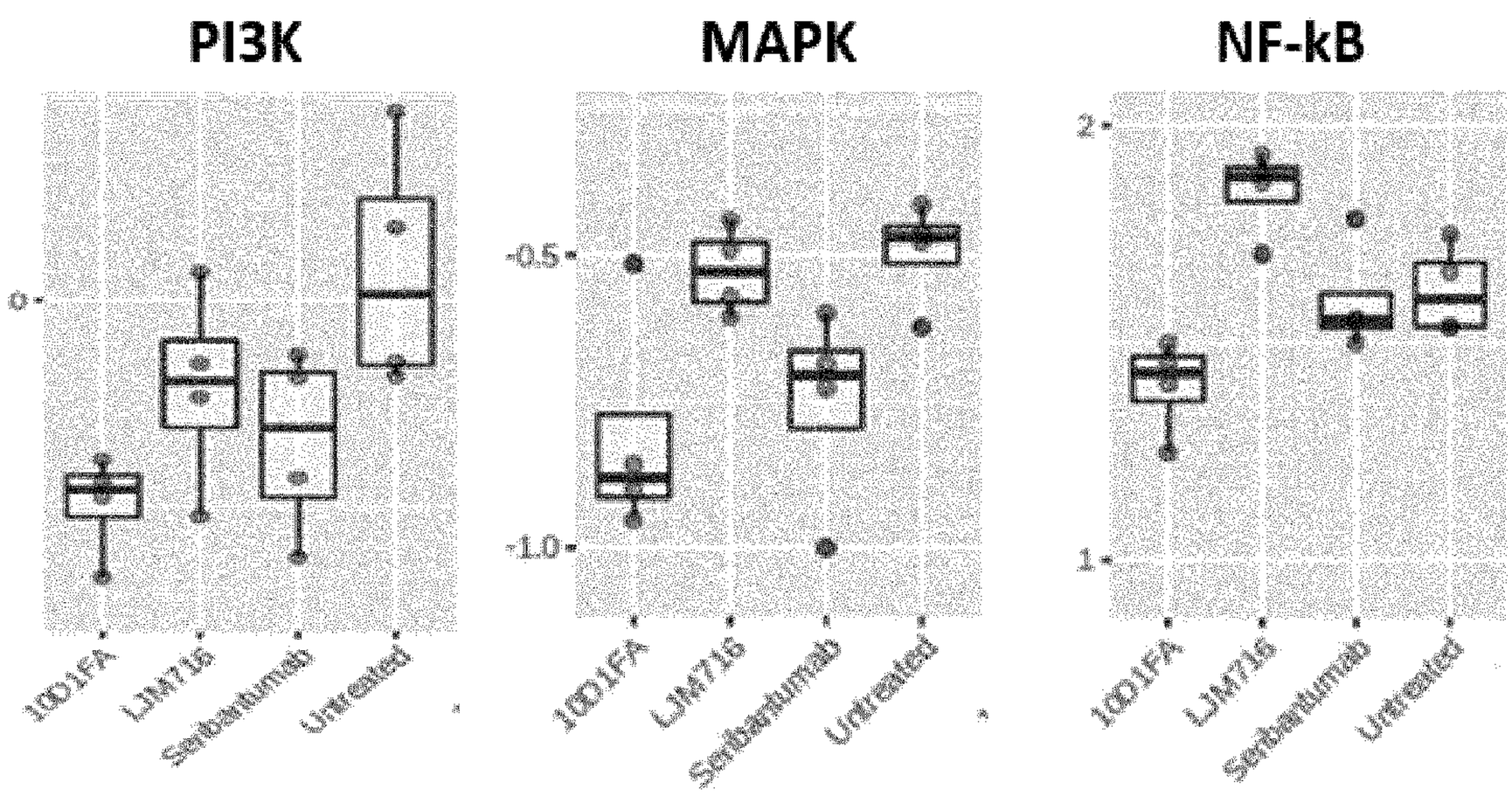


Figure 63A


PI3K
MAPK
NF-kB
0
-0.5
-1.0
2
1
1CD1FA
LJM716
Sertbantumab
Untreated

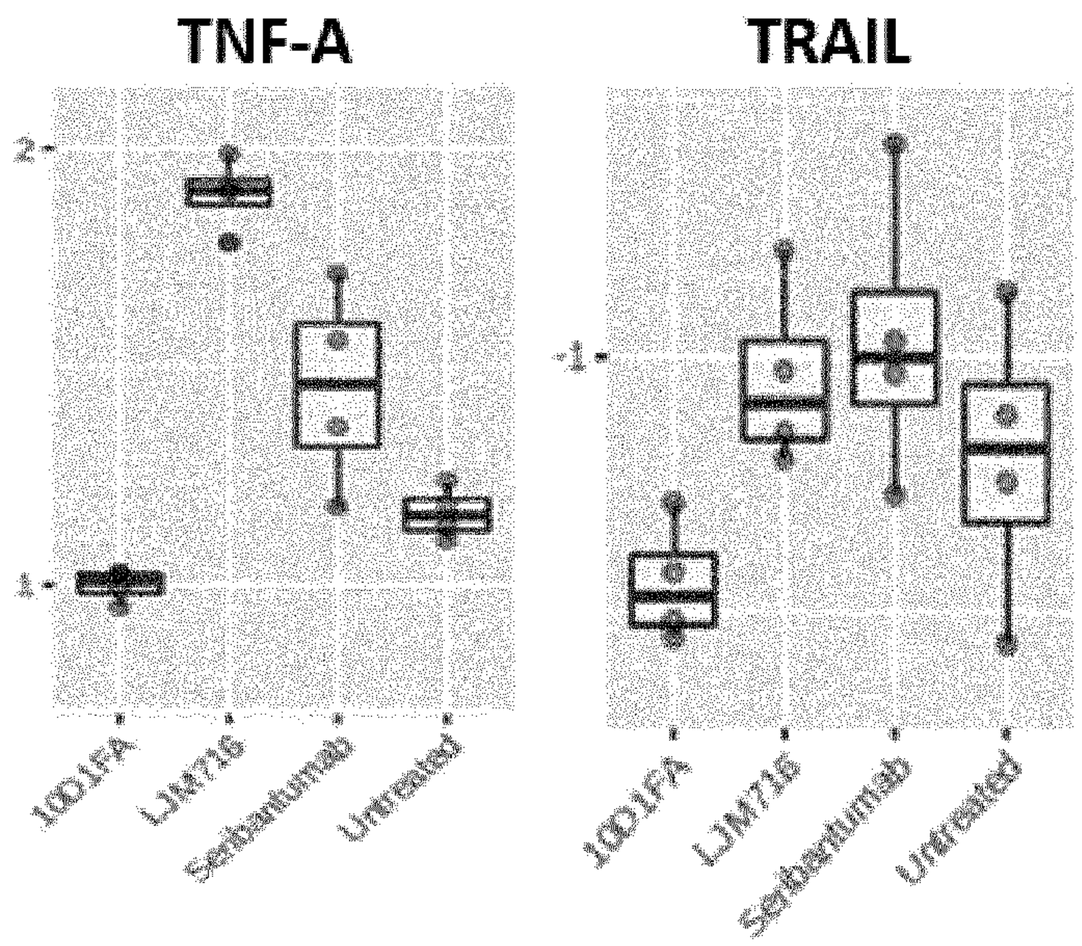

TNF-A
TRAIL
2
1
-1
1CD1FA
LJM716
Sertbantumab
Untreated

Figure 63B

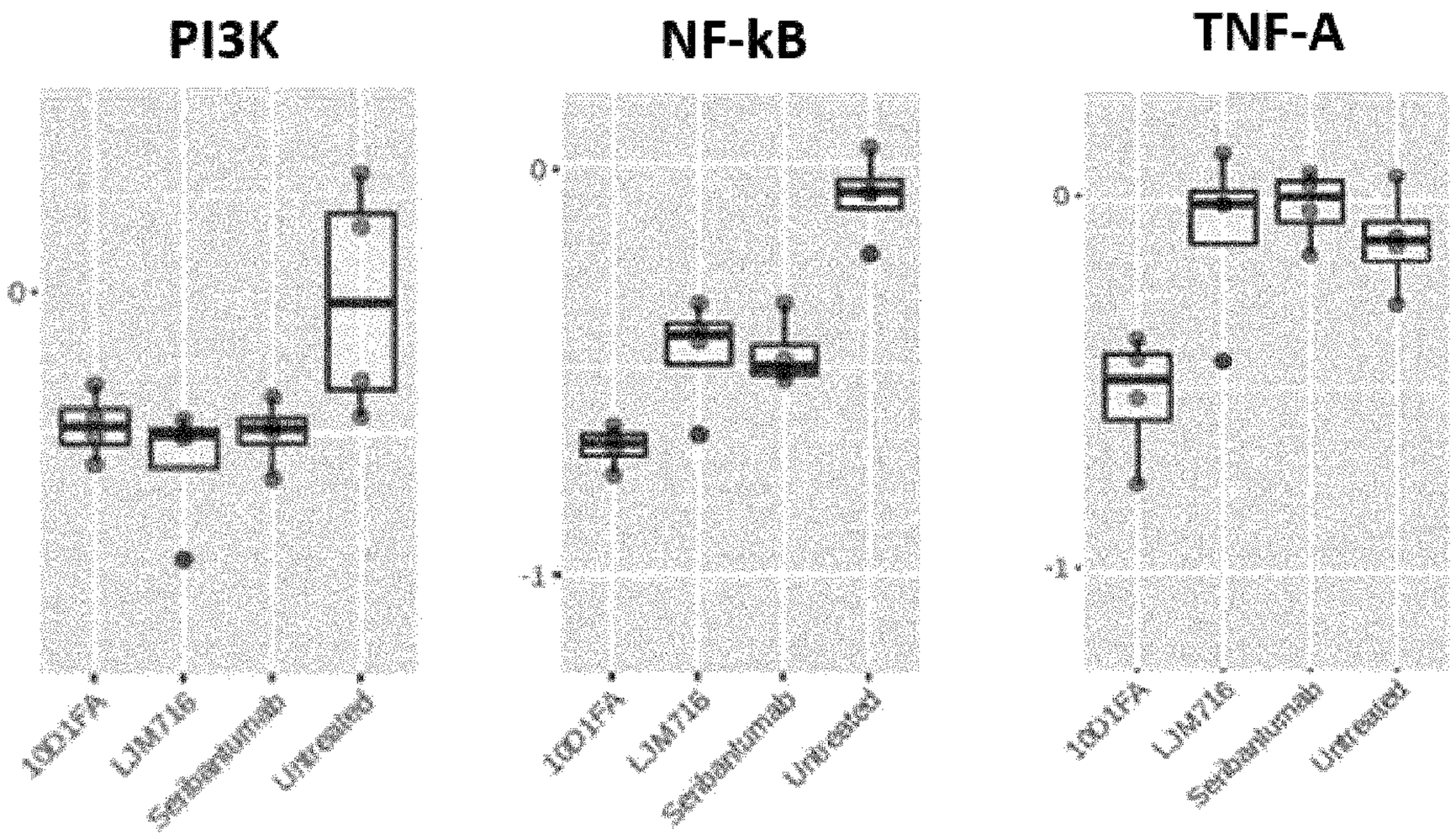
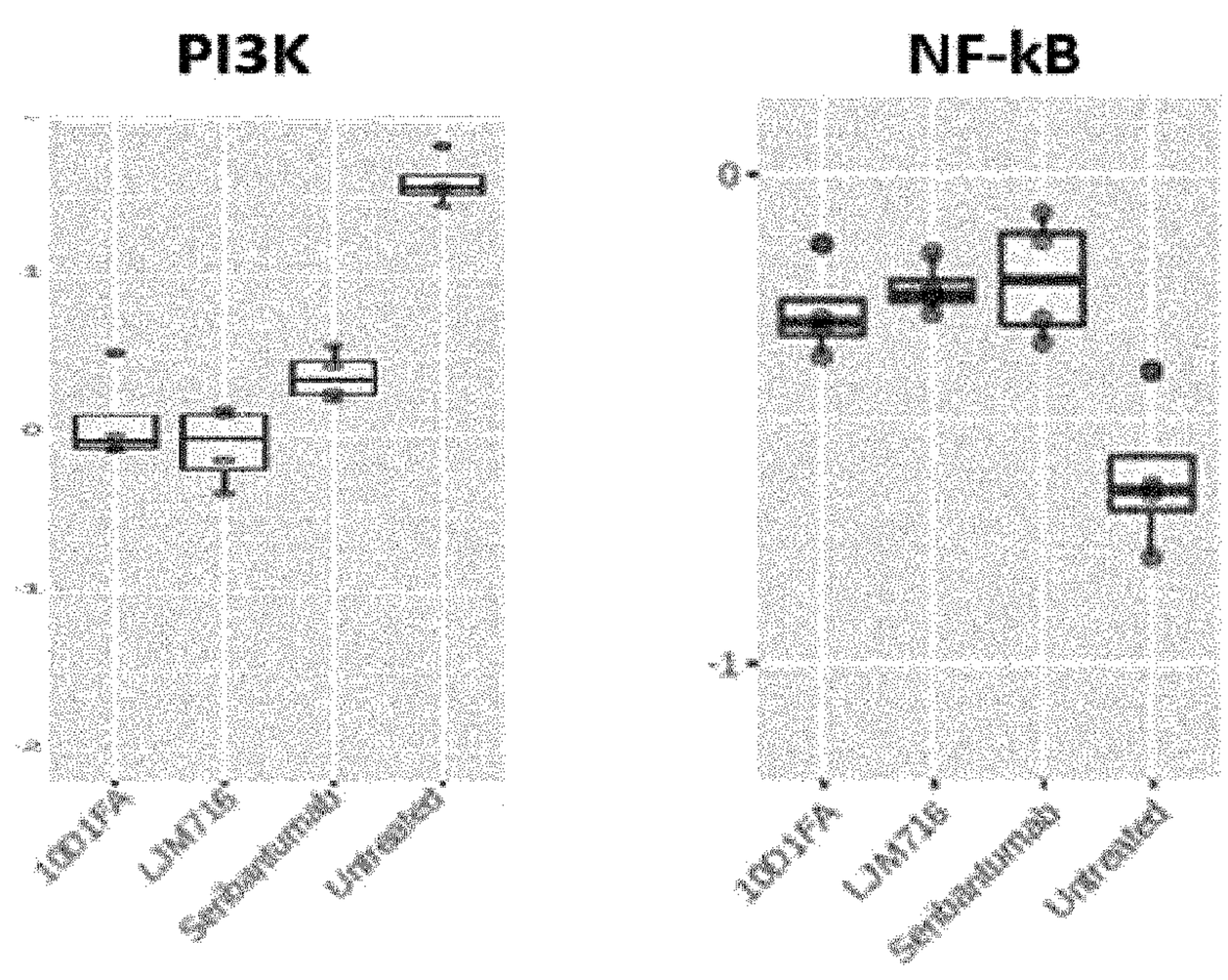
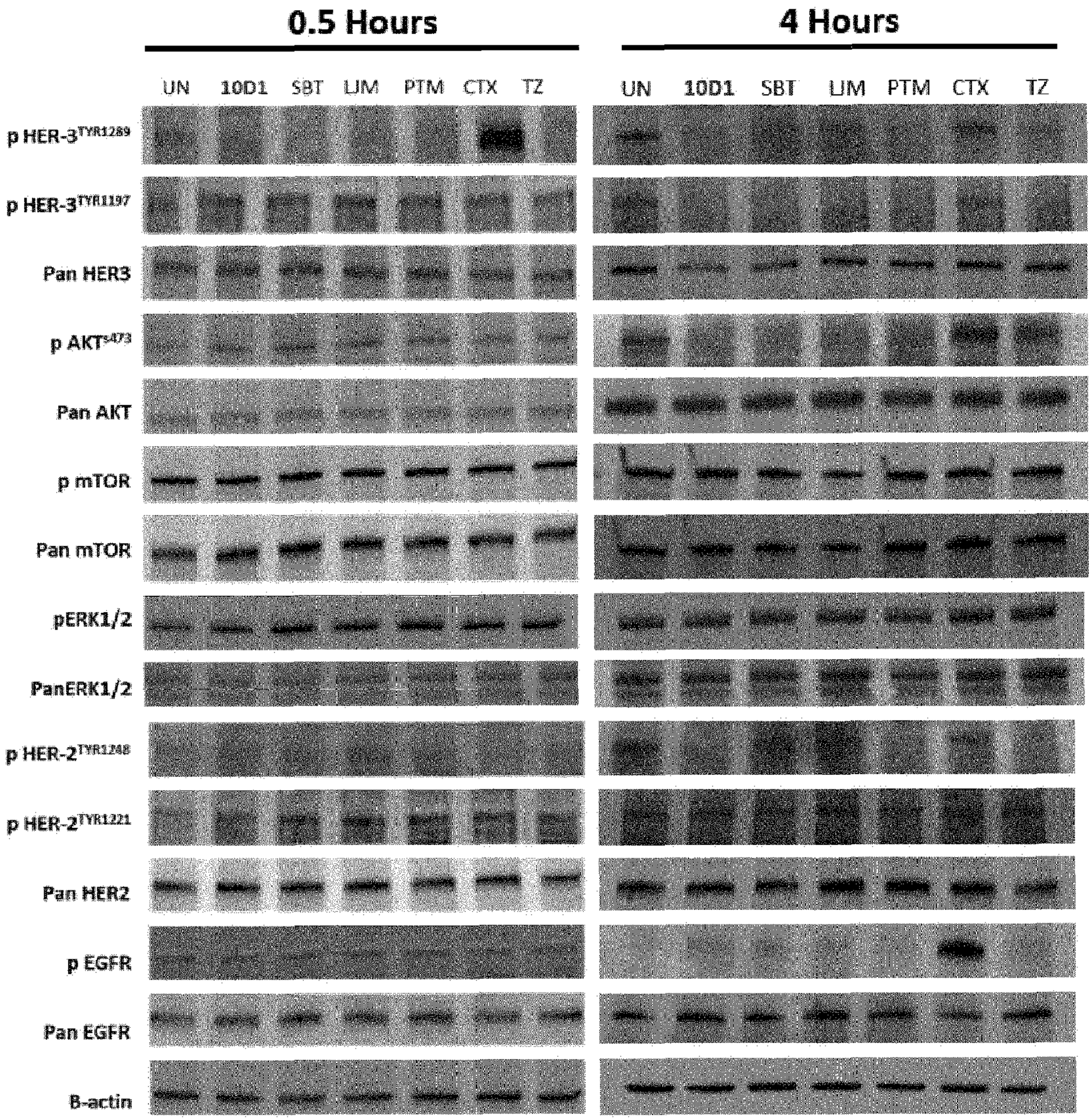


Figure 63C



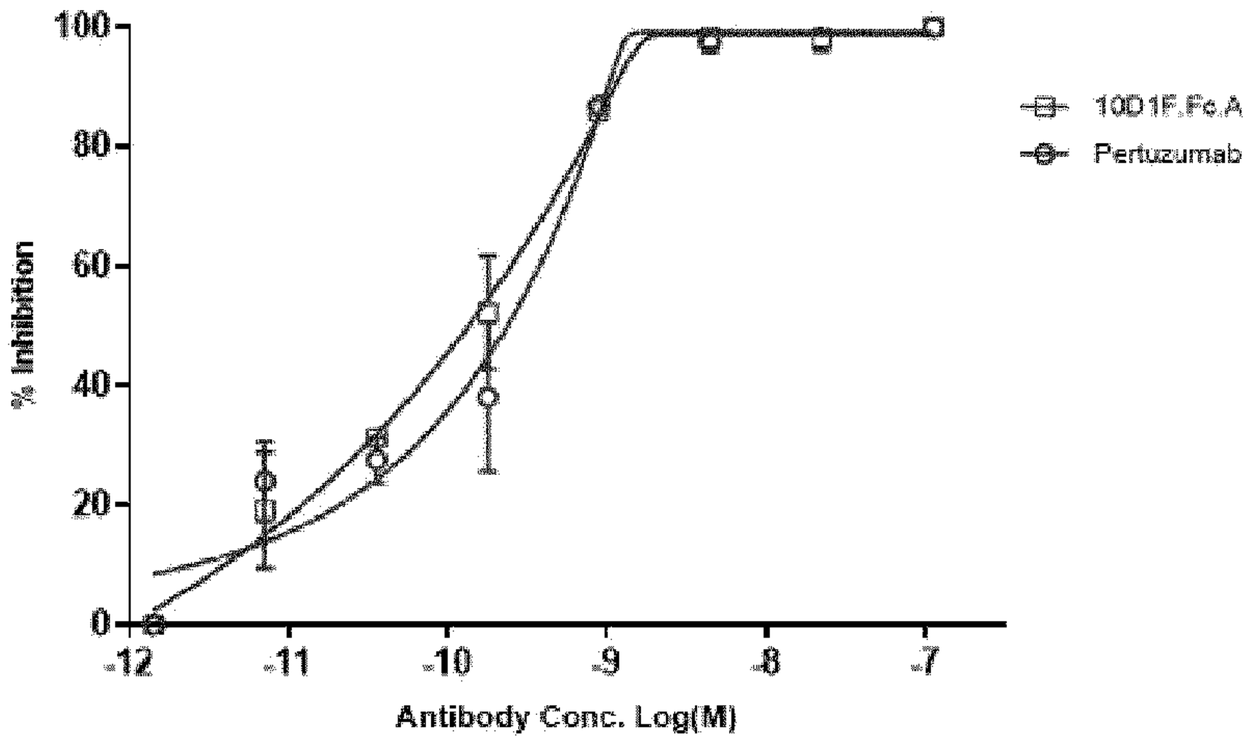
s

Figure 63D



Legend:
UN = Untreated
10D1 = 10D1F.A
SBT = Seribantumab (MM-121)
LJM = Elgemtumab (LJM-716)
PTM = Pertuzumab
CTX = Cetuximab

Figure 64



	10D1F.FcA	Pertuzumab	Isotype
IC_{50} (M)	3.715e-011	2.481e-010	NA

Figure 65

BCPAP

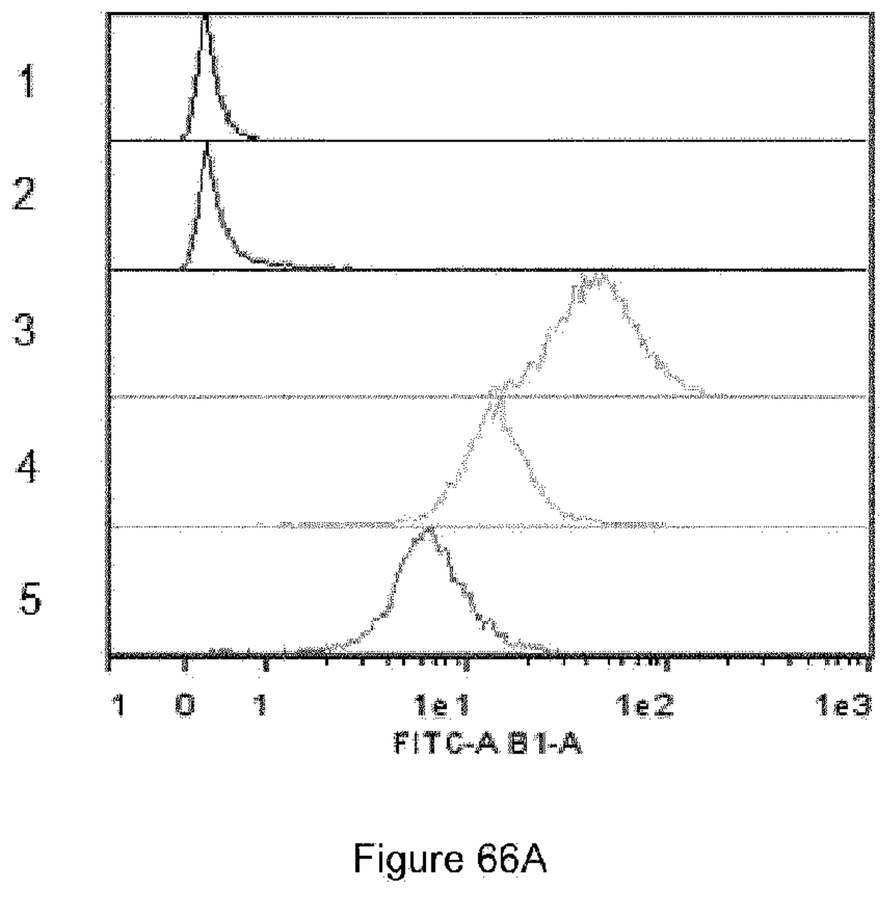


Figure 66A

BHT101

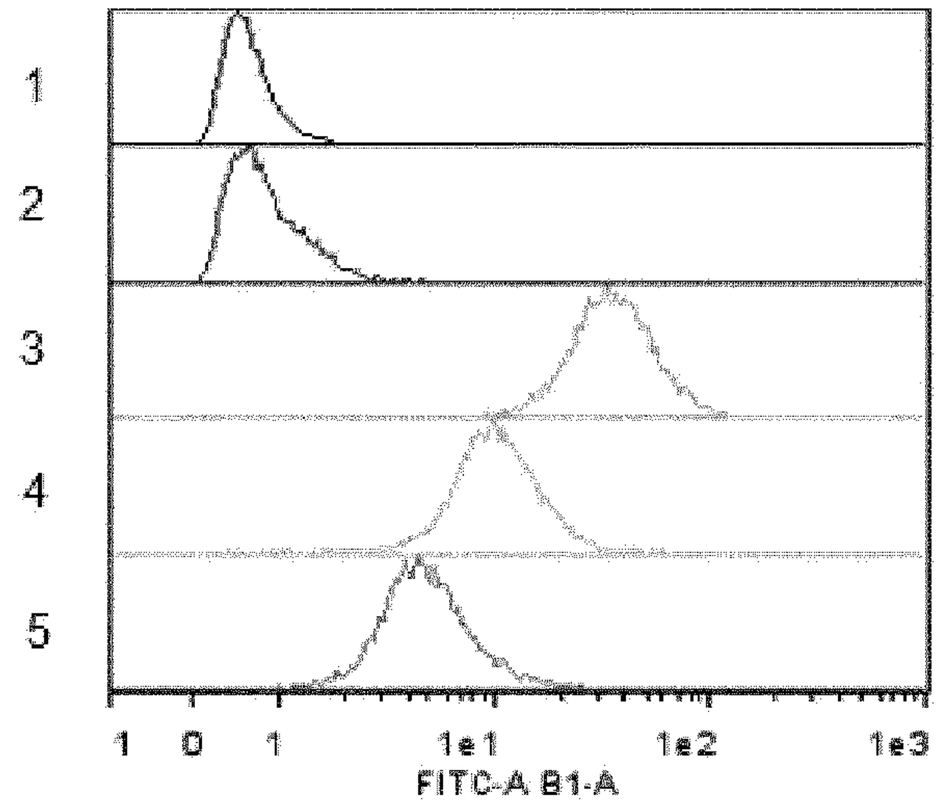


Figure 66B

SW1736

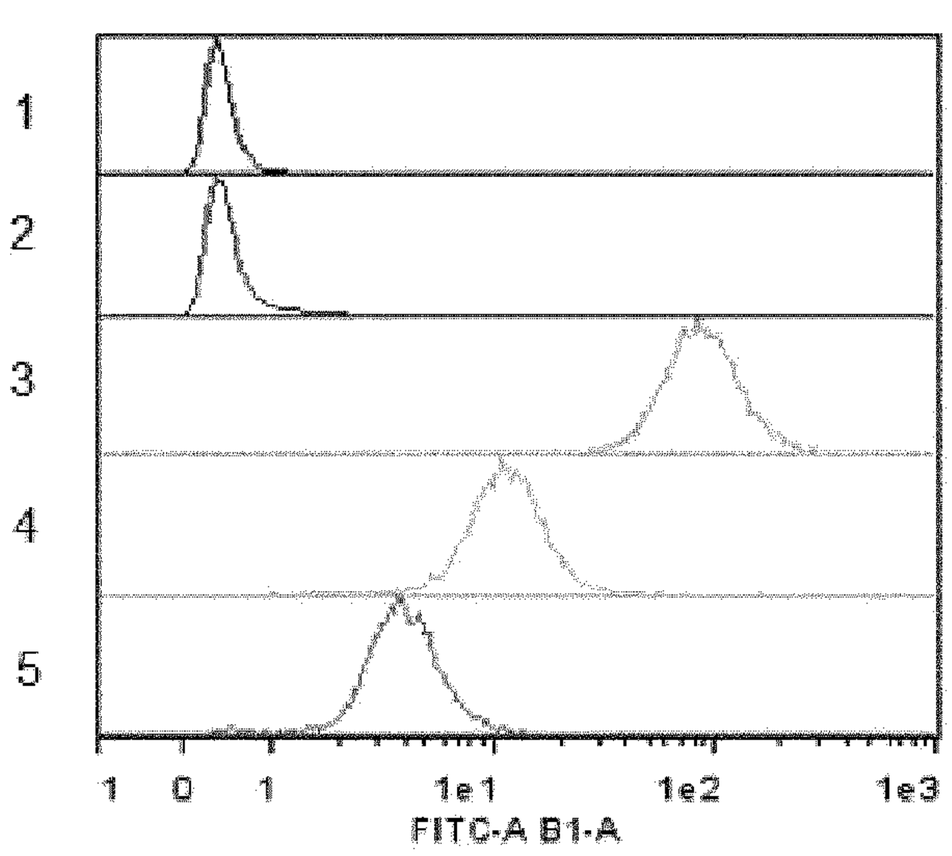


Figure 66C

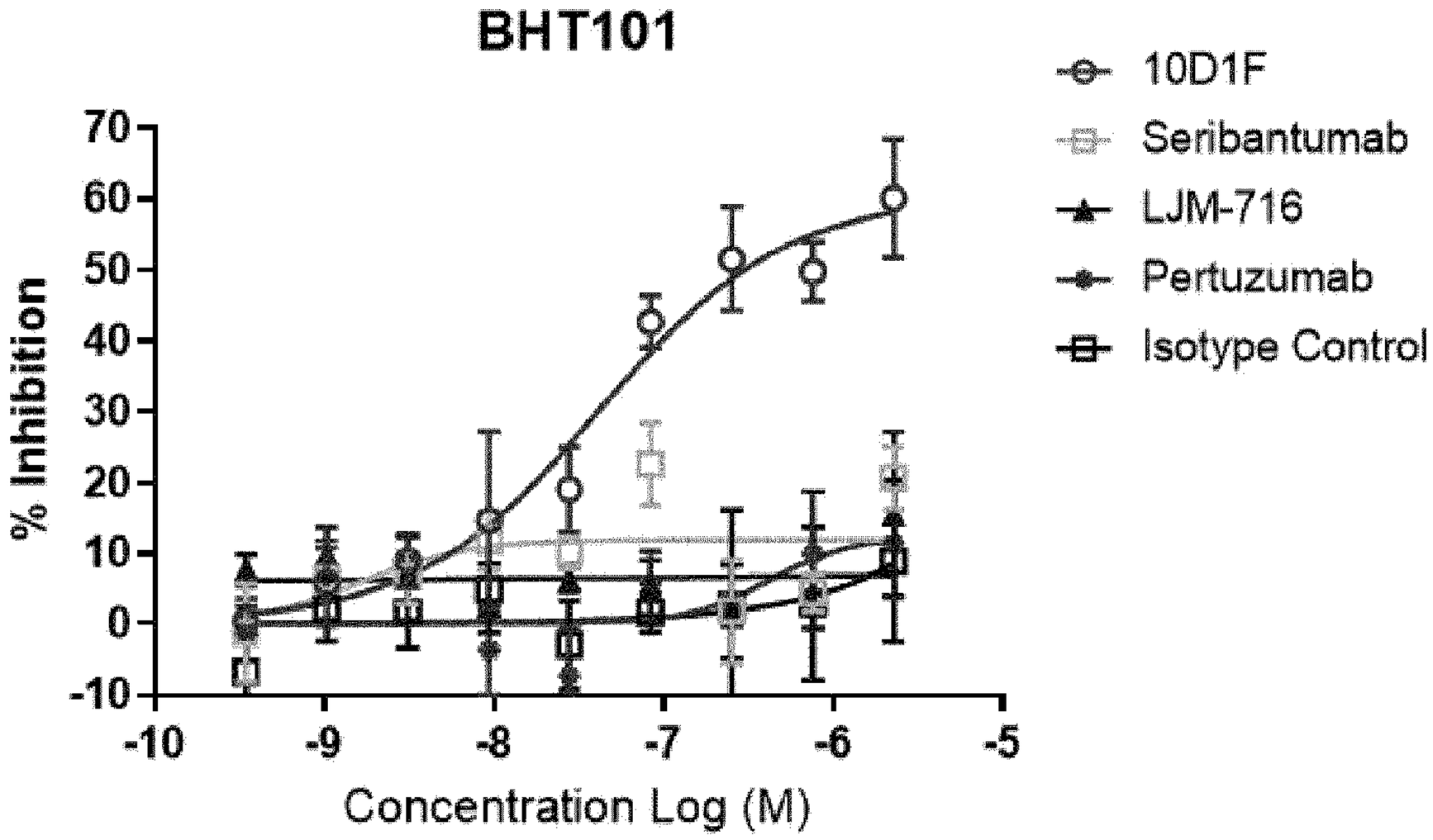


Figure 67A

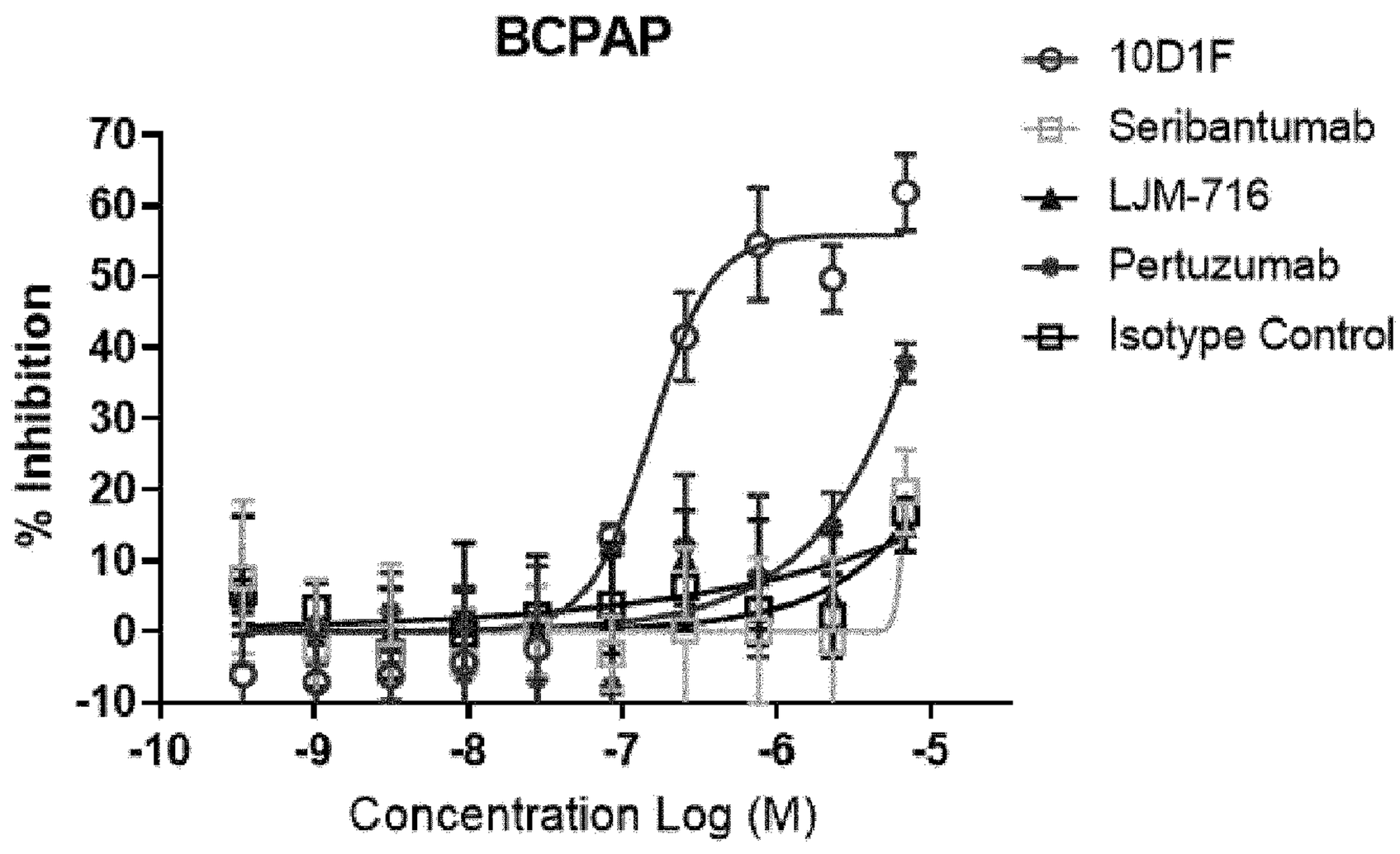


Figure 67B

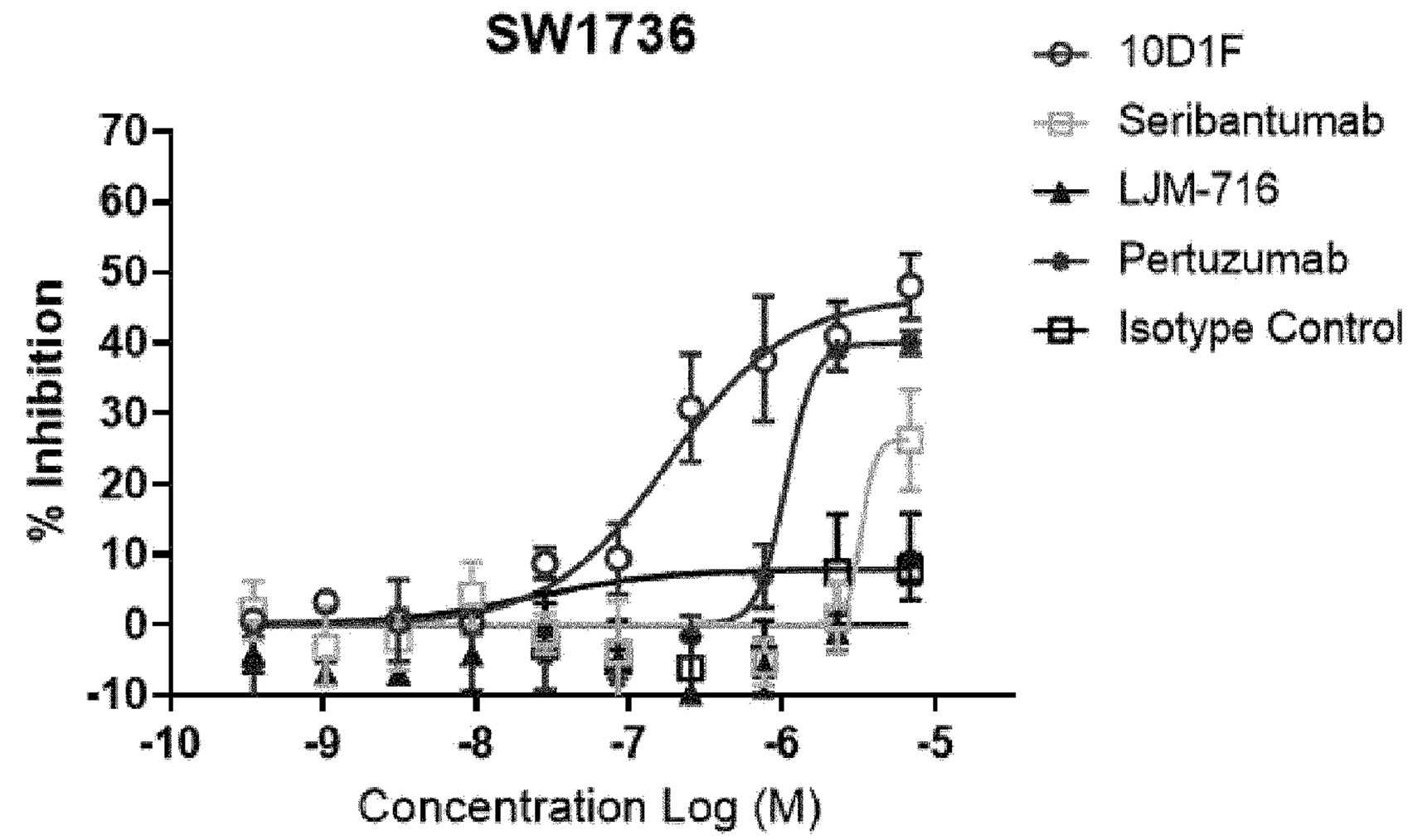


Figure 67C

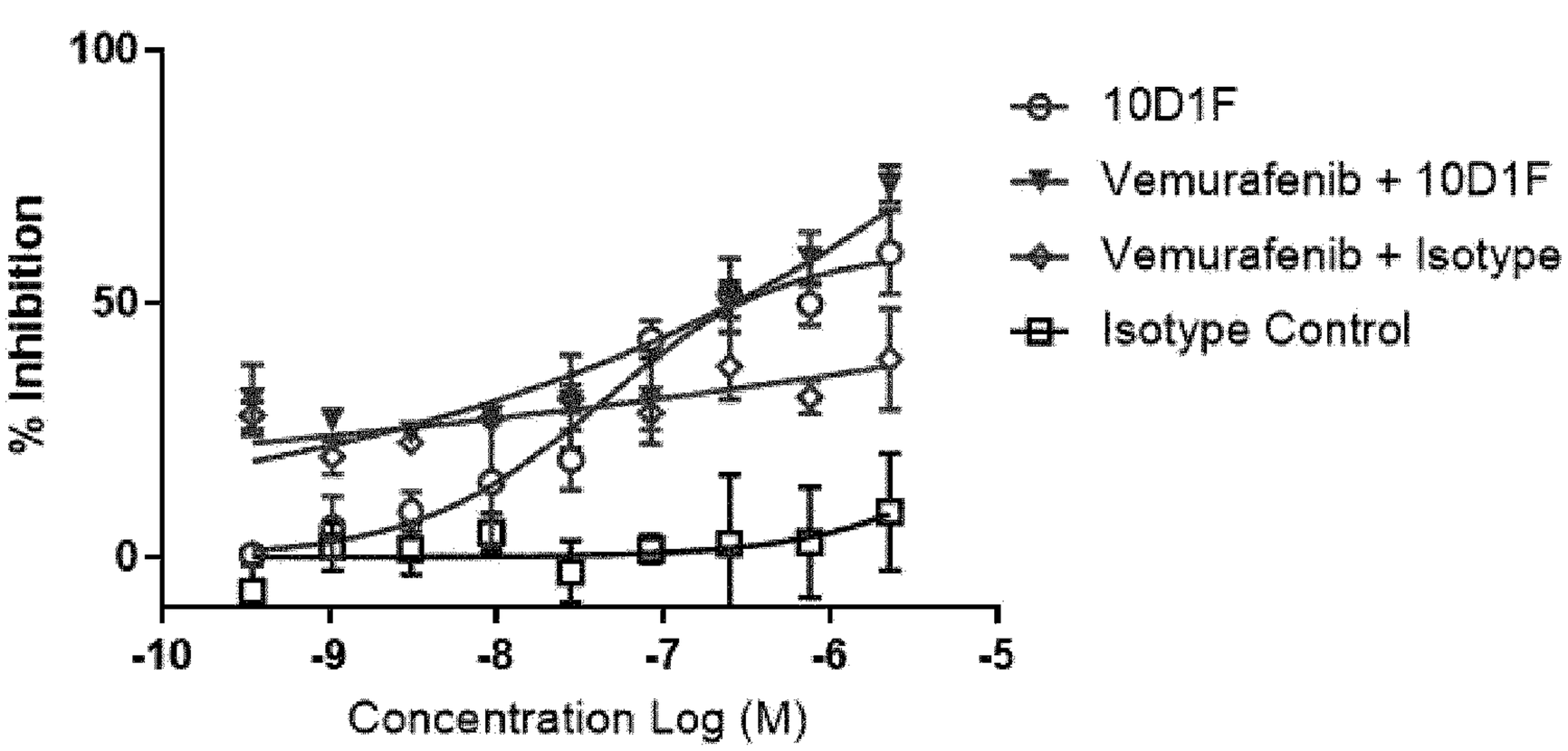


Figure 68A

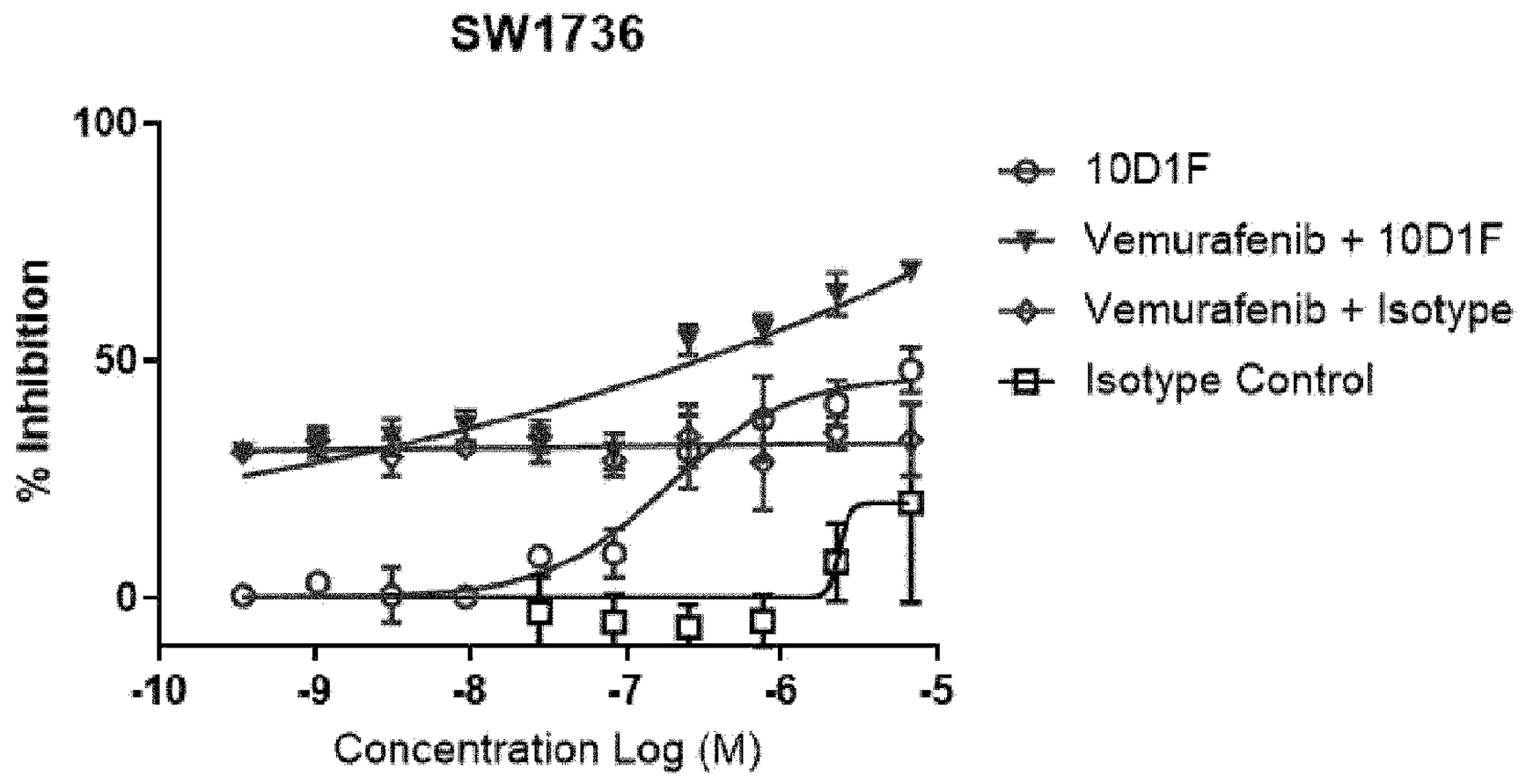


Figure 68B

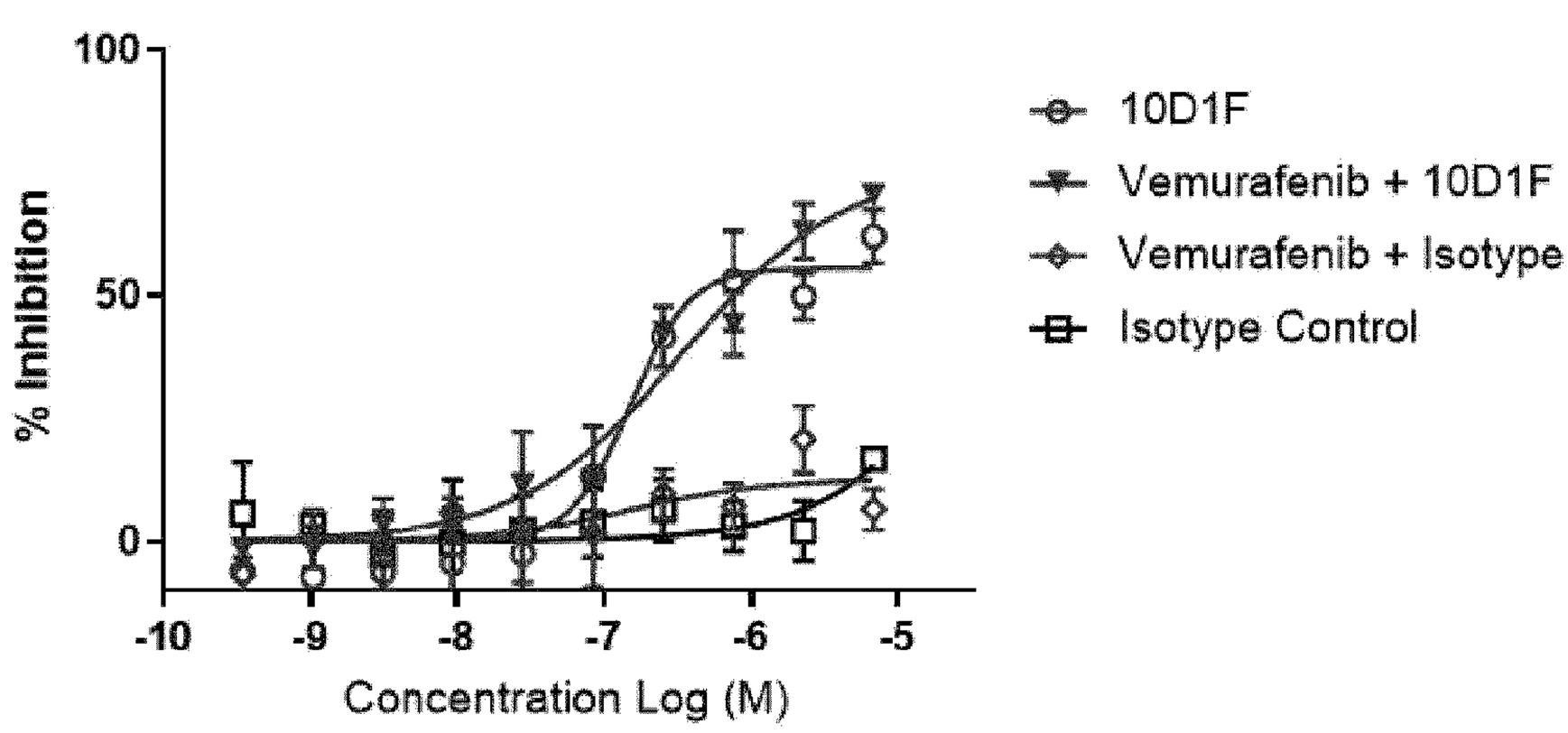


Figure 68C

Treatment Arm	Dose	Red Blood Cell						
					Anemia Parameters			
		RBC Count (10^9/L)	Hemoglobin (g/dl)	Hematocrit (%)	MCV (fml)	MCH (pg)	MCHC (g/dl)	Platelet count (10^9/L)
Vehicle	0	10.59	17.075	52.9275	50	16.125	32.25	490.5
10D1F	10 mg/kg	10.74	17.23	55.97	52.00	16.07	30.87	574.00
	25 mg/kg	10.55	16.97	53.37	50.33	16.10	31.87	555.00
	100 mg/kg	10.16	15.90	51.20	50.33	15.63	31.10	378.00
	250 mg/kg	10.32	16.97	52.13	50.33	16.43	32.53	501.67

Figure 69A

Treatment Arm	Dose	White Blood Cell			
		WBC Count (10^9/ L)	Lymphocyte Count (10^9/ L)	Monocyte Count (10^9/ L)	Neutrophil Count (10^9/ L)
Vehicle	0	7.43	5.58	0.30	1.55
10D1F	10 mg/kg	9.30	7.06	0.14	2.10
	25 mg/kg	8.00	5.94	0.31	1.74
	100 mg/kg	6.92	5.19	0.11	1.31
	250 mg/kg	3.92	2.88	0.29	0.75

Figure 69B

Treatment Arm	Dose	Biochemistry			
		Liver (U/L)		Kidney (mg/dL)	
		ALT	ALP	CREA	BUN
Vehicle	0	25.00	104.50	0.25	13.00
10D1F	10 mg/kg	22.67	109.33	0.30	11.33
	25 mg/kg	48.67	121.00	0.23	12.33
	100 mg/kg	27.00	101.33	0.23	11.00
	250 mg/kg	53.00	101.33	0.27	16.33

Treatment Arm	Dose	Biochemistry					
		Pancreas		Electrolytes			
		GLU (mg/dL)	AMY (U/L)	NA (meq/L)	K (meq/L)	P (mg/dL)	CA (mg/dL)
Vehicle	0	128.75	959.75	144.75	7.35	6.83	10.35
10D1F	10 mg/kg	91.00	904.67	143.00	8.07	6.67	10.30
	25 mg/kg	109.57	938.00	144.33	7.30	6.50	10.77
	100 mg/kg	119.30	862.00	148.33	7.47	5.53	10.57
	250 mg/kg	139.30	1407.67	146.67	7.83	5.33	10.30

Figure 69C

Treatment Arm	Time (hrs)	Red Blood Cell						
					Anemia Parameters			
		RBC Count (10^9/L)	Hemoglobin (g/dl)	Hematocrit (%)	MCV (fml)	MCH (pg)	MCHC (g/dl)	Platelet count (10^9/L)
Vehicle	0	5.30	13.21	54.84	59.33	17.20	28.63	398.0
	6	4.55	8.97	51.38	60.67	16.77	29.90	362.0
	24	5.84	13.59	39.51	56.67	18.03	30.77	411.3
	96	7.76	10.87	52.41	60.67	17.60	30.23	488.7
	168	5.81	11.49	42.31	59.67	17.27	29.90	573.7
	336	7.51	16.41	49.23	60.67	16.83	29.03	685.0
10D1F	0	12.13	13.05	66.59	55.50	17.10	26.20	339.5
	6	11.96	12.95	66.88	57.00	17.35	25.90	392.0
	24	8.05	15.20	49.68	62.00	18.90	30.60	248.5
	96	8.07	15.65	49.34	61.00	19.40	31.80	337.5
	168	6.25	12.40	40.99	65.50	19.80	30.20	577.0
	336	7.35	13.60	47.13	64.00	18.25	28.40	440.0

Figure 70A

Treatment Arm	Time (hrs)	White Blood Cell			
		WBC Count (10^9/ L)	Lymphocyte Count (10^9/ L)	Monocyte Count (10^9/ L)	Neutrophil Count (10^9/ L)
Vehicle	0	13.22	10.12	1.43	3.08
	6	8.09	9.01	1.20	2.57
	24	9.82	9.08	0.89	2.08
	96	7.61	7.59	0.97	1.97
	168	11.02	9.23	1.24	2.05
	336	9.67	6.14	0.64	2.06
10D1F	0	10.61	2.87	0.27	2.47
	6	13.40	5.57	0.99	1.84
	24	10.70	7.55	0.84	2.32
	96	10.24	8.04	0.71	1.49
	168	4.68	3.45	0.18	1.05
	336	11.04	9.02	0.62	1.40

Figure 70B

Treatment Arm	Time (hrs)	Biochemistry			
		Liver (U/L)		Kidney (mg/dL)	
		ALT	ALP	CREA	BUN
Vehicle	0	4.80	6.77	0.40	10.00
	6	5.03	6.37	0.37	12.00
	24	3.87	6.57	0.40	12.33
	96	3.93	6.63	0.40	12.00
	168	4.70	6.90	0.40	10.67
	336	4.97	6.53	0.33	13.33
10D1F	0	5.05	5.55	0.30	13.50
	6	4.40	5.95	0.35	12.50
	24	4.30	7.40	0.40	12.50
	96	4.70	7.00	0.40	12.00
	168	5.00	6.50	0.55	13.50
	336	4.45	6.15	0.30	7.00

Treatment Arm	Time (hrs)	Biochemistry					
		Pancreas		Electrolytes			
		GLU (mg/dL)	AMY (U/L)	NA (meq/L)	K (meq/L)	P (mg/dL)	CA (mg/dL)
Vehicle	0	119.3	514.3	138.3	6.87	6.87	11.50
	6	141.0	537.3	142.7	5.73	5.00	11.50
	24	130.3	594.3	139.7	5.37	7.43	11.53
	96	117.0	503.3	141.3	5.90	7.17	11.60
	168	122.7	562.7	144.0	7.10	6.93	11.30
	336	135.7	643.0	139.7	6.27	7.80	11.17
10D1F	0	125.0	465.5	141.0	6.30	6.70	10.75
	6	123.5	521.0	143.5	6.00	7.25	11.05
	24	131.0	646.5	140.5	7.05	7.85	11.75
	96	111.0	632.5	140.0	6.85	8.05	11.85
	168	146.0	574.0	137.0	5.30	7.05	11.20
	336	100.5	821.5	139.0	5.35	7.30	11.45

Figure 70C

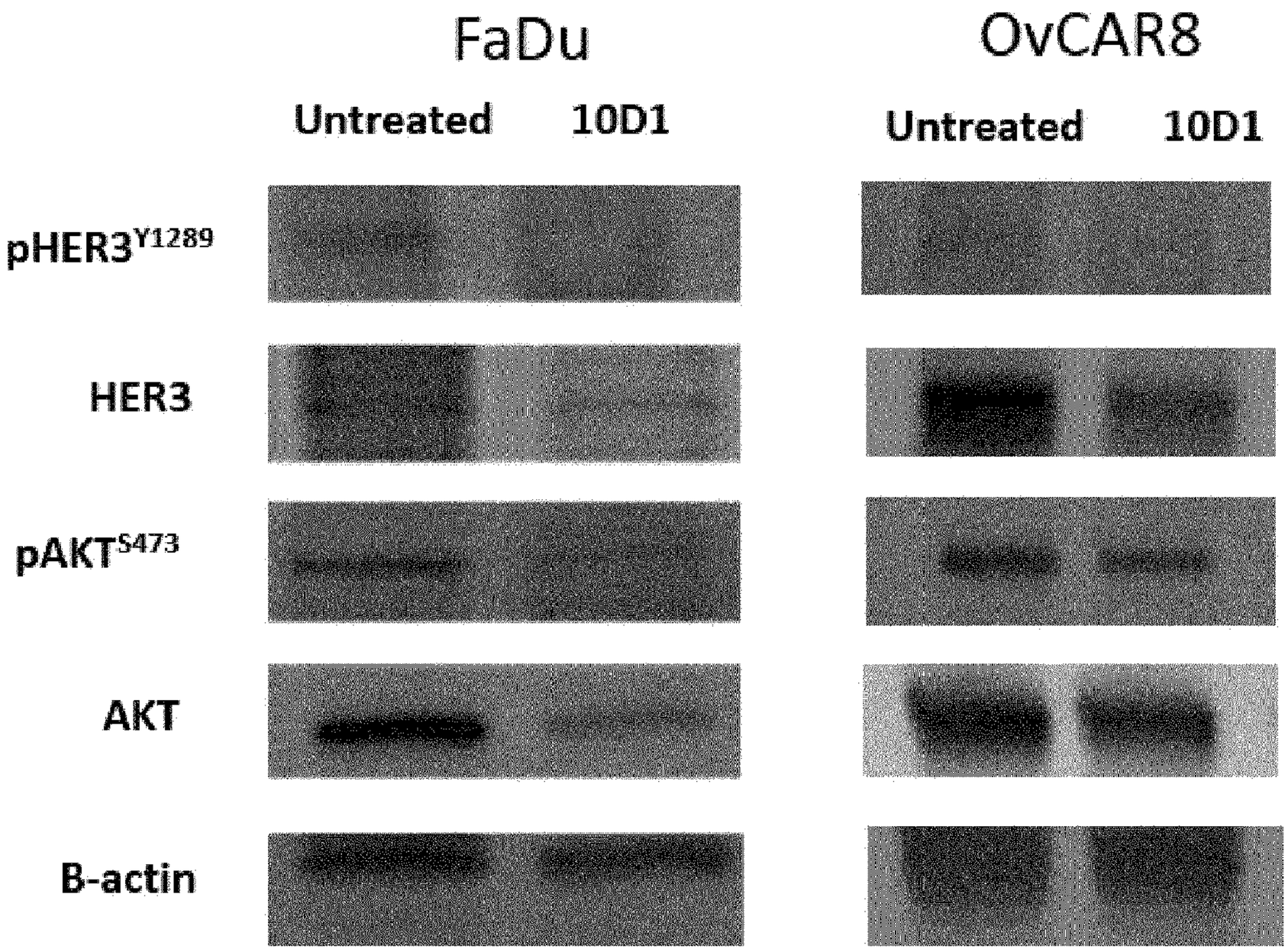

FaDu
OvCAR8
Untreated
10D1
Untreated
10D1
pHER3Y1289
HER3
pAKTS473
AKT
B-actin

Figure 71

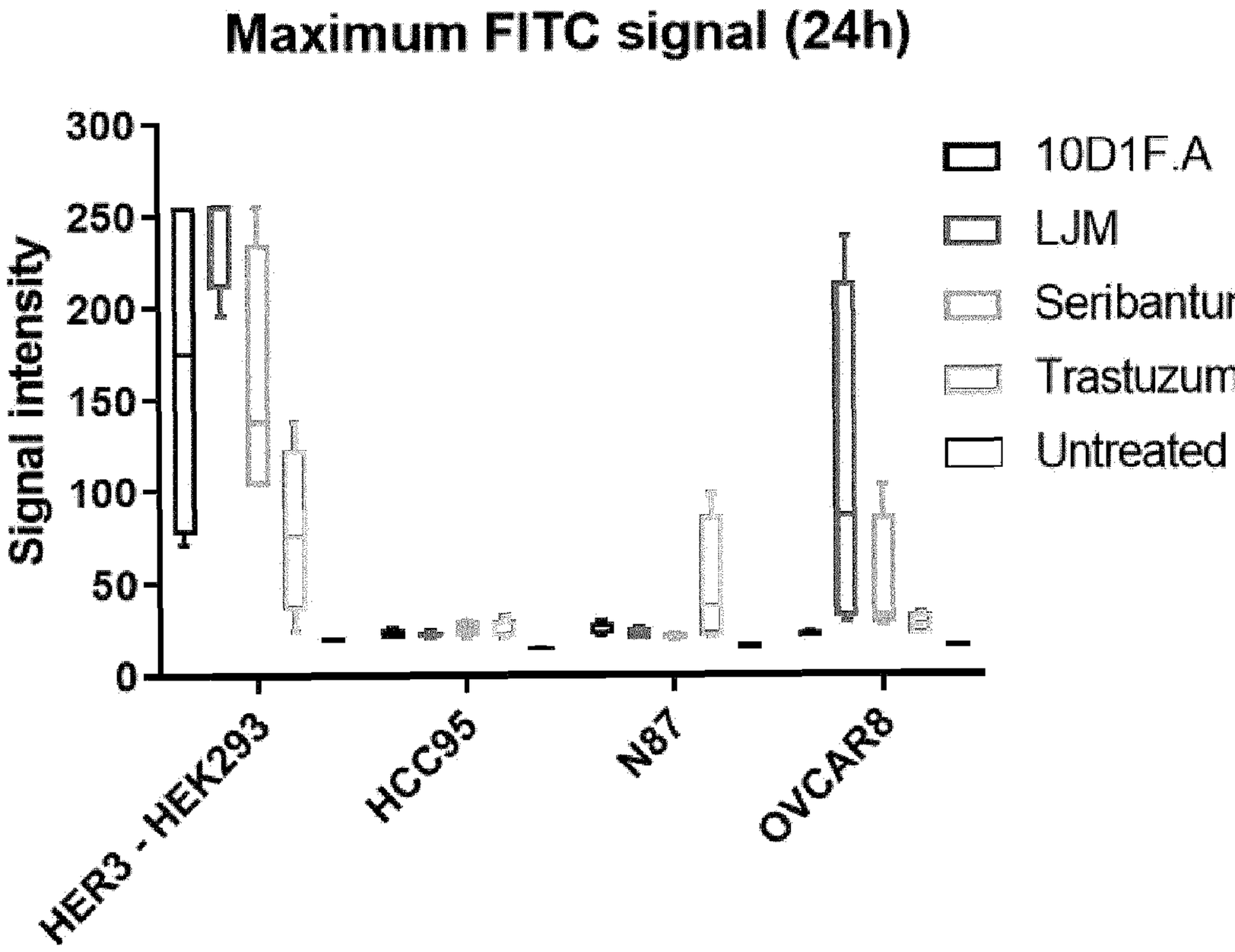

Maximum FITC signal (24h)
Signal intensity
300
250
200
150
100
50
0
HER3 - HEK293
HCC95
N87
OVCAR8
10D1F.A
LJM
Seribantumab
Trastuzumab
Untreated

Figure 72

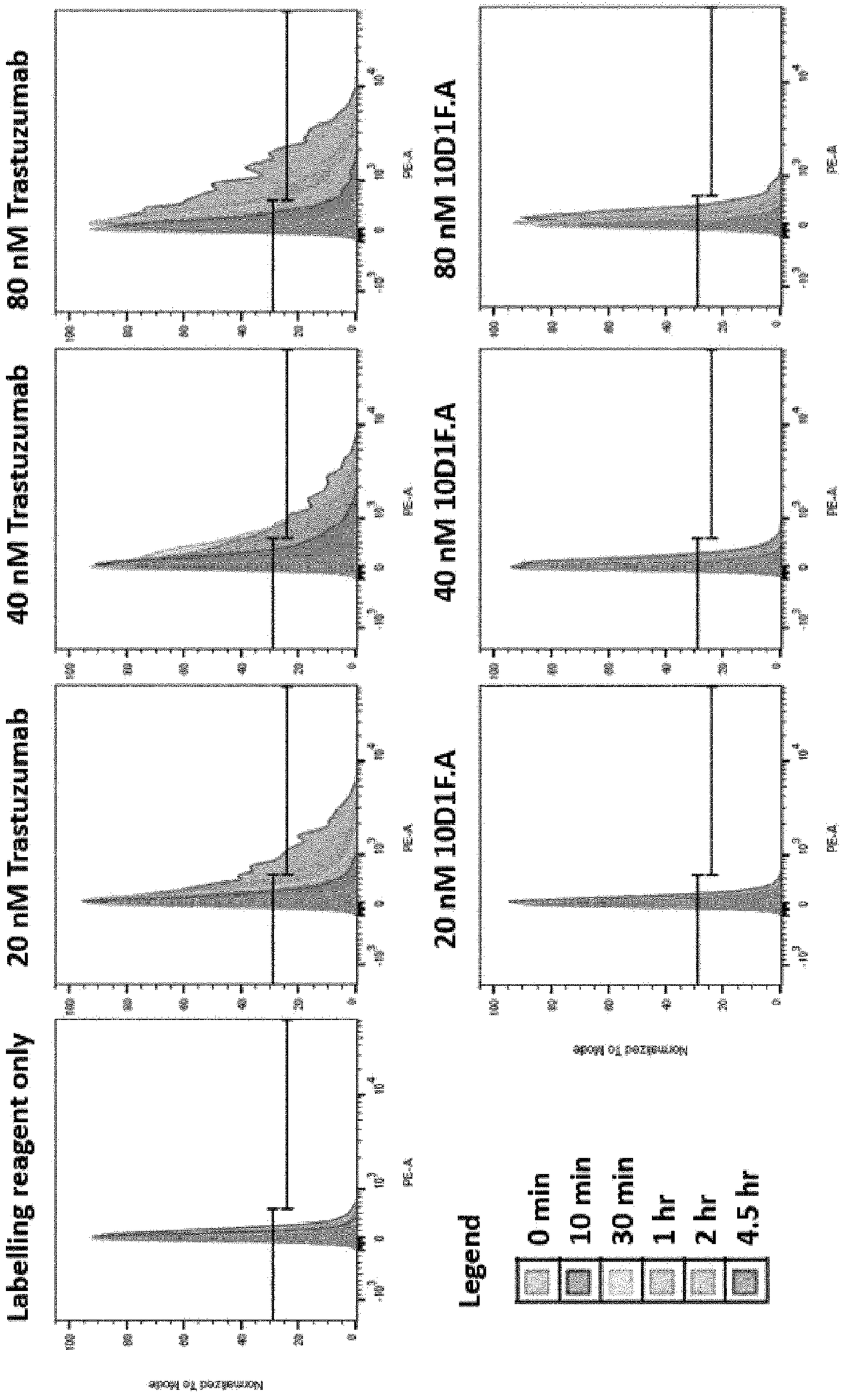

80 nM Trastuzumab
80 nM 10D1F.A
40 nM Trastuzumab
40 nM 10D1F.A
20 nM Trastuzumab
20 nM 10D1F.A
0 nM Trastuzumab
Labelling reagent only
PE-A
Normalized to Mode
Legend
0 min
10 min
30 min
1 hr
2 hr
4.5 hr

Figure 73A

MFI

	0 min	10 min	30 min	1 hr	2 hrs	4.5 hrs
80 nM 10D1F.A	110	108	129	148	184	279
40 nM 10D1F.A	104	114	129	145	178	204
20 nM 10D1F.A	105	110	117	119	127	156
80 nM Trastuzumab	133	270	393	435	528	802
40 nM Trastuzumab	124	298	294	495	465	614
20 nM Trastuzumab	115	194	266	305	354	578
No Ab + 120 nM Zenon	102	116	117	128	143	182

Percent of PE+ cells

	0 min	10 min	30 min	1 hr	2 hrs	4.5 hrs
80 nM 10D1F.A	0.13 %	0 %	0.26 %	0.50 %	0.97 %	6.43 %
40 nM 10D1F.A	0.14 %	0.21 %	0.37 %	0.38 %	1.01 %	1.72 %
20 nM 10D1F.A	0.093 %	0.094 %	0 %	0.18 %	0.22 %	0.43 %
80 nM Trastuzumab	0.90 %	9.64 %	21.7 %	26.9 %	35.6 %	56.0 %
40 nM Trastuzumab	0.49 %	14.4 %	13.2 %	34.3 %	31.4 %	42.5 %
20 nM Trastuzumab	0.14 %	3.73 %	11.1 %	15.2 %	20.3 %	41.8 %
No Ab + 120 nM Zenon	0.039 %	0.086 %	0.35 %	0.18 %	0.26 %	1.06 %

Figure 73B

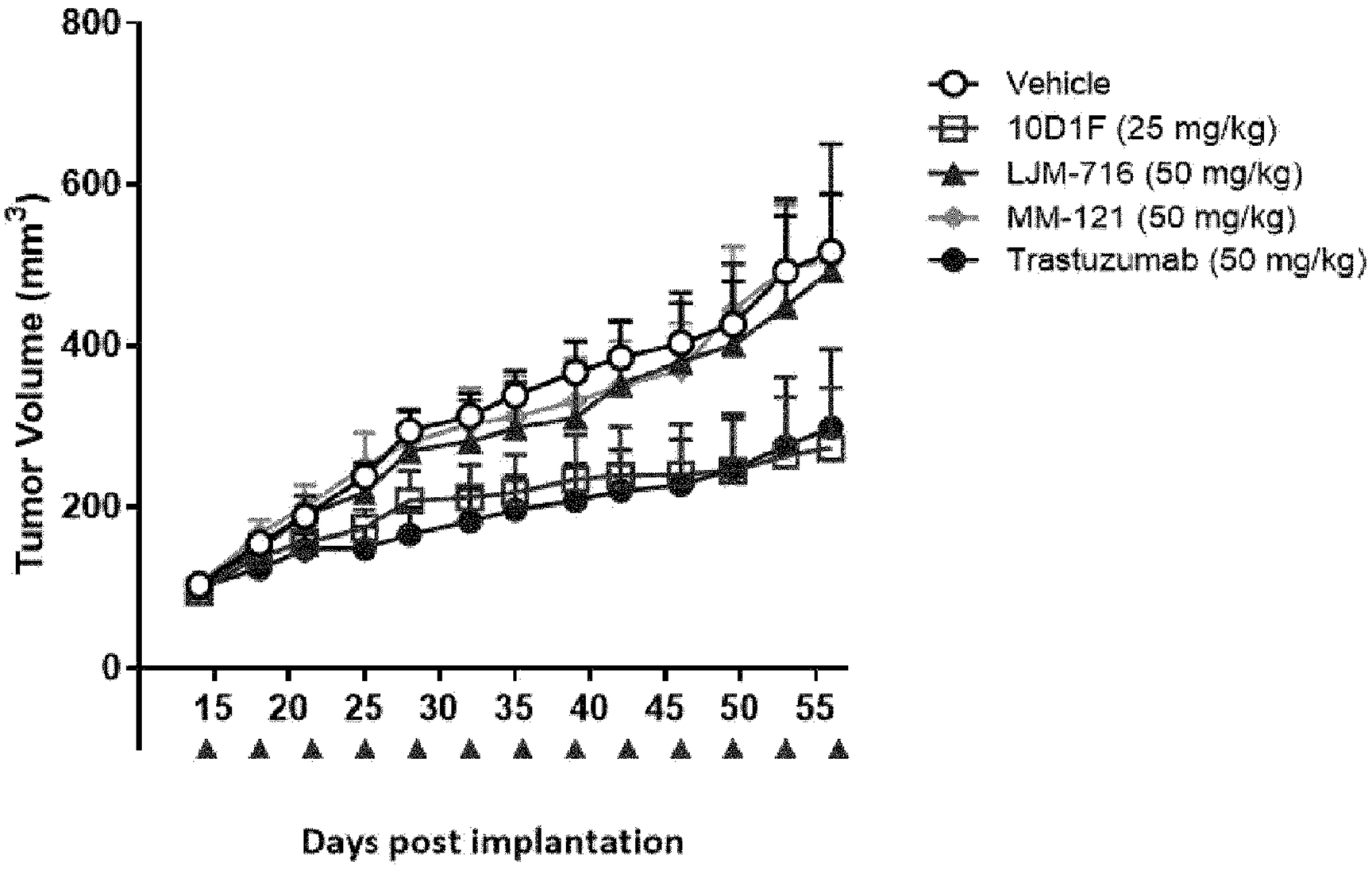

800
600
400
200
0
Tumor Volume (mm3)
15
20
25
30
35
40
45
50
55
Days post implantation
Vehicle
10D1F (25 mg/kg)
LJM-716 (50 mg/kg)
MM-121 (50 mg/kg)
Trastuzumab (50 mg/kg)

Figure 74

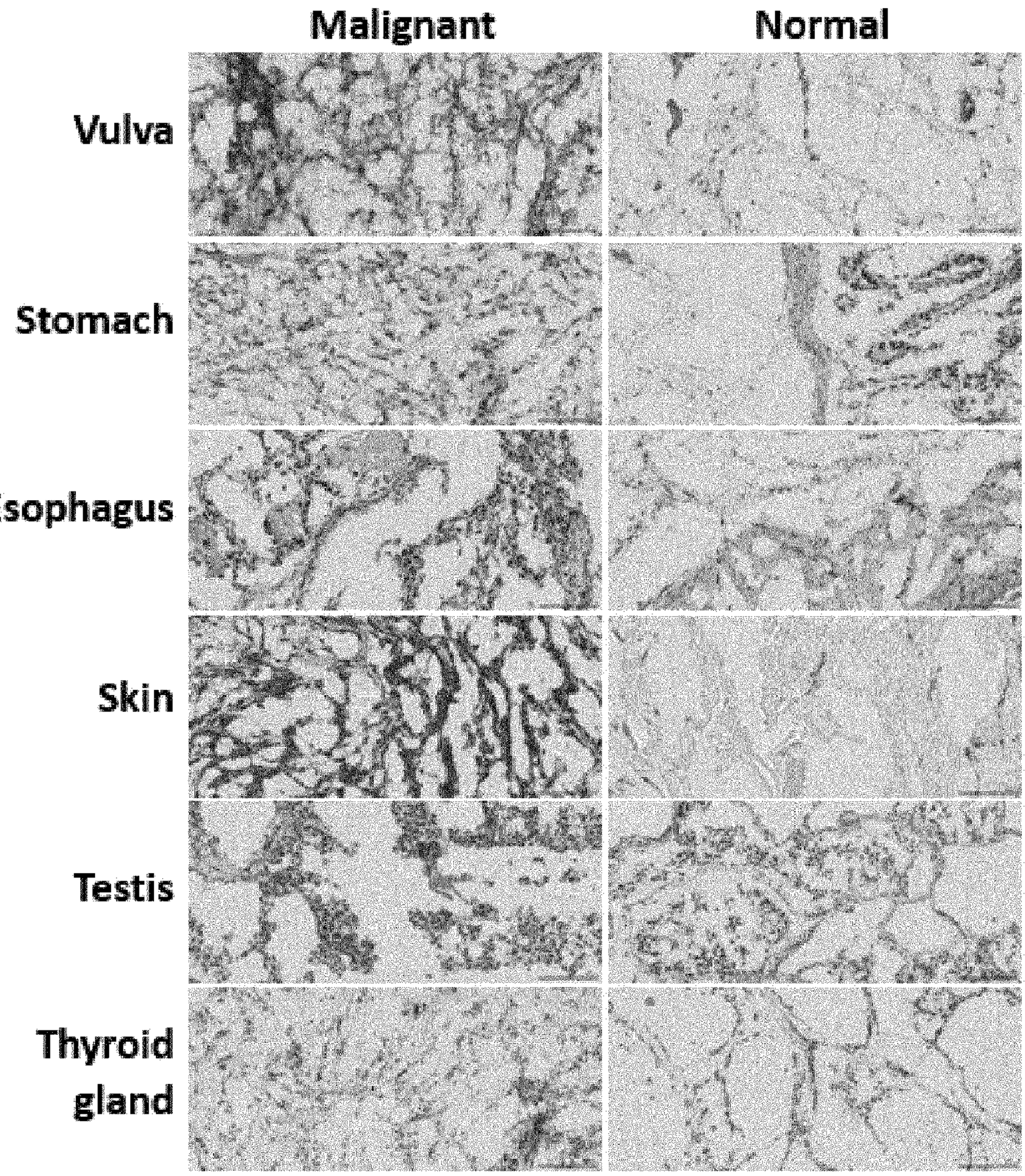

Malignant
Normal
Vulva
Stomach
Esophagus
Skin
Testis
Thyroid gland

Figure 75A

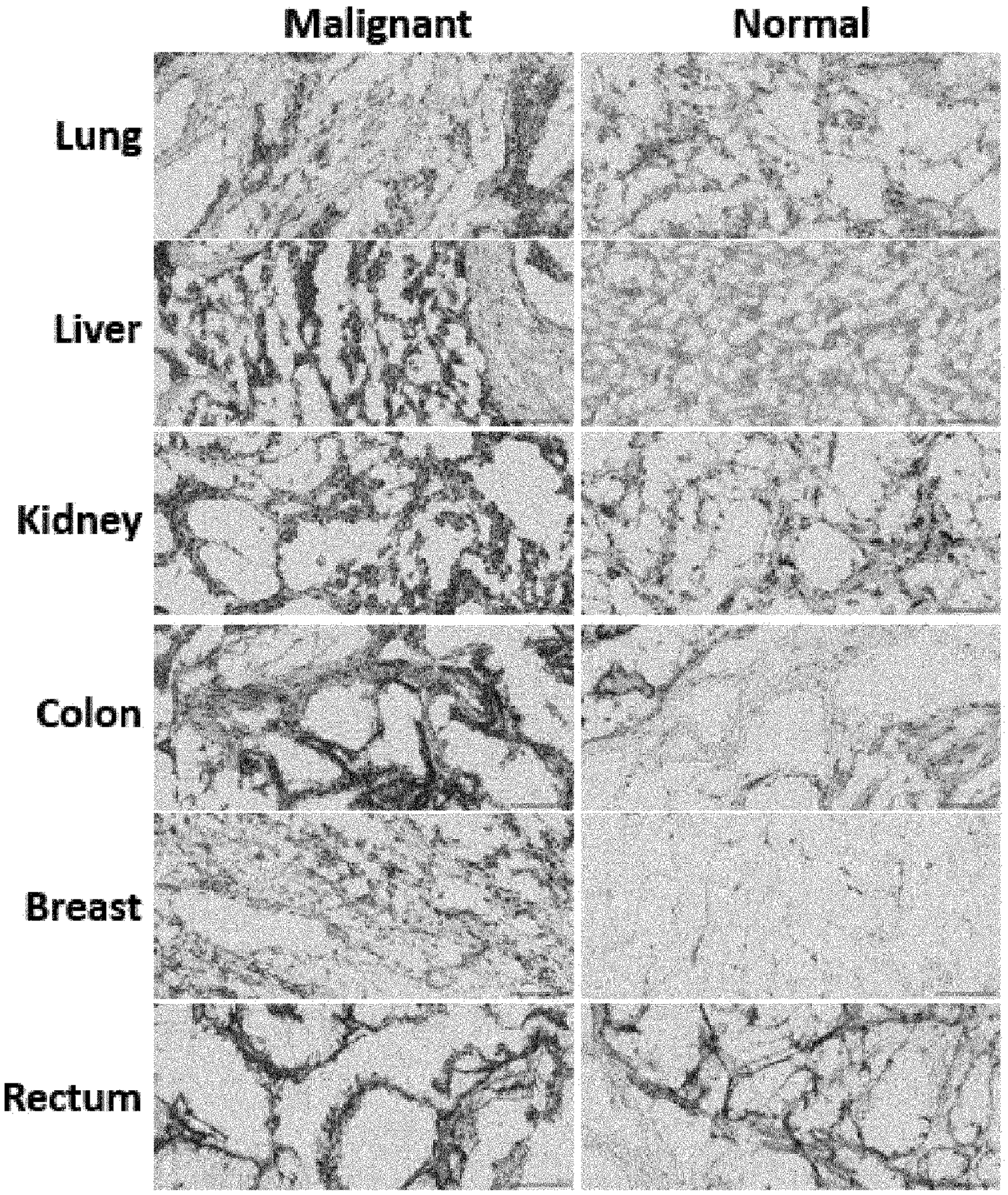


Figure 75B

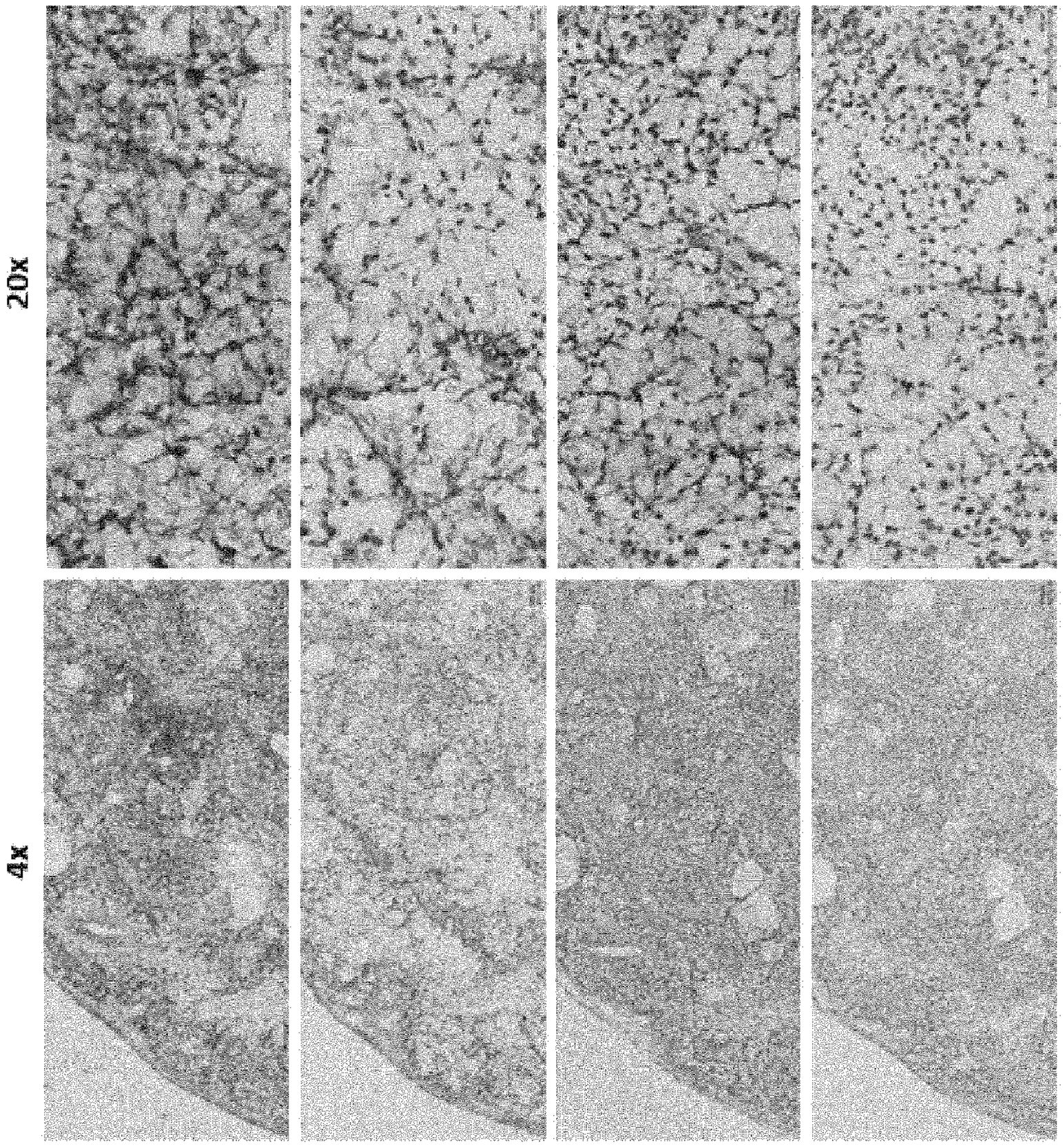

20x
4x
Rabbit anti-HER3 (Sino)
+
Goat anti-rabbit HRP
No primary
+
Goat anti-rabbit HRP
1D1F
+
Goat anti-human HRP
No primary
+
Goat anti-human HRP

Figure 76

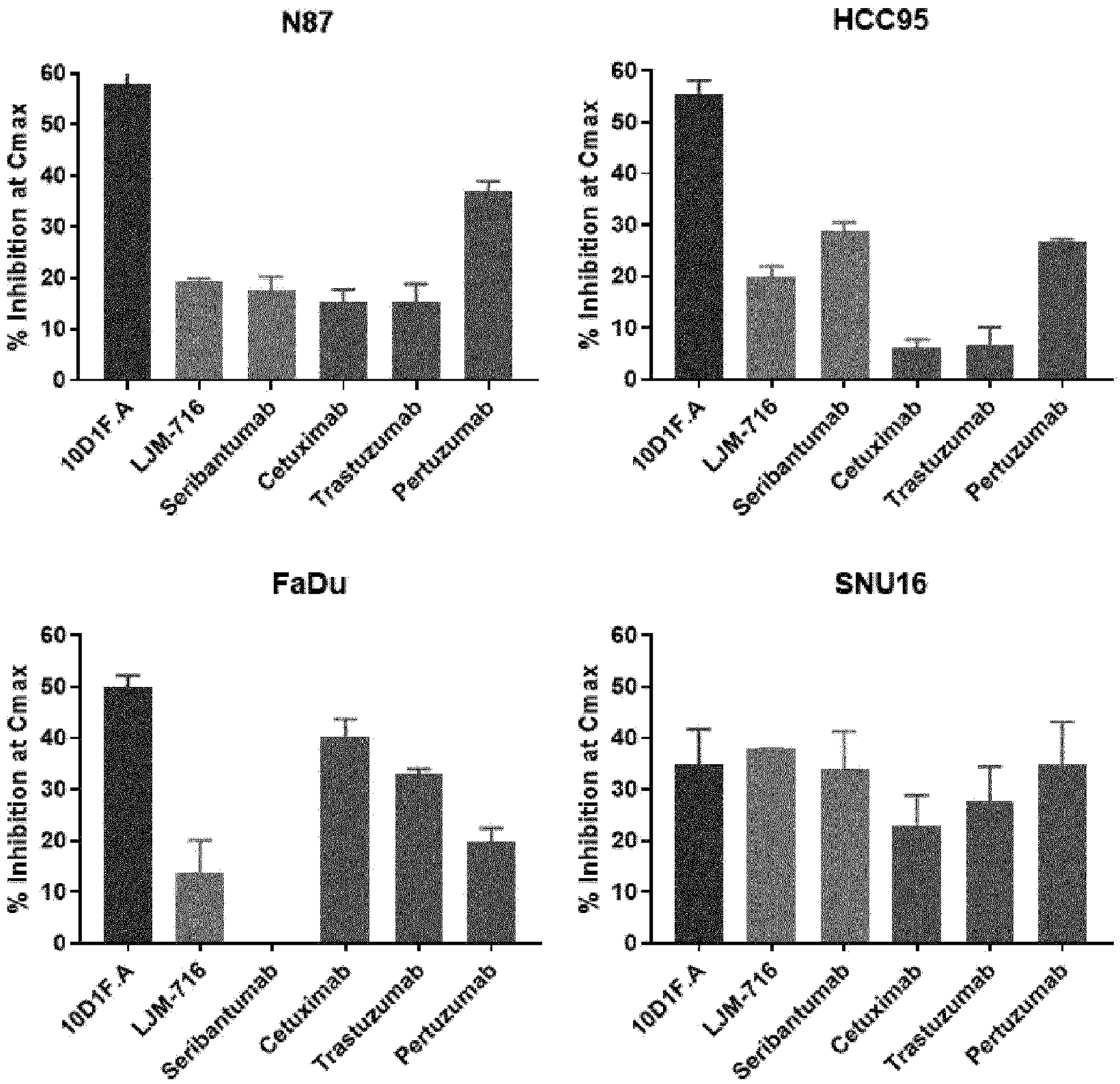

N87
HCC95
FaDu
SNU16
% Inhibition at Cmax
0
10
20
30
40
50
60
10D1F.A
LJM-716
Seribantumab
Cetuximab
Trastuzumab
Pertuzumab

Figure 77A

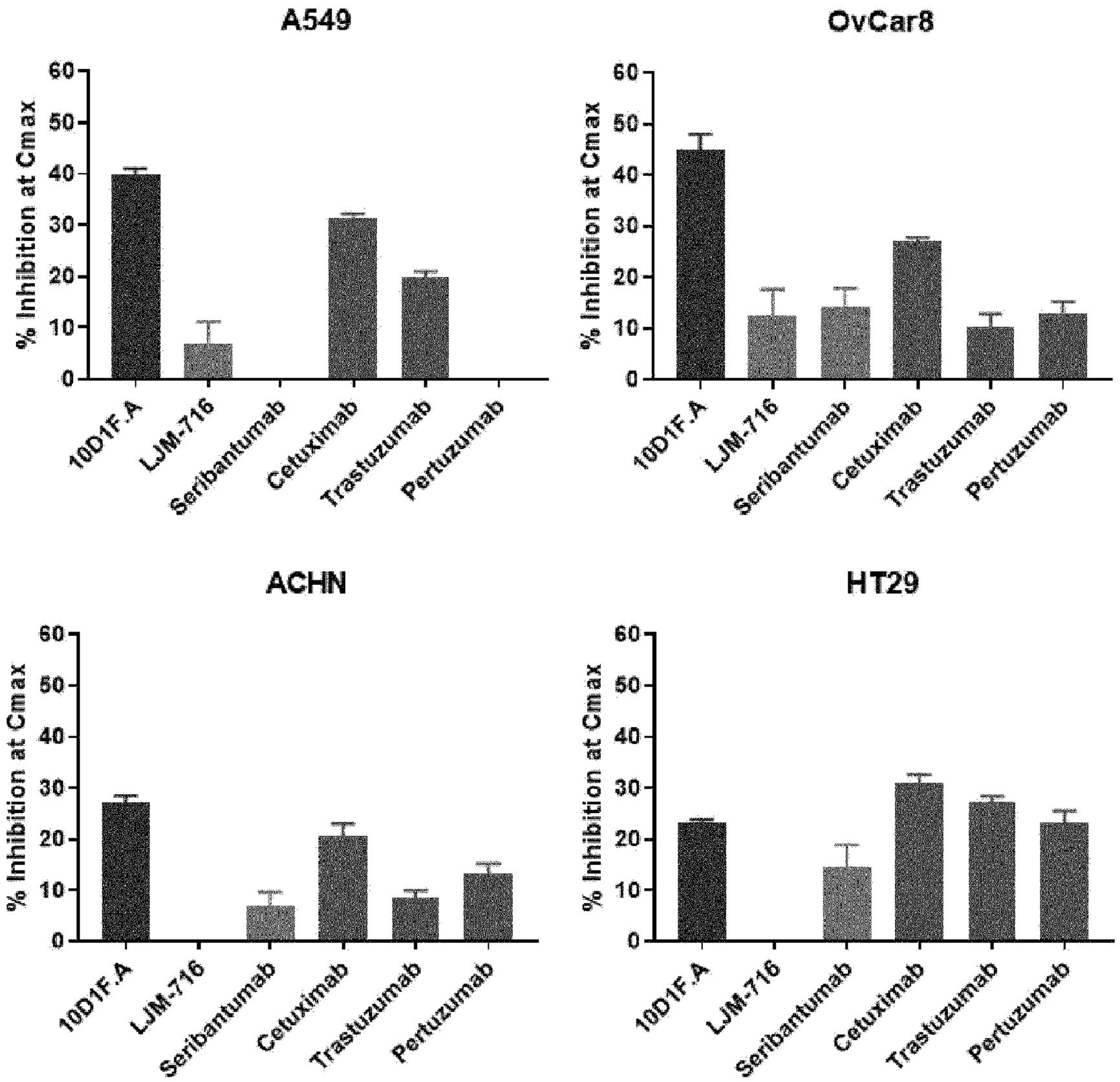

A549
OvCar8
ACHN
HT29
% Inhibition at Cmax
0
10
20
30
40
50
60
10D1F.A
LJM-716
Seribantumab
Cetuximab
Trastuzumab
Pertuzumab

Figure 77B