BISPECIFIC EGFR/c-Met ANTIBODIES

FIELD OF THE INVENTION

The present invention relates to bispecific EGFR/c-Met antibodies and methods of making and using the molecules.

BACKGROUND OF THE INVENTION

Epidermal growth factor receptor (EGFR, ErbBl or HER1) is a Type I transmembrane glycoprotein of 170 kDa that is encoded by the c-erbBl proto-oncogene. EGFR is a member of the human epidermal growth factor receptor (HER) family of receptor tyrosine kinases (RTK) which includes HER2 (ErbB2), HER3 (ErbB3) and HER4 (ErbB4). EGFR signaling is initiated by ligand binding followed by induction of conformational change, homodimerization or heterodimerization of the receptor with other ErbB family members, and trans-autophosphorylation of the receptor (Ferguson *et al.*, Annu Rev Biophys, 37: 353-73, 2008), which initiates signal transduction cascades that ultimately affect a wide variety of cellular functions, including cell proliferation and survival. Increases in expression or kinase activity of EGFR have been linked with a range of human cancers, making EGFR an attractive target for therapeutic intervention (Mendelsohn *et al.*, Oncogene 19: 6550-6565, 2000; Grünwald *et al.*, J Natl Cancer Inst 95: 851-67, 2003; Mendelsohn *et al.*, Semin Oncol 33: 369-85, 2006). Increases in both the EGFR gene copy number and protein expression have been associated with favorable responses to the EGFR tyrosine kinase inhibitor, IRESSA™ (gefitinib), in non-small cell lung cancer (Hirsch *et al.*, Ann Oncol 18:752-60, 2007).

EGFR therapies include both small molecules and anti-EGFR antibodies, approved for treatment of colorectal cancer, pancreatic cancer, head and neck cancer, and non-small cell lung cancer (NSCLC) (Baselga and Arteaga, J Clin Oncol 23:2445-2459 (20005; Gill *et al.*, J Biol Chem, 259:7755-7760, 1984; Goldstein *et al.*, Clin Cancer Res, 1:131 1-1318; 1995; Prewett *et al.*, Clin Cancer Res, 4:2957-2966,1998).

Efficacy of anti-EGFR therapies may depend on tumor type and EGFR mutation/ amplification status in the tumor. Side effects of current therapeutics may include skin toxicity (De Roock *et al.*, Lancet Oncol 11 :753-762, 2010; Linardou *et al.*, Nat Rev Clin Oncol, 6: 352-366, 2009; Li and Perez-Soler, Targ Oncol 4: 107-119, 2009). EGFR tyrosine kinase inhibitors (TKI) are commonly used as 2nd line therapies for non small cell

lung cancer (NSCLC), but often stop working within twelve months due to resistance pathways (Riely *et al.*, Clin Cancer Res 12: 839-44, 2006).

c-Met encodes a transmembrane tyrosine kinase receptor. It was first identified as a proto-oncogene in 1984 after it was found that treatment with a carcinogen resulted in a constitutively active fusion protein TPR-MET (Cooper *et al.*, Nature 311:29-33, 1984). Activation of c-Met by its ligand hepatocyte growth factor (HGF) stimulates a plethora of cell processes including growth, motility, invasion, metastasis, epithelial-mesenchymal transition, angiogenesis/wound healing, and tissue regeneration (Christensen *et al.*, Cancer Lett 225:1-26, 2005; Peters and Adjei, Nat Rev Clin Oncol 9:314-26, 2012). c-Met is synthesized as a single chain protein that is proteolytically cleaved into a 50 kDa alpha- and 140 kDa beta-subunits that are linked by a disulphide bond (Ma *et al.*, Cancer and Metastasis Reviews, 22: 309-325, 2003). c-Met is structurally similar to other membrane receptors such as RON and Sea. The exact stoichiometry of HGF:c-Met binding is unclear, but it is generally believed that two HGF molecules bind to two c-Met molecules leading to receptor dimerization and autophosphorylation at tyrosines 1230, 1234, and 1235 (Stamos *et al.*, The EMBO Journal 23: 2325-2335, 2004). Ligand-independent c-Met autophosphorylation can also occur due to gene amplification, mutation or receptor over-expression.

c-Met is frequently amplified, mutated or over-expressed in many types of cancer including gastric, lung, colon, breast, bladder, head and neck, ovarian, prostate, thyroid, pancreatic, and CNS cancers. Missense mutations typically localized to the kinase domain are commonly found in hereditary papillary renal cell carcinomas (PRCC) and in 13% of sporadic PRCCs (Schmidt *et al.*, Oncogene 18: 2343-2350, 1999). c-Met mutations localized to the semaphorin or juxtamembrane domains of c-Met are frequently found in gastric, head and neck, liver, ovarian, NSCLC and thyroid cancers (Ma *et al.*, Cancer and Metastasis Reviews, 22: 309-325, 2003; Sakakura *et al.*, Chromosomes and Cancer, 1999. 24:299-305). c-Met amplification has been detected in brain, colorectal, gastric, and lung cancers, often correlating with disease progression (Ma *et al.*, Cancer and Metastasis Reviews, 22: 309-325, 2003). Up to 4% and 20% of non-small cell lung cancer (NSCLC) and gastric cancers, respectively, exhibit c-Met amplification (Sakakura *et al.*, Chromosomes and Cancer, 1999. 24:299-305; Sierra and Tsao, Therapeutic Advances in Medical Oncology, 3:S21-35, 2011). Even in the absence of gene amplification, c-Met overexpression is frequently observed in lung cancer (Ichimura *et al.*, Jpn J Cancer Res, 87:1063-9, 1996). Moreover, in clinical samples, nearly half of lung adenocarcinomas exhibited high levels of c-Met and HGF, both of which correlated with enhanced tumor

growth rate, metastasis and poor prognosis (Sierra and Tsao, Therapeutic Advances in Medical Oncology, 3:S21-35, 2011; Siegfried et al., Ann Thorac Surg 66: 1915-8, 1998).

Nearly 60% of all tumors that become resistant to EGFR tyrosine kinase inhibitors increase c-Met expression, amplify c-Met, or increase c-Met only known ligand, HGF (Turke *et al.*, Cancer Cell, 17:77-88, 2010), suggesting the existence of a compensatory pathway for EGFR through c-Met. c-Met amplification was first identified in cultured cells that became resistant to gefitinib, an EGFR kinase inhibitor, and exhibited enhanced survival through the Her3 pathway (Engelman *et al.*, Science, 316:1039-43, 2007). This was further validated in clinical samples where nine of 43 patients with acquired resistance to either erlotinib or gefitinib exhibited c-Met amplification, compared to only two of 62 untreated patients. Four of the nine treated patients also acquired the EGFR activating mutation, T790M, demonstrating simultaneous resistance pathways (Beat *et al.*, Proc Natl Acad Sci U S A, 104:20932-7, 2007).

The individual roles of both EGFR and c-Met in cancer is well established, making these targets attractive for combination therapy. Both receptors signal through the same survival and anti-apoptotic pathways (ERK and AKT); thus, inhibiting the pair in combination may limit the potential for compensatory pathway activation thereby improving overall efficacy. Combination therapies targeting EGFR and c-Met are tested in clinical trials with Tarceva® (erlotinib) in combination with anti-c-Met monovalent antibody for NSCLC (Spigel *et al.*, 2011 ASCO Annual Meeting Proceedings 2011, Journal of Clinical Oncology: Chicago, IL. p. 7505) and Tarceva (erlotinib) in combination with ARQ-197, a small molecule inhibitor of c-Met (Adjei *et al.*, Oncologist, 16:788-99, 2011). Combination therapies or bispecific anti-EGFR/c-Met molecules have been disclosed for example in: Intl. Pat. Publ. Nos. WO2008/127710, WO2009/111691, WO2009/126834, WO2010/039248, WO2010/115551 and U.S. Pat. Publ. No. US2009/0042906.

Current small molecule and large molecule therapeutic approaches to antagonize EGFR and/or c-Met signaling pathways for therapy may be sub-optimal due to possible lack of specificity, potential off-target activity and dose-limiting toxicity that may be encountered with small molecule inhibitors. Typical monospecific bivalent antibodies may result in clustering of membrane bound receptors and unwanted activation of the downstream signaling pathways. Monovalent antibodies having full length heavy chains (half arms) pose significant complexity and cost to the manufacturing process.

Accordingly, the need exists for additional monospecific and bispecific EGFR and/or c-Met inhibitors for both therapeutic and diagnostic purpose.

SUMMARY OF THE INVENTION

One embodiment of the invention is an isolated bispecific epidermal growth factor receptor (EGFR)/ hepatocyte growth factor receptor (c-Met) antibody, comprising:

a first heavy chain (HC1) comprising a HC1 constant domain 3 (HC1 CH3) and a HC1 variable region 1 (VH1);

a second heavy chain (HC2) comprising a HC2 constant domain 3 (HC2 CH3) and a HC2 variable region 2 (VH2);

a first light chain (LC1) comprising a light chain variable region 1 (VL1); and

a second light chain (LC2) comprising a light chain variable region 2 (VL2), wherein the VH1 and the VL1 pair to form a first antigen-binding site that specifically binds EGFR, the VH2 and the VL2 pair to form a second antigen-binding site that specifically binds c-Met, the HC1 comprises at least one substitution in the HC1 CH3 and the HC2 comprises at least one substitution in the HC2 CH3, and the substitution in the HC1 CH3 and the substitution in the HC2 CH3 occur at different amino acid residue positions, when residue numbering is according to the EU index.

In other embodiments, the invention provides for bispecific EGFR/c-Met antibodies, wherein the antibody inhibits phosphorylation of extracellular signal-related kinases 1 and 2 (ERK1/2) in NCI-H292, NCI-H1975 or SKMES-1 cell line with an IC_{50} value that is at least about 10-fold less, at least about 20-fold less, at least about 30-fold less, at least about 40-fold less, at least about 50-fold less or at least about 60-fold less when compared to the IC_{50} value of inhibition of phosphorylation of ERK1/2 in NCI-H292, NCI-H1975 or SKMES-1 cell lines with a mixture of a control monovalent EGFR antibody comprising a heavy chain 3 (HC3) and a light chain 3 (LC3) and a control monovalent c-Met antibody comprising a heavy chain 4 (HC4) and a light chain 4 (LC4), wherein the HC3 and the HC1, the LC3 and the LC1, the HC4 and the HC2, and the LC4 and the LC2 have identical amino acid sequences, respectively, wherein the phosphorylation of ERK1/2 is measured in whole cell lysates using a sandwich immunoassay using an anti-phosphoERK1/2 antibody as a capture antibody and an antibody binding to unphosphorylated and phosphorylated ERK1/2 conjugated with an electrochemiluminescent compound as a detection antibody.

In other embodiments, the invention provides for bispecific EGFR/c-Met antibodies, wherein the antibody inhibits phosphorylation of protein kinase B (AKT) at Ser473 in NCI-H1975 cell line with an IC_{50} value that is at least about 70-fold less when compared to the IC_{50} value of inhibition of phosphorylation of AKT at Ser473 in NCI-H1975 cell line with the mixture of the control monovalent EGFR antibody comprising the HC3 and the LC3 and the control monovalent c-Met antibody comprising the HC4 and the LC4, wherein the HC3 and the HC1, the LC3 and the LC1, the HC4 and the HC2, and the LC4 and the LC2 have identical amino acid sequences, respectively, wherein the phosphorylation of AKT at Ser473 is measured in whole cell lysates using a sandwich immunoassay using an antibody binding to unphosphorylated and phosphorylated AKT as a capture antibody and an anti-phosphoAKT Ser473 antibody conjugated to an electrochemiluminescent compound as a detection antibody.

In other embodiments, the invention provides for bispecific EGFR/c-Met antibodies that bind EGFR of SEQ ID NO: 73 at EGFR residues K489, I491, K467 and S492 and c-Met at residues PEFRDSYPIKYVHAF (SEQ ID NO: 238) and FAQSKPDSAEPMDRSA (SEQ ID NO: 239).

In other embodiments, the invention provides for bispecific EGFR/c-Met antibodies that inhibit growth of NCI-H292 or NCI-H1975 cells with an IC_{50} value that is at least about 300-fold less, at least about 400-fold less, at least about 500-fold less, at least about 600-fold less, at least about 700-fold less or at least about 800-fold less when compared to the IC_{50} value of inhibition of growth of NCI-H292 or NCI-H1975 cells with cetuximab, when NCI-H292 or NCI-H1975 cells are grown in low attachment conditions.

In other embodiments, the invention provides for bispecific EGFR/c-Met antibodies that inhibit growth of HGF-expressing SKMES-1 cell tumor in SCID Beige mice with percentage (%) T/C value of at least 500-fold less on day 36 when compared to cetuximab, when the bispecific antibody and cetuximab are administered at 20 mg/kg dose.

In other embodiments, the invention provides for bispecific EGFR/c-Met antibodies wherein the HC1 CH3 comprises a K409R or a F405L substitution and the HC2 CH3 comprises a K409R or F405L substitution, wherein residue numbering is according to the EU index.

In other embodiments, the invention provides for bispecific EGFR/c-Met antibodies comprising certain heavy and light chain CDR, VH1, VL1, VH2, VL2, HC1, LC1, HC2 and LC2 sequences.

Another embodiment of the invention is an isolated synthetic polynucleotide encoding the HC1, the HC2, the LC1 or the LC2 of the invention.

Another embodiment of the invention is a vector comprising the polynucleotide of the invention.

Another embodiment of the invention is a host cell comprising the vector of the invention.

Another embodiment of the invention is a method of producing the isolated bispecific EGFR/c-Met antibody, comprising:

combining an isolated monospecific bivalent anti-EGFR antibody comprising two heavy chains of SEQ ID NO: 199 and two light chains of SEQ ID NO: 200 and an isolated monospecific bivalent anti-c-Met antibody comprising two heavy chains of SEQ ID NO: 201 and two light chains of SEQ ID NO: 202 in a mixture of about 1:1 molar ratio;

introducing a reducing agent into the mixture;

incubating the mixture about ninety minutes to about six hours;

removing the reducing agent; and

purifying the bispecific EGFR/c-Met antibody that comprises a first heavy chain of SEQ ID NO: 199 and a second heavy chain of SEQ ID NO: 201, a first light chain of SEQ ID NO: 200 and a second light chain of SEQ ID NO: 202, wherein the first heavy chain of SEQ ID NO: 199 pairs with the first light chain of SEQ ID NO: 200 to form the first binding domain that specifically binds EGFR, and the second heavy chain of SEQ ID NO: 201 pairs with the second light chain of SEQ ID NO: 202 to form the second binding domain that specifically binds c-Met.

Another embodiment of the invention is a pharmaceutical composition comprising the bispecific antibody of the invention and a pharmaceutically acceptable carrier.

Another embodiment of the invention is method of treating a subject having cancer, comprising administering a therapeutically effective amount of the bispecific EGFR/c-Met antibody of the invention to a patient in need thereof for a time sufficient to treat the cancer.

Another embodiment of the invention is method of inhibiting growth or proliferation of cells that express EGFR and/or c-Met, comprising contacting the cells with the bispecific antibody of the invention.

Another embodiment of the invention is method of inhibiting growth or metastasis of EGFR and/or c-Met expressing tumor or cancer cells in a subject comprising

administering to the subject an effective amount of the bispecific antibody of the invention to inhibit the growth or metastasis of EGFR and/or c-Met expressing tumor or cancer cells.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A and 1B. Amino acid alignment of the EGFR-binding FN3 domains. The BC and FG loops are boxed at residues 22-28 and 75-86 of SEQ ID NO: 18. Some variants include thermal stability improving L17A, N46K and E86I substitutions (residue numbering according to Tencon SEQ ID NO: 1).

Figure 2. Sequence alignment of the Tencon27 scaffold (SEQ ID NO: 99) and a TCL14 library (SEQ ID NO: 100) having randomized C-CD-F-FG alternative surface. The loop residues are boxed. Loops and strands are indicated above the sequences.

Figure 3. Sequence alignment of the c-Met-binding FN3 domains. The C loop and the CD strand and the F loop and the FG strand are boxed and span residues 29-43 and 65-81.

Figure 4. Inhibition of c-Met phosphorylation in NCI-H292 cells pre-treated with monospecific or bispecific FN3 domain containing molecules and stimulated with HGF is shown. Substantial increase in the potency of the bispecific EGFR/c-Met molecule (ECB1) was observed when compared to a monospecific c-Met-binding FN3 domain (P114AR5P74-A5, shown as A5 in the Figure) on its own or in combination with an EGFR-binding FN3 domain (P54AR4-83v2, shown as 83v2 in the Figure).

Figure 5. Inhibition of EGFR and c-Met phosphorylation in cells pre-treated with monospecific or bispecific FN3 domain containing molecules. In cell lines expressing high levels of EGFR, NCI-H292 (Figure 5A) and H596(Figure 5B), anti-EGFR monospecific and bispecific FN3 domain containing molecules are equally potent at decreasing EGFR phosphorylation. In cell lines expressing low levels of EGFR relative to c-Met, NCI-H441 (Figure 5C), bispecific EGFR/c-Met molecules improve the potency for inhibition of EGFR phosphorylation compared to the monospecific EGFR-binding FN3 domain alone. In cell lines with low levels of c-Met, relative to EGFR, NCI-H292 (Figure 5D) and H596 (Figure 5E), inhibition of c-Met phosphorylation is significantly potentiated with bispecific EGFR/c-Met molecule, compared to monospecific c-Met-binding FN3 domain only. Molecules used in the study were: bispecific ECB5 (shown as 17-A3 in the Figure), monospecific EGFR-binding FN3 domain P53A1R5-17 (shown as "17" in the Figure), bispecific EGFR/c-Met molecule ECB3 (shown as 83-H9 in the Figure), and monospecific c-Met binding FN3 domain P114AR7P93-H9 (shown as H9 in the Figure).

Figure 6. Pharmacodynamic signaling in tumors isolated from mice dosed with bispecific EGFR/c-Met molecules for 6h or 72h. All molecules significantly reduced c-Met, EGFR and ERK phosphorylation at 6h and 72h, the degree if inhibition was dependent on the affinity of the FN3 domains to EGFR and/or c-Met. Bispecific molecules were generated by joining EGFR-binding FN3 domain with a high ("83" in the Figure is p54AR4-83v2) or medium ("17v2" in the Figure is P53A1R5-17v2) affinity to a c-Met-binding FN3 domain with high ("A3" in the Figure is P114AR7P94-A3) or medium ("A5" in the Figure is P114AR5P74-A5) affinity.

Figure 7. Plasma (top) and tumor (bottom) accumulation of bispecific EGFR/cMet molecules of variable affinities linked to an albumin binding domain (ABD) are shown 6h (left) and 72h (right) after IP dosing. Six hours after dosing, tumor accumulation is maximal in mice dosed with a bispecific molecule harboring a medium affinity EGFR-binding FN3 domain (17v2) or high affinity EGFR binding domain (83v2). The bispecific molecules incorporated high or medium affinity EGFR or c-Met binding FN3 domains as follows: 83v2-A5-ABD (ECB18; high/medium for EGFR/cMet) 83v2-A3-ABD (ECB38; high/high) 17v2-A5 (ECB28; medium/medium) 17v2-A3-ABD (ECB39; medium/high). In the figure, 83v2 refers to p54AR4-83v2; 17v2 refers to p53A1R5-17v2; A3 refers to p114AR7P94-A3 and A5 refers to p114AR5P74-A5.

Figure 8. H292-HGF tumor xenografts were implanted into SCID Beige mice. When tumors reached an average volume of approximately 80 mm^3, mice were dosed three times per week with bispecific EGFR/c-Met molecules (25 mg/kg) or PBS vehicle. All bispecific molecules reduced tumor growth, the tumor growth inhibition (TGI) being dependent on the affinities of the molecules for c-Met and EGFR (high EGFR-high cMet refers to p54AR4-83v2-p114AR7P94-A3 (ECB38); high EGFR-med cMet refers to p54AR4-83v2-p114AR5P74-A5 (ECB18); med EGFR-high cMet refers to p53A1R5-17v2-p114AR7P94-A3 (ECB39); med EGFR-med-cMet refers to p53A1R5-17-p114AR5P74-A 5 (ECB28)).

Figure 9. H292-HGF tumor xenografts were implanted into SCID Beige mice and they were treated with different therapies. The anti-tumor activity of the therapies is shown (bispecific EGFR/c-Met molecule refers to p54AR4-83v2-p114AR7P94-A3-ABD (ECB38); the other therapies are crizotinib, erlotinib, cetuximab, and the combination of crizotinib and erlotinib).

Figure 10. SKMES-HGF tumor xenografts were implanted into SCID Beige mice and the mice were treated with different therapies. The anti-tumor activity of the therapies is shown as change in tumor size (mm^3) over time. The bispecific EGFR/c-Met antibody EM1-mAb was dosed intraperitoneally (i.p.) twice a week at either 20 mg/kg, 5 mg/kg, or 1 mg/kg; cetuximab was dosed i.p. twice a week at 20 mg/kg. Arrows in the figure show the administration days. Numbers after the antibodies indicated the administered dose.

Figure 11. HCC827 tumor xenografts were implanted into nude mice and the mice were treated with erlotinib or EM1-mAb at indicated doses. EM1-mAb was dosed biweekly and erlotinib once a day for four weeks. Arrows in the figure show the administration days. The anti-tumor activity of the therapies is shown as change in tumor size (mm^3) over time.

Figure 12. SNU-5 tumor xenografts were implanted into CB17/SCID mice and the mice were treated with 10 mg/kg cetuximab or 10 mg/kg or 1 mg/kg EM1-mAb. Antibodies were dosed biweekly for four weeks. Arrows in the figure show the administration days. The anti-tumor activity of the therapies is shown as change in tumor size (mm^3) over time.

Figure 13. H1975-HGF tumor xenografts were implanted into nude mice and the mice were treated with 10 mg/kg cetuximab, 10 mg/kg EM1-mAb, 50 mg/kg erlotinib, 15 mg/kg afatinib, or a combination of 10 mg/kg EM1-mAb and 15 mg/kg afatinib. Antibodies were dosed biweekly and the small molecules once a day for three weeks. Arrows in the figure show the administration days. The anti-tumor activity of the therapies is shown as change in tumor size (mm^3) over time.

Figure 14. HCC827-ER1 tumor xenografts were implanted into nude mice and the mice were treated with 10 mg/kg EM1-mAb, 25 mg/kg erlotinib, or a combination of the two. EM1-mAb was dosed biweekly and erlotinib once a day for 19 days. Arrows in the figure show the administration days. The anti-tumor activity of the therapies is shown as change in tumor size (mm^3) over time.

Figure 15. Average EGFR and c-Met levels in tumor lysates isolated from H1975 HGF tumor xenografts implanted into SCID Beige mice after administration of a single dose of 20 mg/kg EM1-mAb. Receptor levels are shown as % of PBS control at indicated times post-treatment.

Figure 16. H1975-HGF tumor xenografts were implanted into nude mice and the mice were treated with 10 mg/kg EM1-mAb or 10 mg/kg EM1-mAb variant IgG2 V234A/G237A/P238S/H268A/V309L/A330S/P331S having no Fc receptor binding and

lacking effector functions. Antibodies were dosed biweekly at indicated days. The anti-tumor activity of the therapies is shown as change in tumor size (mm^3) over time.

DETAILED DESCRIPTION OF THE INVENTION

The term "fibronectin type III (FN3) domain" (FN3 domain) as used herein refers to a domain occurring frequently in proteins including fibronectins, tenascin, intracellular cytoskeletal proteins, cytokine receptors and prokaryotic enzymes (Bork and Doolittle, Proc Nat Acad Sci USA 89:8990-8994, 1992; Meinke *et al.*, J Bacteriol 175:1910-1918, 1993; Watanabe *et al.*, J Biol Chem 265:15659-15665, 1990). Exemplary FN3 domains are the 15 different FN3 domains present in human tenascin C, the 15 different FN3 domains present in human fibronectin (FN), and non-natural synthetic FN3 domains as described for example in U.S. Pat. Publ. No. 2010/0216708. Individual FN3 domains are referred to by domain number and protein name, e.g., the 3rd FN3 domain of tenascin (TN3), or the 10th FN3 domain of fibronectin (FN10).

The term "substituting" or "substituted" or 'mutating" or "mutated" as used herein refers to altering, deleting or inserting one or more amino acids or nucleotides in a polypeptide or polynucleotide sequence to generate a variant of that sequence.

The term "randomizing" or "randomized" or "diversified" or "diversifying" as used herein refers to making at least one substitution, insertion or deletion in a polynucleotide or polypeptide sequence.

"Variant" as used herein refers to a polypeptide or a polynucleotide that differs from a reference polypeptide or a reference polynucleotide by one or more modifications for example, substitutions, insertions or deletions.

The term "specifically binds" or "specific binding" as used herein refers to the ability of an FN3 domain, a bispecific agent that specifically binds EGFR and c-Met, or a bispecific EGFR/c-Met antibody of the invention to bind to a predetermined antigen with a dissociation constant (K_D) of about $1x10^{-6}$ M or less, for example about $1x10^{-7}$ M or less, about $1x10^{-8}$ M or less, about $1x10^{-9}$ M or less, about $1x10^{-10}$ M or less, about $1x10^{-11}$ M or less, about $1x10^{-12}$ M or less, or about $1x10^{-13}$ M or less. Typically the FN3 domain, the bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention binds to a predetermined antigen (i.e. EGFR or c-Met) with a K_D that is at least ten fold less than its K_D for a nonspecific antigen (for example BSA or casein) as measured by surface plasmon resonance using for example a Proteon Instrument (BioRad). Thus, the bispecific EGFR/c-Met FN3 domain containing molecule, the

bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention specifically binds to each EGFR and c-Met with a binding affinity (K_D) of at least about $1x10^{-6}$ M or less, for example about $1x10^{-7}$ M or less, about $1x10^{-8}$ M or less, about $1x10^{-9}$ M or less, about $1x10^{-10}$ M or less, about $1x10^{-11}$ M or less, about $1x10^{-12}$ M or less, or about $1x10^{-13}$ M or less. The bispecific EGFR/c-Met FN3 domain containing molecule, the bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention that specifically binds to a predetermined antigen may, however, have cross-reactivity to other related antigens, for example to the same predetermined antigen from other species (homologs).

The term "library" refers to a collection of variants. The library may be composed of polypeptide or polynucleotide variants.

The term "stability" as used herein refers to the ability of a molecule to maintain a folded state under physiological conditions such that it retains at least one of its normal functional activities, for example, binding to a predetermined antigen such as EGFR or c-Met.

"Epidermal growth factor receptor" or "EGFR" as used here refers to the human EGFR (also known as HER1 or ErbB1 (Ullrich *et al.,* Nature 309:418-425, 1984) having the amino acid sequence shown in SEQ ID NO: 73 and in GenBank accession number NP_005219, as well as naturally-occurring variants thereof. Such variants include the well known EGFRvIII and other alternatively spliced variants (e.g., as identified by SwissProt Accession numbers P00533-1 (wild type; identical to SEQ ID NO: 73 and NP_005219), P00533-2 (F404L/L405S), P00533-3 (628-705: CTGPGLEGCP...GEAPNQALLR→PGNESLKAML...SVIITASSCH and 706-1210 deleted), P00533-4 (C628S and 629-1210 deleted), variants GlnQ98, R266, K521, I674, G962, and P988 (Livingston *et al.,* NIEHS-SNPs, environmental genome project, NIEHS ES15478), T790M, L858R/T790M and del(E746, A750).

"EGFR ligand" as used herein encompasses all (e.g., physiological) ligands for EGFR, including EGF, TGFα, heparin binding EGF (HB-EGF), amphiregulin (AR), and epiregulin (EPI).

"Epidermal growth factor" (EGF) as used herein refers to the well known 53 amino acid human EGF having the amino acid sequence shown in SEQ ID NO: 74.

"Hepatocyte growth factor receptor" or "c-Met" as used herein refers to the human c-Met having the amino acid sequence shown in SEQ ID NO: 101 or in GenBank Accession No: NP_001120972 and natural variants thereof.

"Hepatocyte growth factor" (HGF) as used herein refers to the well known human HGF having the amino acid sequence shown in SEQ ID NO: 102 which is cleaved to form a dimer of an alpha and beta chain linked by a disulfide bond.

"Blocks binding" or "inhibits binding", as used herein interchangeably refers to the ability of the FN3 domains, the bispecific EGFR/c-Met FN3 domain containing molecule, the bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention to block or inhibit binding of the EGFR ligand such as EGF to EGFR and/or HGF to c-Met, and encompass both partial and complete blocking/inhibition. The blocking/inhibition of EGFR ligand such as EGF to EGFR and/or HGF to c-Met by the FN3 domains, the bispecific EGFR/c-Met FN3 domain containing molecule, the bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention reduces partially or completely the normal level of EGFR signaling and/or c-Met signaling when compared to the EGFR ligand binding to EGFR and/or HGF binding to c-Met without blocking or inhibition. The FN3 domains, the bispecific EGFR/c-Met FN3 domain containing molecule, the bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention "blocks binding" of the EGFR ligand such as EGF to EGFR and/or HGF to c-Met when the inhibition is at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%. Inhibition of binding can be measured using well known methods, for example by measuring inhibition of binding of biotinylated EGF on EGFR expressing A431 cells exposed to the FN3 domain, the bispecific EGFR/c-Met FN3 domain containing molecule, the bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention using FACS, and using methods described herein, or measuring inhibition of binding of biotinylated HGF on c-Met extracellular domain using well known methods and methods described herein.

The term "EGFR signaling" refers to signal transduction induced by EGFR ligand binding to EGFR resulting in autophosphorylation of at least one tyrosine residue in the EGFR. An exemplary EGFR ligand is EGF.

"Neutralizes EGFR signaling" as used herein refers to the abilityof the FN3 domains, the bispecific EGFR/c-Met FN3 domain containing molecule, the bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention to inhibit EGFR signaling induced by EGFR ligand such as EGF by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% .

The term "c-Met signaling" refers to signal transduction induced by HGF binding to c-Met resulting in autophosphorylation of at least one tyrosine residue in the c-Met. Typically at least one tyrosine residue at positions 1230, 1234, 1235 or 1349 is autophosphorylated upon HGF binding.

"Neutralizes c-Met signaling" as used herein refers to the ability of the FN3 domain, the bispecific EGFR/c-Met FN3 domain containing molecule, the bispecific agent that specifically binds EGFR and c-Met or the bispecific EGFR/c-Met antibody of the invention to inhibit c-Met signaling induced by HGF by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%.

"Overexpress", "overexpressed" and "overexpressing" as used herein interchangeably refer to a cancer or malignant cell that has measurably higher levels of EGFR and/or c-Met on the surface compared to a normal cell of the same tissue type. Such overexpression may be caused by gene amplification or by increased transcription or translation. EGFR and/or c-Met expression and overexpression can be measured using well know assays using for example ELISA, immunofluorescence, flow cytometry or radioimmunoassay on live or lysed cells. Alternatively, or additionally, levels of EGFR and/or c-Met-encoding nucleic acid molecules may be measured in the cell for example using fluorescent *in situ* hybridization, Southern blotting, or PCR techniques. EGFR and/or c-Met is overexpressed when the level of EGFR and/or c-Met on the surface of the cell is at least 1.5-fold higher when compared to the normal cell.

"Tencon" as used herein refers to the synthetic fibronectin type III (FN3) domain having the sequence shown in SEQ ID NO: 1 and described in U.S. Pat. Publ. No. US2010/0216708.

A "cancer cell" or a "tumor cell" as used herein refers to a cancerous, pre-cancerous or transformed cell, either *in vivo*, *ex vivo*, and in tissue culture, that has spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic nucleic acid, or uptake of exogenous nucleic acid, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation/cancer is exemplified by, e.g., morphological changes, immortalization of cells, aberrant growth control, foci formation, proliferation, malignancy, tumor specific marker levels, invasiveness, tumor growth or suppression in suitable animal hosts such as nude mice, and the like, *in vitro*, *in vivo*, and *ex vivo* (Freshney, Culture of Animal Cells: A Manual of Basic Technique (3rd ed. 1994)).

The term "vector" means a polynucleotide capable of being duplicated within a biological system or that can be moved between such systems. Vector polynucleotides typically contain elements, such as origins of replication, polyadenylation signal or selection markers that function to facilitate the duplication or maintenance of these polynucleotides in a biological system. Examples of such biological systems may include a cell, virus, animal, plant, and reconstituted biological systems utilizing biological components capable of duplicating a vector. The polynucleotide comprising a vector may be DNA or RNA molecules or a hybrid of these.

The term "expression vector" means a vector that can be utilized in a biological system or in a reconstituted biological system to direct the translation of a polypeptide encoded by a polynucleotide sequence present in the expression vector.

The term "polynucleotide" means a molecule comprising a chain of nucleotides covalently linked by a sugar-phosphate backbone or other equivalent covalent chemistry. Double and single-stranded DNAs and RNAs are typical examples of polynucleotides.

"Complementary DNA" or "cDNA" refers to a well known synthetic polynucleotide that shares the arrangement of sequence elements found in native mature mRNA species with contiguous exons, with the intervening introns present in genomic DNA are removed. The codons encoding the initiator methionine may or may not be present in cDNA. cDNA may be synthesized for example by reverse transcription or synthetic gene assembly.

"Synthetic" or "non-natural" or "artificial" as used herein refers to a polynucleotide or a polypeptide molecule not present in nature.

The term "polypeptide" or "protein" means a molecule that comprises at least two amino acid residues linked by a peptide bond to form a polypeptide. Small polypeptides of less than about 50 amino acids may be referred to as "peptides".

The term "bispecific EGFR/c-Met molecule" or "bispecific EGFR/c-Met FN3 domain containing molecule" as used herein refers to a molecule comprising an EGFR binding FN3 domain and a distinct c-Met binding FN3 domain that are covalently linked together either directly or via a linker. An exemplary bispecific EGFR/c-Met binding molecule comprises a first FN3 domain specifically binding EGFR and a second FN3 domain specifically binding c-Met.

"Valent" as used herein refers to the presence of a specified number of binding sites specific for an antigen in a molecule. As such, the terms "monovalent", "bivalent",

"tetravalent", and "hexavalent" refer to the presence of one, two, four and six binding sites, respectively, specific for an antigen in a molecule.

"Mixture" as used herein refers to a sample or preparation of two or more FN3 domains not covalently linked together. A mixture may consist of two or more identical FN3 domains or distinct FN3 domains. Mixture as used herein also refers to a sample or preparation of two or more monovalent antibodies that are monovalent towards EGFR and/or monovalent towards c-Met.

The term "bispecific agent that specifically binds EGFR and c-Met" as used herein refers to a molecule comprising a first domain that specifically binds EGFR and a second domain that specifically binds c-Met. An exemplary agent that specifically binds EGFR and c-Met is a bispecific antibody. Another exemplary bispecific agent that specifically binds EGFR and c-Met is a molecule comprising an EGFR binding FN3 domain and a distinct c-Met binding FN3 domain. The bispecific agent that specifically binds EGFR and c-Met may be composed of a single polypeptide or more than one polypeptide.

The term "bispecific anti-EGFR/c-Met antibody" or "bispecific EGFR/c-Met antibody" as used herein refers to a bispecific antibody having a first domain that specifically binds EGFR and a second domain that specifically binds c-Met. The domains specifically binding EGFR and c-Met are typically VH/VL pairs, and the bispecific anti-EGFR/c-Met antibody is monovalent in terms of binding to EGFR and c-Met.

The term "antibodies" as used herein is meant in a broad sense and includes immunoglobulin molecules including polyclonal antibodies, monoclonal antibodies including murine, human, human-adapted, humanized and chimeric monoclonal antibodies, antibody fragments, bispecific or multispecific antibodies, dimeric, tetrameric or multimeric antibodies, and single chain antibodies.

Immunoglobulins can be assigned to five major classes, namely IgA, IgD, IgE, IgG and IgM, depending on the heavy chain constant domain amino acid sequence. IgA and IgG are further sub-classified as the isotypes IgA_1, IgA_2, IgG_1, IgG_2, IgG_3 and IgG_4. Antibody light chains of any vertebrate species can be assigned to one of two clearly distinct types, namely kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

The term "antibody fragments" refers to a portion of an immunoglobulin molecule that retains the heavy chain and/or the light chain antigen binding site, such as heavy chain complementarity determining regions (HCDR) 1, 2 and 3, light chain complementarity determining regions (LCDR) 1, 2 and 3, a heavy chain variable region (VH), or a light

chain variable region (VL). Antibody fragments include a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; a $F(ab)_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; a Fd fragment consisting of the VH and CH1 domains; a Fv fragment consisting of the VL and VH domains of a single arm of an antibody; a domain antibody (dAb) fragment (Ward *et al* (1989) *Nature* 341:544- 546), which consists of a VH domain. VH and VL domains can be engineered and linked together via a synthetic linker to form various types of single chain antibody designs where the VH/VL domains pair intramolecularly, or intermolecularly in those cases when the VH and VL domains are expressed by separate single chain antibody constructs, to form a monovalent antigen binding site, such as single chain Fv (scFv) or diabody; described for example in PCT Intl. Publ. Nos. WO1998/44001, WO1988/01649, WO1994/13804, and WO1992/01047. These antibody fragments are obtained using well known techniques known to those of skill in the art, and the fragments are screened for utility in the same manner as are full length antibodies.

The phrase "isolated antibody" refers to an antibody or antibody fragment that is substantially free of other antibodies having different antigenic specificities (e.g., an isolated bispecific antibody specifically binding EGFR and c-Met is substantially free of antibodies that specifically bind antigens other than human EGFR and c-Met). An isolated antibody that specifically binds EGFR and c-Met, however, can have cross-reactivity to other antigens, such as orthologs of human EGFR and/or c-Met, such as *Macaca fascicularis* (cynomolgus) EGFR and/or c-Met. Moreover, an isolated antibody may be substantially free of other cellular material and/or chemicals.

An antibody variable region consists of a "framework" region interrupted by three "antigen binding sites". The antigen binding sites are defined using various terms: (i) Complementarity Determining Regions (CDRs), three in the VH (HCDR1, HCDR2, HCDR3), and three in the VL (LCDR1, LCDR2, LCDR3), are based on sequence variability (Wu and Kabat ~~(1970)~~ J Exp Med 132:211-50, 1970; Kabat et al Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991). (ii) "Hypervariable regions", "HVR", or "HV", three in the VH (H1, H2, H3) and three in the VL (L1, L2, L3), refer to the regions of an antibody variable domains which are hypervariable in structure as defined by Chothia and Lesk (Chothia and Lesk Mol Biol 196:901-17, 1987). Other terms include "IMGT-CDRs" (Lefranc *et al.*, Dev Comparat Immunol 27:55-77, 2003) and "Specificity Determining Residue Usage" (SDRU) (Almagro Mol Recognit 17:132-43, 2004). The International

ImMunoGeneTics (IMGT) database (http://www_imgt_org) provides a standardized numbering and definition of antigen-binding sites. The correspondence between CDRs, HVs and IMGT delineations is described in Lefranc *et al.*, Dev Comparat Immunol 27:55-77, 2003.

"Chothia residues" as used herein are the antibody VL and VH residues numbered according to Al-Lazikani (Al-Lazikani *et al.*, J Mol Biol 273:927-48, 1997).

"Framework" or "framework sequences" are the remaining sequences of a variable region other than those defined to be antigen binding sites. Because the antigen binding sites can be defined by various terms as described above, the exact amino acid sequence of a framework depends on how the antigen-binding site was defined.

"Humanized antibody" refers to an antibody in which the antigen binding sites are derived from non-human species and the variable region frameworks are derived from human immunoglobulin sequences. Humanized antibodies may include substitutions in the framework regions so that the framework may not be an exact copy of expressed human immunoglobulin or germline gene sequences.

"Human-adapted" antibodies or "human framework adapted (HFA)" antibodies refers to humanized antibodies adapted according to methods described in U.S. Pat. Publ. No. US2009/0118127. Human-adapted antibodies are humanized by selecting the acceptor human frameworks based on the maximum CDR and FR similarities, length compatibilities and sequence similarities of CDR1 and CDR2 loops and a portion of light chain CDR3 loops.

"Human antibody" refers to an antibody having heavy and light chain variable regions in which both the framework and the antigen binding sites are derived from sequences of human origin. If the antibody contains a constant region, the constant region also is derived from sequences of human origin.

Human antibody comprises heavy or light chain variable regions that are "derived from" sequences of human origin if the variable regions of the antibody are obtained from a system that uses human germline immunoglobulin or rearranged immunoglobulin genes. Such systems include human immunoglobulin gene libraries displayed on phage, and transgenic non-human animals such as mice carrying human immunoglobulin loci as described herein. "Human antibody" may contain amino acid differences when compared to the human germline or rearranged immunoglobulin sequences due to for example naturally occurring somatic mutations or intentional introduction of substitutions in the framework or antigen binding sites. Typically, "human antibody" is at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, 99% or 100% identical in amino acid sequence to an amino acid sequence encoded by a human germline or rearranged immunoglobulin gene. In some cases, "human antibody" may contain consensus framework sequences derived from human framework sequence analyses, for example as described in Knappik *et al.,* J Mol Biol 296:57-86, 2000), or synthetic HCDR3 incorporated into human immunoglobulin gene libraries displayed on phage, for example as described in Shi *et al.,* J Mol Biol 397:385-96, 2010 and Intl. Pat. Publ. No. WO2009/085462). Antibodies in which antigen binding sites are derived from a non-human species are not included in the definition of "human antibody".

Isolated humanized antibodies may be synthetic. Human antibodies, while derived from human immunoglobulin sequences, may be generated using systems such as phage display incorporating synthetic CDRs and/or synthetic frameworks, or can be subjected to *in vitro* mutagenesis to improve antibody properties, resulting in antibodies that do not naturally exist within the human antibody germline repertoire *in vivo*.

The term "recombinant antibody" as used herein, includes all antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies isolated from an animal (e.g., a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom (described further below), antibodies isolated from a host cell transformed to express the antibody, antibodies isolated from a recombinant, combinatorial antibody library, and antibodies prepared, expressed, created or isolated by any other means that involve splicing of human immunoglobulin gene sequences to other DNA sequences, or antibodies that are generated *in vitro* using Fab arm exchange.

The term "monoclonal antibody" as used herein refers to a preparation of antibody molecules of single molecular composition. A monoclonal antibody composition displays a single binding specificity and affinity for a particular epitope, or in a case of a bispecific monoclonal antibody, a dual binding specificity to two distinct epitopes.

The term "substantially identical" as used herein means that the two antibody variable region amino acid sequences being compared are identical or have "insubstantial differences". Insubstantial differences are substitutions of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids in an antibody variable region sequence that do not adversely affect antibody properties. Amino acid sequences substantially identical to the variable region sequences disclosed herein are within the scope of the invention. In some embodiments, the sequence identity can be about 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99% or higher. Percent identity can be determined for example by pairwise alignment using the default settings of the AlignX module of Vector NTI v.9.0.0 (Invitrogen, Carlsbad, CA). The protein sequences of the present invention can be used as a query sequence to perform a search against public or patent databases to, for example, identify related sequences. Exemplary programs used to perform such searches are the XBLAST or BLASTP programs (http_//www_ncbi_nlm/nih_gov), or the GenomeQuest™ (GenomeQuest, Westborough, MA) suite using the default settings.

The term "epitope" as used herein means a portion of an antigen to which an antibody specifically binds. Epitopes usually consist of chemically active (such as polar, non-polar or hydrophobic) surface groupings of moieties such as amino acids or polysaccharide side chains and can have specific three-dimensional structural characteristics, as well as specific charge characteristics. An epitope can be composed of contiguous and/or discontiguous amino acids that form a conformational spatial unit. For a discontiguous epitope, amino acids from differing portions of the linear sequence of the antigen come in close proximity in 3-dimensional space through the folding of the protein molecule.

The term "in combination with" as used herein means that two or more therapeutics can be administered to a subject together in a mixture, concurrently as single agents or sequentially as single agents in any order.

The numbering of amino acid residues in the antibody constant region throughout the specification is performed according to the EU index as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991), unless otherwise explicitly stated.

Compositions of matter

The present invention provides bispecific agents that specifically bind EGFR and c-Met. The present invention provides polypeptides and polynucleotides encoding the bispecific agents of the invention or complementary nucleic acids thereof, vectors, host cells, and methods of making and using them.

Monospecific and bispecific EGFR and/or c-Met FN3 domain containing binding molecules

Monospecific EGFR FN3 domain containing binding molecules

The present invention provides fibronectin type III (FN3) domains that bind specifically to epidermal growth factor receptor (EGFR) and block binding of epidermal growth factor (EGF) to EGFR, and thus can be widely used in therapeutic and diagnostic applications. The present invention provides polynucleotides encoding the FN3 domains of the invention or complementary nucleic acids thereof, vectors, host cells, and methods of making and using them.

The FN3 domains of the invention bind EGFR with high affinity and inhibit EGFR signaling, and may provide a benefit in terms of specificity and reduced off-target toxicity when compared to small molecule EGFR inhibitors, and improved tissue penetration when compared to conventional antibody therapeutics.

One embodiment of the invention is an isolated fibronectin type III (FN3) domain that specifically binds epidermal growth factor receptor (EGFR) and blocks binding of epidermal growth factor (EGF) to EGFR.

The FN3 domains of the invention may block EGF binding to the EGFR with an IC_{50} value of less than about $1x10^{-7}$ M, less than about $1x10^{-8}$ M, less than about $1x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $1x10^{-11}$ M, or less than about $1x10^{-12}$ M in a competition assay employing A431 cells and detecting amount of fluorescence from bound biotinylated EGF using streptavidin-phycoerythrin conjugate at 600 nM on A431 cells incubated with or without the FN3 domains of the invention. Exemplary FN3 domains may block EGF binding to the EGFR with an IC_{50} value between about $1x10^{-9}$ M to about $1x10^{-7}$ M, such as EGFR binding FN3 domains having the amino acid sequence of SEQ ID NOs: 18-29, 107-110, or 122-137. The FN3 domains of the invention may block EGF binding to the EGFR by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to binding of EGF to the EGFR in the absence of the FN3 domains of the invention using the same assay conditions.

The FN3 domain of the invention may inhibit EGFR signaling by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to the level of signaling in the absence of the FN3 domains of the invention using the same assay conditions.

Binding of a ligand such as EGF to EGFR stimulates receptor dimerization, autophosphorylation, activation of the receptor's internal, cytoplasmic tyrosine kinase domain, and initiation of multiple signal transduction and transactivation pathways involved in regulation of DNA synthesis (gene activation) and cell cycle progression or division. Inhibition of EGFR signaling may result in inhibition in one or more EGFR

downstream signaling pathways and therefore neutralizing EGFR may have various effects, including inhibition of cell proliferation and differentiation, angiogenesis, cell motility and metastasis.

EGFR signaling may be measured using various well know methods, for example measuring the autophosphorylation of the receptor at any of the tyrosines Y1068, Y1148, and Y1173 (Downward *et al.*, Nature 311:483-5, 1984) and/or phosphorylation of natural or synthetic substrates. Phosphorylation can be detected using well known methods such as an ELISA assay or a western plot using a phosphotyrosine specific antibody. Exemplary assays can be found in Panek *et al.*, J Pharmacol Exp Thera 283:1433-44, 1997 and Batley *et al.*, Life Sci 62:143-50, 1998, and assays described herein.

In one embodiment, the FN3 domain of the invention inhibits EGF-induced EGFR phosphorylation at EGFR residue position Tyrosine 1173 with an IC_{50} value of less than about $2.5x10^{-6}$ M, for example less than about $1x10^{-6}$ M, less than about $1x10^{-7}$ M, less than about $1x10^{-8}$ M, less than about $1x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $1x10^{-11}$ M, or less than about $1x10^{-12}$ M when measured in A431 cells using 50 ng/mL human EGF.

In one embodiment, the FN3 domain of the invention inhibits EGF- induced EGFR phosphorylation at EGFR residue position Tyrosine 1173 with an IC_{50} value between about 1.8×10^{-8} M to about 2.5×10^{-6} M when measured in A431 cells using 50 ng/mL human EGF. Such exemplary FN3 domains are those having the amino acid sequence of SEQ ID NOs: 18-29, 107-110, or 122-137.

In one embodiment, the FN3 domain of the invention binds human EGFR with a dissociation constant (K_D) of less than about $1x10^{-8}$ M, for example less than about $1x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $1x10^{-11}$ M, less than about $1x10^{-12}$ M, or less than about $1x10^{-13}$ M as determined by surface plasmon resonance or the Kinexa method, as practiced by those of skill in the art. In some embodiments, the FN3 domain of the invention binds human EGFR with a K_D of between about $2x10^{-10}$ to about $1x10^{-8}$ M. The affinity of a FN3 domain for EGFR can be determined experimentally using any suitable method. (See, for example, Berzofsky, *et al.*, "Antibody-Antigen Interactions," In *Fundamental Immunology*, Paul, W. E., Ed., Raven Press: New York, NY (1984); Kuby, Janis *Immunology*, W. H. Freeman and Company: New York, NY (1992); and methods described herein). The measured affinity of a particular FN3 domain-antigen interaction can vary if measured under different conditions (e.g., osmolarity, pH). Thus, measurements of affinity and other antigen-binding parameters (e.g., K_D, K_{on}, K_{off}) are

preferably made with standardized solutions of protein scaffold and antigen, and a standardized buffer, such as the buffer described herein.

Exemplary FN3 domains of the invention that bind EGFR include FN3 domains of SEQ ID NOs: 18-29, 107-110, or 122-137.

In one embodiment, the FN3 domain that specifically binds EGFR comprises an amino acid sequence at least 87% identical to the amino acid sequence of SEQ ID NO: 27.

In one embodiment, the FN3 domain that specifically binds EGFR comprises

an FG loop comprising the sequence HNVYKDTNX$_9$RGL (SEQ ID NO: 179) or the sequence LGSYVFEHDVML (SEQ ID NO: 180), wherein X$_9$ is M or I; and

a BC loop comprising the sequence X$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$ (SEQ ID NO: 181), wherein

X$_1$ is A, T, G or D;

X$_2$ is A, D, Y or W;

X$_3$ is P, D or N;

X$_4$ is L or absent;

X$_5$ is D, H, R, G, Y or W;

X$_6$ is G, D or A;

X$_7$ is A, F, G, H or D; and

X$_8$ is Y, F or L.

The FN3 domains of the invention that specifically bind EGFR and inhibit autophosphorylation of EGFR may comprise as a structural feature an FG loop comprising the sequence HNVYKDTNX$_9$RGL (SEQ ID NO: 179) or the sequence LGSYVFEHDVML (SEQ ID NO: 180), wherein X$_9$ is M or I. Such FN3 domains may further comprise a BC loop of 8 or 9 amino acids in length and defined by the sequence X$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$ (SEQ ID NO: 181), and inhibit EGFR autophosphorylation with an IC$_{50}$ value of less than about 2.5x10^{-6} M, or with an IC$_{50}$ value of between about 1.8x10^{-8} M to about 2.5x10^{-6} M when measured in A431 cells using 50 ng/mL human EGF.

The FN3 domains of the invention that specifically bind EGFR and inhibit autophosphorylation of EGFR further comprise the sequence of

LPAPKNLVVSEVTEDSLRLSWX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$DSFLIQYQESEKVGEAINLTVP GSERSYDLTGLKPGTEYTVSIYGVHNVYKDTNX$_9$RGLPLSAEFTT (SEQ ID NO: 182), or the sequence

LPAPKNLVVSEVTEDSLRLSWX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$DSFLIQYQESEKVGEAINLTVP GSERSYDLTGLKPGTEYTVSIYGVLGSYVFEHDVMLPLSAEFTT (SEQ ID NO: 183),

wherein

X_1 is A, T, G or D;

X_2 is A, D, Y or W;

X_3 is P, D or N;

X_4 is L or absent;

X_5 is D, H, R, G, Y or W;

X_6 is G, D or A;

X_7 is A, F, G, H or D;

X_8 is Y, F or L; and

X_9 is M or I

The EGFR binding FN3 domains can be generated and tested for their ability to inhibit EGFR autophosphorylation using well known methods and methods described herein.

Another embodiment of the invention is an isolated FN3 domain that specifically binds EGFR, wherein the FN3 domain comprises the sequence shown in SEQ ID NOs: 18-29, 107-110, or 122-137.

In some embodiments, the EGFR binding FN3 domains comprise an initiator methionine (Met) linked to the N-terminus or a cysteine (Cys) linked to a C-terminus of a particular FN3 domain, for example to facilitate expression and/or conjugation of half-life extending molecules.

Another embodiment of the invention is an isolated fibronectin type III (FN3) domain that specifically binds EGFR and blocks binding of EGF to the EGFR, wherein the FN3 domain is isolated from a library designed based on Tencon sequence of SEQ ID NO: 1.

Monospecific c-Met FN3 domain containing binding molecules

The present invention provides fibronectin type III (FN3) domains that bind specifically to hepatocyte growth factor receptor (c-Met) and block binding of hepatocyte growth factor (HGF) to c-Met, and thus can be widely used in therapeutic and diagnostic applications. The present invention provides polynucleotides encoding the FN3 domains

of the invention or complementary nucleic acids thereof, vectors, host cells, and methods of making and using them.

The FN3 domains of the invention bind c-Met with high affinity and inhibit c-Met signaling, and may provide a benefit in terms of specificity and reduced off-target toxicity when compared to small molecule c-Met inhibitors, and improved tissue penetration when compared to conventional antibody therapeutics. The FN3 domains of the invention are monovalent, therefore preventing unwanted receptor clustering and activation that may occur with other bivalent molecules.

One embodiment of the invention is an isolated fibronectin type III (FN3) domain that specifically binds hepatocyte growth factor receptor (c-Met) and blocks binding of hepatocyte growth factor (HGF) to c-Met.

The FN3 domains of the invention may block HGF binding to c-Met with an IC_{50} value of less than about $1x10^{-7}$ M, less than about $1x10^{-8}$ M, less than about $1x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $1x10^{-11}$ M, or less than about $1x10^{-12}$ M in an assay detecting inhibition of binding of biotinylated HGF to c-Met-Fc fusion protein in the presence of the FN3 domains of the invention. Exemplary FN3 domains may block HGF binding to the c-Met with an IC_{50} value between about $2x10^{-10}$ M to about $6x10^{-8}$ M. The FN3 domains of the invention may block HGF binding to c-Met by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to binding of HGF to c-Met in the absence of the FN3 domains of the invention using the same assay conditions.

The FN3 domain of the invention may inhibit c-Met signaling by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to the level of signaling in the absence of FN3 domains of the invention using the same assay conditions.

Binding of HGF to c-Met stimulates receptor dimerization, autophosphorylation, activation of the receptor's internal, cytoplasmic tyrosine kinase domain, and initiation of multiple signal transduction and transactivation pathways involved in regulation of DNA synthesis (gene activation) and cell cycle progression or division. Inhibition of c-Met signaling may result in inhibition of one or more c-Met downstream signaling pathways and therefore neutralizing c-Met may have various effects, including inhibition of cell proliferation and differentiation, angiogenesis, cell motility and metastasis.

c-Met signaling may be measured using various well know methods, for example measuring the autophosphorylation of the receptor on at least one tyrosine residues Y1230, Y1234,Y1235 or Y1349 and/or phosphorylation of natural or synthetic substrates.

Phosphorylation may be detected, for example, using an antibody specific for phosphotyrosine in an ELISA assay or on a western blot. Assays for tyrosine kinase activity are described for example in: Panek *et al.*, J Pharmacol Exp Thera 283:1433-44, 1997 and Batley *et al.*, Life Sci 62:143-50, 1998, and assays described herein.

In one embodiment, the FN3 domain of the invention inhibits HGF-induced c-Met phosphorylation at c-Met residue position 1349 with an IC_{50} value of less than about $1x10^{-6}$ M, less than about $1x10^{-7}$ M, less than about $1x10^{-8}$ M, less than about $1x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $1x10^{-11}$ M, or less than about $1x10^{-12}$ M when measured in NCI-H441 cells using 100 ng/mL recombinant human HGF.

In one embodiment, the FN3 domain of the invention inhibits HGF-induced c-Met phosphorylation at c-Met tyrosine Y1349 with an IC_{50} value between about $4x10^{-9}$ M to about $1x10^{-6}$ M when measured in NCI-H441 cells using 100 ng/mL recombinant human HGF.

In one embodiment, the FN3 domain of the invention binds human c-Met with an dissociation constant (K_D) of equal to or less than about $1x10^{-7}$ M, $1x10^{-8}$ M, $1x10^{-9}$ M, $1x10^{-10}$ M, $1x10^{-11}$ M, $1x10^{-12}$ M, $1x10^{-13}$ M, $1x10^{-14}$ M, or $1x10^{-15}$ M as determined by surface plasmon resonance or the Kinexa method, as practiced by those of skill in the art. In some embodiments, the FN3 domain of the invention binds human c-Met with a K_D of between about $3x10^{-10}$ M to about $5x10^{-8}$ M. The affinity of a FN3 domain for c-Met may be determined experimentally using any suitable method. (See, for example, Berzofsky, *et al.*, "Antibody-Antigen Interactions," In *Fundamental Immunology*, Paul, W. E., Ed., Raven Press: New York, NY (1984); Kuby, Janis *Immunology*, W. H. Freeman and Company: New York, NY (1992); and methods described herein). The measured affinity of a particular FN3 domain-antigen interaction can vary if measured under different conditions (e.g., osmolarity, pH). Thus, measurements of affinity and other antigen-binding parameters (e.g., K_D, K_{on}, K_{off}) are preferably made with standardized solutions of protein scaffold and antigen, and a standardized buffer, such as the buffer described herein.

Exemplary FN3 domains of the invention that bind c-Met include FN3 domains having the amino acid sequence of SEQ ID NOs: 32-49 or 111-114.

In one embodiment, the FN3 domain that specifically binds c-Met comprises an amino acid sequence at least 83% identical to the amino acid sequence of SEQ ID NO: 41.

In one embodiment, the FN3 domain that specifically binds c-Met comprises

a C strand and a CD loop comprising the sequence $DSFX_{10}IRYX_{11}E$ $X_{12}X_{13}X_{14}X_{15}GX_{16}$ (SEQ ID NO: 184), wherein

X_{10} is W, F or V;

X_{11} is D, F or L;

X_{12} is V, F or L;

X_{13} is V, L or T;

X_{14} is V, R, G, L, T or S;

X_{15} is G, S, A, T or K; and

X_{16} is E or D; and

a F strand and a FG loop comprising the sequence $TEYX_{17}VX_{18}IX_{19}X_{20}V$ $KGGX_{21}X_{22}SX_{23}$ (SEQ ID NO: 185), wherein

X_{17} is Y, W, I, V, G or A;

X_{18} is N, T, Q or G;

X_{19} is L, M, N or I;

X_{20} is G or S;

X_{21} is S, L, G, Y, T, R, H or K;

X_{22} is I, V or L; and

X_{23} is V, T, H, I, P, Y or L.

The FN3 domains of the invention that specifically bind c-Met and inhibit autophosphorylation of c-Met further comprises the sequence:
$LPAPKNLVVSRVTEDSARLSWTAPDAAF\ DSFX_{16}IRYX_{11}E\ X_{12}X_{13}X_{14}X_{15}GX_{16}$ $AIVLTVPGSERSYDLTGLKPGTEYX_{17}VX_{18}IX_{19}X_{20}VKGGX_{21}X_{22}SX_{23}PLSAEFTT$ (SEQ ID NO: 186),
wherein

X_{10} is W, F or V; and

X_{11} is D, F or L;

X_{12} is V, F or L;

X_{13} is V, L or T;

X_{14} is V, R, G, L, T or S;

X_{15} is G, S, A, T or K;

X_{16} is E or D;

X_{17} is Y, W, I, V, G or A;

X_{18} is N, T, Q or G;

X_{19} is L, M, N or I;

X_{20} is G or S;

X_{21} is S, L, G, Y, T, R, H or K;

X_{22} is I, V or L; and

X_{23} is V, T, H, I, P, Y or L.

Another embodiment of the invention is an isolated FN3 domain that specifically binds c-Met, wherein the FN3 domain comprises the sequence shown in SEQ ID NOs: 32-49 or 111-114.

Another embodiment of the invention is an isolated fibronectin type III (FN3) domain that specifically binds c-Met and blocks binding of HGF to the c-Met, wherein the FN3 domain is isolated from a library designed based on Tencon sequence of SEQ ID NO: 1.

Isolation of EGFR or c-Met FN3 domains from a library based on Tencon sequence

Tencon (SEQ ID NO: 1) is a non-naturally occurring fibronectin type III (FN3) domain designed from a consensus sequence of fifteen FN3 domains from human tenascin-C (Jacobs *et al.*, Protein Engineering, Design, and Selection, 25:107-117, 2012; U.S. Pat. Publ. No. 2010/0216708). The crystal structure of Tencon shows six surface-exposed loops that connect seven beta-strands as is characteristic to the FN3 domains, the beta-strands referred to as A, B, C, D, E, F and G, and the loops referred to as AB, BC, CD, DE, EF, and FG loops (Bork and Doolittle, Proc Natl Acad Sci USA 89:8990-8992, 1992; U.S. Pat. No. 6,673,901). These loops, or selected residues within each loop, can be randomized in order to construct libraries of fibronectin type III (FN3) domains that can be used to select novel molecules that bind EGFR or c-Met. Table 1 shows positions and sequences of each loop and beta-strand in Tencon (SEQ ID NO: 1).

Library designed based on Tencon sequence may thus have randomized FG loop, or randomized BC and FG loops, such as libraries TCL1 or TCL2 as described below. The Tencon BC loop is 7 amino acids long, thus 1, 2, 3, 4, 5, 6 or 7 amino acids may be randomized in the library diversified at the BC loop and designed based on Tencon sequence. The Tencon FG loop is 7 amino acids long, thus 1, 2, 3, 4, 5, 6 or 7 amino acids may be randomized in the library diversified at the FG loop and designed based on Tencon sequence. Further diversity at loops in the Tencon libraries may be achieved by insertion and/or deletions of residues at loops. For example, the FG and/or BC loops may be extended by 1-22 amino acids, or decreased by 1-3 amino acids. The FG loop in Tencon is 7 amino acids long, whereas the corresponding loop in antibody heavy chains ranges from 4-28 residues. To provide maximum diversity, the FG loop may be diversified in sequence as well as in length to correspond to the antibody CDR3 length range of 4-28 residues. For example, the FG loop can further be diversified in length by extending the loop by additional 1, 2, 3, 4 or 5 amino acids.

Library designed based on Tencon sequence may also have randomized alternative surfaces that form on a side of the FN3 domain and comprise two or more beta strands, and at least one loop. One such alternative surface is formed by amino acids in the C and the F beta-strands and the CD and the FG loops (a C-CD-F-FG surface). A library design based on Tencon alternative C-CD-F-FG surface and is shown in Figure 1 and detailed generation of such libraries is described in U.S. Pat. Publ. No. US2013/0226834.

Library designed based on Tencon sequence also includes libraries designed based on Tencon variants, such as Tencon variants having substitutions at residues positions 11, 14, 17, 37, 46, 73, or 86 (residue numbering corresponding to SEQ ID NO: 1), and which variants display improved thermal stability. Exemplary Tencon variants are described in US Pat. Publ. No. 2011/0274623, and include Tencon27 (SEQ ID NO: 99) having substitutions E11R, L17A, N46V and E86I when compared to Tencon of SEQ ID NO: 1.

Table 1.

FN3 domain	Tencon (SEQ ID NO: 1)
A strand	1-12
AB loop	13-16
B strand	17-21
BC loop	22-28
C strand	29-37
CD loop	38-43
D strand	44-50
DE loop	51-54
E strand	55-59
EF loop	60-64
F strand	65-74
FG loop	75-81
G strand	82-89

Tencon and other FN3 sequence based libraries can be randomized at chosen residue positions using a random or defined set of amino acids. For example, variants in the library having random substitutions can be generated using NNK codons, which encode all 20 naturally occurring amino acids. In other diversification schemes, DVK codons can be used to encode amino acids Ala, Trp, Tyr, Lys, Thr, Asn, Lys, Ser, Arg, Asp, Glu, Gly, and Cys. Alternatively, NNS codons can be used to give rise to all 20 amino acid residues and simultaneously reducing the frequency of stop codons. Libraries of FN3 domains with biased amino acid distribution at positions to be diversified can be synthesized for example using Slonomics® technology (http://www.sloning.com). This technology uses a library of pre-made double stranded triplets that act as universal building blocks sufficient for thousands of gene synthesis processes. The triplet library represents all possible sequence combinations necessary to build any desired DNA molecule. The codon designations are according to the well known IUB code.

The FN3 domains specifically binding EGFR or c-Met of the invention can be isolated by producing the FN3 library such as the Tencon library using *cis* display to ligate DNA fragments encoding the scaffold proteins to a DNA fragment encoding RepA to generate a pool of protein-DNA complexes formed after *in vitro* translation wherein each protein is stably associated with the DNA that encodes it (U.S. Pat. No. 7,842,476; Odegrip *et al.,* Proc Natl Acad Sci U S A 101, 2806-2810, 2004), and assaying the library for specific binding to EGFR and/or c-Met by any method known in the art and described in the Example. Exemplary well known methods which can be used are ELISA, sandwich immunoassays, and competitive and non-competitive assays (see, e.g., Ausubel *et al.,* eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York). The identified FN3 domains specifically binding EGFR or c-Met are further characterized for their ability to block EGFR ligand such as EGF binding to EGFR, or HGF binding to c-Met, and for their ability to inhibit EGFR and/or c-Met signaling using methods described herein.

The FN3 domains specifically binding to EGFR or c-Met of the invention can be generated using any FN3 domain as a template to generate a library and screening the library for molecules specifically binding EGFR or c-Met using methods provided within. Exemplar FN3 domains that can be used are the 3rd FN3 domain of tenascin C (TN3) (SEQ ID NO: 75), Fibcon (SEQ ID NO: 76), and the 10th FN3 domain of fibronectin (FN10) (SEQ ID NO: 77). Standard cloning and expression techniques are used to clone the libraries into a vector or synthesize double stranded cDNA cassettes of the library, to express, or to translate the libraries *in vitro*. For example ribosome display (Hanes and Pluckthun,

Proc Natl Acad Sci USA, 94, 4937-4942, 1997), mRNA display (Roberts and Szostak, *Proc Natl Acad Sci USA,* 94, 12297-12302, 1997), or other cell-free systems (U.S. Pat. No. 5,643,768) can be used. The libraries of the FN3 domain variants may be expressed as fusion proteins displayed on the surface for example of any suitable bacteriophage. Methods for displaying fusion polypeptides on the surface of a bacteriophage are well known (U.S. Pat. Publ. No. 2011/0118144; Int. Pat. Publ. No. WO2009/085462; U.S. Pat. No. 6,969,108; U.S. Pat. No. 6,172,197; U.S. Pat. No. 5,223,409; U.S. Pat. No. 6,582,915; U.S. Pat. No. 6,472,147).

The FN3 domains specifically binding EGFR or c-Met of the invention can be modified to improve their properties such as improve thermal stability and reversibility of thermal folding and unfolding. Several methods have been applied to increase the apparent thermal stability of proteins and enzymes, including rational design based on comparison to highly similar thermostable sequences, design of stabilizing disulfide bridges, mutations to increase alpha-helix propensity, engineering of salt bridges, alteration of the surface charge of the protein, directed evolution, and composition of consensus sequences (Lehmann and Wyss, Curr Opin Biotechnol, 12, 371-375, 2001). High thermal stability may increase the yield of the expressed protein, improve solubility or activity, decrease immunogenicity, and minimize the need of a cold chain in manufacturing. Residues that can be substituted to improve thermal stability of Tencon (SEQ ID NO: 1) are residue positions 11, 14, 17, 37, 46, 73, or 86, and are described in US Pat. Publ. No. 2011/0274623. Substitutions corresponding to these residues can be incorporated to the FN3 domains or the bispecific FN3 domain containing molecules of the invention.

Another embodiment of the invention is an isolated FN3 domain that specifically binds EGFR and blocks binding of EGF to EGFR, comprising the sequence shown in SEQ ID NOs: 18-29, 107-110, 122-137, further comprising substitutions at one or more residue positions corresponding to positions 11, 14, 17, 37, 46, 73, and 86 in Tencon (SEQ ID NO: 1).

Another embodiment of the invention is an isolated FN3 domain that specifically binds c-Met and blocks binding of HGF to c-Met, comprising the sequence shown in SEQ ID NOs: 32-49 or 111-114, further comprising substitutions at one or more residue positions corresponding to positions 11, 14, 17, 37, 46, 73, and 86 in Tencon (SEQ ID NO: 1).

Exemplary substitutions are substitutions E11N, E14P, L17A, E37P, N46V, G73Y and E86I (numbering according to SEQ ID NO: 1).

In some embodiments, the FN3 domains of the invention comprise substitutions corresponding to substitutions L17A, N46V, and E86I in Tencon (SEQ ID NO: 1).

The FN3 domains specifically binding EGFR (Figure 1) have an extended FG loop when compared to Tencon (SEQ ID NO: 1). Therefore, the residues corresponding to residues 11, 14, 17, 37, 46, 73, and 86 in Tencon (SEQ ID NO: 1) are residues 11, 14, 17, 37, 46, 73 and 91 in EGFR FN3 domains shown in Figure 1A and 1B except for the FN3 domain of SEQ ID NO: 24, wherein the corresponding residues are residues 11, 14, 17, 38, 74, and 92 due to an insertion of one amino acid in the BC loop.

Another embodiment of the invention is an isolated FN3 domain that specifically binds EGFR and blocks binding of EGF to EGFR comprising the amino acid sequence shown in SEQ ID NOs: 18-29, 107-110, or 122-137, optionally having substitutions corresponding to substitutions L17A, N46V, and E86I in Tencon (SEQ ID NO: 1).

Another embodiment of the invention is an isolated FN3 domain that specifically binds c-Met and blocks binding of HGF to c-Met comprising the amino acid sequence shown in SEQ ID NOs: 32-49 or 111-114, optionally having substitutions corresponding to substitutions L17A, N46V, and E86I in Tencon (SEQ ID NO: 1).

Measurement of protein stability and protein lability can be viewed as the same or different aspects of protein integrity. Proteins are sensitive or "labile" to denaturation caused by heat, by ultraviolet or ionizing radiation, changes in the ambient osmolarity and pH if in liquid solution, mechanical shear force imposed by small pore-size filtration, ultraviolet radiation, ionizing radiation, such as by gamma irradiation, chemical or heat dehydration, or any other action or force that may cause protein structure disruption. The stability of the molecule can be determined using standard methods. For example, the stability of a molecule can be determined by measuring the thermal melting ("TM") temperature, the temperature in ° Celsius (°C) at which half of the molecules become unfolded, using standard methods. Typically, the higher the TM, the more stable the molecule. In addition to heat, the chemical environment also changes the ability of the protein to maintain a particular three dimensional structure.

In one embodiment, the FN3 domains binding EGFR or c-Met of the invention exhibit increased stability by at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% or more compared to the same domain prior to engineering measured by the increase in the TM.

Chemical denaturation can likewise be measured by a variety of methods. Chemical denaturants include guanidinium hydrochloride, guanidinium thiocyanate, urea, acetone, organic solvents (DMF, benzene, acetonitrile), salts (ammonium sulfate, lithium

bromide, lithium chloride, sodium bromide, calcium chloride, sodium chloride); reducing agents (e.g. dithiothreitol, beta-mercaptoethanol, dinitrothiobenzene, and hydrides, such as sodium borohydride), non-ionic and ionic detergents, acids (e.g. hydrochloric acid (HCl), acetic acid (CH_3COOH), halogenated acetic acids), hydrophobic molecules (e.g. phosopholipids), and targeted denaturants. Quantitation of the extent of denaturation can rely on loss of a functional property, such as ability to bind a target molecule, or by physiochemical properties, such as tendency to aggregation, exposure of formerly solvent inaccessible residues, or disruption or formation of disulfide bonds.

In one embodiment, the FN3 domain of the invention binding EGFR or c-Met exhibit increased stability by at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% or more compared to the same scaffold prior to engineering, measured by using guanidinium hydrochloride as a chemical denaturant. Increased stability can be measured as a function of decreased tryptophan fluorescence upon treatment with increasing concentrations of guanidine hydrochloride using well known methods.

The FN3 domains of the invention may be generated as monomers, dimers, or multimers, for example, as a means to increase the valency and thus the avidity of target molecule binding, or to generate bi- or multispecific scaffolds simultaneously binding two or more different target molecules. The dimers and multimers may be generated by linking monospecific, bi- or multispecific protein scaffolds, for example, by the inclusion of an amino acid linker, for example a linker containing poly-glycine, glycine and serine, or alanine and proline. Exemplary linker include $(GS)_2$, (SEQ ID NO: 78), $(GGGGS)_5$ (SEQ ID NO: 79), $(AP)_2$ (SEQ ID NO: 80), $(AP)_5$ (SEQ ID NO: 81), $(AP)_{10}$ (SEQ ID NO: 82), $(AP)_{20}$ (SEQ ID NO: 83) and $A(EAAAK)_5AAA$ (SEQ ID NO: 84), linkers. The dimers and multimers may be linked to each other in an N-to C-direction. The use of naturally occurring as well as artificial peptide linkers to connect polypeptides into novel linked fusion polypeptides is well known in the literature (Hallewell *et al., J Biol Chem* 264, 5260-5268, 1989; Alfthan *et al., Protein Eng.* 8, 725-731, 1995; Robinson & Sauer, *Biochemistry* 35, 109-116, 1996; U.S. Pat. No. 5,856,456).

Bispecific agents specifically binding EGFR and c-Met

The bispecific agents that specifically bind EGFR and c-Met of the invention may provide a benefit in terms of specificity and reduced off-target toxicity when compared to small molecule EGFR and/or c-Met inhibitors. The present invention is based at least in part on the surprising finding that the bispecific agents specifically binding EGFR and c-

Met provide a significantly improved synergistic inhibitory effect when compared to a mixture of EGFR-binding and c-Met-binding monospecific agents. The molecules may be tailored to specific affinity towards both EGFR and c-Met to maximize tumor penetration and retention. The bispecific agents that specifically bind EGFR and c-Met provide more efficient inhibition of EGFR and/or c-Met signaling pathways and inhibit tumor growth more efficiently than cetuximab (Erbitux®).

The bispecific agents specifically binding EGFR and c-Met may be formed by any polypeptide or a multimeric polypeptide that comprises an EGFR binding domain and a c-Met binding domain. The EGFR and the c-Met binding domains may be an antigen binding sites of an antibody, a VH/VL pair of an antibody, or another type of binding molecule such as a domain based on fibronectin type III (FN3) domain, a fibronectin type IX (FN9) domain, or any combination thereof.

The EGFR and c-Met binding polypeptides may be derived from existing monospecific EGFR and c-Met binding polypeptides or may be isolated *de novo*.

Bispecific EGFR/c/Met FN3 domain containing molecules

One embodiment of the invention is an isolated bispecific FN3 domain containing molecule comprising a first fibronectin type III (FN3) domain and a second FN3 domain, wherein the first FN3 domain specifically binds epidermal growth factor receptor (EGFR) and blocks binding of epidermal growth factor (EGF) to EGFR, and the second FN3 domain specifically binds hepatocyte growth factor receptor (c-Met) and blocks binding of hepatocyte growth factor (HGF) to c-Met.

The bispecific EGFR/c-Met FN3 domain containing molecules of the invention may be generated by covalently linking any EGFR-binding FN3 domain and any c-Met-binding FN3 domain of the invention directly or via a linker. Therefore, the first FN3 domain of the bispecific molecule may have characteristics as described above for the EGFR-binding FN3 domains, and the second FN3 domain of the bispecific molecule may have characteristics as described above for the c-Met-binding FN3 domains.

In one embodiment, the first FN3 domain of the bispecific EGFR/c-Met FN3 domain containing molecule inhibits EGF-induced EGFR phosphorylation at EGFR residue Tyrosine 1173 with an IC_{50} value of less than about $2.5x10^{-6}$ M when measured in A431 cells using 50 ng/mL human EGF, and the second FN3 domain of the bispecific EGFR/c-Met FN3 domain containing molecule inhibits HGF- induced c-Met phosphorylation at c-Met residue Tyrosine 1349 with an IC_{50} value of less than about $1.5x10^{-6}$ M when measured in NCI-H441 cells using 100 ng/mL human HGF.

In another embodiment, the first FN3 domain of the bispecific EGFR/c-Met FN3 domain containing molecule inhibits EGF-induced EGFR phosphorylation at EGFR residue Tyrosine 1173 with an IC_{50} value of between about 1.8 x 10^{-8} M to about 2.5x10^{-6} M when measured in A431 cells using 50 ng/mL human EGF, and the second FN3 domain of the bispecific EGFR/c-Met FN3 domain containing molecule inhibits HGF- induced c-Met phosphorylation at c-Met residue Tyrosine 1349 with an IC_{50} value between about 4x10^{-9} M to about 1.5x10^{-6} M when measured in NCI-H441 cells using 100 ng/mL human HGF.

In another embodiment, the first FN3 domain of the bispecific EGFR/c-Met FN3 domain containing molecule binds human EGFR with a dissociation constant (K_D) of less than about 1x10^{-8} M, and the second FN3 domain of the bispecific EGFR/c-Met FN3 domain containing molecule binds human c-Met with a K_D of less than about 5 x10^{-8} M.

In the bispecific molecule binding both EGFR and c-Met, the first FN3 domain binds human EGFR with a K_D of between about 2x10^{-10} to about 1x10^{-8} M, and the second FN3 domain binds human c-Met with a K_D of between about 3x10^{-10} to about 5 x10^{-8} M.

The affinity of the bispecific EGFR/c-Met molecule for EGFR and c-Met can be determined as described above for the monospecific molecules.

The first FN3 domain in the bispecific EGFR/c-Met molecule of the invention may block EGF binding to EGFR with an IC_{50} value of between about 1x10^{-9} M to about 1.5x10^{-7} M in an assay employing A431 cells and detecting the amount of fluorescence from bound biotinylated EGF using streptavidin-phycoerythrin conjugate at 600 nM on A431 cells incubated with or without the first FN3 domain. The first FN3 domain in the bispecific EGFR/c-Met molecule of the invention may block EGF binding to the EGFR by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to binding of EGF to EGFR in the absence of the first FN3 domains using the same assay conditions.

The second FN3 domain in the bispecific EGFR/c-Met molecule of the invention may block HGF binding to c-Met with an IC_{50} value of between about 2x10^{-10} M to about 6x10^{-8} M in an assay detecting inhibition of binding of biotinylated HGF to c-Met-Fc fusion protein in the presence of the second FN3 domain. The second FN3 domain in the bispecific EGFR/c-Met molecule may block HGF binding to c-Met by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to binding of HGF to c-Met in the absence of the second FN3 domain using the same assay conditions.

The bispecific EGFR/c-Met molecule of the invention may inhibit EGFR and/or c-Met signaling by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to the level of signaling in the absence of the bispecific EGFR/c-Met molecule of the invention using the same assay conditions.

EGFR and c-Met signaling may be measured using various well know methods as described above for the monospecific molecules.

The bispecific EGFR/c-Met molecules of the invention comprising the first FN3 domain specifically binding EGFR and the second FN3 domain specifically binding c-Met provide a significantly increased synergistic inhibition of EGFR and c-Met signaling and tumor cell proliferation when compared to the synergistic inhibition observed by a mixture of the first and the second FN3 domain. Synergistic inhibition can be assessed for example by measuring inhibition of ERK phosphorylation by the bispecific EGFR/c-Met FN3 domain containing molecules and by a mixture of two monospecific molecules, one binding EGFR and the other c-Met. The bispecific EGFR/c-Met molecules of the invention may inhibit ERK phosphorylation with an at least about 100 fold smaller, for example at least 500, 1000, 5000 or 10,000 fold smaller IC_{50} value when compared to the IC_{50} value for a mixture of two monospecific FN3 domains, indicating at least 100 fold increased potency for the bispecific EGFR/c-Met FN3 domain containing molecules when compared to the mixture of two monospecific FN3 domains. Exemplary bispecific EGFR-c-Met FN3 domain containing molecules may inhibit ERK phosphorylation with and IC_{50} value of about $5x10^{-9}$ M or less. ERK phosphorylation may be measured using standard methods and methods described herein.

The bispecific EGFR/c-Met FN3 domain containing molecule of the invention may inhibit NCI-H292 cell proliferation with an IC_{50} value that is at least 30-fold less when compared to the IC_{50} value of inhibition of NCI-H292 cell growth with a mixture of the first FN3 domain and the second FN3, wherein the cell proliferation is induced with medium containing 10% FBS supplemented with 7.5 ng/mL HGF. The bispecific molecule of the invention may inhibit tumor cell proliferation with an IC_{50} value that is about 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 300, 400, 500, 600, 700, 800, or about 1000 fold less when compared to the IC_{50} value of inhibition of tumor cell proliferation with a mixture of the first FN3 domain and the second FN3 domain. Inhibition of tumor cell proliferation may be measured using standard methods and methods described herein.

Another embodiment of the invention is a bispecific FN3 domain containing molecule comprising a first fibronectin type III (FN3) domain and a second FN3 domain,

wherein the first FN3 domain specifically binds epidermal growth factor receptor (EGFR) and blocks binding of epidermal growth factor (EGF) to EGFR, and the second FN3 domain specifically binds hepatocyte growth factor receptor (c-Met), and blocks binding of hepatocyte growth factor (HGF) to c-Met, wherein

the first FN3 domain comprises

an FG loop comprising the sequence HNVYKDTNX$_9$RGL (SEQ ID NO: 179) or the sequence LGSYVFEHDVML (SEQ ID NO: 180), wherein X$_9$ is M or I; and

a BC loop comprising the sequence X$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$ (SEQ ID NO: 181), wherein

X$_1$ is A, T, G or D;

X$_2$ is A, D, Y or W;

X$_3$ is P, D or N;

X$_4$ is L or absent;

X$_5$ is D, H, R, G, Y or W;

X$_6$ is G, D or A;

X$_7$ is A, F, G, H or D; and

X$_8$ is Y, F or L; and

the second FN3 domain comprises

a C strand and a CD loop comprising the sequence DSFX$_{10}$IRYX$_{11}$E X$_{12}$X$_{13}$X$_{14}$X$_{15}$GX$_{16}$ (SEQ ID NO: 184), wherein

X$_{10}$ is W, F or V;

X$_{11}$ is D, F or L;

X$_{12}$ is V, F or L;

X$_{13}$ is V, L or T;

X$_{14}$ is V, R, G, L, T or S;

X$_{15}$ is G, S, A, T or K; and

X$_{16}$ is E or D; and

a F strand and a FG loop comprising the sequence TEYX$_{17}$VX$_{18}$IX$_{19}$X$_{20}$V KGGX$_{21}$X$_{22}$SX$_{23}$ (SEQ ID NO: 185), wherein

X$_{17}$ is Y, W, I, V, G or A;

X$_{18}$ is N, T, Q or G;

X$_{19}$ is L, M, N or I;

X$_{20}$ is G or S;

X$_{21}$ is S, L, G, Y, T, R, H or K;

X_{22} is I, V or L; and

X_{23} is V, T, H, I, P, Y or L.

In another embodiment, the bispecific molecule comprises the first FN3 domain that binds EGFR comprising the sequence:

LPAPKNLVVSEVTEDSLRLSWX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$DSFLIQYQESEKVGEAINLTVP GSERSYDLTGLKPGTEYTVSIYGVHNVYKDTNX$_9$RGL PLSAEFTT (SEQ ID NO: 182), or the sequence

LPAPKNLVVSEVTEDSLRLSWX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$ DSFLIQYQESEKVGEAINLTVP GSERSYDLTGLKPGTEYTVSIYGV LGSYVFEHDVMLPLSAEFTT (SEQ ID NO: 183),

wherein in the SEQ ID NOs: 182 and 183;

X_1 is A, T, G or D;

X_2 is A, D, Y or W;

X_3 is P, D or N;

X_4 is L or absent;

X_5 is D, H, R, G, Y or W;

X_6 is G, D or A;

X_7 is A, F, G, H or D;

X_8 is Y, F or L; and

X_9 is M or I.

In another embodiment, the bispecific molecule comprises the second FN3 domain that binds c-Met comprising the sequence

LPAPKNLVVSRVTEDSARLSWTAPDAAF DSFX$_{10}$IRYX$_{11}$E X$_{12}$X$_{13}$X$_{14}$X$_{15}$GX$_{16}$ AIVLTVPGSERSYDLTGLKPG TEYX$_{17}$VX$_{18}$IX$_{19}$X$_{20}$VKGGX$_{21}$X$_{22}$SX$_{23}$PLSAEFTT (SEQ ID NO: 186),

wherein

X_{10} is W, F or V; and

X_{11} is D, F or L;

X_{12} is V, F or L;

X_{13} is V, L or T;

X_{14} is V, R, G, L, T or S;

X_{15} is G, S, A, T or K;

X_{16} is E or D;

X_{17} is Y, W, I, V, G or A;

X_{18} is N, T, Q or G;

X_{19} is L, M, N or I;

X_{20} is G or S;

X_{21} is S, L, G, Y, T, R, H or K;

X_{22} is I, V or L; and

X_{23} is V, T, H, I, P, Y, F or L.

Exemplary bispecific EGFR/c-Met FN3 domain containing molecules comprise the amino acid sequence shown in SEQ ID NOs: 50-72, 106, 118-121, or 138-167.

The bispecific EGFR/c-Met molecules of the invention comprise certain structural characteristics associated with their functional characteristics, such as inhibition of EGFR autophosphorylation, such as the FG loop of the first FN3 domain that binds EGFR comprising the sequence HNVYKDTNX_9RGL (SEQ ID NO: 179) or the sequence LGSYVFEHDVML (SEQ ID NO: 180), wherein X_9 is M or I.

In one embodiment, the bispecific EGFR/c-Met FN3 domain containing molecules of the invention

inhibit EGF-induced EGFR phosphorylation at EGFR residues Tyrosine 1173 with an IC_{50} value of less than about $8x10^{-7}$ M when measured in H292 cells using 50 ng/mL human EGF;

inhibit HGF-induced c-Met phosphorylation at c-Met residue Tyrosine 1349 with an IC_{50} value of less than about $8.4x10^{-7}$ M when measured in NCI-H441 cells using 100 ng/mL human HGF;

inhibit HGF-induced NCI-H292 cell proliferation with an IC_{50} value of less than about $9.5x10^{-6}$M wherein the cell proliferation is induced with 10% FBS containing 7.5 ng HGF;

bind EGFR with a K_D of less than about $2.0x10^{-8}$ M; or

bind c-Met with a K_D of less than about $2.0x10^{-8}$ M.

In another embodiment, the bispecific EGFR/c-Met FN3 domain containing molecules of the invention

inhibit EGF-induced EGFR phosphorylation at EGFR residues Tyrosine 1173 with and IC_{50} of between about $4.2x10^{-9}$ M and $8x10^{-7}$ M when measured in H292 cells using 50 ng/mL human EGF;

inhibit HGF-induced c-Met phosphorylation at c-Met residues Tyrosine 1349 with an IC_{50} value of between about $2.4x10^{-8}$ M to about $8.4x10^{-7}$ M when measured in NCI-H441 cells using 100 ng/mL human HGF;

inhibit HGF-induced NCI-H292 cell proliferation with an IC_{50} value between about $2.3x10^{-8}$ M to about $9.5x10^{-6}$M wherein the cell proliferation is induced with 10% FBS containing 7.5 ng HGF;

bind EGFR with a K_D of between about $2x10^{-10}$ M to about $2.0x10^{-8}$ M; or

bind c-Met with a K_D of between about $1x10^{-9}$ M to about $2.0x10^{-8}$ M.

In one embodiment, the bispecific EGFR/c-Met molecules comprise the EGFR-binding FN3 domain comprising the sequence LPAPKNLVVSEVTEDSLRLSWX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$DSFLIQYQESEKVGEAINLTVP GSERSYDLTGLKPGTEYTVSIYGV HNVYKDTNX$_9$RGL PLSAEFTT (SEQ ID NO: 182), wherein

X_1 is D;

X_2 is D;

X_3 is P;

X_4 is absent;

X_5 is H or W;

X_6 is A;

X_7 is F

X_8 is Y; and

X_9 is M or I; and

the c-Met-binding FN3 domain comprising the sequence LPAPKNLVVSRVTEDSARLSWTAPDAAF DSFX$_{10}$IRYX$_{11}$E X$_{12}$X$_{13}$X$_{14}$X$_{15}$GX$_{16}$ AIVLTVPGSERSYDLTGLKPG TEYX$_{17}$VX$_{18}$IX$_{19}$X$_{20}$VKGGX$_{21}$X$_{22}$SX$_{23}$ PLSAEFTT (SEQ ID NO: 186),

wherein

X_{10} is W;

X_{11} is F;

X_{12} is F;

X_{13} is V or L;

X_{14} is G or S;

X_{15} is S or K;

X_{16} is E or D;

X_{17} is V;

X_{18} is N;

X_{19} is L or M;

X_{20} is G or S;

X_{21} is S or K;

X_{22} is I; and

X_{23} is P.

Exemplary bispecific EGFR/c-Met molecules are those having the sequence shown in SEQ ID NOs: 57, 61, 62, 63, 64, 65, 66, 67 and 68.

The bispecific molecules of the invention may further comprise substitutions at one or more residue positions in the first FN3 domain and/or the second FN3 domain corresponding to positions 11, 14, 17, 37, 46, 73 and 86 in Tencon (SEQ ID NO: 1) as described above, and a substitution at position 29. Exemplary substitutions are substitutions E11N, E14P, L17A, E37P, N46V, G73Y, E86I and D29E (numbering according to SEQ ID NO: 1). Skilled in the art will appreciate that other amino acids can be used for substitutions, such as amino acids within a family of amino acids that are related in their side chains as described *infra*. The generated variants can be tested for their stability and binding to EGFR and/or c-Met using methods herein.

In one embodiment, the bispecific EGFR/c-Met FN3 domain containing molecule comprises the first FN3 domain that binds specifically EGFR and the second FN3 domain that binds specifically c-Met, wherein the first FN3 domain comprises the sequence: LPAPKNLVVSX$_{24}$VTX$_{25}$DSX$_{26}$RLSWDDPX$_{27}$AFYX$_{28}$SFLIQYQX$_{29}$SEKVGEAIX$_{30}$LT VPGSERSYDLTGLKPGTEYTVSIYX$_{31}$VHNVYKDTNX$_{32}$RGLPLSAX$_{33}$FTT (SEQ ID NO: 187), wherein

X_{24} is E, N or R;

X_{25} is E or P;

X_{26} is L or A;

X_{27} is H or W;

X_{28} is E or D;

X_{29} is E or P;

X_{30} is N or V;

X_{31} is G or Y;

X_{32} is M or I; and

X_{33} is E or I;

and the second FN3 domain comprises the sequence:

LPAPKNLVVSX$_{34}$VTX$_{35}$DSX$_{36}$RLSWTAPDAAFDSFWIRYFX$_{37}$FX$_{38}$X$_{39}$X$_{40}$GX$_{41}$AIX$_{42}$ LTVPGSERSYDLTGLKPGTEYVVNIX$_{43}$X$_{44}$VKGGX$_{45}$ISPPLSAX$_{46}$FTT (SEQ ID NO: 188); wherein

X$_{34}$ is E, N or R;

X$_{35}$ is E or P;

X$_{36}$ is L or A;

X$_{37}$ is E or P;

X$_{38}$ is V or L;

X$_{39}$ is G or S;

X$_{40}$ is S or K;

X$_{41}$ is E or D;

X$_{42}$ is N or V;

X$_{43}$ is L or M;

X$_{44}$ is G or S;

X$_{45}$ is S or K; and

X$_{46}$ is E or I.

In other embodiments, the bispecific EGFR/c-Met FN3 domain containing molecule comprises the first FN3 domain comprising an amino acid sequence at least 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence of SEQ ID NO: 27, and the second FN3 domain comprising an amino acid sequence at least 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence of SEQ ID NO: 41.

The bispecific EGFR/c-Met FN3 domain containing molecules of the invention may be tailored to a specific affinity towards EGFR and c-Met to maximize tumor accumulation.

Another embodiment of the invention is an isolated bispecific FN3 domain containing molecule comprising a first fibronectin type III (FN3) domain and a second FN3 domain, wherein the first FN3 domain specifically binds epidermal growth factor receptor (EGFR) and blocks binding of epidermal growth factor (EGF) to EGFR, and the second FN3 domain specifically binds hepatocyte growth factor receptor (c-Met), and blocks binding of hepatocyte growth factor (HGF) to c-Met, wherein the first FN3 domain and the second FN3 domain is isolated from a library designed based on Tencon sequence of SEQ ID NO: 1.

The bispecific EGFR/c-Met FN3 domain containing molecule of the invention can be generated by covalently coupling the EGFR-binding FN3 domain and the c-Met binding FN3 domain of the invention using well known methods. The FN3 domains may be linked via a linker, for example a linker containing poly-glycine, glycine and serine, or alanine and proline. Exemplary linker include $(GS)_2$, (SEQ ID NO: 78), $(GGGGS)_5$ (SEQ ID NO: 79), $(AP)_2$ (SEQ ID NO: 80), $(AP)_5$ (SEQ ID NO: 81), $(AP)_{10}$ (SEQ ID NO: 82), $(AP)_{20}$ (SEQ ID NO: 83), $A(EAAAK)_5AAA$ (SEQ ID NO: 84), linkers. The use of naturally occurring as well as artificial peptide linkers to connect polypeptides into novel linked fusion polypeptides is well known in the literature (Hallewell *et al., J Biol Chem* 264, 5260-5268, 1989; Alfthan *et al., Protein Eng.* 8, 725-731, 1995; Robinson & Sauer, *Biochemistry* 35, 109-116, 1996; U.S. Pat. No. 5,856,456). The bispecific EGFR/c-Met molecules of the invention may be linked together from a C-terminus of the first FN3 domain to the N-terminus of the second FN3 domain, or from the C-terminus of the second FN3 domain to the N-terminus of the first FN3 domain. Any EGFR-binding FN3 domain may be covalently linked to a c-Met-binding FN3 domain. Exemplary EGFR-binding FN3 domains are domains having the amino acid sequence shown in SEQ ID NOs: 18-29, 107-110, and 122-137, and exemplary c-Met binding FN3 domains are domains having the amino acid sequence shown in SEQ ID NOs: 32-49 and 111-114. The EGFR-binding FN3 domains to be coupled to a bispecific molecule may additionally comprise an initiator methionine (Met) at their N-terminus.

Variants of the bispecific EGFR/c-Met FN3 domain containing molecules are within the scope of the invention. For example, substitutions can be made in the bispecific EGFR/c-Met FN3 domain containing molecule as long as the resulting variant retains similar selectivity and potency towards EGFR and c-Met when compared to the parent molecule. Exemplary modifications are for example conservative substitutions that will result in variants with similar characteristics to those of the parent molecules. Conservative substitutions are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine, histidine); (3) nonpolar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan); and (4) uncharged polar (glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine). Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. Alternatively, the amino acid repertoire can be grouped as (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine histidine), (3) aliphatic (glycine, alanine, valine, leucine, isoleucine, serine, threonine), with serine and threonine

optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic (phenylalanine, tyrosine, tryptophan); (5) amide (asparagine, glutamine); and (6) sulfur-containing (cysteine and methionine) (Stryer (ed.), Biochemistry, 2nd ed, WH Freeman and Co., 1981). Non-conservative substitutions can be made to the bispecific EGFR/c-Met FN3 domain containing molecule that involves substitutions of amino acid residues between different classes of amino acids to improve properties of the bispecific molecules. Whether a change in the amino acid sequence of a polypeptide or fragment thereof results in a functional homolog can be readily determined by assessing the ability of the modified polypeptide or fragment to produce a response in a fashion similar to the unmodified polypeptide or fragment using the assays described herein. Peptides, polypeptides or proteins in which more than one replacement has taken place can readily be tested in the same manner.

The bispecific EGFR/c-Met FN3 domain containing molecules of the invention may be generated as dimers or multimers, for example, as a means to increase the valency and thus the avidity of target molecule binding. The multimers may be generated by linking one or more EGFR-binding FN3 domain and one or more c-Met-binding FN3 domain to form molecules comprising at least three individual FN3 domains that are at least bispecific for either EGFR or c-Met, for example by the inclusion of an amino acid linker using well known methods.

Another embodiment of the invention is a bispecific FN3 domain containing molecule comprising a first fibronectin type III (FN3) domain and a second FN3 domain, wherein the first FN3 domain specifically binds epidermal growth factor receptor (EGFR) and blocks binding of epidermal growth factor (EGF) to EGFR, and the second FN3 domain specifically binds hepatocyte growth factor receptor (c-Met), and blocks binding of hepatocyte growth factor (HGF) to c-Met comprising the amino acid sequence shown in SEQ ID NOs: 50-72,106 or 138-165.

Half-life extending moieties

The bispecific EGFR/c-Met FN3 domain containing molecules or the monospecific EGFR or c-Met binding FN3 domains of the invention may incorporate other subunits for example via covalent interaction. In one aspect of the invention, the bispecific EGFR/c-Met FN3 domain containing molecules of the invention further comprise a half-life extending moiety. Exemplary half-life extending moieties are albumin,albumin variants, albumin-binding proteins and/or domains, transferrin and

fragments and analogues thereof, and Fc regions. An exemplary albumin-binding domain is shown in SEQ ID NO: 117.

All or a portion of an antibody constant region may be attached to the molecules of the invention to impart antibody-like properties, especially those properties associated with the Fc region, such as Fc effector functions such as C1q binding, complement dependent cytotoxicity (CDC), Fc receptor binding, antibody-dependent cell-mediated cytotoxicity (ADCC), phagocytosis, down regulation of cell surface receptors (e.g., B cell receptor; BCR), and can be further modified by modifying residues in the Fc responsible for these activities (for review; see Strohl, *Curr Opin Biotechnol.* 20, 685-691, 2009).

Additional moieties may be incorporated into the bispecific molecules of the invention such as polyethylene glycol (PEG) molecules, such as PEG5000 or PEG20,000, fatty acids and fatty acid esters of different chain lengths, for example laurate, myristate, stearate, arachidate, behenate, oleate, arachidonate, octanedioic acid, tetradecanedioic acid, octadecanedioic acid, docosanedioic acid, and the like, polylysine, octane, carbohydrates (dextran, cellulose, oligo- or polysaccharides) for desired properties. These moieties may be direct fusions with the protein scaffold coding sequences and may be generated by standard cloning and expression techniques. Alternatively, well known chemical coupling methods may be used to attach the moieties to recombinantly produced molecules of the invention.

A pegyl moiety may for example be added to the bispecific or monospecific molecules of the invention by incorporating a cysteine residue to the C-terminus of the molecule and attaching a pegyl group to the cysteine using well known methods. Exemplary bispecific molecules with the C-terminal cysteine are those having the amino acid sequence shown in SEQ IN NO: 170-178.

Monospecific and bispecific molecules of the invention incorporating additional moieties may be compared for functionality by several well known assays. For example, altered properties of monospecific and/or bispecific molecules due to incorporation of Fc domains and/or Fc domain variants may be assayed in Fc receptor binding assays using soluble forms of the receptors, such as the FcγRI, FcγRII, FcγRIII or FcRn receptors, or using well known cell-based assays measuring for example ADCC or CDC, or evaluating pharmacokinetic properties of the molecules of the invention in *in vivo* models.

Polynucleotides, vectors, host cells

The invention provides for nucleic acids encoding the EGFR-binding or c-Met binding FN3 domains or the bispecific EGFR/c-Met FN3 domain containing molecules of

the invention as isolated polynucleotides or as portions of expression vectors or as portions of linear DNA sequences, including linear DNA sequences used for *in vitro* transcription/translation, vectors compatible with prokaryotic, eukaryotic or filamentous phage expression, secretion and/or display of the compositions or directed mutagens thereof. Certain exemplary polynucleotides are disclosed herein, however, other polynucleotides which, given the degeneracy of the genetic code or codon preferences in a given expression system, encode the EGFR-binding or c-Met binding FN3 domains or the bispecific EGFR/c-Met FN3 domain containing molecules of the invention are also within the scope of the invention.

One embodiment of the invention is an isolated polynucleotide encoding the FN3 domain specifically binding EGFR having the amino acid sequence of SEQ ID NOs: 18-29, 107-110, or 122-137.

One embodiment of the invention is an isolated polynucleotide comprising the polynucleotide sequence of SEQ ID NOs: 97-98 or 168-169.

One embodiment of the invention is an isolated polynucleotide encoding the FN3 domain specifically binding c-Met having the amino acid sequence of the sequence shown in SEQ ID NOs: 32-49 or 111-114.

One embodiment of the invention is an isolated polynucleotide encoding the bispecific EGFR/-c-Met FN3 domain containing molecule having the amino acid sequence of SEQ ID NOs: 50-72, 106, 118-121 or 138-165.

One embodiment of the invention is an isolated polynucleotide comprising the polynucleotide sequence of SEQ ID NOs: 115-116 or 166-167.

The polynucleotides of the invention may be produced by chemical synthesis such as solid phase polynucleotide synthesis on an automated polynucleotide synthesizer and assembled into complete single or double stranded molecules. Alternatively, the polynucleotides of the invention may be produced by other techniques such a PCR followed by routine cloning. Techniques for producing or obtaining polynucleotides of a given known sequence are well known in the art.

The polynucleotides of the invention may comprise at least one non-coding sequence, such as a promoter or enhancer sequence, intron, polyadenylation signal, a *cis* sequence facilitating RepA binding, and the like. The polynucleotide sequences may also comprise additional sequences encoding additional amino acids that encode for example a marker or a tag sequence such as a histidine tag or an HA tag to facilitate purification or detection of the protein, a signal sequence, a fusion protein partner such as RepA, Fc or bacteriophage coat protein such as pIX or pIII.

Another embodiment of the invention is a vector comprising at least one polynucleotide of the invention. Such vectors may be plasmid vectors, viral vectors, vectors for baculovirus expression, transposon based vectors or any other vector suitable for introduction of the polynucleotides of the invention into a given organism or genetic background by any means. Such vectors may be expression vectors comprising nucleic acid sequence elements that can control, regulate, cause or permit expression of a polypeptide encoded by such a vector. Such elements may comprise transcriptional enhancer binding sites, RNA polymerase initiation sites, ribosome binding sites, and other sites that facilitate the expression of encoded polypeptides in a given expression system. Such expression systems may be cell-based, or cell-free systems well known in the art.

Another embodiment of the invention is a host cell comprising the vector of the invention. A monospecific EGFR-binding or c-Met binding FN3 domain or the bispecific EGFR/c-Met FN3 domain containing molecule of the invention can be optionally produced by a cell line, a mixed cell line, an immortalized cell or clonal population of immortalized cells, as well known in the art. See, e.g., Ausubel, *et al.*, ed., Current Protocols in Molecular Biology, John Wiley & Sons, Inc., NY, NY (1987-2001); Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor, NY (1989); Harlow and Lane, Antibodies, a Laboratory Manual, Cold Spring Harbor, NY (1989); Colligan, *et al.*, eds., Current Protocols in Immunology, John Wiley & Sons, Inc., NY (1994-2001); Colligan *et al.*, Current Protocols in Protein Science, John Wiley & Sons, NY, NY, (1997-2001).

The host cell chosen for expression may be of mammalian origin or may be selected from COS-1, COS-7, HEK293, BHK21, CHO, BSC-1, He G2, SP2/0, HeLa, myeloma, lymphoma, yeast, insect or plant cells, or any derivative, immortalized or transformed cell thereof. Alternatively, the host cell may be selected from a species or organism incapable of glycosylating polypeptides, e.g. a prokaryotic cell or organism, such as BL21, BL21(DE3), BL21-GOLD(DE3), XL1-Blue, JM109, HMS174, HMS174(DE3), and any of the natural or engineered *E. coli spp. Klebsiella spp.*, or *Pseudomonas spp* strains.

Another embodiment of the invention is a method of producing the isolated FN3 domain specifically binding EGFR or c-Met of the invention or the isolated bispecific EGFR/c-Met FN3 domain containing molecule of the invention, comprising culturing the isolated host cell of the invention under conditions such that the isolated FN3 domain

specifically binding EGFR or c-Met or the isolated bispecific EGFR/c-Met FN3 domain containing molecule is expressed, and purifying the domain or molecule.

The FN3 domain specifically binding EGFR or c-Met or the isolated bispecific EGFR/c-Met FN3 domain containing molecule of the invention can be purified from recombinant cell cultures by well-known methods, for example by protein A purification, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography, or high performance liquid chromatography (HPLC).

Bispecific EGFR/c-Met antibodies

The bispecific EGFR/c-Met antibodies may be generated *de novo* or may be engineered from existing monospecific anti-EGFR and anti-c-Met antibodies.

Exemplary anti-EGFR antibodies that may be used to engineer bispecific molecules are for example panitumumab (ABX-EGF), nimotuzumab, necitumumab, matuzumab, and those described for example in: U.S. Pat. No. US7,595,378, U.S. Pat. No. US7,247,301, U.S. Pat. Publ. No. US2011/0256142, U.S. Pat. No. US5,891,996, U.S. Pat. No. US5,212,290, U.S. Pat. No. US5,558,864, or U.S. Pat. No. US7,589,180. For example, antibody VH domain having the amino acid sequence shown in SEQ ID NO: 189 or 191 and antibody VL domain having the amino acid sequences shown in SEQ ID NO: 190 or 192 may be used.

Exemplary anti-c-Met antibodies that may be used to engineer bispecific molecules are for example Rilotumumab, Onartuzumab, Ficlatuzumab, and those described for example in PCT Intl. Publ. No. WO2011/110642, US Pat. Publ. No. US2004/0166544, PCT Intl. Publ. No. WO2005/016382, or PCT Intl. Publ. No. WO2006/015371. For example, antibody VH domain having the amino acid sequence shown in SEQ ID NO: 193 or 195 and antibody VL domain having the amino acid sequences shown in SEQ ID NO: 194 or 196 may be used. The heavy and light chain amino acid sequences of the antibodies identified by their United States Adopted Names (USAN) is available via the American Medical Association at http://_www_ama-assn_org or via the CAS registry.

Monospecific EGFR and c-Met biding variable domains may be selected *de novo* from for example a phage display library, where the phage is engineered to express human immunoglobulins or portions thereof such as Fabs, single chain antibodies (scFv), or unpaired or paired antibody variable regions (Knappik *et al.*, J Mol Biol 296:57-86, 2000;

Krebs *et al.,* J Immunol Meth 254:67-84, 2001; Vaughan *et al.,* Nature Biotechnology 14:309-314, 1996; Sheets *et al.,* PITAS (USA) 95:6157-6162, 1998; Hoogenboom and Winter, J Mol Biol 227:381, 1991; Marks *et al.,* J Mol Biol 222:581, 1991), and subsequently engineered into a bispecific format. The monospecific EGFR and c-Met binding variable domains may be isolated for example from phage display libraries expressing antibody heavy and light chain variable regions as fusion proteins with bacteriophage pIX coat protein as described in Shi *et al* (2010) *J. Mol. Biol.* 397:385-96 and PCT Intl. Publ. No. WO09/085462). The antibody libraries are screened for binding to human EGFR or c-Met extracellular domains and the obtained positive clones are further characterized and the Fabs isolated from the clone lysates. Such phage display methods for isolating human antibodies are established in the art. See for example: US Pat. No. 5,223,409; US Pat. No. 5,403,484; and US Pat. No. 5,571,698, US Pat. No. 5,427,908, US Pat. No. 5, 580,717, US Pat. No. 5,969,108, US Pat. No. 6,172,197, US Pat. No. 5,885,793; US Pat. No. 6,521,404; US Pat. No. 6,544,731; US Pat. No. 6,555,313; US Pat. No. 6,582,915 and US Pat. No. 6,593,081. The obtained *de novo* variable regions binding EGFR or c-Met are engineered to bispecific formats using the methods described herein.

Bispecific antibody formats

Antibodies of the present invention have two or more antigen binding sites and are bispecific. Bispecific antibodies of the invention include antibodies having a full length antibody structure.

"Full length antibody" as used herein refers to an antibody having two full length antibody heavy chains and two full length antibody light chains. A full length antibody heavy chain (HC) consists of well known heavy chain variable and constant domains VH, CH1, CH2, and CH3. A full length antibody light chain (LC) consists of well known light chain variable and constant domains VL and CL. The full length antibody may be lacking the C-terminal lysine (K) in either one or both heavy chains.

The term "Fab-arm" or "half molecule" refers to one heavy chain-light chain pair that specifically binds an antigen.

Full length bispecific antibodies of the invention may be generated for example using Fab arm exchange (or half molecule exchange) between two monospecific bivalent antibodies by introducing substitutions at the heavy chain CH3 interface in each half molecule to favor heterodimer formation of two antibody half molecules having distinct

specificity either *in vitro* in cell-free environment or using co-expression. The Fab arm exchange reaction is the result of a disulfide-bond isomerization reaction and dissociation-association of CH3 domains. The heavy- chain disulfide bonds in the hinge regions of the parent monospecific antibodies are reduced. The resulting free cysteines of one of the parent monospecific antibodies form an inter heavy-chain disulfide bond with cysteine residues of a second parent monospecific antibody molecule and simultaneously CH3 domains of the parent antibodies release and reform by dissociation-association. The CH3 domains of the Fab arms may be engineered to favor heterodimerization over homodimerization. The resulting product is a bispecific antibody having two Fab arms or half molecules which each bind a distinct epitope, i.e. an epitope on EGFR and an epitope on c-Met.

"Homodimerization" as used herein refers to an interaction of two heavy chains having identical CH3 amino acid sequences. "Homodimer" as used herein refers to an antibody having two heavy chains with identical CH3 amino acid sequences.

"Heterodimerization" as used herein refers to an interaction of two heavy chains having non-identical CH3 amino acid sequences. "Heterodimer" as used herein refers to an antibody having two heavy chains with non-identical CH3 amino acid sequences.

The "knob-in-hole" strategy (see, e.g., PCT Intl. Publ. No. WO 2006/028936) may be used to generate full length bispecific antibodies. Briefly, selected amino acids forming the interface of the CH3 domains in human IgG can be mutated at positions affecting CH3 domain interactions to promote heterodimer formation. An amino acid with a small side chain (hole) is introduced into a heavy chain of an antibody specifically binding a first antigen and an amino acid with a large side chain (knob) is introduced into a heavy chain of an antibody specifically binding a second antigen. After co-expression of the two antibodies, a heterodimer is formed as a result of the preferential interaction of the heavy chain with a "hole" with the heavy chain with a "knob". Exemplary CH3 substitution pairs forming a knob and a hole are (expressed as modified position in the first CH3 domain of the first heavy chain/ modified position in the second CH3 domain of the second heavy chain): T366Y/F405A, T366W/F405W, F405W/Y407A, T394W/Y407T, T394S/Y407A, T366W/T394S, F405W/T394S and T366W/T366S_L368A_Y407V.

Other strategies such as promoting heavy chain heterodimerization using electrostatic interactions by substituting positively charged residues at one CH3 surface and negatively charged residues at a second CH3 surface may be used, as described in US Pat. Publ. No. US2010/0015133; US Pat. Publ. No. US2009/0182127; US Pat. Publ. No. US2010/028637 or US Pat. Publ. No. US2011/0123532. In other strategies,

heterodimerization may be promoted by following substitutions (expressed as modified position in the first CH3 domain of the first heavy chain/ modified position in the second CH3 domain of the second heavy chain): L351Y_F405A_Y407V/T394W, T366I_K392M_T394W/F405A_Y407V, T366L_K392M_T394W/F405A_Y407V, L351Y_Y407A/T366A_K409F, L351Y_Y407A/T366V_K409F, Y407A/T366A_K409F, or T350V_L351Y_F405A_Y407V/T350V_T366L_K392L_T394W as described in U.S. Pat. Publ. No. US2012/0149876 or U.S. Pat. Publ. No. US2013/0195849

In addition to methods described above, bispecific antibodies of the invention may be generated *in vitro* in a cell-free environment by introducing asymmetrical mutations in the CH3 regions of two monospecific homodimeric antibodies and forming the bispecific heterodimeric antibody from two parent monospecific homodimeric antibodies in reducing conditions to allow disulfide bond isomerization according to methods described in Intl.Pat. Publ. No. WO2011/131746. In the methods, the first monospecific bivalent antibody (e.g., anti-c-Met antibody) and the second monospecific bivalent antibody (e.g., anti-EGFR antibody) are engineered to have certain substitutions at the CH3 domain that promoter heterodimer stability; the antibodies are incubated together under reducing conditions sufficient to allow the cysteines in the hinge region to undergo disulfide bond isomerization; thereby generating the bispecific antibody by Fab arm exchange. The incubation conditions may optimally be restored to non-reducing. Exemplary reducing agents that may be used are 2- mercaptoethylamine (2-MEA), dithiothreitol (DTT), dithioerythritol (DTE), glutathione, tris(2-carboxyethyl)phosphine (TCEP), L-cysteine and beta-mercaptoethanol, preferably a reducing agent selected from the group consisting of: 2- mercaptoethylamine, dithiothreitol and tris(2-carboxyethyl)phosphine. For example, incubation for at least 90 min at a temperature of at least 20°C in the presence of at least 25 mM 2-MEA or in the presence of at least 0.5 mM dithiothreitol at a pH of from 5-8, for example at pH of 7.0 or at pH of 7.4 may be used.

Bispecific EGFR/c-Met antibodies

The bispecific EGFR/c-Met antibodies of the invention may provide a benefit in terms of specificity and reduced off-target toxicity when compared to small molecule EGFR and/or c-Met inhibitors. The present invention is based at least in part on the surprising finding that the bispecific EGFR/c-Met antibodies of the invention provide a significantly improved synergistic inhibitory effect when compared to a mixture of EGFR-binding and c-Met-binding monospecific antibodies or published bispecific EGFR/c-Met

antibodies. Depending on the assay, the synergistic effect observed varied between about 14- to over about 800-fold. The bispecific EGFR/c-Met antibodies of the invention provide more efficient inhibition of EGFR and c-Met signaling pathways and inhibit tumor growth more efficiently than cetuximab (Erbitux®). The bispecific EGFR/c-Met antibodies of the invention inhibit EGFR signaling in tumors and/or tumor cell ines having EGFR activating mutations and/or mutations in EGFR that are known to result in resistance to treatments with tyrosine kinase inhibitors such as gefitinib, and inhibit c-Met signaling pathway, a pathway identified to be upregulated and to provide a compensatory signaling upon treatment with EGFR tyrosine kinase inhibitors in cancers such as NSCLC. The bispecific EGFR/c-Met antibodies of the invention, in addition to directly inhibiting EGFR and c-Met signaling, display antitumor activity through enhanced antibody dependent cell cytotoxicity (ADCC) and degradation of the EGFR and c-Met receptors. Contrary to the current EGFR therapies (cetuximab and panitumumab), the bispecific EGFR/c-Met antibodies of the invention induce, via enhanced ADCC, killing of tumor cells having KRAS mutations.

Int. Pat. Publ. No. WO2010/115551 describes a bispecific EGFR/c-Met antibody (BSAB01) engineered in an IgG-scFv format using the EGFR bindingVH/VL pair of cetuximab, and the c-Met binding VH/VL pair of an antibody 5D5 (MetMab, onartuzumab) currently in Phase III trials. BSAB01 demonstrates approximately two-fold (additive) increased inhibition of A431 cell proliferation when compared to the parental antibodies (Example 7, Figure 8b in WO2010/115551), and a modest additive inhibition of Ovarc-8 cell proliferation (Figure 10a, Example 16 in WO2010/115551) when compared to the combination of the two parental antibodies (15% vs. 10% inhibition). Therefore, surprisingly and unexpectedly, the present invention provides bispecific EGFR/c-Met antibodies that demonstrate a significant synergistic effect in inhibition of EGFR and c-Met signaling, cancer cell survival and tumor growth. By not wishing to be bound by any theory, it is believed that the significant synergistic effect of the bispecific antibodies of the invention at least partially results from the epitope specificity of both the EGFR and the c-Met binding arms, possibly resulting in the inhibition of signaling through not only the EGFR and c-Met homodimers but also the EGFR/HERx heterodimers.

One embodiment of the invention is an isolated bispecific epidermal growth factor receptor (EGFR)/ hepatocyte growth factor receptor (c-Met) antibody, comprising:

a) a first heavy chain (HC1) comprising a HC1 constant domain 3 (HC1 CH3) and a HC1 variable region 1 (VH1);

b) a second heavy chain (HC2) comprising a HC2 constant domain 3 (HC2 CH3) and a HC2 variable region 2 (VH2);

c) a first light chain (LC1) comprising a light chain variable region 1 (VL1); and a second light chain (LC2) comprising a light chain variable region 2 (VL2),

wherein the VH1 and the VL1 pair to form a first antigen-binding site that specifically binds EGFR and the VH2 and the VL2 pair to form a second antigen-binding site that specifically binds c-Met, wherein the HC1 comprises at least one substitution in the HC1 CH3 and the HC2 comprises at least one substitution in the HC2 CH3, wherein the substitution in the HC1 CH3 and the substitution in the HC2 CH3 occur at different amino acid residue positions, when residue numbering is according to the EU index.

In some embodiments described herein, the bispecific EGFR/c-Met antibody inhibits phosphorylation of extracellular signal-related kinases 1 and 2 (ERK1/2) in NCI-H292, NCI-H1975 or SKMES-1 cell line with an IC_{50} value that is at least about 10-fold less, at least about 20-fold less, at least about 30-fold less, at least about 40-fold less, at least about 50-fold less or at least about 60-fold less when compared to the IC_{50} value of inhibition of phosphorylation of ERK1/2 in NCI-H292, NCI-H1975 or SKMES-1 cell line with a mixture of a control monovalent EGFR antibody comprising a heavy chain 3 (HC3) and a light chain 3 (LC3) and a control monovalent c-Met antibody comprising a heavy chain 4 (HC4) and a light chain 4 (LC4), wherein the HC3 and the HC1, the LC3 and the LC1, the HC4 and the HC2, and the LC4 and the LC2 have identical amino acid sequences, respectively, and the phosphorylation of ERK1/2 is measured in whole cell lysates using a sandwich immunoassay using an anti-phosphoERK1/2 antibody as a capture antibody and an antibody binding to unphosphorylated and phosphorylated ERK1/2 conjugated with an electrochemiluminescent compound as a detection antibody. The bispecific EGFR/c-Met antibodies of the invention provide a synergistic more pronounced inhibition of EGFR and c-Met signaling when compared to the combination of monospecific EGFR antibodies and monospecific c-Met antibodies, when inhibition is assessed by inhibition of ERK1/2 phosphorylation. Such exemplary bispecific EGFR/c-Met antibody is the antibody EM1-mAb of the invention.

"Control monospecific EGFR antibody" as used herein refers to an antibody that has a first Fab arm that binds EGFR that is identical in amino acid sequence to the EGFR-binding Fab arm of the bispecific EGFR/c-Met antibody to be tested, and has a second Fab arm that is "inert" and binds an unrelated/irrelevant antigen, human immunodeficiency virus (HIV) gp120. The second Fab arm has a light chain having the sequence of SEQ ID

NO: 209 and a heavy chain having the sequence of SEQ ID NO: 198 in instances when the EGFR binding Fab arm in the bispecific EGFR/c-Met antibody to be tested comprises the F405L substitution. The second Fab arm has a light chain having the sequence of SEQ ID NO: 209 and a heavy chain having the sequence of SEQ ID NO: 197 in instances when the EGFR binding Fab arm in the bispecific EGFR/c-Met antibody to be tested comprises the K409R substitution.

"Control monospecific c-Met antibody" as used herein refers to an antibody that has a first Fab arm that binds c-Met that is identical in amino acid sequence to the c-Met-binding Fab arm of the bispecific EGFR/c-Met antibody to be tested, and has a second Fab arm that is "inert" and binds the unrelated/irrelevant antigen HIV gp120. The second Fab Fab arm has a light chain having the sequence of SEQ ID NO: 209 and a heavy chain having the sequence of SEQ ID NO: 198 in instances when the c-Met binding Fab arm in the bispecific EGFR/c-Met antibody to be tested comprises the F405L substitution. The second inert Fab arm has a light chain having the sequence of SEQ ID NO: 209 and a heavy chain having the sequence of SEQ ID NO: 197 in instances when the c-Met binding Fab arm in the bispecific EGFR/c-Met antibody to be tested comprises the K409R substitution.

In some embodiments described herein, the bispecific EGFR/c-Met antibody inhibits phosphorylation of ERK1/2 with an IC_{50} value of about $2x10^{-9}$ M or less, about $1x10^{-9}$ M or less, or about $1x10^{-10}$ M or less.

In some embodiments described herein, ERK1 is phosphorylated at residues Thr202 and Tyr204, and ERK2 is phosphorylated at residues Thr185 and Tyr197.

In some embodiments described herein, the bispecific EGFR/c-Met antibody inhibits phosphorylation of protein kinase B (AKT) at Ser473 in NCI-H1975 cell line with an IC_{50} value that is at least about 70-fold less when compared to the IC_{50} value of inhibition of phosphorylation of AKT at Ser473 in NCI- H1975 cell line with the mixture of the control monovalent EGFR antibody comprising the HC3 and the LC3 and the control monovalent c-Met antibody comprising the HC4 and the LC4, wherein the HC3 and the HC1, the LC3 and the LC1, the HC4 and the HC2, and the LC4 and the LC2 have identical amino acid sequences, respectively, wherein the phosphorylation of AKT at Ser473 is measured in whole cell lysates using a sandwich immunoassay using an antibody binding to unphosphorylated and phosphorylated AKT as a capture antibody and an anti-phosphoAKT Ser473 antibody conjugated to an electrochemiluminescent compound as a detection antibody.

In some embodiments described herein, the bispecific EGFR/c-Met antibody inhibits phosphorylation of protein kinase B (AKT) at Thr308 in NCI-H1975 cell line with an IC_{50} value that is at least about 100-fold less when compared to the IC_{50} value of inhibition of phosphorylation of AKT at Thr308 in NCI- H1975 cell line with the mixture of the control monovalent EGFR antibody comprising the HC3 and the LC3 and the control monovalent c-Met antibody comprising the HC4 and the LC4, wherein the HC3 and the HC1, the LC3 and the LC1, the HC4 and the HC2, and the LC4 and the LC2 have identical amino acid sequences, respectively, wherein the phosphorylation of AKT at Thr308 is measured in whole cell lysates using a sandwich immunoassay using an antibody binding to unphosphorylated and phosphorylated AKT as a capture antibody and an anti-phosphoAKT Thr308 antibody conjugated to an electrochemiluminescent compound as a detection antibody.

The bispecific EGFR/c-Met antibodies of the invention provide a synergistic more pronounced inhibition of EGFR and c-Met signaling when compared to the combination of monospecific EGFR antibodies and monospecific c-Met antibodies, when inhibition is assessed by inhibition of AKT phosphorylation. Such exemplary bispecific EGFR/c-Met antibody is the antibody EM1-mAb of the invention.

In some embodiments described herein, the bispecific EGFR/c-Met antibody inhibits phosphorylation of AKT at Ser473 or at Thr308 with and IC_{50} value of about $1x10^{-9}$ M or less.

In some embodiments described herein, the bispecific EGFR/c-Met antibody binds EGFR of SEQ ID NO: 73 at EGFR residues K489, I491, K467 and S492 and c-Met at residues PEFRDSYPIKYVHAF (SEQ ID NO: 238) and FAQSKPDSAEPMDRSA (SEQ ID NO: 239). Such an exemplary bispecific antibody is the EM1-mAb. The bispecific EM-1 antibody binds EGFR and c-Met at distinct epitopes when compared to the antibody BSAB01 as described above and in Int. Pat. Publ. No. WO2010/115551. The parental EGFR binding arm (cetuximab) of BSAB01 binds EGFR amino acid residues R353, Q384, Q408, H409, F412, S418, S440, K443, K465, I467, S468, and N473 in mature EGFR, corresponding to residues R367, Q408, Q432, H433, F436, S442, S464, K467, K489, I491, S492 and N497 of full length EGFR of SEQ ID NO: 73 (Li *et al.*, Cancer Cell 7:301-311, 2005). The parental c-Met binding arm of BSAB01 (mAb 5D5) binds c-Met residues 325-340 PGAQLARQIGASLNDD (SEQ ID NO: 240). Epitope mapping of the EGFR binding parental antibody (2F8) of the EM1-mAb is described in US. Pat. Publ. No.

US2011/0256142A1. Cetuximab and the parental 2F8 antibody bind partially overlapping but distinct epitopes.

Epitope mapping can be done using standard methods. For example, when the structures of both individual components are known, *in silico* protein-protein docking can be carried out to identify compatible sites of interaction. Hydrogen-deuterium (H/D) exchange can be carried out with the antigen and antibody complex to map regions on the antigen that may be bound by the antibody. Segment and point mutagenesis of the antigen can be used to locate amino acids important for antibody binding.

In some embodiments described herein, the bispecific EGFR/c-Met antibody neutralizes EGFR and c-Met signaling.

The bispecific EGFR/c-Met antibody of the invention may neutralize EGFR and c-Met signaling by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to the level of signaling in the absence of the bispecific EGFR/c-Met molecule of the invention using the same assay conditions.

Binding of a ligand such as EGF to EGFR stimulates receptor dimerization, autophosphorylation, activation of the receptor's internal, cytoplasmic tyrosine kinase domain, and initiation of multiple signal transduction and transactivation pathways involved in regulation of DNA synthesis (gene activation) and cell cycle progression or division. Neutralization of EGFR signaling may result in inhibition in one or more EGFR downstream signaling pathways and therefore neutralizing EGFR may have various effects, including inhibition of cell proliferation and differentiation, angiogenesis, cell motility and metastasis, and inhibition of downstream signaling pathways.

EGFR signaling and neutralization of EGFR signaling may be measured using various well know methods, for example measuring the autophosphorylation of the receptor at any of the tyrosines Y1068, Y1148, and Y1173 (Downward *et al.,* Nature 311:483-5, 1984) and/or phosphorylation of natural or synthetic substrates, and inhibition of autophosphorylation and/or phosphorylation of natural or synthetic substrates by the bispecific antibodies of the invention. Phosphorylation can be detected using well known methods such as an ELISA assay or a western plot using a phosphotyrosine specific antibody. Exemplary assays can be found in Panek *et al.,* J Pharmacol Exp Thera 283:1433-44, 1997 and Batley *et al.,* Life Sci 62:143-50, 1998, and as described herein.

Binding of HGF to c-Met stimulates receptor dimerization, autophosphorylation, activation of the receptor's cytoplasmic tyrosine kinase domain, and initiation of multiple

signal transduction and transactivation pathways involved in regulation of DNA synthesis (gene activation) and cell cycle progression or division. Inhibition of c-Met signaling may result in inhibition in one or more c-Met downstream signaling pathways and therefore neutralizing c-Met may have various effects, including inhibition of cell proliferation and differentiation, angiogenesis, cell motility and metastasis.

c-Met signaling and neutralization of c-Met signaling may be measured using various well know methods, for example measuring the autophosphorylation of the receptor on at least one tyrosine residues Y1230, Y1234,Y1235 or Y1349, and/or phosphorylation of natural or synthetic substrates. Phosphorylation can be detected, for example, using an antibody specific for phosphotyrosine in an ELISA assay or on a western blot. Exemplary assays can be found in Panek *et al.*, J Pharmacol Exp Thera 283:1433-44, 1997 and Batley *et al.*, Life Sci 62:143-50, 1998, and as described herein.

EGFR and c-Met signaling may be measured using various well know methods as described herein, such as measuring inhibition of ERK1/2 and AKT phosphorylation. Inhibition of ERK1 phosphorylation at Thr202 and Tyr204 and ERK2 phosphorylation at Thr185 and Tyr187 and inhibition of AKT at Ser473 or Thr308 can be measured for example in NCI-H1975 cell lysates utilizing a sandwich assay with capture antibody coated on solid support, and the detection antibody conjugated with an electrohemiluminescent compound such as Meso Scale Discover (MSD) SULFO-TAG label, followed by detection of the signal with a plate reader.

In some embodiments described herein, the bispecific EGFR/c-Met antibody inhibits growth of NCI-H292 or NCI-H1975 cells with an IC_{50} value that is at least about 300-fold less, at least about 400-fold less, at least about 500-fold less, at least about 600-fold less, at least about 700-fold less or at least about 800-fold less when compared to the IC_{50} value of inhibition of growth of NCI-H292 or NCI-H1975 cells with cetuximab, when NCI-H292 or NCI-H1975 cells are grown in low attachment conditions.

Inhibition of cell growth may be assessed by known methods. For example, the cells may be plated in plates coated with hydrogels or biomimetic polymers (for example Ultra Low Attachment plates by Corning) to prevent or reduce cell attachment, and the effect of antibodies on 7.5 ng/mL HGF-induced cell growth can be assessed by measuring percent cell viability after incubation for 72 hours using standard methods.

The bispecific EGFR/c-Met antibodies of the invention provide a synergistic more pronounced inhibition of EGFR and/or c-Met expressing cancer cells when compared to the combination of monospecific EGFR antibodies and monospecific c-Met antibodies and

to the standard of care cetuximab. Such an exemplary bispecific EGFR/c-Met antibody is the antibody EM1-mAb of the invention. The bispecific EGFR/c-Met antibodies of the invention inhibit cancer cells that express the wild type EGFR and the wild type c-Met, and also cancer cells that express the EGFR L858R/T790M mutant, which mutation is identified to contribute to resistance to treatments with small molecule tyrosine kinase inhibitors (TKIs) such as gefitinib. Therefore the bispecific EGFR/c-Met antibodies of the invention may provide a benefit in a broader patient population when compared to cetuximab and TKIs.

In some embodiments described herein, the bispecific EGFR/c-Met antibody inhibits growth of HGF-expressing SKMES-1 cell tumor in SCID Beige mice with a percentage (%) T/C value of at least 500-fold less on day 36 when compared to cetuximab, when the bispecific antibody and cetuximab are administered at 20 mg/kg dose.

Tumor xenograft models using SCID Beige mice are well known. SKMES-1 cells may be engineered to express human HGF using standard methods. Typically, SCID Beige mice may be subcutaneously inoculated with SKMES-1 cells expressing human HGF embedded in extracellular matrix such as Culturex in the dorsal flank of each animal. One week after implantation, mice may be stratified into groups with equivalent tumor volumes, and thereafter dosed for example three times per week with the bispecific EGFR/c-Met antibodies of the invention, control or benchmark antibodies or small molecules. Tumor volumes may be recorded twice weekly, and tumor growth inhibition (TGI) may be observed by calculating the percentage (%) T/C value. The % T/C value is indicative of anti-tumor efficacy. T and C are the mean volumes of the treated and control groups, respectively, on a given day.

The bispecific EGFR/c-Met antibodies of the invention provide a significantly improved efficacy in *in vivo* tumor killing when compared to the standard of care cetuximab, and therefore may provide a benefit in a patient population when compared to cetuximab.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the HC1 and the HC2 of IgG1, IgG2, IgG3 or IgG4 isotype.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the HC1 and the HC2 of IgG1 isotype.

In some embodiments described herein, the bispecific EGFR/c-Met antibody HC1 CH3 comprises at least one, two, three, four, five, six, seven or eight substitutions and the

HC2 CH3 comprises at least one, two, three, four, five, six, seven or eight substitutions at residue positions 350, 366, 368, 370, 399, 405, 407 or 409, when residue numbering is according to the EU index.

In some embodiments described herein, the bispecific EGFR/c-Met antibody HC1 CH3 comprises at least one, two, three or four substitutions and the HC2 CH3 comprises at least one, two, three or four substitutions at residue positions 350, 370, 405 or 409, when residue numbering is according to the EU index.

Antibody domains and numbering are well known. Two CH3 domains (or CH3 regions) are non-identical when they differ with at least one amino acid substitution from each other. An IgG1 CH3 region typically consists of residues 341-446 on IgG1 (residue numbering according to the EU index). An exemplary IgG1 constant region is shown in SEQ ID NO: 203. The CH3 domain spans residues 224-329 of SEQ ID NO: 203, and correspond to residues 341-446 according to EU index.

In some embodiments described herein, the bispecific EGFR/c-Met antibody HC1 CH3 comprises at least one substitution and the HC2 CH3 comprises at least one substitution at residue positions 405 or 409, when residue numbering is according to the EU index.

In some embodiments described herein, the bispecific EGFR/c-Met antibody HC1 CH3 comprises a K409R or a F405L substitution and the HC2 CH3 comprises a K409R or a F405L substitution, wherein residue numbering is according to the EU index.

In some embodiments described herein, the bispecific EGFR/c-Met antibody HC1 CH3 comprises the F405L substitution and the HC2 CH3 comprises the K409R substitution.

In some embodiments described herein, the HC1 CH3 and the HC2 CH3 substitutions are substitutions at position 366, 368, 370, 399, 405, 407 or 409 (numbering according to the EU index). These positions correspond to linear residue positions 248, 250, 252, 281, 287, 289 and 291, respectively, in a heavy chain constant region of SEQ ID NO: 203 and 204.

In some embodiments described herein, the HC1 CH3 position 409 has an amino acid substitution other than Lys, Leu or Met and the HC2 CH3 position 405 has an amino acid substitution other than Phe.

In some embodiments described herein, the HC1 CH3 position 405 has an amino acid substitution other than Phe and the HC2 CH3 position 409 has an amino acid substitution other than Lys, Leu or Met.

In some embodiments described herein, the HC1 CH3 position 409 has an amino acid substitution other than Lys, Leu or Met and the HC2 CH3 position 405 has an amino acid substitution other than Phe, Arg or Gly.

In some embodiments described herein, the HC1 CH3 position 405 has an amino acid substitution other than Phe, Arg or Gly and the HC2 CH3 position 409 has an amino acid substitution other than Lys, Leu or Met

In some embodiments described herein, the HC1 CH3 has Phe at position 405 and an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has an amino acid other than Phe at position 405 and a Lys at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Phe at position 405 and Lys at position 409 and the HC2 CH3 has Phe at position 405 and an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Phe at position 405 and an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has a substitution other than Phe, Arg or Gly at position 405 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has a substitution other than Phe, Arg or Gly at position 405 and Lys at position 409 and the HC2 CH3 has Phe at position 405 and an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Phe at position 405 and an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has Leu at position 405 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has Leu at position 405 and Lys at position 409 and the HC2 CH3 has Phe at position 405 and an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Phe at position 405 and aArg at position 409 and the HC2 CH3 has an amino acid other than Phe, Arg or Gly at position 405 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Phe, Arg or Gly at position 405 and Lys at position 409 and the HC2 CH3 has Phe at position 405 and Arg at position 409.

In some embodiments described herein, the HC1 CH3 has Phe at position 405 and Arg at position 409 and the HC2 CH3 has Leu at position 405 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has Leu at position 405 and Lys at position 409 and the HC2 CH3 has Phe at position 405 and Arg at position 409.

In some embodiments described herein, the HC1 CH3 has Phe at position 405 and Lys at position 409 and the HC2 CH3 has Leu at position 405 and aArg at position 409.

In some embodiments described herein, the HC1 CH3 has Leu at position 405 and aArg at position 409 and the HC2 CH3 has Phe at position 405 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has Lys at position 409, Thr at position 370 and Leu at position 405.

In some embodiments described herein, the HC1 CH3 has Lys at position 409, Thr at position 370 and Leu at position 405 and the HC2 CH3 has an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Arg at position 409 and the HC2 CH3 has Lys at position 409, Thr at position 370 and Leu at position 405.

In some embodiments described herein, the HC1 CH3 has Lys at position 409, Thr at position 370 and Leu at position 405 and the HC2 CH3 has Arg at position 409.

In some embodiments described herein, the HC1 CH3 has Lys at position 370, Phe at position 405 and aArg at position 409 and the HC2 CH3 has Lys at position 409, Thr at position 370 and Leu at position 405.

In some embodiments described herein, the HC1 CH3 has Lys at position 409, Thr at position 370 and Leu at position 405 and the HC2 CH3 has Lys at position 370, Phe at position 405 and Arg at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has an amino acid other than Tyr, Asp, Glu, Phe, Lys, Gln, Arg, Ser or Thr at position 407.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Tyr, Asp, Glu, Phe, Lys, Gln, Arg, Ser or Thr at position 407 and the HC2 CH3 has an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has Ala, Gly, His, Ile, Leu, Met, Asn, Val or Trp at position 407.

In some embodiments described herein, the HC1 CH3 has Ala, Gly, His, Ile, Leu, Met, Asn, Val or Trp at position 407 and the HC2 CH3 has an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has Gly, Leu, Met, Asn or Trp at position 407.

In some embodiments described herein, the HC1 CH3 has Gly, Leu, Met, Asn or Trp at position 407 and the HC2 CH3 has an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Tyr at position 407 and an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has an amino acid other than Tyr, Asp, Glu, Phe, Lys, Gln, Arg, Ser or Thr at position 407 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Tyr, Asp, Glu, Phe, Lys, Gln, Arg, Ser or Thr at position 407 and Lys at position 409 and the HC2 CH3 has Tyr at position 407 and an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Tyr at position 407 and an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has Ala, Gly, His, Ile, Leu, Met, Asn, Val or Trp at position 407 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has Ala, Gly, His, Ile, Leu, Met, Asn, Val or Trp at position 407 and Lys at position 409 and the HC2 CH3 has Tyr at position 407 and an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Tyr at position 407 and an amino acid other than Lys, Leu or Met at position 409 and the HC2 CH3 has Gly, Leu, Met, Asn or Trp at position 407 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has Gly, Leu, Met, Asn or Trp at position 407 and Lys at position 409 and the HC2 CH3 has Tyr at position 407 and an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Tyr at position 407 and Arg at position 409 and the HC2 CH3 has an amino acid other than Tyr, Asp, Glu, Phe, Lys, Gln, Arg, Ser or Thr at position 407 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Tyr, Asp, Glu, Phe, Lys, Gln, Arg, Ser or Thr at position 407 and Lys at position 409 and the HC2 CH3 has Tyr at position 407 and Arg at position 409.

In some embodiments described herein, the HC1 CH3 has Tyr at position 407 and Arg at position 409 and the HC2 CH3 has Ala, Gly, His, Ile, Leu, Met, Asn, Val or Trp at position 407 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has Ala, Gly, His, Ile, Leu, Met, Asn, Val or Trp at position 407 and Lys at position 409 and the HC2 CH3 has Tyr at position 407 and Arg at position 409.

In some embodiments described herein, the HC1 CH3 has Tyr at position 407 and Arg at position 409 and the HC2 CH3 has Gly, Leu, Met, Asn or Trp at position 407 and Lys at position 409.

In some embodiments described herein, the HC1 CH3 has Gly, Leu, Met, Asn or Trp at position 407 and Lys at position 409 and the HC2 CH3 has Tyr at position 407 and Arg at position 409.

In some embodiments described herein, the HC1 CH3 has an amino acid other than Lys, Leu or Met at position 409, and the HC2 CH3 has (i) an amino acid other than Phe, Leu and Met at position 368, or (ii) a Trp at position 370, or (iii) an amino acid other than Asp, Cys, Pro, Glu or Gln at position 399.

In some embodiments described herein, the HC1 CH3 has (i) an amino acid other than Phe, Leu and Met at position 368, or (ii) a Trp at position 370, or (iii) an amino acid other than Asp, Cys, Pro, Glu or Gln at position 399 and the HC2 CH3 has an amino acid other than Lys, Leu or Met at position 409.

In some embodiments described herein, the HC1 CH3 has Arg, Ala, His or Gly at position 409, and the HC2 CH3 has (i) Lys, Gln, Ala, Asp, Glu, Gly, His, Ile, Asn, Arg, Ser, Thr, Val, or Trp at position 368, or (ii) Trp at position 370, or (iii) Ala, Gly, Ile, Leu, Met, Asn, Ser, Thr, Trp, Phe, His, Lys, Arg or Tyr at position 399.

In some embodiments described herein, the HC1 CH3 has (i) Lys, Gln, Ala, Asp, Glu, Gly, His, Ile, Asn, Arg, Ser, Thr, Val, or Trp at position 368, or (ii) Trp at position 370, or (iii) Ala, Gly, Ile, Leu, Met, Asn, Ser, Thr, Trp, Phe, His, Lys, Arg or Tyr at position 399 and the HC2 CH3 has Arg, Ala, His or Gly at position 409.

In some embodiments described herein, the HC1 CH3 has Arg at position 409, and the HC2 CH3 has (i) Asp, Glu, Gly, Asn, Arg, Ser, Thr, Val, or Trp at position 368, or (ii) Trp at position 370, or (iii) Phe, His, Lys, Arg or Tyr at position 399.

In some embodiments described herein, the HC1 CH3 has (i) Asp, Glu, Gly, Asn, Arg, Ser, Thr, Val, or Trp at position 368, or (ii) Trp at position 370, or (iii) Phe, His, Lys, Arg or Tyr at position 399 and the HC2 CH3 has Arg at position 409.

In some embodiments described herein, the HC1 CH3 comprises a K409R substitution or a F405L substitution and the HC2 CH3 comprises a K409R substitution or a F405L substitution, wherein the residue numbering is according to the EU index.

In some embodiments described herein, the HC1 CH3 comprises the F405L substitution and the HC2 CH3 comprises the K409R substitution.

Substitutions are typically made at the DNA level to a molecule such as the constant domain of the antibody using standard methods.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the VH1 and the VL1, wherein

the VH1 comprises the heavy chain complementarity determining region (HCDR) 1 (HCDR1), HCDR 2 (HCDR2) and HCDR 3 (HCDR3) amino acid sequences of SEQ ID NOs: 210, 211 and 212, respectively; and

the VL1 comprises the light chain complementarity determining region (LCDR) 1 (LCDR1), LCDR 2 (LCDR2) and LCDR 3 (LCDR3) amino acid sequences of SEQ ID NOs: 213, 214 and 215, respectively.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the VH2 and the VL2, wherein

the VH2 comprises the HCDR1, the HCDR2, and the HCDR3 amino acid sequences of SEQ ID NOs: 216, 217 and 218, respectively; and

the VL2 comprises the LCDR1, the LCDR2 and the LCDR3 amino acid sequences of SEQ ID NOs: 219, 220 and 221, respectively.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the VH1, the VL1, the VH2 and the VL2 amino acid sequences of SEQ ID NOs: 189, 190, 193 and 194, respectively.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the HC1, the LC1, the HC2 and the LC2 amino acid sequences of SEQ ID NOs: 199, 200, 201 and 202, respectively, optionally having a C-terminal lysine removed from the HC1, the HC2, or both the HC1 and the HC2.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the VH1 and the VL1, wherein

the VH1 comprises the HCDR1, the HCDR2, and the HCDR3 amino acid sequences of SEQ ID NOs: 222, 223 and 224, respectively; and

the VL1 comprises the LCDR1, the LCDR2 and the LCDR3 amino acid sequences of SEQ ID NOs: 225, 226 and 227, respectively.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the VH2 and the VL2, wherein

the VH2 comprises the HCDR1, the HCDR2, and the HCDR3 amino acid sequences of SEQ ID NOs: 228, 229 and 230, respectively; and

the VL2 comprises the LCDR1, the LCDR2 and the LCDR3 amino acid sequences of SEQ ID NOs: 231, 232 and 233, respectively.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the VH1, the VL1, the VH2 and the VL2 amino acid sequences of SEQ ID NOs: 191, 192, 195 and 196, respectively.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the HC1, the LC1, the HC2 and the LC2 amino acid sequences of SEQ ID NOs: 234, 235, 236 and 237, respectively, optionally having the C-terminal lysine removed from the HC1, the HC2, or both the HC1 and the HC2.

In some embodiments described herein, the bispecific EGFR/c-Met antibodies may block EGF binding to the EGFR and HGF binding to c-Met with an IC_{50} value of less than about $1x10^{-8}$ M, less than about $1x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $1x10^{-11}$ M, or less than about $1x10^{-12}$ M in a competition assay employing recombinant human EGFR or recombinant human c-Met extracellular domains coated on plates and incubated with or without the bispecific EGFR/c-Met antibodies of the invention. The bispecific EGFR/c-Met antibodies described herein may block EGF binding to EGFR and HGF binding to c-Met by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% when compared to binding of EGF to the EGFR and HGF binding to c-Met in the absence of the bispecific EGFR/c-Met antibodies of the invention described herein using the same assay conditions.

In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises the HC1, LC1, HC2 and LC2, wherein the HC1, the LC1, the HC2 and the LC2 are encoded by synthetic polynucleotides comprising the sequence of SEQ ID NOs: 205, 206, 207 and 208, respectively.

The bispecific EGFR/c-Met antibodies of the invention may be generated using techniques described herein, such as utilizing CH3 engineering and generating the antibodies using *in vitro* Fab arm exchange. An exemplary bispecific antibody may be generated from two monospecific antibodies by combining about 1-20 mg/mL of each antibody at a 1:1 molar ratio in PBS at pH 7.0 – 7.4 in a buffer having a final concentration of 75 mM 2- mercaptoethanolamine (2-MEA), incubating for 2-6 hours at 25-37ºC, followed by removal of 2-MEA via dialysis, diafiltration, tangential flow filtration, and spinned cell filtration. The yield of the bispecific antibody may be more than about 80%, more than about 90%, more than about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%.

Some embodiments described herein provide for methods of producing the isolated bispecific EGFR/c-Met antibody, comprising:

combining an isolated monospecific bivalent anti-EGFR antibody comprising two heavy chains of SEQ ID NO: 199 and two light chains of SEQ ID NO: 200 and an isolated monospecific bivalent anti-c-Met antibody comprising two heavy chains of SEQ ID NO: 201 and two light chains of SEQ ID NO: 202 in a mixture of about 1:1 molar ratio;

introducing a reducing agent into the mixture;

incubating the mixture about ninety minutes to about six hours;

removing the reducing agent; and

purifying the bispecific EGFR/c-Met antibody that comprises a first heavy chain of SEQ ID NO: 199 and a second heavy chain of SEQ ID NO: 201, a first light chain of SEQ ID NO: 200 and a second light chain of SEQ ID NO: 202, wherein the first heavy chain of SEQ ID NO: 199 pairs with the first light chain of SEQ ID NO: 200 to form the first binding domain that specifically binds EGFR, and the second heavy chain of SEQ ID NO: 201 pairs with the second light chain of SEQ ID NO: 202 to form the second binding domain that specifically binds c-Met.

In some embodiments described herein, the reducing agent is 2-mercaptoethanolamine (2-MEA).

In some embodiments described herein, 2-MEA is present at a concentration of about 25 mM to about 75 mM.

In some embodiments described herein, the incubating step is performed at a temperature of about 25°C to about 37°C.

Some embodiments described herein provide for an isolated bispecific EGFR/-c-Met antibody comprising a HC1, a LC1, a HC2 and a LC2, wherein the HC1 comprises the sequence of SEQ ID NO: 199, the LC1 comprises the sequence of SEQ ID NO: 200, the HC2 comprises the sequence of SEQ ID NO: 201, and the LC2 comprises the sequence of SEQ ID NO: 202, wherein the HC1, the LC1, the HC2 and/or the LC2further comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 conservative amino acid substitutions.

Some embodiments described herein provide for an isolated bispecific EGFR/-c-Met antibody comprising the HC1, the LC1, the HC2 and the LC2, wherein the HC1 comprises the sequence of SEQ ID NO: 234, the LC1 comprises the sequence of SEQ ID

NO: 235, the HC2 comprises the sequence of SEQ ID NO: 236, and the LC2 comprises the sequence of SEQ ID NO: 237, wherein the HC1, the LC1, the HC2 and/or the LC2 further comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 conservative amino acid substitutions.

Bispecific EGFR/c-Met antibodies whose HC1, LC1, HC2 and LC2 amino acid sequences differ insubstantially from those antibodies disclosed herein are encompassed within the scope of the invention. Typically, this involves one or more conservative amino acid substitutions with an amino acid having similar charge, hydrophobic, or stereochemical characteristics in the antigen-binding sites or in the frameworks without adversely altering the properties of the antibody. Conservative substitutions may also be made to improve antibody properties, for example stability or affinity. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acid substitutions may be made for example to the VH1, the VL1, the VH2 and/or the VL2. For example, a "conservative amino acid substitution" may involve a substitution of a native amino acid residue with a nonnative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Furthermore, any native residue in the polypeptide may also be substituted with alanine, as has been previously described for alanine scanning mutagenesis (MacLennan *et al.*, Acta Physiol Scand Suppl 643:55-67, 1998; Sasaki *et al.*, Adv Biophys 35:1-24, 1998). Desired amino acid substitutions may be determined by those skilled in the art at the time such substitutions are desired. For example, amino acid substitutions can be used to identify important residues of the molecule sequence, or to increase or decrease the affinity of the molecules described herein. Exemplary conservative amino acid substitutions are described *supra*.

Amino acid substitutions may be done for example by PCR mutagenesis (U.S. Pat. No. 4,683,195). Libraries of variants may be generated using well known methods, for example using random (NNK) or non-random codons, for example DVK codons, which encode 11 amino acids (Ala, Cys, Asp, Glu, Gly, Lys, Asn, Arg, Ser, Tyr, Trp) and screening the libraries for variants with desired properties.

In some embodiments described herein, amino acid substitutions can be made to the constant region of the antibody. For example different IgG1 allotypes can be used in the bispecific EGFR/c-Met antibodies of the invention, such as well known G1m17 allotype, G1m3 allotype or G1m1 allotype, or a combination thereof.

In some embodiments described herein, pharmacokinetic properties of the bispecific EGFR/c-Met antibodies may be enhanced by substitutions in the Fc domain that modulate antibody halflife. In some embodiments described herein, the bispecific EGFR/c-Met antibody comprises a substitution M252Y/S254T/T256E in the HC1 and/or the HC2, wherein residue numbering is according to the EU index. M252Y/S254T/T256E substitutions have been show to increase antibody half life (Dall'Acqua *et al.*, J Biol Chem 281:23514–24, 2006).

The bispecific EGFR/c-Met antibodies having conservative substitutions and/or additional substitutions in their Fc region are tested for their characteristics using the methods described herein.

In some embodiment described herein, immune effector properties of the bispecific EGFR/c-Met antibodies may be enhanced or silenced through Fc modifications by techniques known to those skilled in the art. For example, Fc effector functions such as C1q binding, complement dependent cytotoxicity (CDC), antibody-dependent cell-mediated cytotoxicity (ADCC), antibody-dependent cell-mediated phagocytosis (ADCP), down regulation of cell surface receptors (e.g., B cell receptor; BCR), etc. may be provided and/or controlled by modifying residues in the Fc responsible for these activities.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a cell-mediated reaction in which non-specific cytotoxic cells that express Fc receptors (FcRs) (e.g. Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and subsequently cause lysis of the target cell.

The ability of monoclonal antibodies to induce ADCC can be enhanced by engineering their oligosaccharide component. Human IgG1 or IgG3 are N-glycosylated at Asn297 with the majority of the glycans in the well known biantennary G0, G0F, G1, G1F, G2 or G2F forms. Antibodies produced by non-engineered CHO cells typically have a glycan fucose content of about at least 85%. The removal of the core fucose from the biantennary complex-type oligosaccharides attached to the Fc regions enhances the ADCC of antibodies via improved FcγRIIIa binding without altering antigen binding or CDC activity. Such mAbs can be achieved using different methods reported to lead to the successful expression of relatively high defucosylated antibodies bearing the biantennary complex-type of Fc oligosaccharides such as control of culture osmolality (Konno *et al.*, Cytotechnology 64(:249-65, 2012), application of a variant CHO line Lec13 as the host cell line (Shields *et al.*, J Biol Chem 277:26733-26740, 2002), application of a variant

CHO line EB66 as the host cell line (Olivier *et al.,* MAbs ;2(4), 2010; Epub ahead of print; PMID:20562582), application of a rat hybridoma cell line YB2/0 as the host cell line (Shinkawa *et al.,* J Biol Chem 278:3466-3473, 2003), introduction of small interfering RNA specifically against the α 1,6-fucosyltrasferase (*FUT8)* gene (Mori *et al.,* Biotechnol Bioeng88:901-908, 2004), or coexpression of β-1,4-*N*-acetylglucosaminyltransferase III and Golgi α-mannosidase II or a potent alpha-mannosidase I inhibitor, kifunensine (Ferrara *et al.,* J Biol Chem281:5032-5036, 2006, Ferrara *et al.,* Biotechnol Bioeng 93:851-861, 2006; Xhou *et al.,* Biotechnol Bioeng 99:652-65, 2008).

In some embodiments described herein, ADCC elicited by the bispecific EGFR/c-Met antibodies may also be enhanced by certain substitutions in the antibody Fc. Exemplary substitutions are for example substitutions at amino acid positions 256, 290, 298, 312, 356, 330, 333, 334, 360, 378 or 430 (residue numbering according to the EU index) as described in U.S. Pat. No. US6737056.

In some embodiments described herein, the bispecific EGFR/c-Met antibody of the invention has a biantennary glycan structure with fucose content of about between 1% to about 15%, for example 15%, 14%, 13%, 12%, 11% 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% or 1% In some embodiments, the bispecific EGFR/c-Met antibody has a glycan structure with fucose content of about 50%, 40%, 45%, 40%, 35%, 30%, 25%, or 20%.

"Fucose content" means the amount of the fucose monosaccharide within the sugar chain at Asn297. . The relative amount of fucose is the percentage of fucose-containing structures related to all glycostructures. These may be characterized and quantified by multiple methods, for example: 1) using MALDI-TOF of N-glycosidase F treated sample (e.g. complex, hybrid and oligo- and high-mannose structures) as described in Int Pat. Publ. No. WO2008/077546 2); 2) by enxymatic release of the Asn297 glycans with subsequent derivatization and detection/ quantitation by HPLC (UPLC) with fluorescence detection and/or HPLC-MS (UPLC-MS); 3) intact protein analysis of the native or reduced mAb, with or without treatment of the Asn297 glycans with Endo S or other enzyme that cleaves between the first and the second GlcNAc monosaccharides, leaving the fucose attached to the first GlcNAc; 4) digestion of the mAb to constituent peptides by enzymatic digestion (e.g., trypsin or endopeptidase Lys-C), and subsequent separation, detection and quantitation by HPLC-MS (UPLC-MS); 5) Separation of the mAb oligosaccharides from the mAb protein by specific enzymatic deglycosylation with PNGase F at Asn 297. The oligosaccharides thus released can be labeled with a fluorophore, separated and identified by various complementary techniques which allow:

fine characterization of the glycan structures by matrix-assisted laser desorption ionization (MALDI) mass spectrometry by comparison of the experimental masses with the theoretical masses, determination of the degree of sialylation by ion exchange HPLC (GlycoSep C), separation and quantification of the oligosacharride forms according to hydrophilicity criteria by normal-phase HPLC (GlycoSep N), and separation and quantification of the oligosaccharides by high performance capillary electrophoresis-laser induced fluorescence (HPCE-LIF).

"Low fucose" or "low fucose content" as used in the application refers to antibodies with fucose content of about between 1%-15%.

"Normal fucose" or 'normal fucose content" as used herein refers to antibodies with fucose content of about over 50%, typically about over 80% or over 85%.

Some embodiments of the invention provide a synthetic nucleic acid encoding the heavy chains and the light chains of the bispecific EGFR/c-Met binding antibodies of the invention as described herein as isolated polynucleotides or as portions of expression vectors or as portions of linear DNA sequences, including linear DNA sequences used for *in vitro* transcription/translation, vectors compatible with prokaryotic, eukaryotic or filamentous phage expression, secretion and/or display of the compositions or directed mutagens thereof.

Some embodiments of the invention provide an isolated polynucleotide comprising the polynucleotide sequence of SEQ ID NOs: 205, 206, 207 or 208.

The polynucleotides of the invention may be produced by chemical synthesis such as solid phase polynucleotide synthesis on an automated polynucleotide synthesizer and assembled into complete single or double stranded molecules. Alternatively, the polynucleotides of the invention may be produced by other techniques such as PCR followed by routine cloning. Techniques for producing or obtaining polynucleotides of a given known sequence are well known in the art.

The polynucleotides of the invention may comprise at least one non-coding sequence, such as a promoter or enhancer sequence, intron, polyadenylation signal, a *cis* sequence facilitating RepA binding, and the like. The polynucleotide sequences may also comprise additional sequences encoding additional amino acids that encode for example a marker or a tag sequence such as a histidine tag or an HA tag to facilitate purification or detection of the protein, a signal sequence, a fusion protein partner such as RepA, Fc or bacteriophage coat protein such as pIX or pIII.

Some embodiments described herein provide for a vector comprising the polynucleotide of the invention. Such vectors may be plasmid vectors, viral vectors, vectors for baculovirus expression, transposon based vectors or any other vector suitable for introduction of the polynucleotide of the invention into a given organism or genetic background by any means. For example, polynucleotides encoding heavy and light chains of the bispecific antibodies of the invention may be inserted into expression vectors. The light and heavy chains may be be cloned in the same or different expression vectors. The DNA segments encoding immunoglobulin chains may be operably linked to control sequences in the expression vector(s) that ensure the expression of immunoglobulin polypeptides. Such control sequences include signal sequences, promoters (e.g. naturally associated or heterologous promoters), enhancer elements, and transcription termination sequences, and may be chosen to be compatible with the host cell chosen to express the antibody. Once the vector has been incorporated into the appropriate host, the host may be maintained under conditions suitable for high level expression of the proteins encoded by the incorporated synthetic polynucleotides.

Suitable expression vectors are typically replicable in the host organisms either as episomes or as an integral part of the host chromosomal DNA. Commonly, expression vectors contain selection markers such as ampicillin-resistance, hygromycin-resistance, tetracycline resistance, kanamycin resistance or neomycin resistance to permit detection of those cells transformed with the desired DNA sequences.

Some embodiments described herein provide for a host cell comprising the vector of the invention. The term "host cell" refers to a cell into which a vector has been introduced. It is understood that the term host cell is intended to refer not only to the particular subject cell but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein. Such host cells may be eukaryotic cells, prokaryotic cells, plant cells or archeal cells.

Exemplary eukaryotic cells may be of mammalian, insect, avian or other animal origins. Mammalian eukaryotic cells include immortalized cell lines such as hybridomas or myeloma cell lines such as SP2/0 (American Type Culture Collection (ATCC), Manassas, VA, CRL-1581), NS0 (European Collection of Cell Cultures (ECACC), Salisbury, Wiltshire, UK, ECACC No. 85110503), FO (ATCC CRL-1646) and Ag653 (ATCC CRL-1580) murine cell lines. An exemplary human myeloma cell line is U266 (ATTC CRL-TIB-196). Other useful cell lines include those derived from Chinese

Hamster Ovary (CHO) cells such as CHO-K1SV (Lonza Biologics, Walkersville, MD), CHO-K1 (ATCC CRL-61) or DG44.

Uses of bispecific EGFR/c-Met FN3 domain containing molecules, bispecific EGFR/-c-Met antibodies and EGFR-binding or c-Met binding FN3 domains of the invention

The bispecific EGFR/c-Met FN3 domain containing molecules, the EGFR binding FN3 domains, the c-Met binding FN3 domains or the bispecific EGFR-c-Met antibodies of the invention may be used to diagnose, monitor, modulate, treat, alleviate, help prevent the incidence of, or reduce the symptoms of human disease or specific pathologies in cells, tissues, organs, fluid, or, generally, a host. The methods of the invention may be used to treat an animal patient belonging to any classification. Examples of such animals include mammals such as humans, rodents, dogs, cats and farm/domestic animals.

One aspect of the invention is a method for inhibiting growth or proliferation of cells that express EGFR and/or c-Met, comprising contacting the cells with the isolated bispecific EGFR/c-Met FN3 domain containing molecule, the EGFR binding FN3 domain, the c-Met binding FN3 domain or the bispecific EGFR/c-Met antibody of the invention.

Another aspect of the invention is a method for inhibiting growth or metastasis of EGFR and/or c-Met -expressing tumor or cancer cells in a subject comprising administering to the subject an effective amount of the isolated bispecific EGFR/c-Met FN3 domain containing molecule, the EGFR binding FN3 domain, the c-Met binding FN3 domain or the bispecific EGFR/c-Met antibody of the invention so that the growth or metastasis of EGFR- and/or c-Met-expressing tumor or cancer cell is inhibited.

Another aspect of the invention is a method of treating a subject having cancer, comprising administering a therapeutically effective amount of the isolated bispecific EGFR/c-Met FN3 domain containing molecule, the EGFR binding FN3 domain, the c-Met binding FN3 domain or the bispecific EGFR/c-Met antibody of the invention to a patient in need thereof for a time sufficient to treat the cancer.

The bispecific EGFR/c-Met FN3 domain containing molecule, the EGFR binding FN3 domain, the c-Met binding FN3 domain or the bispecific EGFR/c-Met antibodies of the invention may be used for treatment of any disease or disorder characterized by abnormal activation or production of EGFR, c-Met, EGF, soluble EGFR, soluble c-Met or other EGFR ligand or HGF, or disorder related to EGFR or c-Met expression, which may or may not involve malignancy or cancer, where abnormal activation and/or production of

EGFR, c-Met, EGF or other EGFR ligand, or HGF is occurring in cells or tissues of a subject having, or predisposed to, the disease or disorder.

The FN3 domains that specifically bind c-Met and block binding of HGF to c-Met of the invention may be for treatment of tumors, including cancers and benign tumors. Cancers that are amenable to treatment by the c-Met binding FN3 domains of the invention include those that overexpress c-Met. Exemplary cancers that are amenable to treatment by the FN3 domains of the invention include epithelial cell cancers, breast cancer, ovarian cancer, lung cancer, colorectal cancer, anal cancer, prostate cancer, kidney cancer, bladder cancer, head and neck cancer, gastric cancer, ovarian cancer, pancreatic cancer, skin cancer, oral cancer, esophageal cancer, vaginal cancer, cervical cancer, cancer of the spleen, testicular cancer, and cancer of the thymus.

The FN3 domains that specifically bind EGFR and blocks binding of EGF to the EGFR of the invention may be used for treatment of tumors, including cancers and benign tumors. Cancers that are amenable to treatment by the FN3 domains of the invention include those that overexpress EGFR or variants. Exemplary cancers that are amenable to treatment by the FN3 domains of the invention include epithelial cell cancers, breast cancer, ovarian cancer, lung cancer, colorectal cancer, anal cancer, prostate cancer, kidney cancer, bladder cancer, head and neck cancer, ovarian cancer, pancreatic cancer, skin cancer, oral cancer, esophageal cancer, vaginal cancer, cervical cancer, cancer of the spleen, testicular cancer, and cancer of the thymus.The bispecific EGFR/c-Met FN3 domain containing molecules or the bispecific EGFR/c-Met antibodies of the invention may be used for treatment of tumors, including cancers and benign tumors. Exemplary cancers that are amenable to treatment by the bispecific EGFR/c-Met FN3 domain containing molecule or the bispecific EGFR/c-Met antibody of the invention include those that over-express EGFR and/or c-Met, cancers associated with elevated EGFR activity and/or expression levels (such as, for example, an EGFR activating mutation, an EGFR gene amplification, or ligand mediated EGFR activation) and elevated c-Met activity and/or expression levels (such as, for example, a c-Met activating mutation, a c-Met gene amplification, or HGF mediated c-Met activation).

Exemplary EGFR activating mutations that may be associated with cancer include point mutations, deletion mutations, insertion mutations, inversions or gene amplifications that lead to an increase in at least one biological activity of EGFR, such as elevated tyrosine kinase activity, formation of receptor homodimers and heterodimers, enhanced ligand binding etc. Mutations can be located in any portion of an EGFR gene or

regulatory region associated with an EGFR gene and include mutations in exon 18, 19, 20 or 21 or mutations in the kinase domain. Exemplary activating EGFR mutations are G719A, L861X (X being any amino acid), L858R, E746K, L747S, E749Q, A750P, A755V, V765M, , L858P or T790M substitutions, deletion of E746-A750, deletion of R748-P753, insertion of Ala between M766 and A767, insertion of SVA (Ser, Val, Ala) between S768 and V769, and insertion of NS (Asn, Ser) between P772 and H773. Other examples of EGFR activating mutations are known in the art (see e.g., U.S. Pat. Publ. No. US2005/0272083). Information about EGFR and other ErbB receptors including receptor homo- and hetero-dimers, receptor ligands, autophosphorylation sites, and signaling molecules involved in ErbB mediated signaling is known in the art (see e.g., Hynes and Lane, Nature Reviews Cancer 5: 341-354, 2005).

Exemplary c-Met activating mutations include point mutations, deletion mutations, insertion mutations, inversions or gene amplifications that lead to an increase in at least one biological activity of a c-Met protein, such as elevated tyrosine kinase activity, formation of receptor homodimers and heterodimers, enhanced ligand binding etc. Mutations can be located in any portion of the c-Met gene or regulatory regions associated with the gene, such as mutations in the kinase domain of c-Met. Exemplary c-Met activating mutations are mutations at residue positions N375, V13, V923, R175, V136, L229, S323, R988, S1058/T1010 and E168. Methods for detecting EGFR and c-Met mutations or gene amplifications are well known.

Exemplary cancers that are amenable to treatment by the bispecific molecules of the invention such as the bispecific EGFR/c-Met antibodies of the invention include epithelial cell cancers, breast cancer, ovarian cancer, lung cancer, non-small cell lung cancer (NSCLC), lung adenocarcinoma, small cell lung cancer, colorectal cancer, anal cancer, prostate cancer, kidney cancer, bladder cancer, head and neck cancer, pharynx cancer, cancer of the nose, pancreatic cancer, skin cancer, oral cancer, cancer of the tongue, esophageal cancer, vaginal cancer, cervical cancer, cancer of the spleen, testicular cancer, gastric cancer, cancer of the thymus, colon cancer, thyroid cancer, liver cancer (hepatocellular carcinoma (HCC)) or sporadic or hereditary papillary renal cell carcinoma (PRCC).

Another aspect of the invention is a method of treating a subject having cancer, comprising administering a therapeutically effective amount of the isolated bispecific EGFR/c-Met antibody of the invention to a patient in need thereof for a time sufficient to treat the cancer, wherein the subject is homozygous for phenylalanine at position 158 of

CD16 (FcγRIIIa-158F/F genotype) or heterozygous for valine and pheynylalanine at position 158 of CD16 (FcγRIIIa-158F/V genotype). CD16 is also known as the Fc gamma receptor IIIa (FcγRIIIa) or the low affinity immunoglobulin gamma Fc region receptor III-A isoform. Valine/phenylalanine (V/F) polymorphism at FcγRIIIa protein residue position 158 has been shown to affect FcγRIIIa affinity to human IgG. Receptor with FcγRIIIa-158F/F or FcγRIIIa-158F/V polymorphisms demonstrates reduced Fc engagement and therefore reduced ADCC when compared to the FcγRIIIa-158V/V. The lack of or low amount of fucose on human N-linked oligosaccharides improves the ability of the antibodies to induce ADCC due to improved binding of the antibodies to human FcγRIIIa (CD16) (Shields *et al.*, J Biol Chem 277:26733-40, 2002). The antibodies of the invention have reduced fucose content of about between 1% to about 10%. In some embodiments, the bispecific EGFR/c-Met antibody has a glycan structure with fucose content of about 50%, 40%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% or 1%. Therefore, the antibodies of the invention may be more efficacious in the treatment of patients with FcγRIIIa-158F/F or FcγRIIIa-158F/V genotypes. Patients can be analyzed for their FcγRIIIa polymorphism using routine methods.

In some methods described herein, the antibodies of the invention may be used to treat a subject having cancer that is resistant or has acquired resistance to treatment with one or more EGFR inhibitors. Exemplary EGFR inhibitors for which cancer may acquire resistance are anti-EGFR antibodies cetuximab (Erbitux®), pantinumumab (Vectibix®), matuzumab, nimotuzumab, small molecule EGFR inhibitors Tarceva® (erlotinib), IRESSA (gefitinib), EKB-569 (pelitinib, irreversible EGFR TKI), pan-ErbB and other receptor tyrosine kinase inhibitors, lapatinib (EGFR and HER2 inhibitor), pelitinib (EGFR and HER2 inhibitor),vandetanib (ZD6474, ZACTIMA™, EGFR, VEGFR2 and RET TKI), PF00299804 (dacomitinib, irreversible pan-ErbB TKI) , CI-1033 (irreversible pan-erbB TKI), afatinib (BIBW2992, irreversible pan-ErbB TKI), AV-412 (dual EGFR and ErbB2 inhibitor), EXEL-7647 (EGFR, ErbB2, GEVGR and EphB4 inhibitor), CO-1686 (irreversible mutant-selective EGFR TKI), AZD9291 (irreversible mutant-selective EGFR TKI),and HKI-272 (neratinib, irreversible EGFR/ErbB2 inhibitor). The methods described herein may be used to treat cancer that is resistant to treatment with gefitinib, erlotinib, afatinib, CO-1686, AZD9291 and/or cetuximab. An exemplary antibody that can be used is EM1-mAb.

Another aspect of the invention is a method of treating a subject having cancer, comprising administering a therapeutically effective amount of the isolated bispecific EGFR/c-Met antibody of the invention to a patient in need thereof for a time sufficient to treat the cancer, wherein the subject is resistant or has acquired resistance to treatment with erlotinib, gefitinib, afatinib, CO-1686, AZD9291 or cetuximab.

Various qualitative and/or quantitative methods may be used to determine if a subject is resistant, has developed or is susceptible to developing a resistance to treatment with an EGFR inhibitor. Symptoms that may be associated with resistance to an EGFR inhibitor include, for example, a decline or plateau of the well-being of the patient, an increase in the size of a tumor, arrested or slowed decline in growth of a tumor, and/or the spread of cancerous cells in the body from one location to other organs, tissues or cells. Re-establishment or worsening of various symptoms associated with cancer may also be an indication that a subject has developed or is susceptible to developing resistance to EGFR inhibitors, such as anorexia, cognitive dysfunction, depression, dyspnea, fatigue, hormonal disturbances, neutropenia, pain, peripheral neuropathy, and sexual dysfunction. The symptoms associated with cancer may vary according to the type of cancer. For example, symptoms associated with cervical cancer may include abnormal bleeding, unusual heavy vaginal discharge, pelvic pain that is not related to the normal menstrual cycle, bladder pain or pain during urination, and bleeding between regular menstrual periods, after sexual intercourse, douching, or pelvic exam. Symptoms associated with lung cancer may include persistent cough, coughing up blood, shortness of breath, wheezing chest pain, loss of appetite, losing weight without trying and fatigue. Symptoms for liver cancer may includeloss of appetite and weight, abdominal pain, especially in the upper right part of abdomen that may extend into the back and shoulder, nausea and vomiting, general weakness and fatigue, an enlarged liver, abdominal swelling (ascites), and a yellow discoloration of the skin and the whites of eyes (jaundice). One skilled in oncology may readily identify symptoms associated with a particular cancer type.

Others means to determine if a subject has developed a resistance to an EGFR inhibitor include examining EGFR phosphorylation, ERK1/2 phosphorylation and/or AKT phosphorylation in cancer cells, where increased phosphorylation may be indicative that the subject has developed or is susceptible to developing resistance to an EGFR inhibitor. Methods of determining EGFR, ERK1/2 and/or AKT phosphorylation are well known and described herein. Identification of a subject who has developed a resistance to an EGFR

inhibitor may involve detection of elevated c-Met expression levels or elevated c-Met activity, for example, arising from increased levels of circulating HGF, an activating mutation of the c-Met gene or a c-Met gene amplification.

Another embodiment of the invention is a method of treating NSCLC in a patient having an NSCLC tumor or tumor metastasis having an activating EGFR mutation or EGFR gene amplification, comprising administering to the patient a therapeutically effective amount of the bispecific EGFR/c-Met antibody of the invention.

The bispecific EGFR/c-Met antibodies of the invention can be used to treat non-small cell lung cancer (NSCLC), which includes squamous cell carcinoma, adenocarcinoma, and large cell carcinoma. In some embodiments, cells of the NSCLC have an epithelial phenotype. In some embodiments, the NSCLC has acquired resistance to treatment with one or more EGFR inhibitors.

In NSCLC, specific mutations in the EGFR gene are associated with high response rates (70-80%) to EGFR tyrosine kinase inhibitors (EGFR-TKIs). A 5 amino acid deletion in exon 19 or the point mutation L858R in EGFR are associated with EGFR-TKI sensitivity (Nakata and Gotoh, Expert Opin Ther Targets 16 :771-781, 2012). These mutations result in a ligand-independent activation of the EGFR kinase activity. Activating EGFR mutations occur in 10-30% of NSCLC patients and are significantly more common in East Asians, women, never smokers, and patients with adenocarcinoma histology (Janne and Johnson Clin Cancer Res 12(14 Suppl): 4416s-4420s, 2006). EGFR gene amplification is also strongly correlated with response after EGFR-TKI treatment (Cappuzzo *et al.*, J Natl Cancer Inst 97:643-55, 2005).

Although the majority of NSCLC patients with EGFR mutations initially respond to EGFR TKI therapy, virtually all acquire resistance that prevents a durable response. 50-60% of patients acquire resistance due to a second-site point mutation in the kinase domain of EGFR (T790M). Nearly 60% of all tumors that become resistant to EGFR tyrosine kinase inhibitors increase c-Met expression, amplify the c-Met gene, or increase its only known ligand, HGF (Turke *et al.*, Cancer Cell, 17:77-88, 2010).

Another embodiments of the invention is a method of treating patient having cancer, comprising administering a therapeutically effective amount of the bispecific EGFR/c-Met antibody of the invention to a patient in need thereof for a time sufficient to treat the cancer, wherein the cancer is associated with an EGFR activating mutation, an

EGFR gene amplification, increased levels of circulating HGF, a c-Met activating mutation, a c-Met gene amplification or a mutant KRAS.

In some embodiments the EGFR activating mutation is G719A, G719X (X being any amino acid), L861X (X being any amino acid), L858R, E746K, L747S, E749Q, A750P, A755V, V765M, L858P or T790M substitution, deletion of E746-A750, deletion of R748-P753, insertion of Ala (A) between M766 and A767, insertion of Ser, Val and Ala (SVA) between S768 and V769, and insertion of Asn and Ser (NS) between P772 and H773.

Another embodiments of the invention is a method of treating patient having cancer, comprising administering a therapeutically effective amount of the bispecific EGFR/c-Met antibody of the invention to a patient in need thereof for a time sufficient to treat the cancer, wherein the cancer is associated with an EGFR mutation L858R, T790M or deletion of residues E746-A750 (del(E746, A750)), EGFR amplification or c-Met amplification.

In some embodiments, the cancer is associated with wild type EGFR and wild type c-Met.

In some embodiments, the cancer is associated with wild type EGFR and c-Met amplification.

In some embodiments, the cancer is associated with EGFR L858R and T790M mutations and wild type c-Met.

In some embodiments, the cancer is associated with EGFR deletion del (E764, A750) and wild type c-Met.

In some embodiments, the cancer is associated with EGFR deletion del(E764, A750) and c-Met amplification.

In some embodiments, the cancer is associated with EGFR deletion del(E764, A750), EGFR amplification and c-Met amplification.

In some embodiments, the patient has a NSCLC associated with EGFR L858R and T790M mutations and wild type c-Met.

In some embodiments, the patient has a NSCLC associated with EGFR amplification and wild type c-Met.

In some embodiments, the patient has a NSCLC associated with EGFR amplification and c-Met amplification.

In some embodiments, the patient has a NSCLC associated with EGFR deletion del(E764, A750) and wild type c-Met.

In some embodiments, the patient has a NSCLC associated with EGFR deletion del(E764, A750) and c-Met amplification.

In some embodiments, the patients are treated with the EM1-mAb of the invention. The EM1-mAb of the invention shows efficacy in *in vivo* tumor animal models, when the tumors are associated with L858R, T790M, del(E746, A750) EGFR, EGFR amplification, wild type c-Met and/or c-Met amplification.Amplification of EGFR or c-Met may be evaluated by standard methods, for example by determining the copy number of the EGFR or c-Met gene by southern blotting, FISH, or comparative genomic hybridization (CGH).

Another embodiments of the invention is a method of treating patient having cancer, comprising administering a therapeutically effective amount of the bispecific EGFR/c-Met antibody of the invention to a patient in need thereof for a time sufficient to treat the cancer, wherein the cancer is associated with EGFR mutations L858R, T790M or deletion of residues E746-A750 (del(E746, A750)), EGFR amplification or c-Met amplification, and mutant KRAS.

In some embodiments, the mutant KRAS has a G12V substitution. KRAS belongs to the family of RAS proto-oncogenes encoding guanosine triphosphatases (GTPases), and mediates EGFR signal transduction downstream of the receptor. Tumors with proto-oncogenic KRAS mutations such as the activating G12V or G12C mutation would therefore not be expected to be treatable by EGFR antibodies. Clinical studies with anti-EGFR antibodies cetuximab or panitumumab demonstrated that patients with KRAS-mutated colorectal tumors do not respond to these agents (Van Cutsem *et al.,* N Eng J Med 360:1408-1417, 2009; Lievre *et al.,* J Clin Oncol 26:374-379, 2008; Amado *et al.,* J Clin Oncol 26:1626-1634m 2008). The bispecific EGFR/c-Met antibodies of the invention mediate KRAS mutant cell line killing via effective ADCC, and therefore, contrary to the current anti-EGFR therapies, may be efficacious in treatment of patients whose cancer is associated with KRAS activating mutations. Such exemplary antibody is the EM1-mAb.

The terms "treat" or "treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) an undesired physiological change or disorder, such as the development or spread of cancer. For purposes of this invention, beneficial or desired clinical results include, but

are not limited to, alleviation of symptoms, diminishment of extent of disease, stabilized (i.e., not worsening) state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, and remission (whether partial or total), whether detectable or undetectable. "Treatment" can also mean prolonging survival as compared to expected survival if not receiving treatment. Those in need of treatment include those already with the condition or disorder as well as those prone to have the condition or disorder or those in which the condition or disorder is to be prevented.

A "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve a desired therapeutic result. A therapeutically effective amount of the bispecific EGFR/c-Met antibody of the invention may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the bispecific EGFR/c-Met antibody of the invention to elicit a desired response in the individual. Exemplary indicators of an effective EGFR/c-Met therapeutic that may decline or abate in association with resistance include, for example, improved well-being of the patient, decrease or shrinkage of the size of a tumor, arrested or slowed growth of a tumor, and/or absence of metastasis of cancer cells to other locations in the body.

Administration/ Pharmaceutical Compositions

The invention provides for pharmaceutical compositions comprising the bispecific EGFR/c-Met antibody of the invention and a pharmaceutically acceptable carrier. For therapeutic use, the bispecific EGFR/c-Met FN3 domain containing molecules, the EGFR-binding FN3 domains, the c-Met-binding FN3 domains or the bispecific EGFR/c-Met antibodies of the invention may be prepared as pharmaceutical compositions containing an effective amount of the domain, molecule or antibody as an active ingredient in a pharmaceutically acceptable carrier. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the active compound is administered. Such vehicles may be liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. For example, 0.4% saline and 0.3% glycine can be used. These solutions are sterile and generally free of particulate matter. They may be sterilized by conventional, well-known sterilization techniques (*e.g.*, filtration). The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, stabilizing, thickening, lubricating and coloring

agents, etc. The concentration of the molecules or antibodies of the invention in such pharmaceutical formulation may vary widely, *i.e.*, from less than about 0.5%, usually to at least about 1% to as much as 15 or 20% by weight and will be selected primarily based on required dose, fluid volumes, viscosities, etc., according to the particular mode of administration selected. Suitable vehicles and formulations, inclusive of other human proteins, e.g., human serum albumin, are described, for example, in e.g. Remington: The Science and Practice of Pharmacy, 21st Edition, Troy, D.B. ed., Lipincott Williams and Wilkins, Philadelphia, PA 2006, Part 5, Pharmaceutical Manufacturing pp 691-1092, See especially pp. 958-989.

The mode of administration for therapeutic use of the bispecific EGFR/c-Met FN3 domain containing molecules, the EGFR-binding FN3 domains, the c-Met-binding FN3 domains or the bispecific EGFR/c-Met antibodies of the invention may be any suitable route that delivers the agent to the host, such as parenteral administration, e.g., intradermal, intramuscular, intraperitoneal, intravenous or subcutaneous, pulmonary, transmucosal (oral, intranasal, intravaginal, rectal), using a formulation in a tablet, capsule, solution, powder, gel, particle; and contained in a syringe, an implanted device, osmotic pump, cartridge, micropump; or other means appreciated by the skilled artisan, as well known in the art. Site specific administration may be achieved by for example intrarticular, intrabronchial, intraabdominal, intracapsular, intracartilaginous, intracavitary, intracelial, intracerebellar, intracerebroventricular, intracolic, intracervical, intragastric, intrahepatic, intracardial, intraosteal, intrapelvic, intrapericardiac, intraperitoneal, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal, intraretinal, intraspinal, intrasynovial, intrathoracic, intrauterine, intravascular, intravesical, intralesional, vaginal, rectal, buccal, sublingual, intranasal, or transdermal delivery.

Thus, a pharmaceutical composition of the invention for intramuscular injection may be prepared to contain 1 ml sterile buffered water, and between about 1 ng to about 100 mg/kg, *e.g.* about 50 ng to about 30 mg/kg or more preferably, about 5 mg to about 25 mg/kg, of the bispecific EGFR/c-Met FN3 domain containing molecules, the EGFR-binding FN3 domains or the c-Met-binding FN3 domains of the invention.

The bispecific EGFR/c-Met antibodies of the invention may be administered to a patient by any suitable route, for example parentally by intravenous (IV) infusion or bolus injection, intramuscularly or subcutaneously or intraperitoneally. IV infusion can be given over as little as 15 minutes, but more often for 30 minutes, 60 minutes, 90 minutes or even 2 or 3 hours. The bispecific EGFR/c-Met antibodies of the invention may also be injected directly into the site of disease (e.g., the tumor itself). The dose given to a patient having a

cancer is sufficient to alleviate or at least partially arrest the disease being treated ("therapeutically effective amount") and may be sometimes 0.1 to 10 mg/kg body weight, for example 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 mg/kg, but may even higher, for example 15, 20, 30, 40, 50, 60, 70, 80, 90 or 100 mg/kg. A fixed unit dose may also be given, for example, 50, 100, 200, 500 or 1000 mg, or the dose may be based on the patient's surface area, e.g., 400, 300, 250, 200, or 100 mg/m^2. Usually between 1 and 8 doses, (e.g., 1, 2, 3, 4, 5, 6, 7 or 8) may be administered to treat cancer, but 10, 12, 20 or more doses may be given. Administration of the bispecific EGFR/c-Met antibody of the invention may be repeated after one day, two days, three days, four days, five days, six days, one week, two weeks, three weeks, one month, five weeks, six weeks, seven weeks, two months, three months, four months, five months, six months or longer. Repeated courses of treatment are also possible, as is chronic administration. The repeated administration may be at the same dose or at a different dose.

For example, a pharmaceutical composition comprising the bispecific EGFR/c-Met antibody of the invention for intravenous infusion may be made up to contain about 200 ml of sterile Ringer's solution, and about 8 mg to about 2400 mg, about 400 mg to about 1600 mg, or about 400 mg to about 800 mg of the bispecific EGFR/c-Met antibody for administration to a 80 kg patient. Methods for preparing parenterally administrable compositions are well known and are described in more detail in, for example, "Remington's Pharmaceutical Science", 15th ed., Mack Publishing Company, Easton, PA.

The bispecific EGFR/c-Met FN3 domain containing molecules, the EGFR-binding FN3 domains, the c-Met-binding FN3 domains or the bispecific EGFR/c-Met antibodies of the invention may be lyophilized for storage and reconstituted in a suitable carrier prior to use. This technique has been shown to be effective with conventional protein preparations and well known lyophilization and reconstitution techniques can be employed.

The bispecific EGFR/c-Met FN3 domain containing molecules, the EGFR-binding FN3 domains, the c-Met-binding FN3 domains or the bispecific EGFR/c-Met antibodies of the invention may be administered in combination with a second therapeutic agent simultaneously, sequentially or separately. The second therapeutic agent may be a chemotherapeutic agent or a targeted anti-cancer therapy.

The bispecific EGFR/c-Met antibody may be administered together with any one or more of the chemotherapeutic drugs or other anti-cancer therapeutics known to those of skill in the art. Chemotherapeutic agents are chemical compounds useful in the treatment of cancer and include growth inhibitory agents or other cytotoxic agents and include alkylating agents, anti-metabolites, anti-microtubule inhibitors, topoisomerase inhibitors,

receptor tyrosine kinase inhibitors, angiogenesis inhibitors and the like. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclosphosphamide (CYTOXAN®); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethylenethiophosphaoramide and trimethylolomelamine; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabicin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-FU; folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogues such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogues such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguazone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2′,2″-trichlorotriethylamine; urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; members of taxoid or taxane family, such as paclitaxel (TAXOL®docetaxel (TAXOTERE®) and analogues thereof; chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogues such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11;

topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoic acid; esperamicins; capecitabine; inhibitors of receptor tyrosine kinases and/or angiogenesis, including sorafenib (NEXAVAR®), sunitinib (SUTENT®), pazopanib (VOTRIENT™), toceranib (PALLADIA™), vandetanib (ZACTIMA™), cediranib (RECENTIN®), regorafenib (BAY 73-4506), axitinib (AG013736), lestaurtinib (CEP-701), erlotinib (TARCEVA®), gefitinib (IRESSA™), BIBW 2992 (TOVOK™), lapatinib (TYKERB®), neratinib (HKI-272), and the like, and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY 117018, onapristone, and toremifene (FARESTON®); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Other conventional cytotoxic chemical compounds as those disclosed in Wiemann et al., 1985, in *Medical Oncology* (Calabresi et aL, eds.), Chapter 10, McMillan Publishing, are also applicable to the methods of the present invention.

Exemplary agents that may be used in combination with the bispecific EGFR/c-Met FN3 domain containing molecules, the EGFR-binding FN3 domains, the c-Met-binding FN3 domains or the bispecific EGFR/c-Met antibodies of the invention include tyrosine kinase inhibitors and targeted anti-cancer therapies such as Iressa® (gefitinib) and Tarceva (erlotinib) and other antagonists of HER2, HER3, HER4 or VEGF. Exemplary HER2 antagonists include CP-724-714, HERCEPTIN™ (trastuzumab), OMNITARG™ (pertuzumab), TAK-165, lapatinib (EGFR and HER2 inhibitor), and GW-282974. Exemplary HER3 antagonists include anti-Her3 antibodies (see e.g., U.S. Pat. Publ. No. US2004/0197332). Exemplary HER4 antagonists include anti-HER4 siRNAs (see e.g., Maatta *et al.,* Mol Biol Cell 17: 67-79, 2006,. An exemplary VEGF antagonist is Bevacizumab (Avastin™).

When a small molecule is used in combination with the bispecific EGFR/c-Met antibody of the invention, it is typically administered more often, preferably once a day, but 2, 3, 4 or more times per day is also possible, as is every two days, weekly or at some other interval. Small molecule drugs are often taken orally but parenteral administration is also possible, e.g., by IV infusion or bolus injection or subcutaneously or intramuscularly. Doses of small molecule drugs may typically be from 10 to 1000 mg, or about 100, 150, 200 or 250 mg.

When the bispecific EGFR/c-Met antibody of the invention is administered in combination with a second therapeutic agent, the combination may take place over any convenient timeframe. For example, the bispecific EGFR/c-Met antibody and the second therapeutic agent may be administered to a patient on the same day, and even in the same intravenous infusion. However, the bispecific EGFR/c-Met antibody and the second therapeutic agent may also be administered on alternating days or alternating weeks, fortnights or months, and so on. In some methods, the bispecific EGFR/c-Met antibody and the second therapeutic agent are administered with sufficient proximity in time that they are simultaneously present (e.g., in the serum) at detectable levels in the patient being treated. In some methods, an entire course of treatment of the bispecific EGFR/c-Met antibody consisting of a number of doses over a time period is followed or preceded by a course of treatment of the second therapeutic agent also consisting of a number of doses. In some methods, treatment with the bispecific EGFR/c-Met antibody administered second is begun if the patient has resistance or develops resistance to the second therapeutic agent administered initially. The patient may receive only a single course or multiple courses of treatment with one or both the bispecific EGFR/c-Met antibody and the second therapeutic agent. A recovery period of 1, 2 or several days or weeks may be used between administration of the bispecific EGFR/c-Met antibody and the second therapeutic agent. When a suitable treatment regiment has already been established for the second therapeutic agent, that regimen may be used in combination with the bispecific EGFR/c-Met antibody of the invention. For example, Tarceva® (erlotinib) is taken as a 100 mg or 150 mg pill once a day, and Iressa® (gefitinib) is taken as 250 mg tablet daily.

The bispecific EGFR/c-Met antibody, optionally in combination with the second therapeutic agent may be administered together with any form of radiation therapy including external beam radiation, intensity modulated radiation therapy (IMRT) and any form of radiosurgery including Gamma Knife, Cyberknife, Linac, and interstitial radiation (e.g. implanted radioactive seeds, GliaSite balloon), and/or with surgery. Combination with radiation therapy can be especially appropriate for head and neck cancer and brain tumors.

While having described the invention in general terms, the embodiments of the invention will be further disclosed in the following examples that should not be construed as limiting the scope of the claims.

Example 1. Construction of Tencon libraries

Tencon (SEQ ID NO: 1) is an immunoglobulin-like scaffold, fibronectin type III (FN3) domain, designed from a consensus sequence of fifteen FN3 domains from human tenascin-C (Jacobs *et al.*, Protein Engineering, Design, and Selection, 25:107-117, 2012; U.S. Pat. Publ. No. 2010/0216708). The crystal structure of Tencon shows six surface-exposed loops that connect seven beta-strands. These loops, or selected residues within each loop, can be randomized in order to construct libraries of fibronectin type III (FN3) domains that can be used to select novel molecules that bind to specific targets.

Tencon:

LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYDLTGLK PGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO 1):

Construction of TCL1 library

A library designed to randomize only the FG loop of Tencon (SEQ ID NO: 1), TCL1, was constructed for use with the *cis*-display system (Jacobs *et al.*, Protein Engineering, Design, and Selection, 25:107-117, 2012). In this system, a single-strand DNA incorporating sequences for a Tac promoter, Tencon library coding sequence, RepA coding sequence, cis-element, and ori element is produced. Upon expression in an *in vitro* transcription/translation system, a complex is produced of the Tencon-RepA fusion protein bound in *cis* to the DNA from which it is encoded. Complexes that bind to a target molecule are then isolated and amplified by polymerase chain reaction (PCR), as described below.

Construction of the TCL1 library for use with *cis*-display was achieved by successive rounds of PCR to produce the final linear, double-stranded DNA molecules in two halves; the 5' fragment contains the promoter and Tencon sequences, while the 3' fragment contains the *repA* gene and the cis- and ori elements. These two halves are combined by restriction digest in order to produce the entire construct. The TCL1 library was designed to incorporate random amino acids only in the FG loop of Tencon, KGGHRSN (SEQ ID NO: 86). NNS codons were used in the construction of this library, resulting in the possible incorporation of all 20 amino acids and one stop codon into the FG loop. The TCL1 library contains six separate sub-libraries, each having a different randomized FG loop length, from 7 to 12 residues, in order to further increase diversity. Design of Tencon-based libraries are shown in Table 2.

Table 2.

Library	BC Loop Design	FG Loop Design
WT Tencon	TAPDAAFD*	KGGHRSN**
TCL1	TAPDAAFD*	XXXXXXX
		XXXXXXXX
		XXXXXXXXX
		XXXXXXXXXX
		XXXXXXXXXXX
		XXXXXXXXXXXX
TCL2	########	#####S##

*TAPDAAFD: residues 22-28 of SEQ ID NO: 1;

**KGGHRSN: SEQ ID NO: 86

X refers to degenerate amino acids encoded by NNS codons.

refers to the "designed distribution of amino acids" described in the text.

To construct the TCL1 library, successive rounds of PCR were performed to append the Tac promoter, build degeneracy into the FG loop, and add necessary restriction sites for final assembly. First, a DNA sequence containing the promoter sequence and Tencon sequence 5' of the FG loop was generated by PCR in two steps. DNA corresponding to the full Tencon gene sequence was used as a PCR template with primers POP2220 (SEQID NO: 2) and TC5'toFG (SEQID NO: 3). The resulting PCR product from this reaction was used as a template for the next round of PCR amplification with primers 130mer (SEQID NO: 4) and Tc5'toFG to complete the appending of the 5' and promoter sequences to Tencon. Next, diversity was introduced into the FG loop by amplifying the DNA product produced in the first step with forward primer POP2222 (SEQID NO: 5), and reverse primers TCF7 (SEQID NO: 6), TCF8 (SEQID NO: 7), TCF9 (SEQID NO: 8), TCF10 (SEQID NO: 9), TCF11 (SEQID N NO: 10), or TCF12 (SEQID NO: 11), which contain degenerate nucleotides. At least eight 100 µL PCR reactions were performed for each sub-library to minimize PCR cycles and maximize the

diversity of the library. At least 5 μg of this PCR product were gel-purified and used in a subsequent PCR step, with primers POP2222 (SEQ ID NO: 5) and POP2234 (SEQID NO: 12), resulting in the attachment of a 6xHis tag and NotI restriction site to the 3' end of the Tencon sequence. This PCR reaction was carried out using only fifteen PCR cycles and at least 500 ng of template DNA. The resulting PCR product was gel-purified, digested with NotI restriction enzyme, and purified by Qiagen column.

The 3' fragment of the library is a constant DNA sequence containing elements for display, including a PspOMI restriction site, the coding region of the *repA* gene, and the cis- and ori elements. PCR reactions were performed using a plasmid (pCR4Blunt) (Invitrogen) containing this DNA fragment with M13 Forward and M13 Reverse primers. The resulting PCR products were digested by PspOMI overnight and gel-purified. To ligate the 5' portion of library DNA to the 3' DNA containing the *repA* gene, 2 pmol of 5' DNA were ligated to an equal molar amount of 3' *repA* DNA in the presence of NotI and PspOMI enzymes and T4 ligase. After overnight ligation at 37°C, a small portion of the ligated DNA was run on a gel to check ligation efficiency. The ligated library product was split into twelve PCR amplifications and a 12-cycle PCR reaction was run with primer pair POP2250 (SEQID NO: 13) and DidLigRev (SEQID NO: 14). The DNA yield for each sub-library of TCL1 library ranged from 32-34 μg.

To assess the quality of the library, a small portion of the working library was amplified with primers Tcon5new2 (SEQID NO: 15) and Tcon6 (SEQID NO: 16), and was cloned into a modified pET vector via ligase-independent cloning. The plasmid DNA was transformed into BL21-GOLD (DE3) competent cells (Stratagene) and 96 randomly picked colonies were sequenced using a T7 promoter primer. No duplicate sequences were found. Overall, approximately 70-85% of clones had a complete promoter and Tencon coding sequence without frame-shift mutation. The functional sequence rate, which excludes clones with STOP codons, was between 59% and 80%.

Construction of TCL2 Library

TCL2 library was constructed in which both the BC and the FG loops of Tencon were randomized and the distribution of amino acids at each position was strictly controlled. Table 3 shows the amino acid distribution at desired loop positions in the TCL2 library. The designed amino acid distribution had two aims. First, the library was biased toward residues that were predicted to be structurally important for Tencon folding

and stability based on analysis of the Tencon crystal structure and/or from homology modeling. For example, position 29 was fixed to be only a subset of hydrophobic amino acids, as this residue was buried in the hydrophobic core of the Tencon fold. A second layer of design included biasing the amino acid distribution toward that of residues preferentially found in the heavy chain HCDR3 of antibodies, to efficiently produce high-affinity binders (Birtalan *et al.*, J Mol Biol 377:1518-28, 2008; Olson *et al.*, Protein Sci 16:476-84, 2007). Towards this goal, the "designed distribution" of Table 3 refers to the distribution as follows: 6% alanine, 6% arginine, 3.9% asparagine, 7.5% aspartic acid, 2.5% glutamic acid, 1.5% glutamine, 15% glycine, 2.3% histidine, 2.5% isoleucine, 5% leucine, 1.5% lysine, 2.5% phenylalanine, 4% proline, 10% serine, 4.5% threonine, 4% tryptophan, 17.3% tyrosine, and 4% valine. This distribution is devoid of methionine, cysteine, and STOP codons.

Table 3.

Residue Position*	WT residues	Distribution in the TCL2 library
22	T	designed distribution
23	A	designed distribution
24	P	50% P + designed distribution
25	D	designed distribution
26	A	20% A + 20% G + designed distribution
27	A	designed distribution
28	F	20% F, 20% I, 20% L, 20% V, 20% Y
29	D	33% D, 33% E, 33% T
75	K	designed distribution
76	G	designed distribution
77	G	designed distribution
78	H	designed distribution
79	R	designed distribution
80	S	100% S
81	N	designed distribution
82	P	50% P + designed distribution

*residue numbering is based on Tencon sequence of SEQ ID NO: 1

The 5' fragment of the TCL2 library contained the promoter and the coding region of Tencon (SEQ ID NO: 1), which was chemically synthesized as a library pool (Sloning Biotechnology). This pool of DNA contained at least 1 x 10^{11} different members. At the end of the fragment, a BsaI restriction site was included in the design for ligation to *RepA*.

The 3' fragment of the library was a constant DNA sequence containing elements for display including a 6xHis tag, the coding region of the *repA* gene, and the cis-element. The DNA was prepared by PCR reaction using an existing DNA template (above), and primers LS1008 (SEQID NO: 17) and DidLigRev (SEQID NO: 14). To assemble the complete TCL2 library, a total of 1 μg of BsaI-digested 5' Tencon library DNA was ligated to 3.5 μg of the 3' fragment that was prepared by restriction digestion with the same enzyme. After overnight ligation, the DNA was purified by Qiagen column and the DNA was quantified by measuring absorbance at 260 nm. The ligated library product was amplified by a 12-cycle PCR reaction with primer pair POP2250 (SEQID NO: 13) and DidLigRev (SEQID NO: 14). A total of 72 reactions were performed, each containing 50 ng of ligated DNA products as a template. The total yield of TCL2 working library DNA was about 100 μg. A small portion of the working library was sub-cloned and sequenced, as described above for library TCL1. No duplicate sequences were found. About 80% of the sequences contained complete promoter and Tencon coding sequences with no frame-shift mutations.

Construction of TCL14 Library

The top (BC, DE, and FG) and the bottom (AB, CD, and EF) loops, e.g., the reported binding surfaces in the FN3 domains are separated by the beta-strands that form the center of the FN3 structure. Alternative surfaces residing on the two "sides" of the FN3 domains having different shapes than the surfaces formed by loops only are formed at one side of the FN3 domain by two anti-parallel beta-strands, the C and the F beta-strands, and the CD and FG loops, and is herein called the C-CD-F-FG surface.

A library randomizing an alternative surface of Tencon was generated by randomizing select surface exposed residues of the C and F strands, as well as portions of the CD and FG loops as shown in Figure 1. A Tencon variant, Tencon27 (SEQ ID NO: 99) having following substitutions when compared to Tencon (SEQ ID NO: 1) was used to

generate the library; E11R L17A, N46V, E86I. A full description of the methods used to construct this library is described in US. Pat. Publ. No. US2013/0226834

Example 2: Selection of fibronectin type III (FN3) domains that bind EGFR and Inhibit EGF Binding

Library screening

Cis-display was used to select EGFR binding domains from the TCL1 and TCL2 libraries. A recombinant human extracellular domain of EGFR fused to an IgG1 Fc (R&D Systems) was biotinylated using standard methods and used for panning (residues 25-645 of full length EGFR of SEQ ID NO: 73). For *in vitro* transcription and translation (ITT), 2-6 μg of library DNA were incubated with 0.1 mM complete amino acids, 1X S30 premix components, and 30 μL of S30 extract (Promega) in a total volume of 100 μL and incubated at 30°C. After 1 hour, 450 μL of blocking solution (PBS pH 7.4, supplemented with 2% bovine serum albumin, 100 μg/mL herring sperm DNA, and 1 mg/mL heparin) were added and the reaction was incubated on ice for 15 minutes. EGFR-Fc:EGF complexes were assembled at molar ratios of 1:1 and 10:1 EGFR to EGF by mixing recombinant human EGF (R&D Systems) with biotinylated recombinant EGFR-Fc in blocking solution for 1 hour at room temperature. For binding, 500 μL of blocked ITT reactions were mixed with 100 μL of EGFR-Fc:EGF complexes and incubated for 1 hour at room temperature, after which bound complexes were pulled down with magnetic neutravidin or streptavidin beads (Seradyne). Unbound library members were removed by successive washes with PBST and PBS. After washing, DNA was eluted from the bound complexes by heating to 65°C for 10 minutes, amplified by PCR, and attached to a DNA fragment encoding RepA by restriction digestion and ligation for further rounds of panning. High affinity binders were isolated by successively lowering the concentration of target EGFR-Fc during each round from 200 nM to 50 nM and increasing the washing stringency. In rounds 4 and 5, unbound and weakly bound FN3 domains were removed by washing in the presence of a 10-fold molar excess of non-biotinylated EGFR-Fc overnight in PBS.

Following panning, selected FN3 domains were amplified by PCR using oligonucleotides Tcon5new2 (SEQID NO: 15) and Tcon6 (SEQID NO: 16), subcloned into a pET vector modified to include a ligase independent cloning site, and transformed into BL21-GOLD (DE3) (Stratagene) cells for soluble expression in *E. coli* using standard

molecular biology techniques. A gene sequence encoding a C-terminal poly-histidine tag was added to each FN3 domain to enable purification and detection. Cultures were grown to an optical density of 0.6-0.8 in 2YT medium supplemented with 100 μg/mL carbenicillin in 1-mL 96-well blocks at 37°C before the addition of IPTG to 1 mM, at which point the temperature was reduced to 30°C. Cells were harvested approximately 16 hours later by centrifugation and frozen at -20°C. Cell lysis was achieved by incubating each pellet in 0.6 mL of BugBuster® HT lysis buffer (Novagen EMD Biosciences) with shaking at room temperature for 45 minutes.

Selection of FN3 domains that Bind EGFR on Cells

To assess the ability of different FN3 domains to bind EGFR in a more physiological context, their ability to bind A431 cells was measured. A431 cells (American Type Culture Collection, cat. #CRL-1555) over-express EGFR with ~2 x 10^6 receptors per cell. Cells were plated at 5,000/well in opaque black 96-well plates and allowed to attach overnight at 37°C, in a humidified 5% CO_2 atmosphere. FN3 domain-expressing bacterial lysates were diluted 1,000-fold into FACS stain buffer (Becton Dickinson) and incubated for 1 hour at room temperature in triplicate plates. Lysates were removed and cells were washed 3 times with 150 μL/well of FACS stain buffer. Cells were incubated with 50 μL/well of anti-penta His-Alexa488 antibody conjugate (Qiagen) diluted 1:100 in FACS stain buffer for 20 minutes at room temperature. Cells were washed 3 times with 150 μL/well of FACS stain buffer, after which wells were filled with 100 μL of FACS stain buffer and read for fluorescence at 488 nm using an Acumen eX3 reader. Bacterial lysates containing FN3 domains were screened for their ability to bind A431 cells (1320 crude bacterial lysates for TCL1 and TCL2 libraries) and 516 positive clones were identified, where binding was ≥10-fold over the background signal. 300 lysates from the TCL14 library were screened for binding, resulting in 58 unique FN3 domain sequences that bind to EGFR.

Selection of FN3 domains that Inhibit EGF Binding to EGFR on Cells

To better characterize the mechanism of EGFR binding, the ability of various identified FN3 domain clones to bind EGFR in an EGF-competitive manner was measured using A431 cells and run in parallel with the A431 binding assay screen. A431 cells were plated at 5,000/well in opaque black 96-well plates and allowed to attach overnight at

37°C in a humidified 5% CO_2 atmosphere. Cells were incubated with 50 µL/well of 1:1,000 diluted bacterial lysate for 1 hour at room temperature in triplicate plates. Biotinylated EGF (Invitrogen, cat. #E-3477) was added to each well for a final concentration of 30 ng/mL and incubated for 10 minutes at room temperature. Cells were washed 3 times with 150 µL/well of FACS stain buffer. Cells were incubated with 50 µL/well of streptavidin-phycoerythrin conjugate (Invitrogen) diluted 1:100 in FACS stain buffer for 20 minutes at room temperature. Cells were washed 3 times with 150 µL/well of FACS stain buffer, after which wells were filled with 100 µL of FACS stain buffer and read for fluorescence at 600 nm using an Acumen eX3 reader.

Bacterial lysates containing the FN3 domains were screened in the EGF competition assay described above. 1320 crude bacterial lysates from TCL1 and TCL2 libraries were screened resulting in 451 positive clones that inhibited EGF binding by > 50%.

Expression and Purification of identified FN3 domains binding EGFR

His-tagged FN3 domains were purified from clarified *E. coli* lysates with His MultiTrap™ HP plates (GE Healthcare) and eluted in buffer containing 20 mM sodium phosphate, 500 mM sodium chloride, and 250 mM imidazole at pH 7.4. Purified samples were exchanged into PBS pH 7.4 for analysis using PD MultiTrap™ G-25 plates (GE Healthcare).

Size Exclusion Chromatography Analysis

Size exclusion chromatography was used to determine the aggregation state of the FN3 domains binding EGFR. Aliquots (10 µL) of each purified FN3 domain were injected onto a Superdex 75 5/150 column (GE Healthcare) at a flow rate of 0.3 mL/min in a mobile phase of PBS pH 7.4. Elution from the column was monitored by absorbance at 280 nm. FN3 domains that exhibited high levels of aggregation by SEC were excluded from further analysis.

Off-Rate of Selected EGFR-binding FN3 domains from EGFR-Fc

Select EGFR-binding FN3 domains were screened to identify those with slow off-rates (k_{off}) in binding to EGFR-Fc on a ProteOn XPR-36 instrument (Bio-Rad) to facilitate selection of high affinity binders. Goat anti-human Fc IgG (R&D systems), at a concentration of 5 μg/mL, was directly immobilized via amine coupling (at pH 5.0) on all 6 ligand channels in horizontal orientation on the chip with a flow rate of 30 μL/min in PBS containing 0.005% Tween-20. The immobilization densities averaged about 1500 Response Units (RU) with less than 5% variation among different channels. EGFR-Fc was captured on the anti-human Fc IgG surface to a density around 600 RU in vertical ligand orientation. All tested FN3 domains were normalized to a concentration of 1 μM and tested for their binding in horizontal orientation. All 6 analyte channels were used for the FN3 domains to maximize screening throughput. The dissociation phase was monitored for 10 minutes at a flow rate of 100 μL/min. The inter-spot binding signals were used as references to monitor non-specific binding between analytes and the immobilized IgG surface, and were subtracted from all binding responses. The processed binding data were locally fit to a 1:1 simple Langmuir binding model to extract the k_{off} for each FN3 domain binding to captured EGFR-Fc.

Inhibition of EGF-Stimulated EGFR Phosphorylation

Purified EGFR-binding FN3 domains were tested for their ability to inhibit EGF-stimulated phosphorylation of EGFR in A431 cells at a single concentration. EGFR phosphorylation was monitored using the EGFR phospho(Tyr1173) kit (Meso Scale Discovery). Cells were plated at 20,000/well in clear 96-well tissue culture-treated plates (Nunc) in 100 μL/well of RPMI medium (Gibco) containing GlutaMAX™ with 10% fetal bovine serum (FBS) (Gibco) and allowed to attach overnight at 37°C in a humidified 5% CO_2 atmosphere. Culture medium was removed completely and cells were starved overnight in 100 μL/well of medium containing no FBS at 37°C in a humidified 5% CO_2 atmosphere. Cells were then treated with 100 μL/well of pre-warmed (37°C) starvation medium containing EGFR-binding FN3 domains at a concentration of 2 μM for 1 hour at 37°C in a humidified 5% CO_2 atmosphere. Controls were treated with starvation medium only. Cells were stimulated by the addition and gentle mixing of 100 μL/well of pre-warmed (37°C) starvation medium containing 100 ng/mL recombinant human EGF (R&D Systems, cat. #236-EG), for final concentrations of 50 ng/mL EGF and 1 μM EGFR-binding FN3 domain, and incubation at 37°C, 5% CO_2 for 15 minutes. One set of control wells was left un-stimulated as negative controls. Medium was completely removed and

cells were lysed with 100 µL/well of Complete Lysis Buffer (Meso Scale Discovery) for 10 minutes at room temperature with shaking, as per the manufacturer's instructions. Assay plates configured for measuring EGFR phosphorylated on tyrosine 1173 (Meso Scale Discovery) were blocked with the provided blocking solution as per the manufacturer's instructions at room temperature for 1.5-2 hours. Plates were then washed 4 times with 200 µL/well of 1X Tris Wash Buffer (Meso Scale Discovery). Aliquots of cell lysate (30 µL/well) were transferred to assay plates, which were covered with plate sealing film (VWR) and incubated at room temperature with shaking for 1 hour. Assay plates were washed 4 times with 200 µL/well of Tris Wash Buffer, after which 25 µL of ice-cold Detection Antibody Solution (Meso Scale Discovery) were added to each well, being careful not to introduce bubbles. Plates were incubated at room temperature with shaking for 1 hour, followed by 4 washes with 200 µL/well of Tris Wash Buffer. Signals were detected by addition of 150 µL/well of Read Buffer (Meso Scale Discovery) and reading on a SECTOR® Imager 6000 instrument (Meso Scale Discovery) using manufacturer-installed assay-specific default settings. Percent inhibition of the EGF-stimulated positive control signal was calculated for each EGFR-binding FN3 domain.

Inhibition of EGF-stimulated EGFR phosphorylation was measured for 232 identified clones from the TCL1 and TCL2 libraries. 22 of these clones inhibited EGFR phosphorylation by $\geq$50% at 1 µM concentration. After removal of clones that either expressed poorly or were judged to be multimeric by size exclusion chromatography, nine clones were carried forward for further biological characterization. The BC and FG loop sequences of these clones are shown in Table 4. Eight of the nine selected clones had a common FG loop sequence (HNVYKDTNMRGL; SEQ ID NO: 95) and areas of significant similarity were seen between several clones in their BC loop sequences.

Table 4.

FN3 Domain		BC Loop		FG Loop	
Clone ID	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
P53A1R5-17	18	ADPHGFYD	87	HNVYKDTNMRGL	95
P54AR4-17	19	TYDRDGYD	88	HNVYKDTNMRGL	95
P54AR4-47	20	WDPFSFYD	89	HNVYKDTNMRGL	95
P54AR4-48	21	DDPRGFYE	90	HNVYKDTNMRGL	95
P54AR4-73	22	TWPYADLD	91	HNVYKDTNMRGL	95
P54AR4-74	23	GYNGDHFD	92	HNVYKDTNMRGL	95
P54AR4-81	24	DYDLGVYD	93	HNVYKDTNMRGL	95
P54AR4-83	25	DDPWDFYE	94	HNVYKDTNMRGL	95
P54CR4-31	26	TAPDAAFD	85	LGSYVFEHDVM	96

Example 3: Characterization of EGFR-binding FN3 domains that Inhibit EGF Binding

Large-scale Expression, Purification, and Endotoxin Removal

The FN3 domains shown in Table 4 were scaled up to provide more material for detailed characterization. An overnight culture containing each EGFR-binding FN3 domain variant was used to inoculate 0.8 L of Terrific broth medium supplemented with 100 μg/mL ampicillin at a 1/80 dilution of overnight culture into fresh medium, and incubated with shaking at 37°C. The culture was induced when the optical density at 600 nm reached ~1.2-1.5 by addition of IPTG to a final concentration of 1 mM and the temperature was reduced to 30°C. After 4 hours, cells were collected by centrifugation and the cell pellet was stored at -80°C until needed.

For cell lysis, the thawed pellet was resuspended in 1X BugBuster® supplemented with 25 U/mL Benzonase® (Sigma-Aldrich) and 1 kU/mL rLysozyme™ (Novagen EMD Biosciences) at a ratio of 5 mL of BugBuster® per gram of pellet. Lysis proceeded for 1 hour at room temperature with gentle agitation, followed by centrifugation at 56,000 x g for 50 minutes at 4°C. The supernatant was collected and filtered through a 0.2 μm filter, then loaded on to a 5-mL HisTrap FF column pre-equilibrated with Buffer A (50 mM Tris-HCl pH 7.5, 500 mM NaCl, 10 mM imidazole) using a GE Healthcare ÄKTAexplorer 100s chromatography system. The column was washed with 20 column volumes of Buffer A and further washed with 16 % Buffer B (50 mM Tris-HCl pH7.5, 500 mM NaCl, 250 mM imidazole) for 6 column volumes. The FN3 domains were eluted with 50% B for 10 column volumes, followed by a gradient from 50-100% B over 6 column volumes. Fractions containing the FN3 domain protein were pooled, concentrated using a Millipore

10K MWCO concentrator, and filtered before loading onto a HiLoad™ 16/60 Superdex™ 75 column (GE Healthcare) pre-equilibrated with PBS. The protein monomer peak eluting from the size exclusion column was retained.

Endotoxins were removed using a batch approach with ActiClean Etox resin (Sterogene Bioseparations). Prior to endotoxin removal, the resin was pre-treated with 1 N NaOH for 2 hours at 37°C (or overnight at 4°C) and washed extensively with PBS until the pH had stabilized to ~7 as measured with pH indicator paper. The purified protein was filtered through a 0.2 μm filter before adding to 1 mL of Etox resin at a ratio of 10 mL of protein to 1 mL of resin. The binding of endotoxin to resin was allowed to proceed at room temperature for at least 2 hours with gentle rotation. The resin was removed by centrifugation at 500 x g for 2 minutes and the protein supernatant was retained. Endotoxin levels were measured using EndoSafe®-PTS™ cartridges and analyzed on an EndoSafe®-MCS reader (Charles River). If endotoxin levels were above 5 EU/mg after the first Etox treatment, the above procedure was repeated until endotoxin levels were decreased to ≥5 EU/mg. In cases where the endotoxin level was above 5 EU/mg and stabilized after two consecutive treatments with Etox, anion exchange or hydrophobic interaction chromatography conditions were established for the protein to remove the remaining endotoxins.

Affinity Determination of Selected EGFR-binding FN3 domains to EGFR-Fc (EGFR-Fc Affinity)

Binding affinity of selected EGFR-binding FN3 domains to recombinant EGFR extracellular domain was further characterized by surface Plasmon resonance methods using a Proteon Instrument (BioRad). The assay set-up (chip preparation, EGFR-Fc capture) was similar to that described above for off-rate analysis. Selected EGFR binding FN3 domains were tested at 1 μM concentration in 3-fold dilution series in the horizontal orientation. A buffer sample was also injected to monitor the baseline stability. The dissociation phase for all concentrations of each EGFR-binding FN3 domain was monitored at a flow rate of 100 μL/min for 30 minutes (for those with k_{off} ~10^{-2} s^{-1} from off-rate screening), or 1 hour (for those with k_{off} ~10^{-3} s^{-1} or slower). Two sets of reference data were subtracted from the response data: 1) the inter-spot signals to correct for the non-specific interactions between the EGFR-binding FN3 domain and the immobilized IgG surface; 2) the buffer channel signals to correct for baseline drifting due to the

dissociation of captured EGFR-Fc surface over time. The processed binding data at all concentrations for each FN3 domain were globally fit to a 1:1 simple Langmuir binding model to extract estimates of the kinetic (k_{on}, k_{off}) and affinity (K_D) constants. Table 5 shows the kinetic constants for each of the constructs, with the affinity varying from 200 pM to 9.6 nM.

Binding of Selected EGFR-binding FN3 domains to EGFR on Cells ("A431 Cell Binding Assay")

A431 cells were plated at 5,000/well in opaque black 96-well plates and allowed to attach overnight at 37°C, in a humidified 5% CO_2 atmosphere. Purified EGFR-binding FN3 domains (1.5 nM to 30 μM) were added to the cells (in 50 uL) for 1 hour at room temperature in triplicate plates. Supernatant was removed and cells were washed 3 times with 150 μL/well of FACS stain buffer. Cells were incubated with 50 μL/well of anti-penta His-Alexa488 antibody conjugate (Qiagen) diluted 1:100 in FACS stain buffer for 20 minutes at room temperature. Cells were washed 3 times with 150 μL/well of FACS stain buffer, after which wells were filled with 100 μL of FACS stain buffer and read for fluorescence at 488 nm using an Acumen eX3 reader. Data were plotted as raw fluorescence signal against the logarithm of the FN3 domain molar concentration and fitted to a sigmoidal dose-response curve with variable slope using GraphPad Prism 4 (GraphPad Software) to calculate EC_{50} values. Table 5 reports the EC_{50} for each of the constructs ranging from 2.2 nM to > 20 μM.

Inhibition of EGF Binding to EGFR on Cells using Selected EGFR-binding FN3 domains (A431 cell EGF competition assay)

A431 cells were plated at 5,000/well in opaque black 96-well plates and allowed to attach overnight at 37°C, in a humidified 5% CO_2 atmosphere. Purified EGFR-binding FN3 domains (1.5 nM to 30 μM) were added to the cells (50 μL/well) for 1 hour at room temperature in triplicate plates. Biotinylated EGF (Invitrogen, Cat #: E-3477) was added to each well to give a final concentration of 30 ng/mL and incubated for 10 minutes at room temperature. Cells were washed 3 times with 150 μL/well of FACS stain buffer. Cells were incubated with 50 μL/well of streptavidin-phycoerythrin conjugate (Invitrogen) diluted 1:100 in FACS stain buffer for 20 minutes at room temperature. Cells were washed 3 times with 150 μL/well of FACS stain buffer, after which wells were filled with

100 μL of FACS stain buffer and read for fluorescence at 600 nm using an Acumen eX3 reader. Data were plotted as the raw fluorescence signal against the logarithm of FN3 domain molar concentration and fitted to a sigmoidal dose-response curve with variable slope using GraphPad Prism 4 (GraphPad Software) to calculate IC_{50} values. Table 5 reports the IC_{50} values ranging from 1.8 nM to 121 nM.

Inhibition of EGF-Stimulated EGFR Phosphorylation (Phoshpo EGFR assay)

Select FN3 domains that significantly inhibited EGF-stimulated EGFR phosphorylation were assessed more completely by measuring IC_{50} values for inhibition. Inhibition of EGF-stimulated EGFR phosphorylation was assessed at varying FN3 domain concentrations (0.5 nM to 10 μM) as described above in "inhibition of EGF stimulated EGFR phosphorylation". Data were plotted as electrochemiluminescence signal against the logarithm of the FN3 domain molar concentration and IC_{50} values were determined by fitting data to a sigmoidal dose response with variable slope using GraphPad Prism 4 (GraphPad Software). Table 5 shows the IC_{50} values which ranged from 18 nM to >2.5 μM.

Inhibition of Human Tumor Cell Growth (NCI-H292 growth and NCI-H322 growth assay)

Inhibition of EGFR-dependent cell growth was assessed by measuring viability of the EGFR over-expressing human tumor cell lines, NCI-H292 and NCI-H322 (American Type Culture Collection, cat. #CRL-1848 & #CRL-5806, respectively), following exposure to EGFR-binding FN3 domains. Cells were plated at 500 cells/well (NCI-H292) or 1,000 cells/well (NCI-H322) in opaque white 96-well tissue culture-treated plates (Nunc) in 100μL/well of RPMI medium (Gibco) containing GlutaMAX™ and 10mM HEPES, supplemented with 10% heat inactivated fetal bovine serum (Gibco) and 1% penicillin/streptomycin (Gibco), and allowed to attach overnight at 37°C in a humidified 5% CO_2 atmosphere. Cells were treated by addition of 5μL/well of phosphate-buffered saline (PBS) containing a concentration range of EGFR-binding FN3 domains. Controls were treated with 5μL/well of PBS only or 25 mM ethylenediaminetetraacetic acid in PBS. Cells were incubated at 37°C, 5% CO_2 for 120 hours. Viable cells were detected by addition of 75μL/well of CellTiter-Glo® reagent (Promega), followed by mixing on a plate shaker for 2 minutes, and incubation in the dark at room temperature for a further 10

minutes. Plates were read on a SpectraMax M5 plate reader (Molecular Devices) set to luminescence mode, with a read time of 0.5 seconds/well against a blank of medium only. Data were plotted as a percentage of PBS-treated cell growth against the logarithm of FN3 domain molar concentration. IC_{50} values were determined by fitting data to the equation for a sigmoidal dose response with variable slope using GraphPad Prism 4 (GraphPad Software). Table 5 shows IC_{50} values ranging from 5.9 nM to 1.15 μM and 9.2 nM to > 3.1 μM, using the NCI-H292 and NCI-H322 cells respectively. Table 5 shows the summary of biological properties of EGFR-binding FN3 domains for each assay.

Table 5.

FN3 Domain Clone ID	SEQ ID NO:	EGFR-Fc Affinity (nM)	A431 Cell Binding	A431 Cell EGF Competition	Phospho-EGFR	NCI-H292 Growth	NCI-H322 Growth
			EC_{50} (nM)	IC_{50} (nM)	IC_{50} (nM)	IC_{50} (nM)	IC_{50} (nM)
P53A1R5-17	18	1.89	4.0	9.8	>2500	86	65
P54AR4-17	19	9.62	16	21	184	ND	ND
P54AR4-47	20	2.51	8.6	7.1	295	44	39
P54AR4-48	21	7.78	12	9.8	170	ND	ND
P54AR4-73	22	0.197	9.4	4.6	141	83	73
P54AR4-74	23	ND	77	ND	ND	ND	ND
P54AR4-81	24	ND	84	121	ND	ND	ND
P54AR4-83	25	0.255	2.2	1.8	18	5.9	9.2
P54CR4-31	26	0.383	>20000	55	179	1150	>3073

Example 4: Engineering of EGFR-Binding FN3 domains

A subset of the EGFR binding FN3 domains was engineered to increase the conformational stability of each molecule. The mutations L17A, N46V, and E86I which have been shown to improve FN3 domain stability (described in US Pat. Publ. No. US2011/0274623) were incorporated into clones P54AR4-83, P54CR4-31, and P54AR4-37 by DNA synthesis. The new mutants, P54AR5-83v2, P54CR431-v2, and P54AR4-37v2 were expressed and purified as described above. Differential scanning calorimetry in PBS was used to assess the stability of each mutant in order to compare it to that of the corresponding parent molecule. Table 6 shows that each variant molecule was stabilized significantly, with an average increase in the T_m of 18.5°C.

Table 6.

FN3 domain Clone	SEQID NO:	T_m (°C)
P54AR4-83	25	50.6
P54AR4-83v2	27	69.8
P54CR4-31	26	60.9
P54CR4-31v2	28	78.9
P54AR4-37	22	45.9
P54AR4-37v2	29	64.2

Example 5: Selection of fibronectin type III (FN3) domains that bind c-Met and Inhibit HGF Binding

Panning on human c-Met

The TCL14 library was screened against biotinylated-human c-Met extracellular domain (bt-c-Met) to identify FN3 domains capable of specifically binding c-Met. For selections, 3 µg of TCL14 library was *in vitro* transcribed and translated (IVTT) in *E. Coli* S30 Linear Extract (Promega, Madison, WI) and the expressed library blocked with Cis

Block (2% BSA (Sigma-Aldrich, St. Louis, MO), 100 µg/ml Herring Sperm DNA (Promega), 1 mg/mL heparin (Sigma-Aldrich)). For selections, bt-c-Met was added at concentrations of 400 nM (Round 1), 200 nM (Rounds 2 and 3) and 100 nM (Rounds 4 and 5). Bound library members were recovered using neutravidin magnetic beads (Thermo Fisher, Rockford, IL) (Rounds 1, 3, and 5) or streptavidin magnetic beads (Promega) (Rounds 2 and 4) and unbound library members were removed by washing the beads 5-14 times with 500 uL PBS-T followed by 2 washes with 500 µL PBS.

Additional selection rounds were performed to identify FN3 domains molecules with improved affinities. Briefly, outputs from round 5 were prepared as described above and subjected to additional iterative rounds of selection with the following changes: incubation with bt-c-Met was decreased from 1 hour to 15 minutes and bead capture was decreased from 20 minutes to 15 minutes, bt-c-Met decreased to 25 nM (Rounds 6 and 7) or 2.5 nM (Rounds 8 and 9), and an additional 1 hour wash was performed in the presence of an excess of non-biotinylated c-Met. The goal of these changes was to simultaneously select for binders with a potentially faster on-rate and a slower off-rate yielding a substantially lower K_D.

Rounds 5, 7 and 9 outputs were PCR cloned into a modified pET15 vector (EMD Biosciences, Gibbstown, NJ) containing a ligase independent cloning site (pET15-LIC) using TCON6 (SEQID No. 30) and TCON5 E86I short (SEQID No. 31) primers, and the proteins were expressed as C-terminal His6-tagged proteins after transformations and IPTG induction (1 mM final, 30°C for 16 hours) using standard protocols. The cells were harvested by centrifugation and subsequently lysed with Bugbuster HT (EMD Biosciences) supplemented with 0.2 mg/mL Chicken Egg White Lysozyme (Sigma-Aldrich). The bacterial lysates were clarified by centrifugation and the supernatants were transferred to new 96 deep-well plates.

Screening for FN3 domains that Inhibit HGF Binding to c-Met

FN3 domains present in *E. coli* lysates were screened for their ability to inhibit HGF binding to purified c-Met extracellular domain in a biochemical format. Recombinant human c-Met Fc chimera (0.5 µg/mL in PBS, 100 µL/well) was coated on 96-well White Maxisorp Plates (Nunc) and incubated overnight at 4°C. The plates were washed two times with 300 µl/well of Tris-buffered saline with 0.05% Tween 20 (TBS-T, Sigma-Aldrich) on a Biotek plate washer. Assay plates were blocked with StartingBlock

T20 (200 µL/well, Thermo Fisher Scientific, Rockland, IL) for 1 hour at room temperature (RT) with shaking and again washed twice with 300 µl of TBS-T. FN3 domain lysates were diluted in StartingBlock T20 (from 1:10 to 1:100,000) using the Hamilton STARplus robotics system. Lysates (50 µL/well) were incubated on assay plates for 1 hour at RT with shaking. Without washing the plates, bt-HGF (1 µg/mL in StartingBlock T20, 50 µL/well, biotinylated) was added to the plate for 30 min at RT while shaking. Control wells containing Tencon27 lysates received either Starting Block T20 or diluted bt-HGF. Plates were then washed four times with 300 µl/well of TBS-T and incubated with 100 µl/well of Streptavidin-HRP (1:2000 in TBS-T, Jackson Immunoresearch, West Grove, PA) for 30-40 minutes at RT with shaking. Again the plates were washed four times with TBS-T. To develop signal, POD Chemiluminescence Substrate (50 µL/well, Roche Diagnostics, Indianapolis, IN), prepared according to manufacturer's instructions, was added to the plate and within approximately 3 minutes luminescence was read on the Molecular Devices M5 using SoftMax Pro. Percent inhibition was determined using the following calculation: $100-((RLU_{sample}-\text{Mean } RLU_{\text{No bt-HGF control}})/(\text{Mean } RLU_{\text{bt-HGF control}}-\text{Mean } RLU_{\text{No bt-HGF control}})*100)$. Percent inhibition values of 50% or greater were considered hits.

High-throughput Expression and Purification of FN3 domains

His-tagged FN3 domains were purified from clarified *E. coli* lysates with His MultiTrap™ HP plates (GE Healthcare) and eluted in buffer containing 20 mM sodium phosphate, 500 mM sodium chloride, and 250 mM imidazole at pH 7.4. Purified samples were exchanged into PBS pH 7.4 for analysis using PD MultiTrap™ G-25 plates (GE Healthcare).

IC_{50} determination of Inhibition of HGF Binding to c-Met

Select FN3 domains were further characterized in the HGF competition assay. Dose response curves for purified FN3 domains were generated utilizing the assay described above (starting concentrations of 5 µM). Percent inhibition values were calculated. The data were plotted as % inhibition against the logarithm of FN3 domain molar concentrations and IC_{50} values were determined by fitting data to a sigmoidal dose response with variable slope using GraphPad Prism 4.

35 unique sequences were identified from Round 5 to exhibit activity at dilutions of 1:10, with IC_{50} values ranging from 0.5 to 1500 nM. Round 7 yielded 39 unique sequences with activity at dilutions of 1:100 and IC_{50} values ranging from 0.16 to 2.9 nM. 66 unique sequences were identified from Round 9, where hits were defined as being active at dilutions of 1:1000. IC_{50} values as low as 0.2 nM were observed in Round 9 (Table 8).

Affinity Determination of Selected c-Met-binding FN3 domains to c-Met-Fc (EGFR-Fc Affinity)

Affinities were determined for select c-Met binding FN3 domains as is described in Example 3 for affinity determination fo selected EGFR-binding FN3 domains, except that c-Met-Fc was used in the assays.

Example 6: Characterization of FN3 domains that Bind c-Met and Inhibit HGF Binding

FN3 domains were expressed and purified as described above in Example 2. Size exclusion chromatography and kinetic analysis was done as described above in Examples 1 and 2, respectively. Table 7 shows the sequences of the C-strand, CD loop, F-strand, and FG loop, and a SEQ ID NO: for the entire amino acid sequence for each domain.

Table 7.

Clone		C loop	CD strand	F loop	FG strand
Name	SEQ ID NO:				
P114AR5P74-A5	32	FDSFWIRYDE	VVVGGE	TEYYVNILGV	KGGSISV
P114AR5P75-E9	33	FDSFFIRYDE	FLRSGE	TEYWVTILGV	KGGLVST
P114AR7P92-F3	34	FDSFWIRYFE	FLGSGE	TEYIVNIMGV	KGGSISH
P114AR7P92-F6	35	FDSFWIRYFE	FLGSGE	TEYVVNILGV	KGGGLSV
P114AR7P92-G8	36	FDSFVIRYFE	FLGSGE	TEYVVQILGV	KGGYISI
P114AR7P92-H5	37	FDSFWIRYLE	FLLGGE	TEYVVQIMGV	KGGTVSP
P114AR7P93-D11	38	FDSFWIRYFE	FLGSGE	TEYVVGINGV	KGGYISY
P114AR7P93-G8	39	FDSFWIRYFE	FLGSGE	TEYGVTINGV	KGGRVST

P114AR7P93-H9	40	FDSFWIRYFE	FLGSGE	TEYVVQIIGV	KGGHISL
P114AR7P94-A3	41	FDSFWIRYFE	FLGSGE	TEYVVNIMGV	KGGKISP
P114AR7P94-E5	42	FDSFWIRYFE	FLGSGE	TEYAVNIMGV	KGGRVSV
P114AR7P95-B9	43	FDSFWIRYFE	FLGSGE	TEYVVQILGV	KGGSISV
P114AR7P95-D3	44	FDSFWIRYFE	FLGSGE	TEYVVNIMGV	KGGSISY
P114AR7P95-D4	45	FDSFWIRYFE	FLGSGE	TEYVVQILGV	KGGYISI
P114AR7P95-E3	46	FDSFWIRYFE	FLGSGE	TEYVVQIMGV	KGGTVSP
P114AR7P95-F10	47	FDSFWIRYFE	FTTAGE	TEYVVNIMGV	KGGSISP
P114AR7P95-G7	48	FDSFWIRYFE	LLSTGE	TEYVVNIMGV	KGGSISP
P114AR7P95-H8	49	FDSFWIRYFE	FVSKGE	TEYVVNIMGV	KGGSISP

C loop residues correspond to residues 28-37 of indicated SEQ ID NO

CD strand residues correspond to residues 38-43 of indicated SEQ ID NO

F loop residues correspond to residues 65-74 of indicated SEQ ID NO

FG strand residues correspond to residues 75-81 of indicated SEQ ID NO

Binding of Selected c-Met-binding FN3 domains to c-Met on Cells ("H441 Cell Binding Assay")

NCI-H441 cells (Cat # HTB-174, American Type Culture Collection, Manassas, VA) were plated at 20,000 cells per well in Poly-D-lysine coated black clear bottom 96-well plates (BD Biosciences, San Jose, CA) and allowed to attach overnight at 37°C, 5% CO_2. Purified FN3 domains (50 µL/well; 0 to 1000 nM) were added to the cells for 1 hour at 4°C in duplicate plates. Supernatant was removed and cells were washed three times with FACS stain buffer (150 µL/well, BD Biosciences, cat # 554657). Cells were incubated with biotinylated-anti HIS antibody (diluted 1:160 in FACS stain buffer, 50 µL/well, R&D Systems, cat # BAM050) for 30 minutes at 4°C. Cells were washed three times with FACS stain buffer (150 µL/well), after which wells were incubated with anti mouse IgG1-Alexa 488 conjugated antibody (diluted 1:80 in FACS stain buffer, 50 µL/well, Life Technologies, cat # A21121) for 30 minutes at 4°C. Cells were washed three times with FACS stain buffer (150 µL/well) and left in FACS stain buffer (50 µL/well). Total fluorescence was determined using an Acumen eX3 reader. Data were plotted as raw fluorescence signal against the logarithm of the FN3 domain molar concentration and fitted to a sigmoidal dose-response curve with variable slope using GraphPad Prism 4 (GraphPad Software) to calculate EC_{50} values. FN3 domains were found to exhibit a

range of binding activities, with EC_{50} values between 1.4 nM and 22.0 nM, as shown in Table 8.

Inhibition of HGF-Stimulated c-Met Phosphorylation

Purified FN3 domains were tested for their ability to inhibit HGF-stimulated phosphorylation of c-Met in NCI-H441, using the c-Met phospho(Tyr1349) kit from Meso Scale Discovery (Gaithersburg, MD). Cells were plated at 20,000/well in clear 96-well tissue culture-treated plates in 100 µL/well of RPMI medium (containing Glutamax and HEPES, Life Technologies) with 10% fetal bovine serum (FBS; Life Technologies) and allowed to attach overnight at 37°C, 5% CO_2. Culture medium was removed completely and cells were starved overnight in serum-free RPMI medium (100 µL/well) at 37°C, 5% CO_2. Cells were then replenished with fresh serum-free RPMI medium (100 µL/well) containing FN3 domains at a concentration of 20 µM and below for 1 hour at 37°C, 5% CO_2. Controls were treated with medium only. Cells were stimulated with 100 ng/mL recombinant human HGF (100 µL/well, R&D Systems cat # 294-HGN) and incubated at 37°C, 5% CO_2 for 15 minutes. One set of control wells was left un-stimulated as negative controls. Medium was then completely removed and cells were lysed with Complete Lysis Buffer (50 µL/well, Meso Scale Discovery) for 10 minutes at RT with shaking, as per manufacturer's instructions. Assay plates configured for measuring phosphorylated c-Met were blocked with the provided blocking solution as per the manufacturer's instructions at room temperature for 1 hour. Plates were then washed three times with Tris Wash Buffer (200 µL/well, Meso Scale Discovery). Cell lysates (30 µL/well) were transferred to assay plates, and incubated at RT with shaking for 1 hour. Assay plates were then washed four times with Tris Wash Buffer, after which ice-cold Detection Antibody Solution (25 µL/well, Meso Scale Discovery) was added to each well for 1hr at RT with shaking. Plates were again rinsed four times with Tris Wash Buffer. Signals were detected by addition of 150 Read Buffer (150 µL/well, Meso Scale Discovery) and reading on a SECTOR® Imager 6000 instrument (Meso Scale Discovery) using manufacturer-installed assay-specific default settings. Data were plotted as electrochemiluminescence signal against the logarithm of FN3 domain molar concentration and IC_{50} values were determined by fitting data to a sigmoidal dose response with variable slope using GraphPad Prism 4. FN3 domains were found to inhibit phosphorylated c-Met with IC_{50} values ranging from 4.6 nM to 1415 nM as shown in Table 8.

Inhibition of Human Tumor Cell Growth or Viability

Inhibition of c-Met-dependent cell growth was assessed by measuring viability of U87-MG cells (American Type Culture Collection, cat # HTB-14), following exposure to c-Met-binding FN3 domains. Cells were plated at 8000 cells per well in opaque white 96-well tissue culture-treated plates (Nunc) in 100 µL/well of RPMI medium, supplemented with 10% FBS and allowed to attach overnight at 37°C, 5% CO_2. Twenty-four hours after plating, medium was aspirated and cells were replenished with serum-free RPMI medium. Twenty-four hours after serum starvation, cells were treated by addition of serum-free medium containing c-Met-binding FN3 domains (30 µL/well). Cells were incubated at 37°C, 5% CO_2 for 72 hours. Viable cells were detected by addition of 100 µL/well of CellTiter-Glo® reagent (Promega), followed by mixing on a plate shaker for 10 minutes. Plates were read on a SpectraMax M5 plate reader (Molecular Devices) set to luminescence mode, with a read time of 0.5 seconds/well. Data were plotted as raw luminescence units (RLU) against the logarithm of FN3 domain molar concentration. IC_{50} values were determined by fitting data to an equation for a sigmoidal dose response with variable slope using GraphPad Prism 4. Table 8 reports IC_{50} values ranging from 1 nM to >1000 nM. Characteristics of the c-Met binding FN3 domains are summarized in Table 8.

Table 8.

Clone		Affinity (Kd, nM)	HGF competition IC_{50} (nM)	H441 Cell binding (EC_{50}, nM)	pMet inhibition in H441 cells (IC_{50}, nM)	Inhbibition of Proliferation of U87-MG cells (IC_{50}, nM)
Name	SEQ ID NO:					
P114AR5P74-A5	32	10.1	5.2	18.7	1078	464.4
P114AR5P75-E9	33	45.8	51.9	ND	1415	1193.9
P114AR7P92-F3	34	0.4	0.2	1.5	8.3	2.7
P114AR7P92-F6	35	3.1	2.2	4.9	165.3	350.5
P114AR7P92-G8	36	1.0	1.6	5.9	155.3	123.9
P114AR7P92-H5	37	11.6	ND	22.0	766.4	672.3
P114AR7P93-D11	38	ND	ND	2.3	16	14.4
P114AR7P93-G8	39	6.9	1	3.8	459.5	103.5
P114AR7P93-H9	40	3.3	2.9	12.9	288.2	269.9

P114AR7P94-A3	41	0.4	0.2	1.4	5	9.3
P114AR7P94-E5	42	4.2	0.7	3.4	124.3	195.6
P114AR7P95-B9	43	0.5	0.3	ND	9.8	17.4
P114AR7P95-D3	44	0.3	0.2	1.5	4.6	1.7
P114AR7P95-D4	45	0.4	ND	1.4	19.5	19.4
P114AR7P95-E3	46	1.5	ND	3.2	204.6	209.2
P114AR7P95-F10	47	4.2	1.4	4.4	187.6	129.7
P114AR7P95-G7	48	20.0	ND	11.3	659.3	692
P114AR7P95-H8	49	3.7	ND	4.1	209.8	280.7

Thermal stability of c-Met –binding FN3 domains

Differential scanning calorimetry in PBS was used to assess the stability of each FN3 domain. Results of the experiment are shown in Table 9.

Table 9.

Clone		Thermal Stability (Tm, C)
Name	SEQ ID NO:	
P114AR5P74-A5	32	74.1
P114AR5P75-E9	33	ND
P114AR7P92-F3	34	81.5
P114AR7P92-F6	35	76.8
P114AR7P92-G8	36	90.9
P114AR7P92-H5	37	87
P114AR7P93-D11	38	ND
P114AR7P93-G8	39	76.8
P114AR7P93-H9	40	88.2
P114AR7P94-A3	41	86.2
P114AR7P94-E5	42	80
P114AR7P95-B9	43	86.3
P114AR7P95-D3	44	82
P114AR7P95-D4	45	85.3
P114AR7P95-E3	46	94.2
P114AR7P95-F10	47	85.2
P114AR7P95-G7	48	87.2
P114AR7P95-H8	49	83

Example 7. Generation and Characterization of Bispecific anti-EGFR/c-Met molecules

Generation of bispecific EGFR/c-Met molecules

Numerous combinations of the EGFR and c-Met-binding FN3 domains described in Examples 1-6 were joined into bispecific molecules capable of binding to both EGFR and c-Met. Additionally, EGFR-binding FN3 domains having amino acid sequences shown in SEQ ID NOs: 107-110 and c-Met binding FN3 domains having amino acid sequences shown in SEQ ID NOs: 111-114 were made and joined into bispecific molecules. Synthetic genes were created to encode for the amino acid sequences described in SEQ ID NOs: 50-72 and 106 (Table 10) such that the following format was maintained: EGFR-binding FN3 domain followed by a peptide linker followed by a c-Met-binding FN3 domain. A poly-histidine tag was incorporated at the C-terminus to aid purification. In addition to those molecules described in Table 10, the linker between the two FN3 domains was varied according to length, sequence composition and structure according to those listed in Table 11. It is envisioned that a number of other linkers could be used to link such FN3 domains Bispecific EGFR/c-Met molecules were expressed and purified from *E. coli* as described for monospecific EGFR or c-Met FN3 domains using IMAC and gel filtration chromatography steps.

Table 10.

Bispecifcic EGFR/c-Met molecule		EGFR-binding FN3 comain		cMET-binding FN3 domain		Linker	
Clone ID	SEQ ID NO:	Clone ID	SEQ ID NO:	Clone ID	SEQ ID NO:	Sequence	SEQ ID NO:
ECB1	50	P54AR4-83v2	27	P114AR5P74-A5	32	$(GGGGS)_4$	79
ECB2	51	P54AR4-83v2	27	P114AR7P94-A3	41	$(GGGGS)_4$	79
ECB3	52	P54AR4-83v2	27	P114AR7P93-H9	40	$(GGGGS)_4$	79
ECB4	53	P54AR4-83v2	27	P114AR5P75-E9	33	$(GGGGS)_4$	79
ECB5	54	P53A1R5-17v2	107	P114AR7P94-A3	41	$(GGGGS)_4$	79
ECB6	55	P53A1R5-17v2	107	P114AR7P93-H9	40	$(GGGGS)_4$	79
ECB7	56	P53A1R5-17v2	107	P114AR5P75-E9	33	$(GGGGS)_4$	79
ECB15	57	P54AR4-83v2	27	P114AR7P94-A3	41	$(AP)_5$	81
ECB27	58	P54AR4-83v2	27	P114AR5P74-A5	32	$(AP)_5$	81
ECB60	59	P53A1R5-17v2	107	P114AR7P94-A3	41	$(AP)_5$	81
ECB37	60	P53A1R5-17v2	107	P114AR5P74-A5	32	$(AP)_5$	81
ECB94	61	P54AR4-83v22	108	P114AR7P94-A3v22	111	$(AP)_5$	81
ECB95	62	P54AR4-83v22	108	P114AR9P121-A6v2	112	$(AP)_5$	81
ECB96	63	P54AR4-83v22	108	P114AR9P122-A7v2	113	$(AP)_5$	81
ECB97	64	P54AR4-83v22	108	P114AR7P95-C5v2	114	$(AP)_5$	81
ECB106	65	P54AR4-83v23	109	P114AR7P94-A3v22	111	$(AP)_5$	81
ECB107	66	P54AR4-83v23	109	P114AR9P121-A6v2	112	$(AP)_5$	81
ECB108	67	P54AR4-83v23	109	P114AR9P122-A7v2	113	$(AP)_5$	81
ECB109	68	P54AR4-83v23	109	P114AR7P95-C5v2	114	$(AP)_5$	81
ECB118	69	P53A1R5-17v22	110	P114AR7P94-A3v22	111	$(AP)_5$	81
ECB119	70	P53A1R5-17v22	110	P114AR9P121-A6v2	112	$(AP)_5$	81
ECB120	71	P53A1R5-17v22	110	P114AR9P122-A7v2	113	$(AP)_5$	81
ECB121	72	P53A1R5-17v22	110	P114AR7P95-C5v2	114	$(AP)_5$	81
ECB91	106	P54AR4-83v22	108	P114AR7P95-C5v2	114	$(AP)_5$	81
ECB18	118	P54AR4-83v2	27	P114AR5P74-A5	32	$(AP)_5$	81
ECB28	119	P53A1R5-17v2	107	P114AR5P74-A5	32	$(AP)_5$	81
ECB38	120	P54AR4-83v2	27	P114AR7P94-A3	41	$(AP)_5$	81
ECB39	121	P53A1R5-17v2	107	P114AR7P94-A3	41	$(AP)_5$	81

Table 11.

Linker	SEQ ID NO:	Linker length in amino acids	Structure
GS	78	2	Disordered
GGGGS	105	5	Disordered
$(GGGGS)_4$	79	20	Disordered
$(AP)_2$	80	4	Rigid
$(AP)_5$	81	5	Rigid
$(AP)_{10}$	82	20	Rigid

$(AP)_{20}$	83	40	Rigid
$A(EAAAK)_5AAA$	84	29	α-helical

Bispecific EGFR/c-Met molecules enhance potency compared to monospecific molecules alone, suggesting avidity

NCI-H292 cells were plated in 96 well plates in RPMI medium containing 10% FBS. 24 hours later, medium was replaced with serum free RPMI. 24 hours after serum starvation, cells were treated with varying concentrations of FN3 domains: either a high affinity monospecific EGFR FN3 domain (P54AR4-83v2), a weak affinity monospecific c-Met FN3 domain (P114AR5P74-A5), the mixture of the two monospecific EGFR and c-Met FN3 domains, or a bispecific EGFR/c-Met molecules comprised of the low affinity c-Met FN3 domain linked to the high affinity EGFR FN3 domain (ECB1). Cells were treated for 1h with the monospecific or bispecific molecules and then stimulated with EGF, HGF, or a combination of EGF and HGF for 15 minutes at 37°C, 5% CO_2. Cells were lysed with MSD Lysis Buffer and cell signaling was assessed using appropriate MSD Assay plates, according to manufacturer's instructions, as described above.

The low affinity c-Met FN3 domain inhibited phosphorylation of c-Met with an IC_{50} of 610 nM (Figure 4). As expected the EGFR FN3 domain was not able to inhibit c-Met phosphorylation and the mixture of the mono-specific molecules looked identical to the c-Met FN3 domain alone. However, the bi-specific EGFR/c-Met molecule inhibited phosphorylation of c-Met with an IC_{50} of 1 nM (Figure 4), providing more than a 2-log shift in improving potency relative to the c-Met monospecific alone.

The potential for the bispecific EGFR/c-Met molecule to enhance the inhibition of c-Met and/or EGFR phosphorylation through an avidity effect was evaluated in multiple cell types with variable c-Met and EGFR densities and ratios (Figure 5). NCI-H292, NCI-H441, or NCI-H596 cells were plated in 96 well plates in RPMI medium containing 10% FBS. 24 hours later, medium was replaced with serum free RPMI. 24 hours after serum starvation, cells were treated with varying concentrations of either monospecific EGFR-binding FN3 domain, monospecific c-Met FN3 domain, or a bispecific EGFR/c-Met molecule (ECB5, comprised of P53A1R5-17v2 and P114AR7P94-A3). Cells were treated for 1h with the monospecific or bispecific molecules and then stimulated with EGF, HGF, or a combination of EGF and HGF for 15 minutes at 37°C, 5% CO_2. Cells were lysed

with MSD Lysis Buffer and cell signaling was assessed using appropriate MSD Assay plates, according to manufacturer's instructions, as described above.

Figure 5 (A-C) shows the inhibition of EGFR using a monospecific EGFR-binding FN3 domain compared to a bispecific EGFR/cMet molecule in three different cell lines. To assess avidity in an EGFR phosphorylation assay, a medium affinity EGFR-binding FN3 domain (1.9 nM) (P53A1R5-17v2) was compared to a bispecific EGFR/c-Met molecule containing the same EGFR-binding FN3 domain linked to a high-affinity c-Met-binding FN3 domain (0.4 nM) (P114AR7P94-A3). In NCI-H292 and H596 cells, inhibition of phosphorylation of EGFR was comparable for the monospecific and bispecific molecules (Figures 5A and 5B), likely because these cell lines have a high ratio of EGFR to c-Met receptors. To test this theory, inhibition of EGFR phosphorylation was evaluated in NCI-H441 cells which exhibit more c-Met receptors than EGFR. Treatment of NCI-H441 cells with the bispecific EGFR/c-Met molecule decreased the IC_{50} for inhibition of EGFR phosphorylation compared to the monospecific EGFR-binding FN3 domain by 30-fold (Figure 5C).

The potential for enhanced potency with a bi-specific EGFR/c-Met molecule was evaluated in a c-Met phosphorylation assay using a molecule with a high affinity to EGFR (0.26 nM) and medium affinity to c-Met (10.1 nM). In both NCI-H292 and NCI-H596 cells, the inhibition of phosphorylation of c-Met was enhanced with the bispecific molecule compared to the monospecific c-Met-binding FN3 domain, by 134 and 1012 fold, respectively (Figure 3D and 3E).

It was verified that the enhanced potency for inhibition of EGFR and c-Met phosphorylation with the bispecific EGFR/c-Met molecules translated into an enhanced inhibition of signaling and proliferation. For these experiments, the mixture of FN3 EGFR-binding and c-Met-binding FN3 domains was compared to a bispecific EGFR/c-Met molecule. As described in Tables 12 and 13, the IC_{50} values for ERK phosphorylation (Table 12) and proliferation of NCI-H292 cells (Table 13) were decreased when cells were treated with the bispecific EGFR/c-Met molecule compared to the mixture of the monospecific binders. The IC_{50} for inhibition of ERK phosphorylation for the bi-specific EGFR/c-Met molecule was 143-fold lower relative to the mixture of the two monospecific EGFR and c-Met FN3 domains, showing the effect of avidity to the potency of the molecules in this assay. In Table 12, the monospecific EGFR- and c-Met binding FN3 domains do not fully inhibit activity and therefore the IC_{50} values shown should be considered lower limits. The proliferation assay was completed using different combinations EGFR and c-Met binding FN3 domains either as a mixture or linked in a

bispecific format. The IC_{50} for inhibition of proliferation for the bispecific EGFR/c-Met molecule was 34-236-fold lower relative to the mixture of the monospecific parent EGFR or c-Met binding FN3 domains. This confirmed that the avidity effect observed at the level of the receptors (Figure 4 and Figure 5) translates into an improvement in inhibiting cell signaling (Table 12) and cell proliferation (Table 13).

Table 12.

Specificity of the FN3-domain molecule	Clone name	Type	IC_{50} (nM) (ERK phosphorylation)
EGFR	P54AR4-83v2	monospecific	>10,000
c-Met	P114AR5P74-A5	monospecific	2366
EGFR or c-Met	P54AR4-83v2 + P114AR5P74-A5	mixture of monospecific molecules	798.4
EGFR and c-Met	ECB1	bispecific	5.6

Table 13.

EGFR-binding FN3 domain (affinity)	c-Met binding FN3 domain (affinity)	IC_{50} for mixture of monospecific molecules (nM)	IC_{50} for bispecific molecule (nM)	Fold increase in IC_{50} for mixture of monospecific/ bispecific
P54AR4-83v2 (0.26 nM)	P114ARP94-A3 (0.4 nM)	36.5	1.04	35

P54AR4-83v2 (0.26 nM)	P114AR7P93-H9 (3.3 nM)	274.5	8.05	34
P54AR4-83v2 (0.26 nM)	P114AR5P74-A5 (10.1 nM)	1719	7.29	236

***In vivo* tumor xenografts: PK/PD**

In order to determine efficacy of the monospecific and bispecific FN3 domain molecules *in vivo*, tumor cells were engineered to secrete human HGF (murine HGF does not bind to human c-Met). Human HGF was stably expressed in NCI-H292 cells using lentiviral infection (Lentiviral DNA vector expressing human HGF (Accession #X16322) and lentiviral packaging kit from Genecopoeia). After infection, HGF-expressing cells were selected with 4 μg/mL puromycin (Invitrogen). Human HGF protein was detected in the conditioned medium of pooled cells using assay plates from MesoScale Discovery.

SCID Beige mice were subcutaneously inoculated with NCI-H292 cells expressing human HGF ($2.0x10^6$ cells in Cultrex (Trevigen) in a volume of 200 μL) on the dorsal flank of each animal. Tumor measurements were taken twice weekly until tumor volumes ranged between 150-250 mm^3. Mice were then given a single i.p. dose of bispecific EGFR/c-Met molecules (linked to an albumin binding domain to increase half-life) or PBS vehicle. At 6h or 72h after dosing, tumors were extracted and immediately frozen in liquid nitrogen. Blood samples were collected via cardiac puncture into 3.8% citrate containing protease inhibitors. Immediately after collection, the blood samples were centrifuged and the resulting plasma was transferred to sample tubes and stored at -80°C. Tumors were weighed, cut into small pieces, and lysed in Lysing Matrix A tubes (LMA) containing RIPA buffer with HALT protease/phosphatase inhibitors (Pierce), 50 mM sodium fluoride (Sigma), 2 mM activated sodium orthovanadate (Sigma), and 1 mM PMSF (MesoScale Discovery). Lysates were removed from LMA matrix and centrifuged to remove insoluble protein. The soluble tumor protein was quantified with a BCA protein assay and diluted to equivalent protein levels in tumor lysis buffer. Phosphorylated c-Met, EGFR and ERK were measured using assay plates from MesoScale Discovery (according to Manufacturer's protocol and as described above).

Figure 6 shows the results of the experiments. Each bispecific EGFR/c-Met molecule significantly reduced the levels of phosphorylated c-Met, EGFR, and ERK at both 6h and 72h. The data presented in Figure 6 show the importance of inhibiting both c-

Met and EGFR simultaneously and how the affinity of the bispecific EGFR/c-Met molecule for each receptor plays a role in inhibition of downstream ERK. The molecules containing the high affinity EGFR-binding FN3 domains (P54AR4-83v2; shown as "8" in the Figure, K_D=0.26 nM) inhibited phosphorylation of EGFR to a larger extent compared to those containing the medium affinity EGFR-binding FN3 domains (P53A1R5-17v2; shown as "17" in the figure K_D =1.9 nM) at both 6h and 72h. All four bispecific molecules tested completely inhibited phosphorylation of ERK at the 6 hour time point, regardless of affinity. At the 72 hour time point, the molecules containing the tight affinity c-Met-binding domain (P114AR7P94-A3; shown as "A3" in the figure K_D =0.4 nM) significantly inhibited phosphorylation of ERK compared to the medium affinity c-Met-binding FN3 domain (P114AR5P74-A5; shown as "A5" in the Figure; K_D =10.1 nM; Figure 6).

The concentration of each bispecific EGFR/c-Met molecule was measured at 6 and 72 hours after dosing in the blood and in the tumor (Figure 7). Interestingly, the bispecific molecule with the medium affinity EGFR-binding domain (P53A1R5-17v2 ; K_D =1.9 nM) but high affinity c-Met-binding FN3 domain (P114AR7P94-A3; K_D =0.4 nM) had significantly more tumor accumulation at 6 hours relative to the other molecules, while the difference is diminished by 72 hours. It can be hypothesized that cells outside the tumor have lower levels of both EGFR and c-Met surface expression and therefore the medium affinity EGFR molecule doesn't bind to normal tissue as tightly compared to the higher affinity EGFR-binding FN3 domain. Therefore there is more free medium affinity EGFR-binding FN3 domain available to bind in the tumor. Therefore, identifying the appropriate affinities to each receptor may allow for identification of a therapeutic with decreased systemic toxicities and increased tumor accumulation.

Tumor efficacy studies with bispecific EGFR/c-Met molecules

SCID Beige mice were subcutaneously inoculated with NCI-H292 cells expressing human HGF ($2.0x10^6$ cells in Cultrex (Trevigen) in 200 µL) in the dorsal flank of each animal. One week after implantation, mice were stratified into groups with equivalent tumor volumes (mean tumor volume=77.9+/-1.7mm^3). Mice were dosed three times per week with the bispecific molecules and tumor volumes were recorded twice weekly. Tumor growth inhibition (TGI) was observed with four different bispecific molecules, with variable affinities for c-Met and EGFR. Figure 8 shows the benefit of inhibiting both c-Met and EGFR as a delay in tumor growth was observed in the mice

treated with molecules containing the high affinity EGFR-binding FN3 domain compared to the medium affinity EGFR-binding FN3 domain when the c-Met-binding FN3 domain was medium affinity (open vs. closed triangles, P54AR4-83v2- P114AR5P74-A5 compared to P53A1R5-17- P114AR5P74-A5). In addition, the data shows the importance of having a high affinity c-Met-binding FN3 domain as bispecific molecules containing either the high or medium affinity EGFR-binding FN3 domain but high affinity c-Met-binding FN3 domain showed the most efficacy (dotted gray and black lines, P54AR4-83v2- P114AR7P94-A3 and P53A1R5-17v2- P114AR7P94-A3).

Efficacy of bispecific molecule and other inhibitors of EGFR and c-Met

The *in vivo* therapeutic efficacies of a bispecific EGFR/c-Met molecule (ECB38) and the small molecule inhibitors crizotinib (c-Met inhibitor) and erlotinib (EGFR inhibitor), cetuximab (anti-EGFR antibody), each as a single agent, and the combination of crizotinib and erlotinib were evaluated in the treatment of subcutaneous H292-HGF human lung cancer xenograft model in SCID/Beige mice.

The H292-HGF cells were maintained *in vitro* in RPMI1640 medium supplemented with fetal bovine serum (10% v/v), and L-glutamine (2 mM) at 37°C in an atmosphere of 5% CO_2 in air. The cells were routinely subcultured twice weekly by trypsin-EDTA treatment. The cells growing in an exponential growth phase were harvested and counted for tumor inoculation.

Each mouse was inoculated subcutaneously at the right flank region with H292-HGF tumor cells (2×10^6) in 0.1 ml of PBS with Cultrex (1:1) for tumor development. The treatments were started when the mean tumor size reached 139 mm^3. The test article administration and the animal numbers in each study group were shown in the following experimental design table. The date of tumor cell inoculation was denoted as day 0. Table 14 shows the treatment groups.

Table 14.

Group	N	Treatment	Dose (mg/kg)	Dosing Route	Planned Schedule	Actual Schedule
1	10	Vehicle Control	0	*i.p.*	QD×3 weeks	QD×3 weeks
2	10	bispecific EGFR/c-Met molecule	25	*i.p.*	3 times/week ×3 weeks	3 times/week ×3 weeks

3	10	crizotinib	50	*p.o.*	QD×3 weeks	QD×17 days
4	10	erlotinib	50	*p.o.*	QD×2 weeks	QD×3 weeks
5	10	crizotinib	50	*p.o.*	QD×3 weeks	QD×3 weeks
6	10	cetuximab	1 mg/mouse	*i.p.*	Q4d*6	Q4d*6

N: animal number; *p.o.*: oral administration; *i.p.*: intraperitoneal injection 3 times/week: doses were given on days 1, 3 and 5 of the week.
QD: once daily Q4d: once every four days; the interval of the combination of crizotinib and erlotinib was 0.5hrs; dosing volume was adjusted based on body weight (10 l/g); a: dosing was not given on day 14 post grouping.

Before commencement of treatment, all animals were weighed and the tumor volumes were measured. Since the tumor volume can affect the effectiveness of any given treatment, mice were assigned into groups using randomized block design based upon their tumor volumes. This ensures that all the groups are comparable at the baseline. The randomized block design was used to assign experimental animals to groups. First, the experimental animals were divided into homogeneous blocks according to their initial tumor volume. Secondly, within each block, randomization of experimental animals to treatments was conducted. Using randomized block design to assign experimental animals ensured that each animal had the same probability of being assigned to a given treatment and therefore systematic error was reduced.

At the time of routine monitoring, the animals were checked for any effects of tumor growth and treatments on normal behavior, such as mobility, visual estimation of food and water consumption, body weight gain/loss (body weights were measured twice weekly), eye/hair matting and any other abnormal effect.

The endpoint was whether tumor growth can be delayed or tumor bearing mice can be cured. Tumor size was measured twice weekly in two dimensions using a caliper, and the volume was expressed in mm^3 using the formula: $V = 0.5\ a \times b^2$ where a and b are the long and short diameters of the tumor, respectively. The tumor size was then used for calculations of both T-C and T/C values. T-C was calculated with T as the time (in days) required for the mean tumor size of the treatment group to reach 1000 mm^3, and C was the time (in days) for the mean tumor size of the control group to reach the same size. The T/C value (in percent) was an indication of antitumor efficacy; T and C were the mean tumor volume of the treated and control groups, respectively, on a given day. Complete

tumor regression (CR) is defined as tumors that are reduced to below the limit of palpation (62.5 mm^3). Partial tumor regression (PR) is defined as tumors that are reduced from initial tumor volume. A minimum duration of CR or PR in 3 or more successive tumor measurements is required for a CP or PR to be considered durable.

Animals for which the body weight loss exceeded 20%, or for which the mean tumor size of the group exceeds 2000 mm^3 were euthanized. The study was terminated after two weeks of observation after the final dose.

Summary statistics, including mean and the standard error of the mean (SEM), are provided for the tumor volume of each group at each time point are shown in Table 15. Statistical analyses of difference in tumor volume among the groups were evaluated using a one-way ANOVA followed by individual comparisons using Games-Howell (equal variance not assumed). All data were analyzed using SPSS 18.0. $p < 0.05$ was considered to be statistically significant.

Table 15

Days	Tumor volume (mm^3)a					
	Vehicle	bispecific EGFR/c-Met molecule at 25mg/kg	crizotinib at 50mg/kg	erlotinib at 50mg/kg	crizotinib; erlotinib at 50mg/kg; 50mg/kg	cetuximab at 1 mg/mouse
7	139±7	137±7	140±9	141±8	139±8	139±10
9	230±20	142±7	217±20	201±19	134±9	168±13
13	516±45	83±6	547±43	392±46	109±10	212±20
16	808±104	44±7	914±92	560±70	127±15	252±28
20	1280±209	30±6	1438±239	872±136	214±30	371±48
23	1758±259	23±7	2102±298	1122±202	265±40	485±61
27	2264±318	21±5	--	1419±577	266±42	640±82
30	--	23±6	--	1516±623	482±61	869±100

The mean tumor size of the vehicle treated group (Group 1) reached 1,758 mm^3 at day 23 after tumor inoculation. Treatment with the bispecific EGFR/c-Met molecule at 25 mg/kg dose level (Group 2) led to complete tumor regression (CR) in all mice which were durable in >3 successive tumor measurements (average TV=23 mm^3, T/C value = 1%, p= 0.004 compared with the vehicle group at day 23).

Treatment with crizotinib as a single agent at 50 mg/kg dose level (Group 3) showed no antitumor activity; the mean tumor size was 2,102 mm^3 at day 23 (T/C value =120%, p= 0.944 compared with the vehicle group).

Treatment with erlotinib as a single agent at 50 mg/kg dosing level (Group 4) showed minor antitumor activity, but no significant difference was found compared with the vehicle group; the mean tumor size was 1,122 mm^3 at day 23 (T/C value =64%, p= 0.429 compared with the vehicle group), with 4 days of tumor growth delay at tumor size of 1,000 mm^3 compared with the vehicle group.

The combination of crizotinib (50 mg/kg, Group 5) and erlotinib (50 mg/kg, Group 5) showed significant antitumor activity; the mean tumor size was 265 mm^3 at day 23 (T/C=15%; p= 0.008), with 17 days of tumor growth delay at tumor size of 1,000 mm^3 compared with the vehicle group.

Cetuximab at 1 mg/mouse dosing level as a single agent (Group 6) showed significant antitumor activities; the mean tumor size was 485 mm^3 at day 23 (T/C=28%; p=0.018), with 17 days of tumor growth delay at tumor size of 1,000 mm^3 compared with the vehicle group. Figure 15 and Table 16 show the anti-tumor activities of the various therapies.

Table 16

Treatment	Tumor Size (mm^3) at day 23	T/C (%)	T-C (days) at 1000 mm^3	*P value*
Vehicle	1758±259	--	--	--
bispecific EGFR/c-Met molecule (25mg/kg)	23±7	1	--	0.004
crizotinib (50mg/kg)	2102±298	120	-1	0.944
erlotinib (50mg/kg)	1122±202	64	4	0.429
crizotinib+ erlotinib (50mg/kg+50mg/kg)	265±40	15	17	0.008
cetuximab (1 mg/mouse)	485±61	28	17	0.018

Medium to severe body weight loss was observed in the vehicle group which might be due to the increasing tumor burden; 3 mice died and 1 mouse were euthanized when BWL>20% by day 23. Slight toxicity of the bispecific EGFR/c-Met molecule was observed in Group 2; 3 mice were euthanized when BWL>20% during the treatment period; the body weight was gradually recovered when the treatment was withdrawn

during the 2 weeks of observation period. More severe body weight loss was observed in the crizotinib or erlotinib monotherapy group compared to the vehicle group, suggesting the treatment related toxicity. The combination of crizotinib and erlotinib was generally tolerated during the dosing phase, but severe body weight loss was observed at the end of the study, which might be due to the resumption of the fast tumor growth during the non-treatment period. The monotherapy of cetuximab was well tolerated in the study; body weight loss was only observed at the end of the study due to the resume of the tumor growth.

In summary, the bispecific EGFR/c-Met molecule at 25 mg/kg (3 times/week x 3 weeks) produced a complete response in H292-HGF human lung cancer xenograft model in SCID/Beige mice. The treatment was tolerated in 7 out of 10 mice, and resulted in severe body weight loss in 3 out of 10 mice. Figure 9 shows the impact of the various therapies on tumor size during the time points after treatment.

Example 8: Half-life extension of the bispecific EGFR/c-Met molecules

Numerous methods have been described to reduce kidney filtration and thus extend the serum half-life of proteins including modification with polyethylene glycol (PEG) or other polymers, binding to albumin, fusion to protein domains which bind to albumin or other serum proteins, genetic fusion to albumin, fusion to IgG Fc domains, and fusion to long, unstructured amino acid sequences.

Bispecific EGFR/c-Met molecules were modified with PEG in order to increase the hydrodynamic radius by incorporating a free cysteine at the C-terminus of the molecule. Most commonly, the free thiol group of the cysteine residue is used to attach PEG molecules that are functionalized with maleimide or iodoacetemide groups using standard methods. Various forms of PEG can be used to modify the protein including linear PEG of 1000, 2000, 5000, 10,000, 20,000, or 40,000 kDa. Branched PEG molecules of these molecular weights can also be used for modification. PEG groups may also be attached through primary amines in the bispecific EGFR/c-Met molecules in some instances.

In addition to PEGylation, the half-life of bispecific EGFR/c-Met molecules was extended by producing these proteins as fusion molecules with a naturally occurring 3-helix bundle serum albumin binding domain (ABD) or a consensus albumin binding domain (ABDCon). These protein domains were linked to the C-terminus of the c-Met-binding FN3 domain via any of the linkers described in Table 12. The ABD or ABDCon domain may also be placed between the EGFR-binding FN3 domain and the c-Met

binding FN3 domain in the primary sequence.

Example 9: Characterization of select bispecific EGFR/c-Met molecules

Select bispecific EGFR/c-Met molecules were characterized for their affinity to both EGFR and c-Met, their ability to inhibit EGFR and c-Met autophosphorylation, and their effect on proliferation of HGF cells. Binding affinity of the bispecific EGFR/c-Met molecules to recombinant EGFR and/or c-Met extracellular domain was further evaluated by surface Plasmon resonance methods using a Proteon Instrument (BioRad) according to protocol described in Example 3. Results of the characterization are shown in Table 17.

Table 17.

	K_D (EGFR, nM)	K_D (c-Met, nM)	pMet inhibition in H441 cells (IC_{50}, nM)	H292 pEGFR inhibition in H292 cells (IC_{50}, nM)	H292-HGF Proliferation inhibition in HGF-induced H292 cells (IC_{50}, nM)
ECB15	0.2	2.6	n/a	4.2	23
ECB94	1	4.3	53.8	5.1	29.6
ECB95	1.1	6.2	178.8	13.6	383.4
ECB96	1.6	22.1	835.4	24.7	9480
ECB97	1.3	1.7	24.2	16.6	31.0
ECB106	16.7	5.1	53.3	367.4	484.5
ECB107	16.9	9	29.9	812.3	2637
ECB108	15.3	25.5	126.2	814.4	11372
ECB109	17.3	2.1	26	432	573.6

Example 10. Generation of bispecific EGFR/cMet antibodies

Several monospecific EGFR and c-Met antibodies were expressed as IgG1, kappa, having Fc substitutions K409R or F405L (numbering according to the EU index) in their Fc regions. The monospecific antibodies were expressed in two CHO cell lines, one cell

line having reduced fucosylation ability resulting in antibodies with 1-15% fucose content in the antibody polysaccharide chain.

The monospecific antibodies were purified using standard methods using a Protein A column (HiTrap MabSelect SuRe column). After elution, the pools were dialyzed into D-PBS, pH 7.2

Bispecific EGFR/c-Met antibodies were generated by combining a monospecific EGFR mAb and a monospecific c-Met mAb in *in vitro* Fab arm exchange (as described in WO2011/131746). Briefly, at about 1-20 mg/ml at a molar ratio of 1:1 of each antibody in PBS, pH 7-7.4 and 75 mM 2-mercaptoethanolamine (2-MEA) was mixed together and incubated at 25-37ºC for 2-6 h, followed by removal of the 2-MEA via dialysis, diafiltration, tangential flow filtration and/or spinned cell filtration using standard methods.

Several monospecific anti-EGFR antibodies and anti-c-Met antibodies were combined in matrix in *in vitro* Fab arm exchange to generate bispecific antibodies that were subsequently characterized further. The generated bispecific antibodies were ranked using a four step strategy using assays as follows: Step 1: binding to NCI-H441, NCI-H1975 and A549 cells in a FACS assay. Step 2: inhibition of pMet phosphorylation in A549 cells. Step 3: inhibition of proliferation in NCI-H1975, KP4 and NCI-H441 cells. Step 4: inhibition of EGFR phosphorylation in A549 and SNU-5 cells. Noteworthy, the characteristics of the parental antibodies were not preserved in the bispecific antibody. For example, the presence of certain EGFR binding arms in the bispecific antibody resulted in a loss or reduced inhibition, or enhanced c-Met phosphorylation. Based on the characterization studies select pairs were chosen.

A monospecific bivalent anti-EGFR antibody E1-K409R was generated comprising the VH and VL regions of an anti-EGFR antibody 2F8 having the VH of SEQ ID NO: 189 and the VL of SEQ ID NO: 190 (antibody 2F8 is described in Int. Pat. Publ. No. WO2002/100348) and an IgG1 constant region with a K409R substitution.

A monospecific bivalent anti-EGFR antibody E1-F405L was generated comprising the VH and VL regions of an anti-EGFR antibody 2F8 having the VH of SEQ ID NO: 189 and the VL of SEQ ID NO: 190 (antibody 2F8 is described in Int. Pat. Publ. No. WO2002/100348) and an IgG1 constant region with a F405L substitution.

A monospecific bivalent anti-EGFR antibody E2-K409R was generated comprising the VH and VL regions of an anti-EGFR antibody 018 having the VH of SEQ

ID NO: 191 and the VL of SEQ ID NO: 192 (antibody 018 is described in Int. Pat. Publ. No. WO2009/030239) and an IgG1 constant region with a K409R substitution.

A monospecific bivalent anti-EGFR antibody E2-F405L was generated comprising the VH and VL regions of an anti-EGFR antibody 018 having the VH of SEQ ID NO: 191 and the VL of SEQ ID NO: 192 (antibody 018 is described in Int. Pat. Publ. No. WO2009/030239) and an IgG1 constant region with a F405L substitution.

A monospecific bivalent anti-c-Met antibody M1-K409R was generated comprising the VH and VL regions of an anti-c-Met antibody 069 having the VH of SEQ ID NO: 193 and the VL of SEQ ID NO: 194 (antibody 069 is described in WO2011/110642) and an IgG1 constant region with a K409R substitution.

A monospecific bivalent anti-c-Met antibody M1-F405L was generated comprising the VH and VL regions of an anti-c-Met antibody 069 having the VH of SEQ ID NO: 193 and the VL of SEQ ID NO: 194 (antibody 069 is described in WO2011/110642) and an IgG1 constant region with a F405L substitution.

A monospecific anti-c-Met antibody M2-K409R was generated comprising the VH and VL regions of an anti-c-Met antibody 058 having the VH of SEQ ID NO: 195 and the VL of SEQ ID NO: 196 (antibody 058 is described in WO2011/110642) and an IgG1 constant region with a K409R substitution.

A monospecific anti-c-Met antibody M2-F405L was generated comprising the VH and VL regions of an anti-c-Met antibody 058 having the VH of SEQ ID NO: 195 and the VL of SEQ ID NO: 196 (antibody 058 is described in WO2011/110642) and an IgG1 constant region with a F405L substitution.

The VH, VL, HC and LC sequences of the antibodies are shown below:

>SEQ ID NO: 189 EGFR mAb E1 VH
QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWD
DGSYKYYGDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGITMVRGV
MKDYFDYWGQGTLVTVSS

>SEQ ID NO: 190EGFR mAb E1 VL
AIQLTQSPSSLSASVGDRVTITCRASQDISSALVWYQQKPGKAPKLLIYDASSLESG
VPSRFSGSESGTDFTLTISSLQPEDFATYYCQQFNSYPLTFGGGTKVEIK

>SEQ ID NO: 191 EGFR mAb E2 VH

EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMNWVRQA PGKGLEWVAN IKKDGSEKYY VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDL GWGWGWYFDL WGRGTLVTVSS

>SEQ ID NO: 192 EGFR mAb E2 VL

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPARFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPPTFGQ GTKVEIK

>SEQ ID NO: 193 cMet mAb M1 VH

QVQLVQSGAEVKKPGASVKVSCETSGYTFTSYGISWVRQAPGHGLEWMGWISAY NGYTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFD YWGQGTLVTVSS

>SEQ ID NO: 194 cMet mAb M1VL

DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWFQHKPGKAPKLLIYAASSLLS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP-ITFGQGTRLEIK

>SEQ ID NO: 195 cMet mAb M2 VH

EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDD GSYTYYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAREGLYYYGSGS YYNQDYWGQGTLVTVSS

>SEQ ID NO: 196 cMet mAb M2 VL

QLTQSPSSLSASVGDRVTITCRASQGLSSALAWYRQKPGKAPKLLIYDASSLESGV PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFTSYPQITFGQGTRLEIK

>SEQ ID NO: 199EM1-mAb H1 (anti-EGFR,405L)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWD DGSYKYYGDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGITMVRGV MKDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS

DIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>SEQ ID NO: 200EM-1 mAb L1
AIQLTQSPSSLSASVGDRVTITCRASQDISSALVWYQQKPGKAPKLLIYDASSLESG
VPSRFSGSESGTDFTLTISSLQPEDFATYYCQQFNSYPLTFGGGTKVEIKRTVAAPS
VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>SEQ ID NO: 201 EM-1 mAb H2 (K409R, anti-cMet)
QVQLVQSGAEVKKPGASVKVSCETSGYTFTSYGISWVRQAPGHGLEWMGWISAY
NGYTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFD
YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVE
PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEALHNH
YTQKSLSLSPGK

>SEQ ID NO: 202 EM-1 mAb L2
DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWFQHKPGKAPKLLIYAASSLLS
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPITFGQGTRLEIKRTVAAPS
VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>SEQ ID NO: 234 E2 mAb HC1 (EGFR-F405L)
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMNWVRQA PGKGLEWVAN
IKKDGSEKYY VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDL
GWGWGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP
SNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

>SEQ ID NO: 235E2 mAb LC1 (EGFR)

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD
ASNRATGIPARFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPPTFGQ
GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC

>SEQ ID NO: 236 E2 mAb HC2 (c-Met- K409R)

EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDD
GSYTYYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAREGLYYYGSGS
YYNQDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

>SEQ ID NO: 237

E2 mAb LC2 (cMet)

QLTQSPSSLSASVGDRVTITCRASQGLSSALAWYRQKPGKAPKLLIYDASSLESGV
PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFTSYPQITFGQGTRLEIKRTVAAPSV
FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

The generated monospecific anti-EGFR and c-Met antibodies were mixed for *in vitro* Fab arm exchange in matrix and characterized in various assays. The bispecific antibody EM1-mAb comprises the EGFR binding arm of mAb E1-F405L and the c-Met binding arm of mAb M1-K409R. The bispecific antibody EM2-mAb comprises the EGFR binding arm of mAb E2-F405L and the c-Met binding arm of mAb M2-K409R. The bispecific antibody EM3-mAb comprises the EGFR binding arm of mAb E1-K409R and the c-Met binding arm of mAb M1-F405L. The bispecific antibody EM4-mAb comprises the EGFR binding arm of mAb E2-K409R and the c-Met binding arm of mAb M2-F405L. EM1-mAb and EM3-mAb had comparable characteristics.

The bispecific EM1-mAb was cultured in a CHO cell line having reduced fucosylation ability of glycoproteins, and hence have a fucosyl content of about 1-15%. The removal of the core fucose from the biantennary complex-type oligosaccharides

attached to the Fc regions significantly enhances the ADCC of antibodies via improved FcγRIIIa binding without altering antigen binding or CDC activity. Such mAbs can be achieved using different methods reported to lead to the successful expression of relatively high defucosylated therapeutic antibodies bearing the biantennary complex-type of Fc oligosaccharides and are described *supra*.

Example 11. Purification of bispecific EGFR/c-Met antibodies

The bispecific EM1-mAb was further purified after the *in vitro* Fab-arm exchange using hydrophobic interaction chromatography to minimize residual parental c-Met and EGFR antibodies using standard methods.

Example 12. Characterization of bispecific EGFR/c-Met antibodies

The EGFR/c-Met bispecific antibody EM1-mAb was tested in various assays for its characteristics including inhibition of EGF-stimulated EGFR phosphorylation, HGF-stimulated c-Met phosphorylation, ERK1/2 phosphorylation, AKT phosphorylation, inhibition of ligand binding and cell viability. The characteristics of the EM1-mAb was compared to control monovalent EGFR- or c-Met binding antibodies, and to known EGFR inhibitors such as erlotinib (CAS 183321-74-6; tyrosine kinase inhibitor) and cetuximab (CAS 205923-56-4).

As the parent antibodies of the EM-1 mAb antibodies are bivalent, control monovalent EGFR and c-Met antibodies were generated in a bispecific format combined with a Fab arm that binds to an unrelated/irrelevant antigen to accurately compare the synergy and avidity of a bispecific EM-1 mAb in comparison to a mixture of corresponding control monovalent molecules.

To generate the control monovalent EGFR and c-Met antibodies, a monospecific anti-HIV gp120 antibody gp120-K409R was generated comprising heavy chain of SEQ ID NO: 198 and a light chain of SEQ ID NO: 209. A monospecific anti-HIV gp120 antibody gp120-F405L was generated comprising the heavy chain of SEQ ID NO: 197 and the light chain of SEQ ID NO: 209.

The control monovalent anti-EGFR mAb E1-F405L-gp120-K409R was generated by *in vitro* Fab arm exchange between E1-F405L and gp120-K409R, and the control monovalent anti-cMet mAb M1- K409R -gp120- F405L was generated by *in vitro* Fab-arm exchange between M1- K409R and gp120- F405L and purified as described earlier.

The following cell lines were used in characterization of the bispecific antibodies: NCI-H292 (American Type Culture Collection (ATCC), Cat. No. CRL-1848), NCI-H1975 (ATCC Cat. No.CRL-5908), SKMES-1 (ATCC Cat. No.HTB-58), A431 (ATCC Cat. No. CRL-1555), NCI-H441 (ATCC Cat. No.HTB-174), NCI-H3255 (DCTD tumor/ cell line repository, NCI, Frederick, NCI-Navy Medical oncology Cell Line supplement. J Cell Biochem suppl 24, 1996; Tracy S. cancer Res 64:7241-4, 2004; Shimamura T. cancer Res 65:6401-8, 2005) and HCC-827 (ATCC Cat. No. CRL-2868). NCI-H292 and SKMES-1 cells express both wild type EGFR and wild type c-Met. NCI-3255 expresses mutant L858R EGFR and displays EGFR and c-Met amplification. H1975 expresses mutant L858R/T790M EGFR and wild type c-Met. HCC-827 expresses Δ (E746, A750) EGFR and displays EGFR amplification. Cell line NCI-H292, NCI-H975, NCI-H441 and NCI-H3255 are interchangeably referred to as H292, H975, H441 and H3255, respectively, in the specification.

Binding of bispecific EGFR/cMet antibodies to EGFR and c-Met on Cells (A431 Cell Binding Assay)

The bispecific EGFR/c-Met antibody EM1-mAb was tested for binding to EGFR and c-Met on cells using protocol described in Example 3 ("A431 Cell Binding Assay") and Example 6 ("H441 Cell Binding Assay"). Cetuximab and a control antibody monovalent towards EGFR E1-F405L-gp120-K409R were used as controls for the A431 cells. Cetuximab had an EC_{50} value of 5.0 nM. Table 18 shows the EC_{50} values for binding. EM1-mAb demonstrated a 1.9-fold (A431 cells) and 2.3-fold (H441 cells) decrease in binding when compared to the bivalent monospecific parental control antibodies. Cetuximab was comparable to the bivalent parental control antibodies. EM1-mAb displays higher EC_{50} binding values than the values for the parental mAbs due to the monovalent binding of EGFR and c-Met. EM1-mAb has similar binding EC_{50} values as the single arm E1/inert arm and E2/inert arm bispecific monovalent mAbs.

Table 18.

	EC_{50} (nM) binding to cells		
	EM1-mAb	Parental mAbs	E1-F405L-gp120-K409R (A431 cells) or M1-K409R -gp120- F405L

			(H441 cells)
A431 (assay for EGFR binding)	9.6 ± 3	5.1 ± 0.3	10.1 ± 0.6
H441 (assay for c-Met binding)	1.5 ± 0.7	0.65 ± 0.1	1.0 ± 0.3

Inhibition of ligand binding to the receptor

The bispecific antibodies were tested for their ability to block binding of EGF to EGFR extracellular domain and HGF to c-Met extracellular domain in an ELISA assay. Recombinant human EGF R-Fc (R&D Systems, Cat #: 344-ER-050) or human HGF (R&D Systems, Cat #: 294-HGN-025/CF) was coated onto MSD HighBind plates (Meso Scale Discovery, Gaithersburg, MD) for 2 hr at room temperature. MSD Blocker A buffer (Meso Scale Discovery, Gaithersburg, MD) was added to each well and incubated for 2 hr at room temperature. Plates were washed three times with 0.1 M HEPES buffer, pH 7.4, followed by the addition of a mixture of either flurescent dy labeled (MSD) EGF or biotinylated HGF proteins with different concentrations of antibodies. Ruthenium-labeled EGF protein was incubated for 30 min at RT with increasing concentrations of different antibodies, from 1 nM to 4 μM. After 2-hour incubation with gentle shaking at room temperature, the plates were washed 3 times with 0.1M HEPES buffer (pH 7.4). MSD Read Buffer T was diluted and dispensed and the signals were analyzed with a SECTOR Imager 6000. The HGF inhibition assays were performed as the EGF/EGFR inhibition assays except that 10 nM of biotinylated HGF was incubated for 30 min at RT with increasing concentrations of different antibodies, from 1 nM to 2 μM.

EM1-mAb inhibited EGF binding to EGFR with an IC_{50} value of 10.7 nM ± 1.2 in the presence of 50 nM EGF and with an IC_{50} value of 10.6 ± 1.5 nM in the presence of 80 nM EGF. The parental bivalent antibody inhibited EGF binding to EGFR with an IC_{50} value of 0.14 ± 1.5 nM in the presence of 50 nM EGF and with an IC_{50} value of 1.7 ± 1.4 nM in the presence of 80 nM EGF. EM1 mAb had a weaker inhibition of EGF binding to the EGFR extracellular domain because of the monovalent binding of EM1 mAb as compared to the parental bivalent mAb.

EM1-mAb inhibited HGF binding to c-Met with an IC_{50} value of 29.9 ± 1.5 nM. The parental bivalent antibody inhibited HGF binding to c-Met with and IC_{50} of 14.8 ± 1.6

nM. EM1 mAb had a weaker inhibition of HGF binding to the cMet extracellular domain because of the monovalent binding of EM1-mAb as compared to the parental bivalent mAb.

Inhibition of EGF-Stimulated EGFR Phosphorylation and HGF-Stimulated c-Met Phosphorylation

Antibodies were tested to determine IC_{50} values for inhibition of EGFR and c-Met phosphorylation. Inhibition of EGF-stimulated EGFR phosphorylation and HGF-stimulated c-Met phosphorylation were assessed at varying antibody concentrations (0.035 – 700 nM final) as described in Example 2 ("Inhibition of EGF-Stimulated EGFR Phosphorylation") and Example 6 ("Inhibition of HGF-Stimulated c-Met Phosphorylation"). In some experiments, both EGF and HGF were added to the cells so the same cell lysate could be used to detect both EGFR and c-Met phosphorylation.

The control anti-EGFR mAb E1-F405L-gp120-K409R monovalent for EGFR and the parental bivalent anti-EGFR antibody with low fucose content were used as control antibodies. Table 19 shows the IC_{50} values of the assays.

Table 19.

	pEGFR (IC_{50}, nM)		pMet (IC_{50}, nM)	
Cell line	H292	H1975	H292	H1975
Antibody				
EM1-mAb	8.6-29	1.5	0.55 – 0.83	0.64
E1-F405L-gp120-K409R	10.9-13.1	ND	0.7-4	ND
Parental EGFR (F405L)mAb*	1.5	ND	No effect	ND

*Antibody had low fucose content

Enhanced Inhibition of pERK and pAKT With EM1-mAb Compared to Mixture of Monovalent Antibodies (mAb pERK assay) (mAb pAKT assay)

The potential for enhanced potency with a bispecific EGFR/c-Met antibody was evaluated by assessing mAb effects on pERK and pAKT downstream signaling. For these experiments, the mixture of monovalent control EGFR and monovalent control c-Met antibodies was compared to the bispecific EM1-mAb. Cells were plated in clear 96-well tissue culture-treated plates (Nunc) in 100 µL/well of RPMI medium containing GlutaMAX and 25 mM Hepes (Invitrogen), supplemented with 1 mM sodium pyruvate (Gibco), 0.1mM NEAA (Gibco), 10% heat inactivated fetal bovine serum (Gibco), and 7.5 ng/mL HGF (R&D Systems cat # 294-HGN) and allowed to attach overnight at 37°C in a humidified 5% CO_2 atmosphere. Cells were not serum-starved. Cells were treated for 30 min (pERK assay) or 1 hour (pAkt assay) with varying concentrations (0.11 – 700 nM final) of monovalent control antibodies or EM1-mAb.

Cells were assessed for pERK or pAKT levels using the following kits and according to manufacturer's instructions from Meso Scale Discovery: Phospho-ERK1/2 (Thr202/Tyr204; Thr185/Tyr187) Assay Whole Cell Lysate Kit (cat# K151DWD, Phospho-Akt (Ser473) Assay Whole Cell Lysate Kit (cat#K151CAD), Phospho-Akt (Thr308) Assay Whole Cell Lysate Kit (cat#K151DYD). For the pERK assay, cells were lysed, and whole cell lysates were added to plates coated with anti-phospho-ERK1/2 antibody (recognizing ERK1 phosphoryated at residues Thr202 and Tyr204 and ERK2 phosphorylated at residues Thr185 and Tyr187), and phosphorylated ERK1/2 was detected with anti-total ERK1/2 antibody conjugated with MSD SULFO-TAG™ reagent. For the pAKT Ser473 assay, the capture antibody was anti-totalAKT antibody and the detection antibody anti-pAKT Ser473 antibody conjugated with MSD SULFO-TAG™ reagent. For the pAKT Thr308 assay, the capture antibody was anti-totalAKT antibody and the detection antibody anti-pAKT Thr308 antibody conjugated with MSD SULFO-TAG™ reagent.

Plates were read on a SECTOR® Imager 6000 instrument (Meso Scale Discovery) using manufacturer-installed assay-specific default settings. Data were plotted as electrochemiluminescence signal against the logarithm of antibody concentration and IC_{50} values were determined by fitting the data to a sigmoidal dose response with variable slope using GraphPad Prism 5 software. NCI-H292, H1975 and SKMES-1 cell lines were used in these assays.

The IC_{50} for inhibition of ERK phosphorylation by the bispecific EM1-mAb was about 14-63 fold lower relative to the mixture of the two monovalent control antibodies, depending on a cell line tested (Table 20). The improved potency of the EM1-mAb compared to the mixture of two monovalent control antibodies suggests a cooperative or avidity effect due to enhanced binding of EM1-mAb to these cell lines. The IC_{50} for inhibition of Ser475 (pAKTS475) and Thr308 (pAKTT308) AKT phosphorylation in NCI-H1975 cell line was about 75-fold and 122-fold lower, respectively, when compared to the mixture of the two monovalent control antibodies (Table 21). The improved potency of the EM1-mAb compared to the mixture of two monovalent control antibodies suggests a cooperative or avidity effect due to enhanced binding of EM1-mAb to these cell lines. Thus, the bispecific nature of the EM1-mAb resulted in an enhanced effect on downstream signaling effectors.

Table 20.

	IC_{50} (nM) pERK		
	Antibody		
Cell line	Bispecific EM1-mAb	Mixture of E1-F405L-gp120-K409R and M1-K409R-gp120-F405L	Fold change bispecific vs. mixture of two monovalent control antibodies
H292	0.64	34.94	55
H1975	1.67	106	63
SKMES-1	0.54	7.63	14

Table 21.

Antibody	IC_{50} (nM) pAKTS473	IC_{50} (nM) pAKTT308
Bispecific EM1-mAb	0.87	0.96
Mixture of E1-F405L-gp120-K409R and M1-K409R-gp120-F405L	65	117
Fold change mixture of two monovalent vs. bispecific	75	122

Inhibition of Human Tumor Cell Growth or Viability by Antibodies

Inhibition of c-Met-dependent cell growth was assessed by measuring viability of various tumor cells following exposure to the bispecific EM1-mAb. NCI-H292, SKMES-1, NCI-H1975 and NCI-H3255 cells were used in the studies.

Cells were cultured in standard 2D and low attachment formats. Erlotinib and cetuximab were used as controls. Table 22 summarizes the IC_{50} values for the assay.

Inhibition of Human Tumor Cell Growth or Viability by Antibodies – Standard 2D format

The inhibition of cell growth was assessed by measuring the viability of NCI-H292 and NCI-H1975 following exposure to antibodies in two formats. For the standard 2D format cells were plated in opaque white 96-well tissue culture-treated plates (PerkinElmer) in RPMI medium containing GlutaMAX and 25 mM Hepes (Invitrogen), supplemented with 1 mM sodium pyruvate (Gibco), 0.1mM NEAA (Gibco), and 10% heat inactivated fetal bovine serum (Gibco), and allowed to attach overnight at 37°C, 5% CO_2. Cells were treated with varying concentrations of antibodies (0.035 – 700 nM final), along with HGF (7.5 ng/mL, R&D Systems cat #294-HGF), then incubated at 37°C, 5% CO_2 for 72 hours. Some wells were left untreated with either HGF or antibodies as controls. Viable cells were detected using CellTiter-Glo® reagent (Promega), and data were

analyzed as described in Example 3 in "Inhibition of Human Tumor Cell Growth (NCI-H292 growth and NCI-H322 growth assay)".

Inhibition of Human Tumor Cell Growth or Viability by Antibodies – Low attachment format

To assess survival in low attachment conditions, cells were plated in Ultra Low Attachment 96-well plates (Corning Costar) in 50 µL/well of RPMI medium (Invitrogen) containing GlutaMAX and 25mM Hepes, supplemented with 1 mM sodium pyruvate (Gibco), 0.1 mM NEAA (Gibco), and 10% heat inactivated fetal bovine serum (Gibco), and allowed to attach overnight at 37°C, 5% CO_2. Cells were treated with varying concentrations of antibodies (0.035 – 700 nM final), along with HGF (7.5 ng/mL, R&D Systems cat# 294-HGN), then incubated at 37°C, 5% CO_2 for 72 hours. Some wells were left untreated with either HGF or antibodies as controls. Viable cells were detected using CellTiter-Glo® reagent (Promega), and data were analyzed as described above in "Inhibition of Human Tumor Cell Growth (NCI-H292 growth and NCI-H322 growth assay)" in Example 3, except that lysates were transferred to opaque white 96-well tissue culture-treated plates (PerkinElmer) prior to reading luminescence.

In the standard 2D culture, EM1-mAb inhibited NCI-H292 growth with an IC_{50} of 31 nM, and in low attachment conditions with an IC_{50} of 0.64 nM. EM-1 mAb inhibited NCI-H1975 cell growth with an IC_{50} of >700 nM and 0.8-1.35 nM in standard 2D and low attachment culture, respectively. In NCI-H292 cells expressing both wild type EGFR and cMet, EM1-mAb had over 22 fold improved potency in the standard 2D and about 330-fold improved potency in the low attachment culture conditions when compared to cetuximab. In NCI-H1975 cell, which express L858R, T790M EGFR mutant and wild type cMet, EM-1 mAb had at least a 518-fold improved potency when compared to cetuximab in low attachment culture conditions. Table 22 shows the summary of the assays.

Table 22.

Cell line	EGFR state	cMet state	EM1-mAb Standard 2D culture	EM1-mAb Low attachment	Cetuximab Standard 2D culture	Cetuximab Low attachment

			IC_{50} (nM)	IC_{50} (nM)	IC_{50} (nM)	IC_{50} (nM)
NCI-H292	WT	WT	31	0.64	>700	212
NCI-H1975	L858R, T790M	WT	>700	0.8-1.35	>700	>700

Combination of Erlotinib and EM1-mAb is efficient in inhibition of growth of EGFR mutant cell lines

The inhibition of cell growth by the combination of erlotinib plus EM1-mAb was evaluated in both standard 2D culture conditions and in the low attachment format. NCI-H3255 and HCC-827 cells were plated as described above in "Inhibition of Human Tumor Cell Growth or Viability by Antibodies". HGF (7.5 ng/mL, R&D Systems cat # 294-HGN) was added to cells along with treatment with antibodies. Cells were treated with varying concentrations of antibodies (0.11 – 700 nM final), or erlotinib (0.46 – 3000 nM final), or the combination of erlotinib plus antibody, using increasing amounts of each in a fixed ratio (e.g. lowest concentration of combination = lowest concentration of antibody (0.11 nM) + lowest concentration of erlotinib (0.46 nM)). Some wells were left untreated with either HGF or antibodies as controls. Cells were incubated at 37°C, 5% CO_2 for 72 hours, then viable cells were detected using CellTiter-Glo® reagent (Promega), and data were analyzed as described above in "Inhibition of Human Tumor Cell Growth (NCI-H292 growth and NCI-H322 growth assay)". Table 23 summarizes the results of the experiment. In the table, the IC_{50} values for the combinations are relative to either the antibody, or erlotinib, depending on what is indicated in parentheses.

In both NCI-H3255 and HCC-827 cells (EGFR mutant cell lines) the addition of EM1-mAb to erlotinib both increased the potency of inhibition of cell viability and was more effective resulting in fewer viable cells overall. In the NCI-H3255 cells using standard 2D conditions, the IC_{50} for erlotinib alone was 122 nM, whereas the combination was 49 nM. Similarly, in HCC-827 cells, the IC_{50} for erlotinib alone was 27 nM, whereas the combination was 15 nM. Also, the combination of erlotinib plus EM1-mAb was more effective than the combination of erlotinib plus cetuximab. Thus, in the presence of HGF, addition of EM1-mAb increased the effectiveness of erlotinib in this assay.

NCI-H3255 cells express L858R mutant EGFR and amplified cMet. HCC-827 cells express EGFR mutants with deletions at amino acid positions 746 and 750 and wild

type c-Met. EM1-mAb has stronger effects in the viability of HCC-827 and NCI-3255 in the presence of erlotinib than erlotinib alone in either standard or low attachment cultures.

Table 23.

Samples	EM1 mAb + erlotinib IC_{50} (nM)	erlotinib IC_{50} (nM)
NCI-H3255, standard 2D culture	49.0	122
NCI-H3255, low attachment culture	10.6	47.1
HCC-827, standard 2D culture	14.6	27.4
HCC-827 , low attachment culture	3.5	9.5

Example 13. Antibody mediated cellular cytotoxicity (ADCC) of EM1-mAb in *in vitro* cell lines.

ADCC assays were performed as previously described (Scallon *et al.,* Mol Immunol 44:1524-1534 2007). Briefly, PBMCs were purified from human blood by Ficoll gradients and used as effector cells for ADCC assays. NCI-H292, NCI-H1975 or NCI-H441 cells were used as target cells with a ratio of 1 target cell to 50 effector cells. Target cells were pre-labeled with BATDA (PerkinElmer) for 20 minutes at 37°C, washed twice and resuspended in DMEM, 10% heat-inactivated FBS, 2mM L-glutamine (all from Invitrogen). Target ($1x10^4$ cells) and effector cells ($0.5x10^6$ cells) were combined and 100µl of cells were added to the wells of 96-well U-bottom plates. An additional 100µl was added with or without wild type and protease-resistant mAb constructs. All samples were performed in duplicate. The plates were centrifuged at 200g for 3 minutes, incubated at 37°C for 2 hours, and then centrifuged again at 200g for 3 minutes. A total of 20µl of supernatant was removed per well and cell lysis was measured by the addition of 200µl of the DELPHIA Europium-based reagent (PerkinElmer). Fluorescence was measured using an Envision 2101 Multilabel Reader (PerkinElmer). Data were normalized to maximal cytotoxicity with 0.67% Triton X-100 (Sigma Aldrich) and minimal control determined by spontaneous release of BATDA from target cells in the absence of any antibody using the following equation: (experimental release – spontaneous release)/(maximal release –

spontaneous release) x 100%. Data were fit to a sigmoidal dose-response model using GraphPad Prism v5.

The ADCC results for the EM1 mAbs and comparators are summarized in the Table 24 (NCI-H292 cells), Table 25 (NCI-H1975 cells) and Table 26 (NCI-H441 cells) and Table 27 (NCI-H1993 cells) list the EC_{50} values and maximum lysis achieved. NCI-H292 cells express wild type (WT) EGFR, WT c-Met, and WT KRAS; NCI-H1975 cells express mutant EGFR (L858R T790M), WT cMet and WT KRAS; NCI-H441 express WT EGFR, WT cMet, and mutant KRAS (G12V), and NCI-H1993 cells express WT EGFR, amplified cMet, WT KRAS. KRAS is also known as GTPase KRas and as V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog.

The EM1-mAb has higher potency of ADCC responses than cetuximab and the normal fucose version of EM1-mAb as indicated by having lower EC_{50} values. The EM1 mAb has higher efficacy in terms of maximum lysis achieved than cetuximab and the normal fucose bispecific mAb. From profiles of on Tables 24-27, the EM-1 mAb has ADCC activity on cells that have mutant and WT EGFR, WT with normal and amplified levels of cMet, and WT and mutant KRAS.

Table 24.

mAb	Potency (EC_{50} µg/ml)	R^2	Efficacy (maximum lysis achieved)
EM1 mAb	0.0058	0.93	19%
Anti-EGFR x cMet normal fucose bispecific mAb	0.22	0.85	13%
Cetuximab	0.0064	0.94	12%

Table 25.

mAb	Potency (EC_{50} µg/ml)	R^2	Efficacy (maximum lysis achieved)
EM1 mAb	0.022	0.91	19%

Anti-EGFR x cMet normal fucose bispecific mAb	1.8	0.79	13%
Cetuximab	0.029	0.70	11%

Table 26.

mAb	Potency (EC_{50} µg/ml)	R^2	Efficacy (maximum lysis achieved)
EM1 mAb	0.022	0.97	24%
Anti-EGFR x cMet normal fucose bispecific mAb	0.52	0.87	7.9%
Cetuximab	0.013	0.85	15%

Table 27.

mAb	Potency (EC_{50} µg/ml)	R^2	Efficacy (maximum lysis achieved)
EM1 mAb	0.0013	0.95	27%
Anti-EGFR x cMet normal fucose bispecific mAb	0.054	0.87	17%
Cetuximab	0.0042	0.76	21%

Example 14. Tumor efficacy studies with the EM1-mAb

The efficacy of the EM1 mAb against tumor growth was conducted as described in Example 7 "Tumor efficacy studies with bispecific EGFR/c-Met molecules". In brief, NCI-H292-HGF cells were implanted subcutaneously (s.c.) with Cultrex at $2x10^6$ into female SCID Beige mice. The mice were stratified by tumor volume 7 days after implant into 5 Groups with 10 mice per group. The dosing began after the starting mean tumor

volume per group ranged from 62-66mm^3 (small tumors). PBS or therapeutic were dosed intraperitoneally (i.p.) 2 times per week.

The evaluation of the efficacy also employed SKMES-HGF, a human squamous cell carcinoma that was transfected with human HGF (hepatic growth factor). These cells were implanted s.c. at 10x10^6 into female SCID Beige mice. These mice were stratified by tumor volume 12 days after implant into 5 groups with 8 mice per group. The first study began with starting mean tumor volume per group ranged from 98-101 mm^3 (large tumors). PBS or therapeutic mAbs were- dosed i.p. 2x/week for 4 weeks. In the larger sized tumor study, the mice that were stratified after the tumor volumes were about 200-300mm^3 by splitting into 2 groups. These mice were then treated with either cetuximab (20 mg/kg) or EM1-mAb (20 mg/kg), i.p., 2x/week (3 weeks).

The summary of the data is shown in Table 28. Figure 10 shows the efficacy of the molecules over time. EM1-mAb has an improved tumor suppression profile when compared to cetuximab in H292-HGF small tumor model and in SKMES-HGF small and large tumor models.

Table 28.

Sample and time	Cell line	Dosing at mg per kg	Partial regression	Complete regression
EM1 at day 35	H292-HGF small tumor	20	10/10	10/10
		5	10/10	10/10
		1	0/10	0/10
Cetuximab at day 35	H292-HGF small tumor	20	0/10	0/10
EM1 at day 67	SKMES - HGF small tumor	20	0/8	8/8
		5	1/8	6/8
		1	2/8	4/8
Cetuximab at day 67		20	0/8	6/8
EM1 at day 70	SKMES – HGF large tumor	20	4/7	3/7
Cetuximab at day 35		20	0/7	0/7

Table 29 shows the tumor sizes in treatment groups from the SKMES-HGF tumors, and table 30 shows the anti-tumor activity.

EM1-mAb inhibited tumor growth in the SKMES-HGF model 97% or more at multiple doses down to 1 mg/kg. While initially cetuximab was very effective (88% TGI at 20 mg/kg), after dosing ended the cetuximab-treated tumors grew back. In contrast, the tumors treated with EM1-mAb at either 5 or 20 mg/kg did not grow back over the course of the study (> 2 months).

Table 29

Days	Tumor volume (mm^3)				
	Vehicle	bispecific EM1 at 20mg/kg	bispecific EM1 at 5mg/kg	bispecific EM1 at 1mg/kg	Cetuximab at 20mg/kg
1	99±6	99±7	101±6	101±6	98±5
8	146±14	48±10	49±9	49±10	60±8
15	192±21	9±1	22±10	41±13	44±23
22	326±43	3±2	17±12	33±15	42±23
29	577±55	2±1	15±9	38±17	85±60
36	994±114	0.2±0.1	13±9	26±14	125±62
50	--	0.04±0.04	10±7	18±9	423±115
57	--	0.1±0.2	3±2	21±10	650±116
67	--	0±0	8±7	34±22	1257±151

Table 30

Treatment	Tumor Size (mm^3)a at day 36	T/C (%)	T-C (days) at 1000 mm^3	*P value*
Vehicle	994±114	--	--	--
bispecific EM1 at 20mg/kg	0.19±0.12	0.02	--	
bispecific EM1 at 5mg/kg	13±9	1.3	--	

bispecific EM1 at 1mg/kg	26±14	2.6	--	
Cetuximab (20mg/kg)	125±62	13	31	

Example 15. Inhibition of cell migration with EM1-mAb *in vitro*

Method

Effect of the EM- mAb and the control monovalent antibodies on inhibition of tumor cell migration was assessed in NIH-1650 cells. EGFR mutant cell line H1650 (Lung Bronchioloalveolar carcinoma cells harboring an exon 19 mutation [deletion E746, A750]) was cultured in tissue culture flasks under normal culture conditions (37°C, 5% CO_2, 95% humidity). All media and supplementation were as suggested by the supplier of the cells (American Type Culture Collection, Manassas, VA, USA).

Spheroids were generated by plating H1650 lung tumor cells at 10,000 cells/well into "U" bottom Ultra Low Adherence (ULA) 96-well plates (Corning, Tewksbury, USA) at 200 µl/well. These plates stimulate spontaneous formation of a single spheroid of cells within 24 hours (upon incubation at 37°C, 5%CO_2) and the spheroids were grown for four days under normal culture conditions.

Round bottom 96-well plates (BD Bioscience) were coated with 0.1% gelatin (EMD Millipore, Billerica, USA) in sterile water for 1 h at 37°C. For compound evaluation studies, day 4 10,000 cell tumor spheroids (H1650 and NCI-H1975) were transferred to the coated round bottom plates and treated with the EM1-mAb, the control monovalent anti-EGFR mAb E1-F405L-gp120-K409R having low fucose content, the control monovalent anti-cMet mAb M1- K409R -gp120- F405L having low fucose content, and a combination of the two monovalent antibodies E1-F405L-gp120-K409R and M1- K409R -gp120- F405L (produced in low fucose) in a dilution series with 20 ng/ml of HGF (R&D systems). Controls were treated with vehicle which was IgG_1 kappa isotype control (concentration equal to highest drug-treated cells). Effects of compounds were analyzed at 48 hrs by measuring the area covered by migrating cells using bright field images in a fully automated Operetta high content imaging system (Perkin Elmer) with a 2x objective. Inhibition of cell migration (total area) due to treatment effect was assessed by normalizing data by dividing by media only control to create a percentage cell migration to control. Thus, a value less than 1 would be inhibitory to cell migration.

Results

The EM1-mAb demonstrated potent synergistic inhibition of cell migration in H1650 (L858R EGFR mutant) and H1975 (L858R/T790M EGFR mutant) cells when compared to a combination of the control monovalent anti-EGRF and anti-c-Met antibodies E1-F405L-gp120-K409R and M1- K409R -gp120- F405L. In H1650 cells, the six highest concentrations of the EM1-mAb significantly inhibited cell migration ($p<0.001$) compared to the isotype control. The EC_{50} value for the EM1-mAb was 0.23 nM, whereas the EC_{50} value for the combination of the monospecific control antibodies was 4.39 nM. The EM1-mAb therefore was about 19 fold more efficient in inhibiting H1650 cell migration when compared to the combination of the monovalent control antibodies. The level of cell migration inhibition of EM1-mAb was superior to the combination of monospecific control mAbs for H1650 and H1975 cells. Table 31 shows the EC_{50} values for the assay.

Table 31.

Samples	H1650		H1975
	EC_{50} (nM)	Inhibition at 30 nM	Inhibition at 30 nM
EM1-mAb	0.23	64%	38%
Mixture of E1-F405L-gp120-K409R* and M1-K409R-gp120-F405L*	4.39	59%	20%
E1-F405L - gp120-K409R*	5.44	15%	7%
M1-K409R-gp120-F405L*	7.36	43	10%

*antibodies have low fucose content

Example 16. Epitope mapping of anti-c-Met antibody 069 and 5D5

The anti-c-Met mAb 069 binding epitope was mapped using the linear and constrained CLIPS peptide technology. The peptides scanned the SEMA, PSI, and Ig domains of human cMet. The linear and CLIPS peptides were synthesized using the amino acid sequence of the aforementioned cMet using standard Fmoc chemistry and

deprotected using trifluoric acid with scavengers. The constrained peptides were synthesized on chemical scaffolds in order to reconstruct conformational epitopes using Chemically linked Peptides on Scaffolds (CLIPS) Technology (Timmerman *et al.*, J Mol Recognition 20:283, 2007). The linear and constrained peptides were coupled to PEPSCAN cards and screened using a PEPSCAN based ELISA (Slootstra *et al.*, Molecular Diversity 1, 87-96, 1996). The anti-c-Met mab 069 binding epitope is a discontinuous epitope consisting of c-Met amino acids 239-253 PEFRDSYPIKYVHAF (SEQ ID NO: 238) and 346-361 FAQSKPDSAEPMDRSA (SEQ ID NO: 239). c-Met amino acid sequence is shown in SEQ ID NO: 201.

Similar methods were used to map mAb 5D5 (MetMab, Onartuzumab) epitope. mAb 5D5 binds c-Met residues 325-340 PGAQLARQIGASLNDD (SEQ ID NO: 240).

Example 17. *In vivo* tumor efficacy studies with EM1-mAb

The efficacy of EM1 mAb against tumor growth was conducted as described in Example 7 "Tumor efficacy studies with bispecific EGFR/c-Met molecules" and Example 14 employing additional tumor cell lines with EGFR mutation or EGFR and/or c-Met amplifications. In brief, SNU-5, H1975, HCC827 cells, H1975 cells expressing human HGF, or a clone of HCC827 cells selected for its incrased resistance to erlotinib (HCC827-ER1 cells) were implanted subcutaneously (s.c.) into female nude mice, except that SNU-5 cells were implanted in CR17/SCID mice. Mice were dosed intraperitoneally with PBS or EM1-mAb, cetuximab (CAS 205923-56-4), erlotinib (CAS 183321-74-6), afatinib (CAS 439081-18-2), or a combination of EM-1 mAb and afatinib and EM-1 mAb and erlotinib at indicated dosage and schedule shown in Table 32. Antitumor efficacy was measured as %TGI (tumor growth inhibition) calculated as 100- %T/C (T=mean tumor size of the treatment group; C=mean tumor size of the control group on a given day as described in Example 7).

In tumors with primary EGFR activating mutations (no resistance to EGFR TKIs): (HCC827 tumor, EGFR del(E746, A750)), EM1-mAb dosed 10 mg/kg inhibited tumor growth by 82%. Erlotinib was similarly effective in this model, as was the combination of erlotinib and EM1-mAb. Figure 11 shows efficacy of the therapeutics over time in the HCC827 tumor model.

In tumors with wild type EGFR and c-Met gene amplification (gastric cancer model SNU-5), EM1-mAb showed antitumor activity with full tumor regression (98% TGI, at day 34 $p<0.01$, compared to vehicle using one-way ANOVA followed by

individual comparisons using Games-Howell). Antitumor activity of anti-EGFR mAb cetuximab was less, 49% at day 34, in this model. Figure 12 shows the efficacy of the therapeutics over time in the SNU-5 model.

EM1-mAb was tested in a NSCLC model containing primary EGFR activating mutation and the T790M EGFR mutation which renders tumors resistant to 1st generation EGFR TKIs (H1975 model). EM1-mAb inhibited tumor growth with a 57% TGI in the H1975 cell line model implanted in nude mice ($p<0.0001$, compared to PBS vehicle using Logrank analysis with Prism 3.03). As expected, erlotinib was not effective in this model with the T790M mutation. Afatinib was equally effective as the EM1-mAb (57% TGI). Cetuximab and the combination of EM1-mAb with afatinib were the most effective, regressing tumors with 91% and 96% tumor growth inhibition, respectively , ($p<0.0001$ for both cetuximab compared to PBS and EM1-mAb + afatinib compared to the PBS + afatinib vehicles group using Logrank analysis with Prism 3.03). c-Met signaling pathways are not activated in this model as the mouse HGF does not bind to human c-Met.

EM1-mAb was tested in several models that were engineered to express human HGF using a lentiviral transduction system. This allows modeling of ligand activation of the c-Met pathway *in vivo* because mouse HGF does not activate the human c-Met on the implanted human tumor cells. Results with SKMES-HGF model are shown in Example 14 and Figure 10, and the %TGI summarized in Table 32. EM1-mAb inhibited tumor growth in the H1975-HGF model 71% ($p<0.0001$, compared to PBS vehicle using Logrank analysis with Prism 3.03). Afatinib, erlotinib and cetuximab were less efficacious in this model. The combination of EM1-mAb and afatinib was very effective (96% TGI, $p<0.0001$, compared to the PBS + afatinib vehicles group using Logrank analysis with Prism 3.03). Figure 13 shows the efficacy of the molecules over time in the H1975-HGF model. Erlotinib, afatinib and cetuximab thus lose their antitumor efficacy in tumor models in which c-Met pathway is activated.

EM1-mAb was tested in a tumor model characterized by primary EGFR activating mutation and increased resistance to 1st generation EGFR TKI (erlotinib) due to c-Met gene amplification (HCC827-ER1 model). EM1-mAb dosed at 10 mg/kg partially regressed HCC827-ER1 tumors implanted with 86% TGI at day 25, and was more efficacious than erlotinib alone (65% TGI at day 25). Combination of EM1-mAb and erlotinib did not further improve efficacy. Figure 14 shows the efficacy of the molecules over time.

EM1-mAb thus demonstrates efficacy in tumor models with wild type EGFR, with primary activating EGFR mutations, with the EGFR mutation T790M associated with resistance to EGFR therapeutics, as well as in models where c-Met is activated in either a ligand-dependent (autocrine HGF expression) or ligand-independent (c-Met gene amplification) manner. Combination of EM1-mAb with erlotinib or afatinib may improve efficacy in some tumor models.

Table 32.

Tumor Type	EGFR	cMet	Treatment (dose in mg/kg), schedule	% TGI (day of study); compared to PBS vehicle
SKMES-HGF lung squamous	WT	WT	EM1-mAb (20), BIWx4wk	100 (36)
			cetuximab (20), BIWx4wk	88 (36)
SNU-5 gastric	WT	AMP	EM1-mAb (10), BIWx4wk	98 (34)
			cetuximab (10), BIWx4wk	49 (34)
H1975 NSCLC	L858R; T790M	WT	EM1-mAb (10), BIWx3wk	57 (18)
			cetuximab (10), BIWx3wk	91 (18)
			erlotinib (50), QDx21d	9 (18)
			afatinib (15), QDx21d	57 (18)
			EM1-mAb (10), BIWx3wk + afatinib (15), QDx21d	96 (18)
H1975-HGF NSCLC	L858R; T790M	WT	EM1-mAb (10), BIWx3wk	71 (16)
			cetuximab (10), BIWx3wk	42 (16)

			erlotinib (50), QDx21d	20 (16)
			afatinib (15), QDx21d	29 (16)
			EM1-mAb (10), BIWx3wk + afatinib (15), QDx21d	96 (16)
HCC827 NSCLC	del (E746, A750); AMP	WT	EM1-mAb (10), BIWx4wk	82 (35)
			erlotinib (25), QDx28d	79 (35)
			EM1-mAb (10), BIWx3wk + erlotinib (25), QDx28d	78 (35)
HCC827-ER1 NSCLC	del (E746, A750); AMP	AMP	EM1-mAb (10), BIWx4wk	86 (25)
			erlotinib (25), QDx28d	65 (25)
			EM1-mAb (10), BIWx3wk + erlotinib (25), QDx28d	87 (25)

BIW= biweekly

QD= once per day

WT= wild tpe

AMP=amplified

Example 18. EM1 mAb induced degradation of EGFR and c-Met *in vivo*

To demonstrate engagement of both EGFR and c-Met by EM1-mAb in the tumor, samples were taken from H1975-HGF tumors at various times after a single dose of 20 mg/kg EM1-mAb Tumor lysates were prepared, normalized to total protein, and samples run on SDS-PAGE gels. Gels were transferred to nitrocellulose and Western blotted for either EGFR (Mouse (mAb) Anti-human EGFR (EGF-R2); Santa Cruz Biotechnology, Cat# sc-73511) or c-Met (Mouse (mAb) Anti-human Met (L41G3); Cell Signaling Technology, Cat# 3148). EGFR levels were normalized to GAPDH; c-Met levels were normalized to actin. The levels of receptors from EM1-mAb treated tumors were compared to those of PBS-treated tumors to get % total receptor. EM1-mAb treatment decreased the total EGFR and cMet receptor levels in H1975-HGF tumors to between 20% to 60% of control, depending on the time point analyzed. Figure 15 shows the average

receptor levels compared to PBS over time. pEGFR, pc-Met and pAKT were also decreased at 72 hours after the single dose of EM1.

Example 19. Anti-Tumor Activity Comparing IgG_1 and $IgG_{2\sigma}$ variant isoforms of EGFR/c-Met bispecific mAbs

To better understand the contribution of effector function to the efficacy observed in the H1975-HGF model, a comparison was performed between EM1-mAb and a variant of EM1-mAb having an IgG2 Fc with effector silencing substitutions V234A/G237A/P238S/H268A/V309L/A330S/P331S on IgG2 (substitutions described in Intl. Pat. Appl. No. WO2011/066501) (numbering according to the EU index). An IgG2 antibody with V234A/G237A/P238S/H268A/V309L/A330S/P331S substitutions does not interact with Fc receptors or effector cells (such as NK cells and macrophages). Any loss of activity observed with the IgG2 V234A/G237A/P238S/H268A/V309L/A330S/P331S variant of the EM1-mAb may thus represent antitumor activity contributed by effector-mediated mechanisms such as ADCC and/or ADCP. After 32 day post tumor cell implant in the H1975-HGF model described above, there is an indication of loss of antitumor activity with the IgG2 V234A/G237A/P238S/H268A/V309L/A330S/P331S variant of the EM1-mAb when compared to the parental EM1-mAb, suggesting that effector-mediated mechanisms contribute to the function of EM-1 mAb. Figure 16 shows the antitumor activity of the molecules.

SEQUENCE LISTING

SEQ ID NO:	Type	Species	Description	Sequence
1	PRT	Artificial	Tencon	LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLT VPGSERSYDLTGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT
2	DNA	Artificial	POP2220	GGAAACAGGATCTACCATGCTGCCGGCGCCGAAAAACCTGGTTGT TTCTGAAGTTACC
3	DNA	Artificial	TC5'loFG	AACACCGTAGATAGAAACGGT
4	DNA	Artificial	130mer	CGGCGGTTAGAACGCGGCTACAATTAATACATAACCCCATCCCCC TGTTGACAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGC GGATAACAATTTCACACAGGAAACAGGATCTACCATGCTG
5	DNA	Artificial	POP2222	CGGCGGTTAGAACGCGGCTAC
6	DNA	Artificial	TCF7	GGTGGTGAATTCCGCAGACAGCGGSNNSNNSNNSNNSNNSNNSNN AACACCGTAGATAGAAACGGT
7	DNA	Artificial	TCF8	GGTGGTGAATTCCGCAGACAGCGGSNNSNNSNNSNNSNNSNNSNN SNNAACACCGTAGATAGAAACGGT
8	DNA	Artificial	TCF9	GGTGGTGAATTCCGCAGACAGCGGSNNSNNSNNSNNSNNSNNSNN SNNSNNAACACCGTAGATAGAAACGGT
9	DNA	Artificial	TCF10	GGTGGTGAATTCCGCAGACAGCGGSNNSNNSNNSNNSNNSNNSNN SNNSNNSNNAACACCGTAGATAGAAACGGT
10	DNA	Artificial	TCF11	GGTGGTGAATTCCGCAGACAGCGGSNNSNNSNNSNNSNNSNNSNN SNNSNNSNNSNNAACACCGTAGATAGAAACGGT
11	DNA	Artificial	TCF12	GGTGGTGAATTCCGCAGACAGCGGSNNSNNSNNSNNSNNSNNSNN SNNSNNSNNSNNSNNAACACCGTAGATAGAAACGGT
12	DNA	Artificial	POP2234	AAGATCAGTTGCGGCCGCTAGACTAGAACCGCTGCCATGGTGATG GTGATGGTGACCGCCGGTGGTGAATTCCGCAGACAG
13	DNA	Artificial	POP2250	CGGCGGTTAGAACGCGGCTACAATTAATAC
14	DNA	Artificial	DidLigRev	CATGATTACGCCAAGCTCAGAA
15	DNA	Artificial	Tcon5new 2	GAGCCGCCGCCACCGGTTTAATGGTGATGGTGATGGT GACCACCGGTGGTGAATTCCGCAGACAG
16	DNA	Artificial	Tcon6	AAGAAGGAGAACCGGTATGCTGCCGGCGCCGAAAAAC
17	DNA	Artificial	LS1008	TTTGGGAAGCTTCTAGGTCTCGGCGGTCACCATCACC ATCACCATGGCAGCGGTTCTAGTCTAGCGGCCCCAAC TGATCTTCACCAAAC
18	PRT	Artificial	P53A1R5-17 without met	LPAPKNLVVSEVTEDSLRLSWADPHGFYDSFLIQYQES EKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAEFTT

19	PRT	Artificial	P54AR4-17 without met	LPAPKNLVVSEVTEDSLRLSWTYDRDGYDSFLIQYQES EKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAEFTT
20	PRT	Artificial	P54AR4-47 without met	LPAPKNLVVSEVTEDSLRLSWGYNGDHFDSFLIQYQES EKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAEFTT
21	PRT	Artificial	P54AR4-48 without met	LPAPKNLVVSEVTEDSLRLSWDDPRGFYESFLIQYQES EKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAEFTT
22	PRT	Artificial	P54AR4-37 without met	LPAPKNLVVSEVTEDSLRLSWTWPYADLDSFLIQYQES EKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAEFTT
23	PRT	Artificial	54AR4-74 without met	LPAPKNLVVSEVTEDSLRLSWGYNGDHFDSFLIQYQES EKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAEFTT
24	PRT	Artificial	P54AR4-81 without met	LPAPKNLVVSEVTEDSLRLSWDYDLGVYFDSFLIQYQE SEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHN VYKDTNMRGLPLSAEFTT
25	PRT	Artificial	P54AR4-83 without met	LPAPKNLVVSEVTEDSLRLSWDDPWAFYESFLIQYQES EKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAEFTT
26	PRT	Artificial	P54CR4-31 without Met	LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESE KVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVLGSY VFEHDVMLPLSAEFTT
27	PRT	Artificial	P54AR4-83v2 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAIFTT
28	PRT	Artificial	P54CR4-31v2 without Met	LPAPKNLVVSEVTEDSARLSWTAPDAAFDSFLIQYQESE KVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVLGSY VFEHDVMLPLSAIFTT
29	PRT	Artificial	P54AR4-73v2 wihtout Met	LPAPKNLVVSEVTEDSLRLSWTWPYADLDSFLIQYQES EKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIYGVHNV YKDTNMRGLPLSAEFTT
30	DNA	Artificial	TCON6	AAG AAG GAG AAC CGG TAT GCT GCC GGC GCC GAA AAA C
31	DNA	Artificial	TCON5 E86Ishort	GAG CCG CCG CCA CCG GTT TAA TGG TGA TGG TGA TGG TGA CCA CCG GTG GTG AAG ATC GCA GAC AG
32	PRT	Artificial	P114AR5P74-A5	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYDEV VVGGEAIVLTVPGSERSYDLTGLKPGTEYYVNILGVKGG SISVPLSAIFTT
33	PRT	Artificial	P114AR5P75-E9	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFFIRYDEFL RSGEAIVLTVPGSERSYDLTGLKPGTEYWVTILGVKGGL VSTPLSAIFTT
34	PRT	Artificial	P114AR7P92-F3	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYIVNIMGVKGGSI SHPLSAIFTT

35	PRT	Artificial	P114AR7P92-F6	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGGL SVPLSAIFTT
36	PRT	Artificial	P114AR7P92-G8	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFVIRYFEFLG SGEAIVLTVPGSERSYDLTGLKPGTEYVVQILGVKGGYISI PLSAIFTT
37	PRT	Artificial	P114AR7P92-H5	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYLEFLL GGEAIVLTVPGSERSYDLTGLKPGTEYVVQIMGVKGGTVS PPLSAIFTT
38	PRT	Artificial	P114AR7P93-D11	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVGINGVKGGYI SYPLSAIFTT
39	PRT	Artificial	P114AR7P93-G8	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTDLKPGTEYGVTINGVKGGRV STPLSAIFTT
40	PRT	Artificial	P114AR7P93-H9	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVQIIGVKGGHIS LPLSAIFTT
41	PRT	Artificial	P114AR7P94-A3	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGGKI SPPLSAIFTT
42	PRT	Artificial	P114AR7P94-E5	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYAVNIMGVKGGRV SVPLSAIFTT
43	PRT	Artificial	P114AR7P95-B9	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVQILGVKGGSI SVPLSAIFTT
44	PRT	Artificial	P114AR7P95-D3	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGGSI SYPLSAIFTT
45	PRT	Artificial	P114AR7P95-D4	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVQILGVKGGYI SIPLSAIFTT
46	PRT	Artificial	P114AR7P95-E3	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVQIMGVKGGTV SPPLSAIFTT
47	PRT	Artificial	P114AR7P95-F10	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFTT AGEAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGGSIS PPLSAIFTT
48	PRT	Artificial	P114AR7P95-G7	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFELLS TGEAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGGSIS PPLSAIFTT

49	PRT	Artificial	P114AR7P95-H8	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFV SKGEAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGGSI SPPLSAIFTT
50	PRT	Artificial	ECB1	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTGGGGSGGGGSGGGGSGGGGSM LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYDEVV VGGEAIVLTVPGSERSYDLTGLKPGTEYYVNILGVKGGSIS VPLSAIFTT
51	PRT	Artificial	ECB2	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTGGGGSGGGGSGGGGSGGGGSL PAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLG SGEAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGGKIS PPLSAIFTT
52	PRT	Artificial	ECB3	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTGGGGSGGGGSGGGGSGGGGSM LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVQIIGVKGGHIS LPLSAIFTT
53	PRT	Artificial	ECB4	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTGGGGSGGGGSGGGGSGGGGSM LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFFIRYDEFLR SGEAIVLTVPGSERSYDLTGLKPGTEYWVTILGVKGGLVS TPLSAIFTT
54	PRT	Artificial	ECB5	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTGGGGSGGGGSGGGGSGGGGSM LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGGKI SPPLSAIFTT
55	PRT	Artificial	ECB6	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTGGGGSGGGGSGGGGSGGGGSM LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVQIIGVKGGHIS LPLSAIFTT
56	PRT	Artificial	ECB7	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTGGGGSGGGGSGGGGSGGGGSM LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFL GSGEAIVLTVPGSERSYDLTGLKPGTEYVVQIIGVKGGHIS LPLSAIFTT

57	PRT	Artificial	ECB15	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSERS YDLTGLKPGTEYVVNIMGVKGGKISPPLSAIFTT
58	PRT	Artificial	ECB27	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYDEVVVGGEAIVLTVPGSER SYDLTGLKPGTEYYVNILGVKGGSISVPLSAIFTT
59	PRT	Artificial	ECB60	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTAPAPAPAPAPMLPAPKNLVVSRVT EDSARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSE RSYDLTGLKPGTEYVVNIMGVKGGKISPPLSAIFTT
60	PRT	Artificial	ECB37	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNMRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYDEVVVGGEAIVLTVPGSER SYDLTGLKPGTEYYVNILGVKGGSISVPLSAIFTT
61	PRT	Artificial	ECB94	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSERS YDLTGLKPGTEYVVNILGVKGGKISPPLSAIFTT
62	PRT	Artificial	ECB95	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFVGSGEAIVLTVPGSER SYDLTGLKPGTEYVVNILGVKGGSISPPLSAIFTT
63	PRT	Artificial	ECB96	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFVSKGDAIVLTVPGSERS YDLTGLKPGTEYVVNILGVKGGSISPPLSAIFTT
64	PRT	Artificial	ECB97	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSERS YDLTGLKPGTEYVVNILSVKGGSISPPLSAIFTT

65	PRT	Artificial	ECB106	MLPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSERS YDLTGLKPGTEYVVNILGVKGGKISPPLSAIFTT
66	PRT	Artificial	ECB107	MLPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFVGSGEAIVLTVPGSER SYDLTGLKPGTEYVVNILGVKGGSISPPLSAIFTT
67	PRT	Artificial	ECB108	MLPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFVSKGDAIVLTVPGSERS YDLTGLKPGTEYVVNILGVKGGSISPPLSAIFTT
68	PRT	Artificial	ECB109	MLPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSERS YDLTGLKPGTEYVVNILSVKGGSISPPLSAIFTT
69	PRT	Artificial	ECB118	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSERS YDLTGLKPGTEYVVNILGVKGGKISPPLSAIFTT
70	PRT	Artificial	ECB119	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFVGSGEAIVLTVPGSER SYDLTGLKPGTEYVVNILGVKGGSISPPLSAIFTT
71	PRT	Artificial	ECB120	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFVSKGDAIVLTVPGSERS YDLTGLKPGTEYVVNILGVKGGSISPPLSAIFTT
72	PRT	Artificial	ECB121	MLPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQES EKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYGVHNVY KDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNLVVSRVTED SARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSERS YDLTGLKPGTEYVVNILSVKGGSISPPLSAIFTT

SEQ ID NO: 73, PRT, Homo Sapiens, EGFR (includes signal sequence of 24 aa. Mature protein starts at residue 25)

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  1 MRPSGTAGAA LLALLAALCP ASRALEEKKV CQGTSNKLTQ LGTFEDHFLS LQRMFNNCEV
 61 VLGNLEITYV QRNYDLSFLK TIQEVAGYVL IALNTVERIP LENLQIIRGN MYYENSYALA
121 VLSNYDANKT GLKELPMRNL QEILHGAVRF SNNPALCNVE SIQWRDIVSS DFLSNMSMDF
181 QNHLGSCQKC DPSCPNGSCW GAGEENCQKL TKIICAQQCS GRCRGKSPSD CCHNQCAAGC
```

241 TGPRESDCLV CRKPRDEATC KDTCPPLMLY NPTTYQMDVN PEGKYSFGAT CVKKCPRNYV
301 VTDHGSCVRA CGADSYEMEE DGVRKCKKCE GPCRKVCNGI GIGEFKDSLS INATNIKHFK
361 NCTSISGDLH ILPVAFRGDS FTHTPPLDPQ ELDILKTVKE ITGFLLIQAW PENRTDLHAF
421 ENLEIIRGRT KQHGQFSLAV VSLNITSLGL RSLKEISDGD VIISGNKNLC YANTINWKKL
481 FGTSGQKTKI ISNRGENSCK ATGQVCHALC SPEGCWGPEP RDCVSCRNVS RGRECVDKCN
541 LLEGEPREFV ENSECIQCHP ECLPQAMNIT CTGRGPDNCI QCAHYIDGPH CVKTCPAGVM
601 GENNTLVWKY ADAGHVCHLC HPNCTYGCTG PGLEGCPTNG PKIPSIATGM VGALLLLLVV
661 ALGIGLFMRR RHIVRKRTLR RLLQERELVE PLTPSGEAPN QALLRILKET EFKKIKVLGS
721 GAFGTVYKGL WIPEGEKVKI PVAIKELREA TSPKANKEIL DEAYVMASVD NPHVCRLLGI
781 CLTSTVQLIT QLMPFGCLLD YVREHKDNIG SQYLLNWCVQ IAKGMNYLED RRLVHRDLAA
841 RNVLVKTPQH VKITDFGLAK LLGAEEKEYH AEGGKVPIKW MALESILHRI YTHQSDVWSY
901 GVTVWELMTF GSKPYDGIPA SEISSILEKG ERLPQPPICT IDVYMIMVKC WMIDADSRPK
961 FRELIIEFSK MARDPQRYLV IQGDERMHLP SPTDSNFYRA LMDEEDMDDV VDADEYLIPQ
1021 QGFFSSPSTS RTPLLSSLSA TSNNSTVACI DRNGLQSCPI KEDSFLQRYS SDPTGALTED
1081 SIDDTFLPVP EYINQSVPKR PAGSVQNPVY HNQPLNPAPS RDPHYQDPHS TAVGNPEYLN
1141 TVQPTCVNST FDSPAHWAQK GSHQISLDNP DYQQDFFPKE AKPNGIFKGS TAENAEYLRV
1201 APQSSEFIGA

74	PRT	Homo sapiens	EGF	NSDSECPLSHDGYCLHDGVCMYIEALDKYACNCVVGYIG ERCQYRDLKWWELR

SEQ ID NO: 75, PRT, Homo Sapiens, Tenascin-C

1 mgamtqllag vflaflalat eggvikkvir hkrqsgvnat lpeenqpvvf nhvyniklpv
61 gsqcsvdles asgekdlapp sepsesfqeh tvdgenqivf thriniprra cgcaaapdvk
121 ellsrleele nlvsslreqc tagagcclqp atgrldtrpf csgrgnfste gcgcvcepgw
181 kgpncsepec pgnchlrgrc idgqcicddg ftgedcsqla cpsdcndqgk cvngvcicfe
241 gyagadcsre icpvpcseeh gtcvdglcvc hdgfagddcn kplclnncyn rgrcvenecv
301 cdegftgedc selicpndcf drgrcingtc yceegftged cgkptcphac htqgrceegq
361 cvcdegfagv dcsekrcpad chnrgrcvdg rcecddgftg adcgelkcpn gcsghgrcvn
421 gqcvcdegyt gedcsqlrcp ndchsrgrcv egkcvceqgf kgydcsdmsc pndchqhgrc
481 vngmcvddg ytgedcrdrq cprdcsnrgl cvdgqcvced gftgpdcael scpndchgqg
541 rcvngqcvch egfmgkdcke qrcpsdchgq grcvdgqcic hegftgldcg qhscpsdcnn
601 lgqcvsgrci cnegysgedc sevsppkdlv vtevteetvn lawdnemrvt eylvvytpth
661 eggiemqfrv pgdqtstiiq elepgveyfi rvfailenkk sipvsarvat ylpapegikf
721 ksiketsvev ewdpldiafe tweiifrnmn kedegeitks lrrpetsyrq tglapgqeye
781 islhivknnt rgpglkrvtt tnldapsqie vkdvtdttal itwfkplaei dgieltygik
841 dvpgdrttid ltedenqysi gnlkpdteye vslisrrgdm ssspaketft tgidaprnlr

901 rvsqtdnsit lewrngkaai dsyrikyapi sggdhaevdv pksqqattkt tltglrpgtc

961 ygigvsavke dkesnpatin aateidtpkd lqvsetaets ltliwktpla kfdryrlnys

1021 iptgqwvgvq lpnttsyvl rgiepgqeyn vlltaekgrh kskparvkas teqapeleni

1081 tvtevgwdgl rinwtaadqa yehfiiqvqe ankveaaml tvpgslravd ipglkaatpy

1141 tvsiygviqg yrtpvlsaea stgetpnlge vvvaevgwda ikinwtapeg ayeyffiqvq

1201 eadtveaaqn ltvpgglrst dlpglkaath ytitirgvtq dfsttplsve vtteevpdmg

1261 nltvtevswd alrlnwttpd gtydqftiqv qeadqveeah nltvpgslrs meipglragt

1321 pytvtlhgev rghstrplav evvtedlpql gdlavsevgw dglrlnwtaa dnayehfviq

1381 vqevnkveaa qnltlpgslr avdipglesa tpyrvsiygv irgyrtpvls aeastakepe

1441 ignlnvsdit pesfnlswma tdgifetfti eudsnrlle tveynisgae rtahisglpp

1501 stdfivylsg lapsirtkti satattealp llenltisdi npygftvswm asenafdsfl

1561 vtvvdsgkll dpqefllsgt qrklelrgli tgigyevmvs gftqghqtkp lraeivteae

1621 pevdnllvsd atpdgfilsw tadegvfdnf vlkirdtkkq sepleitlla pertrditgl

1681 reateyeiel ygiskgrrsq tvsaiattam gspkevifsd itensatvsw raptaqvesf

1741 rityvpitgg tpsmvtvdgt ktqtrlvkli pgveylvsii amkgfeesep vsgsfttald

1801 gpsglvtani tdsealarwq paiatvdsyv isytgekvpe itrtvsgntv eyaltdlepa

1861 teytlrifae kgpqksstit akfttdldsp rdltatevqs etalltwrpp rasvtgyllv

1921 yesvdgtvke vivgpdttsy sladlspsth ytakiqaing plrsnmiqti fttigllypf

1981 pkdcsqamln gdttsglyti ylngdkaeal evfcdmtsdg ggwivfirk ngrentyqnw

2041 kayaagfgdr reefwlgldn lnkitaqgqy elrvdlrdhg etafavydkf svgdaktryk

2101 lkvegysgta gdsmayhngr sfstfdkdtd saitncalsy kgafwyrnch rvnlmgrygd

2161 nnhsqgvnwf hwkghehsiq faemklrpsn frnlegrrkr a

76	PRT	Artificial	Fibcon	Ldaptdlqvtnvtdtsitvswtppsatitgyritytpsngpgepkeltvppsstsv titgltpgveyvvsiyalkdnqespplvgtqtt
77	PRT	Artificial	10th FN3 domain of fibronectin (FN10)	VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPV QEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINY RT
78	PRT	Artificial	Linker	GSGS
79	PRT	Artificial	Linker	GGGGSGGGGSGGGGSGGGGSGGGGS
80	PRT	Artificial	Linker	APAP
81	PRT	Artificial	Linker	APAPAPAPAP
82	PRT	Artificial	Linker	APAPAPAPAPAPAPAPAPAP
83	PRT	Artificial	Linker	APAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPA PAP

84	PRT	Artificial	Linker	AEAAAKEAAAKEAAAKEAAAKEAAAKAAA
85	PRT	Artificial	Tencon BC loop	TAPDAAFD
86	PRT	Artificial	Tencon GF loop	KGGHRSN
87	PRT	Artificial	P53A1R5-17 BC loop	ADPHGFYD
88	PRT	Artificial	P54AR4-17 BC loop	TYDRDGYD
89	PRT	Artificial	P54AR4-47 BC loop	WDPFSFYD
90	PRT	Artificial	P54AR4-48 BC loop	DDPRGFYE
91	PRT	Artificial	P54AR4-73 BC loop	TWPYADLD
92	PRT	Artificial	P54AR4-74 BC loop	GYNGDHFD

93	PRT	Artificial	P54AR4-81 BC loop	DYDLGVYD
94	PRT	Artificial	P54AR4-83 BC loop	DDPWDFYE
95	PRT	Artificial	FG loops of EGFR	HNVYKDTNMRGL
96	PRT	Artificial	FG loops of EGFR	LGSYVFEHDVM
97	DNA	Artificial	>EGFR part ECB97; P54AR4-83v22	Atgttgccagcgccgaagaacctggtagttagcgaggttactgaggac agcgcgcgtctgagctgggacgatccgtgggcgttctacgagagctttct gatccagtatcaagagagcgagaaagtcggtgaagcgattgtgctgac cgtcccgggctccgagcgttcctacgacctgaccggtttgaagccgggt accgagtatacggtgagcatctacggtgttcacaatgtctataaggaca ctaatatccgcggtctgcctctgagcgccatttttcaccacc
98	DNA	Artificial	>EGFR part ECB15; P54AR4-83v2	Atgctgccagcccctaagaatctggtcgtgagcgaagtaaccgagga cagcgcccgcctgagctgggacgacccgtgggcgttctatgagtctttcc tgattcagtatcaagaaagcgaaaaagttggcgaagcgatcgtcctga ccgtcccgggtagcgagcgctcctacgatctgaccggcctgaaaccgg gtacggagtacacggtgtccatttacggtgttcacaatgtgtataaagac accaacatgcgtggcctgccgctgtcggcgattttcaccacc
99	PRT	Artificial	tencon 27	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VKGGHRSNPLSAIFTT
100	PRT	Artificial	TCL14 library	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFXIXYX EXXXXGEAIVLTVPGSERSYDLTGLKPGTEYXVXIXG VKGGXXSXPLSAIFTT

>SEQ ID NO: 101
PRT
Homo sapiens
cMet

1 mkapavlapg ilvlftlvq rsngeckeal aksemnvnmk yqlpnftaet piqnvilheh

61 hifigatnyi yvlneedlqk vaeyktgpvl ehpdcfpcqd csskanisgg vwkdninmal

121 vvdtyyddql isegsvnrgt cqrhvfphnh tadiqsevhc ifspqieeps qepdcvvsal

181 gakvlssvkd rfinffvgnt inssyfpdhp lhsisvrrlk etkdgfmflt dqsyidvlpe

241 frdsypikyv hafesnnfiy fltvqretld aqtfhtrnir fcsinsglhs ymemplecil

301 tekrkkrstk kevfnilqaa yvskpgaqla rqigaslndd ilfgvfaqsk pdsaepmdrs

361 amcafpikyv ndffnkivnk nnvrclqhfy gpnhehcfnr tlirnssgce arrdeyrtef

421 ttalqrvdlf mgqfsevllt sistfikgdl tianlgtseg rfmqvvvsrs gpstphvnfl

481 ldshpvspev ivehtlnqng ytlvitgkki tkiplngigc rhfqscsqcl sappfvqcgw

541 chdkcvrsee clsgtwtqqi clpaiykvfp nsapleggtr liicgwdfgf rrnnkfdlkk

601 trvlignesc tltlsestmn tlketvgpam nkhfnmsiii snghgttqys tfsyvdpvit
661 sispkygpma ggtiltltgn yinsgnsrhi siggktctik svsnsilecy tpaqtistef
721 avklkidlan retsifsyre dpivyeihpt ksfistwwke plnivstlfc fasggstitg
781 vgknlnsvsv prmvinvhea grnftvacqh rsnseiicct tpslqqlnlq lpiktkaffm
841 ldgilskyfd iiyvhnpvfk pfekpvmism gnenvieikg ndidpeavkg evikvgnksc
901 enihlhseav letvpndllk lnselniewk qaisstvlgk vivqpdqnft gliagvvsis
961 talliiigff lwlkkrkqik digselvryd arvhtphldr ivsarsvspt temvsnesvd
1021 yratfpedqf pnssqngscr qvqypltdms piltsgdsdi sspliqntvh idlsalnpel
1081 vqavqhvvig psslivhfne vigrghfgcv yhgtlldndg kkihcavksl nritdigevs
1141 qfltegiimk dfshpnvlsl lgiclrsegs plvvlpymkh gdlrnfirne thnptvkdli
1201 gfglqvakgm kylaskkfvh rdlaarncml dekftvkvad fglardmydk eyysvhnktg
1261 aklpvkwmal eslqtqkftt ksdvwsfgvl lwelmtrgap pypdvntfdi tvyllqgrri
1321 lqpeycpdpl yevmlkcwhp kaemrpsfse lvsrisaifs tfigehyvhv natyvnvkcv
1381 apypsllsse dnaddevdtr pasfwets

102	PRT	Homo sapiens	HGF	QRKRRNTIHEFKKSAKTTLIKIDPALKIK TKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMS SGVKKEFGHEFDLYE NKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRG KDLQENYCRNP RGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDH TESGKICQRWDHQTP HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAI TCADNTMNDTDVPL ETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKC KDLRENYCRNPDGS ESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMGNLSQT RSGLTCSMWDKNME DLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPIS RCEGDTTPTIVNL DHPVISCAKTKQLRVVNGIPTRTNIGWMVSLRYRNKHICGGSLIKESW VLTARQCFPSRD LKDYEAWLGIHDVHGRGDEKCKQVLNVSQLVYGPEGSDLVLMKLAR PAVLDDFVSTIDLP NYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRG KVTLNESEICAG AEKIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFV RVAYYAKWIHKII LTYKVPQS
103	DNA	Artificial	>cMET part ECB97 P114AR7P95-C5v2	Ctgccggctccgaagaacttggtggtgagccgtgttaccgaagatagc gcacgcctgagctggacggcaccggatgcggcgttcgatagcttctgg attcgctatttgagtttctgggtagcggtgaggcaattgttctgacggtgcc gggctctgaacgctcctacgatttgaccggtctgaaaccgggcaccga gtatgtggtgaacattctgagcgttaagggcggtagcatcagcccaccg ctgagcgcgatcttcacgactggtggttgc
104	DNA	Artificial	>cMET part ECB15 P114AR7P94-A3	Ctgccggcaccgaagaacctggttgtcagccgtgtgaccgaggatag cgcacgtttgagctggaccgctccggatgcagcctttgacagcttctgga ttcgttacttttgaatttctgggtagcggtgaggcgatcgttctgacggtgccg ggctctgaacgcagctatgatttgacgggcctgaagccgggtactgagt acgtggttaacatcatgggcgttaagggtggtaaaatcagcccgccatt gtccgcgatctttaccacg
105	PRT	Artificial	linker	GGGGS
106	PRT	Artificial	ECB91	mlpapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltvpgse rsydltglkpgteytvsiygvhnvykdtnirglpisaifttapapapapapLPAP KNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTV PGSERSYDLTGLKPGTEYVVNILSVKGGSISPPLSAIFTT
107	PRT	Artificial	P53A1R5-17v2	lpapknlvvsevtedsarlswadphgfydsfliqyqesekvgeaivltvpgsersy dltglkpgteytvsiygvhnvykdtnmrglpisaiftt

108	PRT	Artificial	P54AR4-83v22	ipapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltvpgsersydltglkpgteytvsiygvhnvykdtnirglplsaiftt
109	PRT	Artificial	P54AR4-83v23	ipapknlvvsevtedsarlswddphafyesfliqyqesekvgeaivltvpgsersydltglkpgteytvsiygvhnvykdtnirglplsaiftt
110	PRT	Artificial	P53A1RS-17v22	ipapknlvvsevtedsarlswadphgfydsfliqyqesekvgeaivltvpgsersydltglkpgteytvsiygvhnvykdtnirglplsaiftt
111	PRT	Artificial	P114AR7P94-A3v22	ipapknlvvsrvtedsarlswtapdaafdsfwiryfeflgsgeaivltvpgsersydltglkpgteyvvnilgvkggkispplsaiftt
112	PRT	Artificial	P114AR9P121-A6v2	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVGSGEAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSISPPLSAIFTT
113	PRT	Artificial	P114AR9P122-A7v2	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVSKGDAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSISPPLSAIFTT
114	PRT	Artificial	P114AR7P95-C5v2	LPAPKNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVPGSERSYDLTGLKPGTEYVVNILSVKGGSISPPLSAIFTT
115	DNA	Artificial	ECB97	atgttgccagcgccgaagaacctggtagttagcgaggttactgaggacagcgcgcgtctgagctgggacgatccgtgggcgttctacgagagctttctgatccagtatcaagagagcgagaaagtcggtgaagcgattgtgctgaccgtcccgggctccgagcgttcctacgacctgaccggtttgaagccgggtaccgagtatacggtgagcatctacggtgttcacaatgtctataaggacactaatatccgcggtctgcctctgagcgccatttttcaccaccgcaccggcaccggctccggctcctgccccgctgccggctccgaagaacttggtggtgagccgtgttaccgaagatagcgcacgcctgagctggacggcaccggatgcggcgttcgatagcttctggattcgctattttgagtttctgggtagcggtgaggcaattgttctgacggtgccgggctctgaacgctcctacgatttgaccggtctgaaaccgggcaccgagtatgtggtgaacattctgagcgttaagggcggtagcatcagcccaccgctgagcgcgatcttcacgactggtggttgc
116	DNA	Artificial	ECB15	atgctgccagccccctaagaatctggtcgtgagcgaagtaaccgaggacagcgcccgcctgagctgggacgacccgtgggcgttctatgagtctttcctgattcagtatcaagaaagcgaaaaagttggcgaagcgatcgtcctgaccgtcccgggtagcgagcgctcctacgatctgaccggcctgaaaccgggtacggagtacacggtgtccatttacggtgttcacaatgtgtataaagacaccaacatgcgtggcctgccgctgtcggcgattttcaccaccgcgcctgccagcgcctgcaccggctccgctgccggcaccgaagaacctggttgtcagccgtgtgaccgaggatagcgcacgtttgagctggaccgctccggatgcagcctttgacagcttctggattcgttactttgaatttctgggtagcggtgaggcgatcgttctgacggtgccgggctctgaacgcagctatgatttgacggcctgaagccgggtactgagtacgtggttaacatcatgggcgttaagggtggtaaaatcagcccgccattgtccgcgatcttlaccacg
117	PRT	Artificial	albumin binding domain	tidewllkeakekaieelkkagitsdyyfdlinkaktvegvnalkdeilka

118	PRT	Artificial	ECB18	mlpapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltv pgsersydltglkpgteytvsiygvhnvykdtnmrglplsaifttapapapa paplpapknlvvsrvtedsarlswtapdaafdsfwirydevvvggeaivlt vpgsersydltglkpgteyyvnilgvkggsisvplsaifttapapapapapl aeakvlanreldkygvsdyyknlinnaktvegvkalideilaalp
119	PRT	Artificial	ECB28	mlpapknlvvsevtedsarlswadphgfydsfliqyqesekvgeaivltv pgsersydltglkpgteytvsiygvhnvykdtnmrglplsaifttapapapa paplpapknlvvsrvtedsarlswtapdaafdsfwirydevvvggeaivlt vpgsersydltglkpgteyyvnilgvkggsisvplsaifttapapapapapl aeakvlanreldkygvsdyyknlinnaktvegvkalideilaalp
120	PRT	Artificial	ECB38	mlpapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltv pgsersydltglkpgteytvsiygvhnvykdtnmrglplsaifttapapapa paplpapknlvvsrvtedsarlswtapdaafdsfwiryfeflgsgeaivltv pgsersydltglkpgteyvvnimgvkggkispplsaifttapapapapapl aeakvlanreldkygvsdyyknlinnaktvegvkalideilaalp
121	PRT	Artificial	ECB39	mlpapknlvvsevtedsarlswadphgfydsfliqyqesekvgeaivltv pgsersydltglkpgteytvsiygvhnvykdtnmrglplsaifttapapapa paplpapknlvvsrvtedsarlswtapdaafdsfwiryfeflgsgeaivltv pgsersydltglkpgteyvvnimgvkggkispplsaifttapapapapapl aeakvlanreldkygvsdyyknlinnaktvegvkalideilaalp
122	PRT	Artificial	P53A1R5-17 wthMet	MLPAPKNLVVSEVTEDSLRLSWADPHGFYDSFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAEFTT
123	PRT	Artificial	P54AR4-17 with Met	MLPAPKNLVVSEVTEDSLRLSWTYDRDGYDSFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAEFTT
124	PRT	Artificial	P54AR4-47 with Met	MLPAPKNLVVSEVTEDSLRLSWGYNGDHFDSFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAEFTT
125	PRT	Artificial	P54AR4-48 with Met	MLPAPKNLVVSEVTEDSLRLSWDDPRGFYESFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAEFTT
126	PRT	Artificial	P54AR4-73 with Met	MLPAPKNLVVSEVTEDSLRLSWTWPYADLDSFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAEFTT
127	PRT	Artificial	54AR4-74 with Met	MLPAPKNLVVSEVTEDSLRLSWGYNGDHFDSFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAEFTT
128	PRT	Artificial	P54AR4-81 with Met	MLPAPKNLVVSEVTEDSLRLSWDYDLGVYFDSFLIQ YQESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSI YGVHNVYKDTNMRGLPLSAEFTT
129	PRT	Artificial	P54AR4-83 with Met	MLPAPKNLVVSEVTEDSLRLSWDDPWAFYESFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAEFTT

130	PRT	Artificial	P54CR4-31 with Met	MLPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVLGSYVFEHDVMLPLSAEFTT
131	PRT	Artificial	P54AR4-83v2 with Met	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAIFTT
132	PRT	Artificial	P54CR4-31v2 with Met	MLPAPKNLVVSEVTEDSARLSWTAPDAAFDSFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVLGSYVFEHDVMLPLSAIFTT
133	PRT	Artificial	P54AR4-73v2 withMet	MLPAPKNLVVSEVTEDSLRLSWTWPYADLDSFLIQY QESEKVGEAINLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNMRGLPLSAEFTT
134	PRT	Artificial	P53A1R5-17v2 with Met	mlpapknlvvsevtedsarlswadphgfydsfliqyqesekvgeaivltvpgser sydltglkpgteytvsiygvhnvykdtnmrglplsaiftt
135	PRT	Artificial	P54AR4-83v22 with Met	mlpapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltvpgse rsydltglkpgteytvsiygvhnvykdtnirglplsaiftt
136	PRT	Artificial	P54AR4-83v23 with Met	mlpapknlvvsevtedsarlswddphafyesfliqyqesekvgeaivltvpgser sydltglkpgteytvsiygvhnvykdtnirglplsaiftt
137	PRT	Artificial	P53A1R5-17v22 with Met	mlpapknlvvsevtedsarlswadphgfydsfliqyqesekvgeaivltvpgser sydltglkpgteytvsiygvhnvykdtnirglplsaiftt
138	PRT	Artificial	ECB1 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTGGGGSGGGGSGGGG SGGGGSMLPAPKNLVVSRVTEDSARLSWTAPDAAF DSFWIRYDEVVVGGEAIVLTVPGSERSYDLTGLKPG TEYYVNILGVKGGSISVPLSAIFTT
139	PRT	Artificial	ECB2 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTGGGGSGGGGSGGGG SGGGGSLPAPKNLVVSRVTEDSARLSWTAPDAAFD SFWIRYFEFLGSGEAIVLTVPGSERSYDLTGLKPGT EYVVNIMGVKGGKISPPLSAIFTT
140	PRT	Artificial	ECB3 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTGGGGSGGGGSGGGG SGGGGSMLPAPKNLVVSRVTEDSARLSWTAPDAAF DSFWIRYFEFLGSGEAIVLTVPGSERSYDLTGLKPG TEYVVQIIGVKGGHISLPLSAIFTT

141	PRT	Artificial	ECB4 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTGGGGSGGGGSGGGG SGGGGSMLPAPKNLVVSRVTEDSARLSWTAPDAAF DSFFIRYDEFLRSGEAIVLTVPGSERSYDLTGLKPGT EYWVTILGVKGGLVSTPLSAIFTT
142	PRT	Artificial	ECB5 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTGGGGSGGGGSGGGG SGGGGSMLPAPKNLVVSRVTEDSARLSWTAPDAAF DSFWIRYFEFLGSGEAIVLTVPGSERSYDLTGLKPG TEYVVNIMGVKGGKISPPLSAIFTT
143	PRT	Artificial	ECB6 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTGGGGSGGGGSGGGG SGGGGSMLPAPKNLVVSRVTEDSARLSWTAPDAAF DSFWIRYFEFLGSGEAIVLTVPGSERSYDLTGLKPG TEYVVQIIGVKGGHISLPLSAIFTT
144	PRT	Artificial	ECB7 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTGGGGSGGGGSGGGG SGGGGSMLPAPKNLVVSRVTEDSARLSWTAPDAAF DSFWIRYFEFLGSGEAIVLTVPGSERSYDLTGLKPG TEYVVQIIGVKGGHISLPLSAIFTT
145	PRT	Artificial	ECB15 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGGKI SPPLSAIFTT
146	PRT	Artificial	ECB27 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYDEVVVGG EAIVLTVPGSERSYDLTGLKPGTEYYVNILGVKGGSI SVPLSAIFTT
147	PRT	Artificial	ECB60 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTAPAPAPAPAPMLPAPK NLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGS GEAIVLTVPGSERSYDLTGLKPGTEYVVNIMGVKGG KISPPLSAIFTT
148	PRT	Artificial	ECB37 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNMRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYDEVVVGG EAIVLTVPGSERSYDLTGLKPGTEYYVNILGVKGGSI SVPLSAIFTT

149	PRT	Artificial	ECB94 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGE AIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGKIS PPLSAIFTT
150	PRT	Artificial	ECB95 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSI SPPLSAIFTT
151	PRT	Artificial	ECB96 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVSKGD AIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSIS PPLSAIFTT
152	PRT	Artificial	ECB97 without Met	LPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGE AIVLTVPGSERSYDLTGLKPGTEYVVNILSVKGGSISP PLSAIFTT
153	PRT	Artificial	ECB106 without Met	LPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGE AIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGKIS PPLSAIFTT
154	PRT	Artificial	ECB107 without Met	LPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSI SPPLSAIFTT
155	PRT	Artificial	ECB108 without Met	LPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVSKGD AIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSIS PPLSAIFTT
156	PRT	Artificial	ECB109 without Met	LPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGE AIVLTVPGSERSYDLTGLKPGTEYVVNILSVKGGSISP PLSAIFTT

157	PRT	Artificial	ECB118 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGE AIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGKIS PPLSAIFTT
158	PRT	Artificial	ECB119 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSI SPPLSAIFTT
159	PRT	Artificial	ECB120 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVSKGD AIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSIS PPLSAIFTT
160	PRT	Artificial	ECB121 without Met	LPAPKNLVVSEVTEDSARLSWADPHGFYDSFLIQYQ ESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIYG VHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKNL VVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGE AIVLTVPGSERSYDLTGLKPGTEYVVNILSVKGGSISP PLSAIFTT
161	PRT	Artificial	ECB91 without Met	lpapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltvpgsers ydltglkpgteytvsiygvhnvykdtnirglplsaifttapapapapapLPAPK NLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTVP GSERSYDLTGLKPGTEYVVNILSVKGGSISPPLSAIFTT
162	PRT	Artificial	ECB18 without Met	lpapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltvp gsersydltglkpgteytvsiygvhnvykdtnmrglplsaifttapapapap aplpapknlvvsrvtedsarlswtapdaafdsfwirydevvvggeaivltv pgsersydltglkpgteyyvnilgvkggsisvplsaifttapapapapapla eakvlanreldkygvsdyyknlinnaktvegvkalldeilaalp
163	PRT	Artificial	ECB28 without Met	lpapknlvvsevtedsarlswadphgfydsfliqyqesekvgeaivltvpg sersydltglkpgteytvsiygvhnvykdtnmrglplsaifttapapapapa plpapknlvvsrvtedsarlswtapdaafdsfwirydevvvggeaivltvp gsersydltglkpgteyyvnilgvkggsisvplsaifttapapapapaplae akvlanreldkygvsdyyknlinnaktvegvkalldeilaalp
164	PRT	Artificial	ECB38 without Met	lpapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltvp gsersydltglkpgteytvsiygvhnvykdtnmrglplsaifttapapapap aplpapknlvvsrvtedsarlswtapdaafdsfwiryfefigsgeaivltvp gsersydltglkpgteyvvnimgvkggkisppisaifttapapapapapla eakvlanreldkygvsdyyknlinnaktvegvkalldeilaalp

165	PRT	Artificial	ECB39 without Met	lpapknlvvsevtedsarlswadphgfydsfliqyqesekvgeaivltvpg sersydltglkpgteytvsiygvhnvykdtnmrglplsaifttapapapapa ptpapknlvvsrvtedsariswtapdaafdsfwiryfefigsgeaivltvpg sersydltglkpgteyvvnimgvkggkispplsaifttapapapapaplae akvlanreldkygvsdyyknlinnaktvegvkalldeilaalp
166	DNA	Artificial	ECB97 without Met	ttgccagcgccgaagaacctggtagttagcgaggttactgaggacagc gcgcgtctgagctgggacgatccgtgggcgttctacgagagctttctgat ccagtatcaagagagcgagaaagtcggtgaagcgattgtgctgaccgt cccgggctccgagcgttcctacgacctgaccggtttgaagccgggtacc gagtatacggtgagcatctacggtgttcacaatgtctataaggacactaa tatccgcggtctgcctctgagcgccatttttcaccaccgcaccggcaccg gctccggctcctgccccgctgccggctccgaagaacttggtggtgagcc gtgttaccgaagatagcgcacgcctgagctggacggcaccggatgcg gcgttcgatagcttctggattcgctatttttgagtttctgggtagcggtgaggc aattgttctgacggtgccgggctctgaacgctcctacgatttgaccggtct gaaaccgggcaccgagtatgtggtgaacattctgagcgttaagggcggt agcatcagcccaccgctgagcgcgatcttcacgactggtggttgc
167	DNA	Artificial	ECB15 without Met	ctgccagcccctaagaatctggtcgtgagcgaagtaaccgaggacag cgcccgcctgagctgggacgacccgtgggcgttctatgagtctttcctga ttcagtatcaagaaagcgaaaaagttggcgaagcgatcgtcctgaccg tcccgggtagcgagcgctcctacgatctgaccggcctgaaaccgggta cggagtacacggtgtccatttacggtgttcacaatgtgtataaagacacc aacatgcgtggcctgccgctgtcggcgattttcaccaccgcgcctgcgc cagcgcctgcaccggctccgctgccggcaccgaagaacctggttgtca gccgtgtgaccgaggatagcgcacgtttgagctggaccgctccggatg cagcctttgacagcttctggattcgttactttgaatttctgggtagcggtgag gcgatcgttctgacggtgccgggctctgaacgcagctatgatttgacggg cctgaagccgggtactgagtacgtggttaacatcatgggcgttaagggtg gtaaaatcagcccgccattgtccgcgatctttaccacg
168	DNA	Artificial	>EGFR part ECB97; P54AR4-83v22 without met	ttgccagcgccgaagaacctggtagttagcgaggttactgaggacagc gcgcgtctgagctgggacgatccgtgggcgttctacgagagctttctgat ccagtatcaagagagcgagaaagtcggtgaagcgattgtgctgaccgt cccgggctccgagcgttcctacgacctgaccggtttgaagccgggtacc gagtatacggtgagcatctacggtgttcacaatgtctataaggacactaa tatccgcggtctgcctctgagcgccatttttcaccacc
169	DNA	Artificial	>EGFR part ECB15; P54AR4-83v2 without Met	ctgccagcccctaagaatctggtcgtgagcgaagtaaccgaggacag cgcccgcctgagctgggacgacccgtgggcgttctatgagtctttcctga ttcagtatcaagaaagcgaaaaagttggcgaagcgatcgtcctgaccg tcccgggtagcgagcgctcctacgatctgaccggcctgaaaccgggta cggagtacacggtgtccatttacggtgttcacaatgtgtataaagacacc aacatgcgtggcctgccgctgtcggcgattttcaccacc
170	PRT	Artificial	ECB94 with C-ter cysteine	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGKI SPPLSAIFTTC
171	PRT	Artificial	ECB95 with C-ter cysteine	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSI SPPLSAIFTTC

172	PRT	Artificial	ECB96 with C-ter cysteine	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVSKG DAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSI SPPLSAIFTTC
173	PRT	Artificial	ECB97 with C-ter cysteine	MLPAPKNLVVSEVTEDSARLSWDDPWAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILSVKGGSIS PPLSAIFTTC
174	PRT	Artificial	ECB106 with C-ter cysteine	MLPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGKI SPPLSAIFTTC
175	PRT	Artificial	ECB107 with C-ter cysteine	MLPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSI SPPLSAIFTTC
176	PRT	Artificial	ECB108 with C-ter cysteine	MLPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFVSKG DAIVLTVPGSERSYDLTGLKPGTEYVVNILGVKGGSI SPPLSAIFTTC
177	PRT	Artificial	ECB109 with C-ter cysteine	MLPAPKNLVVSEVTEDSARLSWDDPHAFYESFLIQY QESEKVGEAIVLTVPGSERSYDLTGLKPGTEYTVSIY GVHNVYKDTNIRGLPLSAIFTTAPAPAPAPAPLPAPKN LVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSG EAIVLTVPGSERSYDLTGLKPGTEYVVNILSVKGGSIS PPLSAIFTTC
178	PRT	Artificial	ECB91 with C-ter cysteine	mlpapknlvvsevtedsarlswddpwafyesfliqyqesekvgeaivltvpgse rsydltglkpgteytvsiygvhnvykdtnirglplsaifttapapapapaplPAP KNLVVSRVTEDSARLSWTAPDAAFDSFWIRYFEFLGSGEAIVLTV PGSERSYDLTGLKPGTEYVVNILSVKGGSISPPLSAIFTTC

>SEQ ID NO: 179

PRT

Artificial

An FG loop of EGFR binding FN3 domain

HNVYKDTNX$_9$RGL;
wherein X$_9$ is M or I

>SEQ ID NO: 180
PRT
Artificial
A FG loop of EGFR binding FN3 domain
LGSYVFEHDVML (SEQ ID NO: 180),

>SEQ ID NO: 181
PRT
Artificial
a BC loop of EGFR binding FN3 domain
X$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$ (SEQ ID NO: 181), wherein
X$_1$ is A, T, G or D;
X$_2$ is A, D, Y or W;
X$_3$ is P, D or N;
X$_4$ is L or absent;
X$_5$ is D, H, R, G, Y or W;
X$_6$ is G, D or A;
X$_7$ is A, F, G, H or D; and
X$_8$ is Y, F or L.

>SEQ ID NO: 182
PRT
Artificial
EGFR binding FN3 domain
LPAPKNLVVSEVTEDSLRLSWX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$DSFLIQYQESEKVGEAINLTVP
GSERSYDLTGLKPGTEYTVSIYGVHNVYKDTNX$_9$RGLPLSAEFTT (SEQ ID NO:
182),
X$_1$ is A, T, G or D;
X$_2$ is A, D, Y or W;
X$_3$ is P, D or N;
X$_4$ is L or absent;

X_5 is D, H, R, G, Y or W;

X_6 is G, D or A;

X_7 is A, F, G, H or D;

X_8 is Y, F or L; and

X_9 is M or I

>SEQ ID NO: 183

PRT

Artificial

EGFR binding FN3 domain

LPAPKNLVVSEVTEDSLRLSWX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$DSFLIQYQESEKVGEAINLTVP GSERSYDLTGLKPGTEYTVSIYGVLGSYVFEHDVMLPLSAEFTT (SEQ ID NO: 183),

wherein

X_1 is A, T, G or D;

X_2 is A, D, Y or W;

X_3 is P, D or N;

X_4 is L or absent;

X_5 is D, H, R, G, Y or W;

X_6 is G, D or A;

X_7 is A, F, G, H or D; and

X_8 is Y, F or L.

>SEQ ID NO: 184

PRT

Artificial

A C-met binding FN3 domain C strand and a CD loop sequence

DSFX$_{10}$IRYX$_{11}$E X$_{12}$X$_{13}$X$_{14}$X$_{15}$GX$_{16}$ (SEQ ID NO: 184), wherein

X_{10} is W, F or V;

X_{11} is D, F or L;

X_{12} is V, F or L;

X_{13} is V, L or T;

X_{14} is V, R, G, L, T or S;

X_{15} is G, S, A, T or K; and

X_{16} is E or D; and

>SEQ ID NO: 185

PRT

Artificial

A c-Met binding FN3 domain F strand and a FG loop

TEYX_{17}VX_{18}I$X_{19}X_{20}$V KGG$X_{21}X_{22}$SX_{23} (SEQ ID NO: 185), wherein

X_{17} is Y, W, I, V, G or A;

X_{18} is N, T, Q or G;

X_{19} is L, M, N or I;

X_{20} is G or S;

X_{21} is S, L, G, Y, T, R, H or K;

X_{22} is I, V or L; and

X_{23} is V, T, H, I, P, Y or L.

>SEQ ID NO: 186

PRT

Artificial

a c-Met binding FN3 domain

LPAPKNLVVSRVTEDSARLSWTAPDAAF DSFX_{10}IRYX_{11}E $X_{12}X_{13}X_{14}X_{15}$GX_{16} AIVLTVPGSERSYDLTGLKPGTEYX_{17}VX_{18}I$X_{19}X_{20}$VKGG$X_{21}X_{22}$SX_{23}PLSAEFTT (SEQ ID NO: 186),

wherein

X_{10} is W, F or V; and

X_{11} is D, F or L;

X_{12} is V, F or L;

X_{13} is V, L or T;

X_{14} is V, R, G, L, T or S;

X_{15} is G, S, A, T or K;

X_{16} is E or D;

X_{17} is Y, W, I, V, G or A;

X_{18} is N, T, Q or G;

X_{19} is L, M, N or I;

X_{20} is G or S;

X_{21} is S, L, G, Y, T, R, H or K;

X_{22} is I, V or L; and

X_{23} is V, T, H, I, P, Y or L.

>SEQ ID NO: 187

PRT

Artificial

EGFR FN3 domain of a bispecific EGFR/c-Met FN3 domain containing molecule

LPAPKNLVVSX$_{24}$VTX$_{25}$DSX$_{26}$RLSWDDPX$_{27}$AFYX$_{28}$SFLIQYQX$_{29}$SEKVGEAIX$_{30}$LT VPGSERSYDLTGLKPGTEYTVSIYX$_{31}$VHNVYKDTNX$_{32}$RGLPLSAX$_{33}$FTT (SEQ ID NO: 187), wherein

X_{24} is E, N or R;

X_{25} is E or P;

X_{26} is L or A;

X_{27} is H or W;

X_{28} is E or D;

X_{29} is E or P;

X_{30} is N or V;

X_{31} is G or Y;

X_{32} is M or I; and

X_{33} is E or I;

>SEQ ID NO: 188

c-Met FN3 domain of a bispecific EGFR/c-Met FN3 domain containing molecule

LPAPKNLVVSX$_{34}$VTX$_{35}$DSX$_{36}$RLSWTAPDAAFDSFWIRYFX$_{37}$FX$_{38}$X$_{39}$X$_{40}$GX$_{41}$AIX$_{42}$ LTVPGSERSYDLTGLKPGTEYVVNIX$_{43}$X$_{44}$VKGGX$_{45}$ISPPLSAX$_{46}$FTT (SEQ ID NO: 188); wherein

X_{34} is E, N or R;

X_{35} is E or P;

X_{36} is L or A;

X_{37} is E or P;

X_{38} is V or L;

X_{39} is G or S;

X_{40} is S or K;

X_{41} is E or D;

X_{42} is N or V;

X_{43} is L or M;

X_{44} is G or S;

X_{45} is S or K; and

X_{46} is E or I.

>SEQ ID NO: 189

EGFR mAb E1 VH

QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWD

DGSYKYYGDSVKGRFTISRDNSKNTLY

LQMNSLRAEDTAVYYCARDGITMVRGVMKDYFDYWGQGTLVTVSS

>SEQ ID NO: 190

EGFR mAb E1 VL

AIQLTQSPSSLSASVGDRVTITCRASQDISSALVWYQQKPGKAPKLLIYDASSLESG

VPSRFSGSESGTDFTLTISSLQP

EDFATYYCQQFNSYPLTFGGGTKVEIK

>SEQ ID NO: 191

EGFR mAb E2 VH

1 EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMNWVRQA
PGKGLEWVAN IKKDGSEKYY
61 VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDL
GWGWGWYFDL WGRGTLVTVS
121 S

>SEQ ID NO: 192

EGFR mAb E2 VL

1 EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD
ASNRATGIPA
61 RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPPTFGQ GTKVEIK

>SEQ ID NO: 193

cMet mAb M1 VH

QVQLVQSGAEVKKPGASVKVSCETSGYTFTSYGISWVRQAPGHGLEWMGWISAY
NGYTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFD
YWGQGTLVTVSS

>SEQ ID NO: 194
cMet mAb M1VL
DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWFQHKPGKAPKLLIYAASSLLS
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP-ITFGQGTRLEIK

>SEQ ID NO: 195
cMet mAb M2 VH
EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDD
GSYTYYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAREGLYYYGSGS
YYNQDYWGQGTLVTVSS

>SEQ ID NO: 196
cMet mAb M2 VL
QLTQSPSSLSASVGDRVTITCRASQGLSSALAWYRQKPGKAPKLLIYDASSLESGV
PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFTSYPQITFGQGTRLEIK

>SEQ ID NO: 197
Gp120 heavy chain with F405L
qvqlvqsgaevkkpgasvkvscqasgyrfsnfvihwvrqapgqrfewmgwinpyngnkefsakfqdrvtftadtsantay
melrslrsadtavyycarvgpyswddspqdnyymdvwgkgttvivssastkgpsvfplapsskstsggtaalgclvkdyfp
epvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrvepkscdkthtcppcpapell
ggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwln
gkeykckvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttpp
vldsdgsfllyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk

>SEQ ID NO: 198
Gp120 heavy chain with K409R
qvqlvqsgaevkkpgasvkvscqasgyrfsnfvihwvrqapgqrfewmgwinpyngnkefsakfqdrvtftadtsantay
melrslrsadtavyycarvgpyswddspqdnyymdvwgkgttvivssastkgpsvfplapsskstsggtaalgclvkdyfp
epvtvswnsgaltsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrvepkscdkthtcppcpapell

ggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwln
gkeykckvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttpp
vldsdgsfflysrltvdksrwqqgnvfscsvmhealhnhytqkslslspgk

>SEQ ID NO: 199
EM1-mAb H1 (anti-EGFR,405L)
QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWD
DGSYKYYGDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGITMVRGV
MKDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>SEQ ID NO: 200
EM-1 mAb L1
AIQLTQSPSSLSASVGDRVTITCRASQDISSALVWYQQKPGKAPKLLIYDASSLESG
VPSRFSGSESGTDFTLTISSLQPEDFATYYCQQFNSYPLTFGGGTKVEIKRTVAAPS
VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>SEQ ID NO: 201
EM-1 mAb H2 (K409R, anti-cMet)
QVQLVQSGAEVKKPGASVKVSCETSGYTFTSYGISWVRQAPGHGLEWMGWISAY
NGYTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFD
YWGQGTLVTVSS
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>SEQ ID NO: 202

EM-1 mAb L2

DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWFQHKPGKAPKLLIYAASSLLS
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPITFGQGTRLEIK
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES
VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>SEQ ID NO: 203

H1 constant region

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>SEQ ID NO: 204

H2 constant region

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFLLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>SEQ ID NO: 205

EM1-mAb H1 cDNA pdr000015499

caggtgcagctggtcgagagcggcggagggggtggtgcagcccggcagaagcctgaggctgtcctgcgccgccagcggcttc
accttcagcacctacggcatgcactgggtgcggcaggccccaggcaagggcctggagtgggtggccgtgatctgggacgacg
gcagctacaagtactacggcgacagcgtgaagggcaggttcaccatcagcagggacaacagcaagaacaccctgtacctgca
gatgaacagcctgagggccgaggacaccgccgtgtactactgcgccagggacggcatcaccatggtgcggggcgtgatgaag
gactacttcgactactggggccagggcaccctggtgaccgtgagcagcgccagcaccaagggcccaagcgtgttccccctggc
ccccagcagcaagagcaccagcggcggcacagccgccctgggctgcctggtgaaggactacttccccgagccagtgaccgtg

tcctggaactctggcgccctgacctccggcgtgcacaccttcccgccgtgctgcagagcagcggcctgtacagcctgagcagc
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acaagagagtggagcccaagagctgcgacaagacccacacctgccccccctgcccagccccagagctgctgggcggaccca
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gccacgaggacccagaggtgaagttcaactggtacgtggacggcgtggaggtgcacaacgccaagaccaagcccagagagg
agcagtacaacagcacctacagggtggtgtccgtgctgaccgtgctgcaccaggactggctgaacggcaaggaatacaagtgc
aaggtctccaacaaggccctgccagccccatcgaaaagaccatcagcaaggccaagggccagccacgggagccccaggtg
tacaccctgccccccagccgggaggagatgaccaagaaccaggtgtccctgacctgtctggtgaagggcttctaccccagcgac
atcgccgtggagtgggagagcaacggccagccccgagaacaactacaagaccacccccccagtgctggacagcgacggcagc
ttcctcctgtacagcaagctgaccgtggacaagtccaggtggcagcagggcaacgtgttcagctgcagcgtgatgcacgaggcc
ctgcacaaccactacacccagaagtccctgagcctgagccccggcaaatga

>SEQ ID NO: 206

EM1-mAb L1 cDNA pDR000015499

atccagctgacccagagccccagcagcctgagcgccagcgtgggcgaccgggtgaccatcacctgccgggccagccaggac
atcagcagcgccctggtctggtatcagcagaagcccggcaaggccccaagctgctgatctacgacgccagctccctggaaag
cggcgtgcccagccggttcagcggcagcgagagcggcaccgacttcaccctgaccatcagcagcctgcagccccgaggactic
gccacctactactgccagcagttcaacagctaccccctgaccttttggcggcggaacaaaggtggagatcaagcgtacggtggcc
gctcccagcgtgttcatcttccccccagcgacgagcagctgaagagcggcaccgccagcgtggtgtgcctgctgaacaacttct
acccccgggaggccaaggtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggagagcgtcaccgagcag
gacagcaaggactccacctacagcctgagcagcaccctgaccctgtccaaggccgactacgagaagcacaaggtgtacgcctg
cgaggtgacccaccagggcctgtccagccccgtgaccaagagcttcaacaggggcgagtgctga

>SEQ ID NO: 207

EM-1 mAb H2 cDNA pDR000016584

caggttcagctggtgcagtctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcgagacttctggttacacctt
taccagctatggtatcagctgggtgcgacaggcccctggacacgggcttgagtggatgggatggatcagcgcttacaatggttac
acaaactatgcacagaagctccagggcagggtcaccatgaccacagacacatccacgagcacagcctacatggagctgagga
gcctgagatctgacgacacggccgtgtattactgtgcgagagatctgagaggaactaactactttgactactggggccagggaac
cctggtcaccgtctcctcagcctccaccaagggcccaagcgtgttccctctggccccagcagcaagagcacatctggcggaac
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gcacaccttccagccgtgctgcagagcagcggcctgtacagcctgtccagcgtggtgaccgtgcccagcagctccctgggcac
ccagacctacatctgcaacgtgaaccacaagcccagcaacaccaaggtggacaagcgggtggaacccaagagctgcgacaag

acccacacctgtccccctgccctgccctgaactgctgggcggaccctccgtgttcctgttcccccaaagcccaaggacaccc
tgatgatcagccggacccccgaagtgacctgcgtggtggtggacgtgtcccacgaggaccctgaagtgaagttcaattggtacgt
ggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagtacaacagcacctaccgggtggtgtccgtgctg
acagtgctgcaccaggactggctgaacggcaaagagtacaagtgcaaggtctccaacaaggccctgcctgctcccatcgagaa
aaccatcagcaaggccaagggccagccccgcgagcctcaggtgtacacactgcctcccagccgggaagagatgaccaagaa
ccaggtgtccctgacctgtctggtgaaaggcttctaccccagcgatatcgccgtggaatgggagagcaacggacagccccgagaa
caactacaagaccacccccccctgtgctggacagcgacggctccttcttcctgtactctcggctgaccgtggacaagagccggtgg
cagcagggaaacgtgttcagctgcagcgtgatgcacgaggccctgcacaaccactacacccagaagtccctgagcctgagccc
cgggaagtga

>SEQ ID NO: 208

EM-1 mAb L2 cDNA pDR000016584

gacatccagatgacccagtccccctcctccgtgtccgcctctgtgggcgacagagtgaccatcacctgtcgggcctcccagggc
atctccaactggctggcctggttccagcacaagcccggcaaggccccaagctgctgatctacgccgcctcctccctgctgtccg
gcgtgccctccagattctccggctctggctccggcaccgacttcaccctgaccatctccagcctgcagccccgaggacttcgccac
ctactactgccagcaggccaactccttccccatcaccttcggccagggcacccggctggaaatcaagcgtacggtggccgctcc
cagcgtgttcatcttccccccagcgacgagcagctgaagagcggcaccgccagcgtggtgtgcctgctgaacaacttctaccc
ccgggaggccaaggtgcagtggaaggtggacaacgccctgcagagcggcaacagccaggagagcgtcaccgagcaggaca
gcaaggactccacctacagcctgagcagcaccctgaccctgtccaaggccgactacgagaagcacaaggtgtacgcctgcgag
gtgacccaccagggcctgtccagccccgtgaccaagagcttcaacaggggcgagtgctga

>SEQ ID NO: 209

Gp120 light chain

Eivltqspgtlslspgeratfscrsshsirsrrvawyqhkpgqaprlvihgvsnrasgisdrfsgsgsgtdftltitrvepedfalyy
cqvygassytfgqgtklerkrtvaapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsgnsqesvteqdskd
styslsstltlskadyekhkvyacevthqglsspvtksfnrgec

>SEQ ID NO: 210

E1 HC1 HCDR1

TYGMH

>SEQ ID NO: 211

E1 HC1 HCDR2

VIWDDGSYKYYGDSVKG

>SEQ ID NO: 212
E1 HC1 HCDR3
DGITMVRGVMKDYFDY

>SEQ ID NO: 213
E1 LC1 LCDR1
RASQDISSALV

>SEQ ID NO: 214
E1 LC1 LCDR2
DASSLES

>SEQ ID NO: 215
E1 LC1 LCDR3
QQFNSYPLT

>SEQ ID NO: 216
E1 HC2 HCDR1
SYGIS

>SEQ ID NO: 217
E1 HC2 HCDR2
WISAYNGYTNYAQKLQG

>SEQ ID NO: 218
E1 HC2 HCDR3
DLRGTNYFDY

>SEQ ID NO: 219
E1 LC2 LCDR1
RASQGISNWLA

>SEQ ID NO: 220
E1 LC2 LCDR2

AASSLLS

>SEQ ID NO: 221
E1 LC2 LCDR3
QQANSFPIT

>SEQ ID NO: 222
E2 mAB HC1 HCDR1
SYWMN

>SEQ ID NO: 223
E2 mAb HC1 HCDR2
NIKKDGSEKYYVDSVKG

>SEQ ID NO: 224
E2 mAb HC1 HCDR3
DLGWGWGWYFDL

>SEQ ID NO: 225
E2 mAB LC1 LCDR1
RASQSVSSYLA

>SEQ ID NO: 226
E2 mAb LC1 LCDR2
DASNRAT

>SEQ ID NO: 227
E2 mAb LC1 LCDR3
QQRSNWPPT

>SEQ ID NO: 228
E2 mAB HC2 HCDR1
DYYMY

>SEQ ID NO: 229

E2 mAb HC2 HCDR2

TISDDGSYTYYPDSVKG

>SEQ ID NO: 230

E2 mAb HC2 HCDR3

EGLYYYGSGSYYNQDY

>SEQ ID NO: 231

E2 mAB LC2 LCDR1

RASQGLSSALA

>SEQ ID NO: 232

E2 mAb LC2 LCDR2

DASSLES

>SEQ ID NO: 233

E2 mAb LC2 LCDR3

QQFTSYPQIT

>SEQ ID NO: 234

E2 mAb HC1 (EGFR-F405L)

EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMNWVRQA PGKGLEWVAN IKKDGSEKYY
VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDL GWGWGWYFDL WGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK

>SEQ ID NO: 235

E2 mAb LC1 (EGFR)

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA
RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPPTFGQ GTKVEIK
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>SEQ ID NO: 236
E2 mAb HC2 (c-Met- K409R)
EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDD
GSYTYYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAREGLYYYGSGS
YYNQDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

>SEQ ID NO: 237
E2 mAb LC2 (cMet)
QLTQSPSSLSASVGDRVTITCRASQGLSSALAWYRQKPGKAPKLLIYDASSLESGV
PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFTSYPQITFGQGTRLEIK
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES
VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>SEQ ID NO: 238
c-Met discontinuous epitope of mAb 069
PEFRDSYPIKYVHAF

>SEQ ID NO: 239
c-Met discontinuous epitope of mAb 069
FAQSKPDSAEPMDRSA

>SEQ ID nO: 240
5D5 mAb epitope
PGAQLARQIGASLNDD

WHAT IS CLAIMED

1. An isolated bispecific epidermal growth factor receptor (EGFR)/ hepatocyte growth factor receptor (c-Met) antibody, comprising:
   a) a first heavy chain (HC1) comprising a HC1 constant domain 3 (HC1 CH3) and a HC1 variable region 1 (VH1);
   b) a second heavy chain (HC2) comprising a HC2 constant domain 3 (HC2 CH3) and a HC2 variable region 2 (VH2);
   c) a first light chain (LC1) comprising a light chain variable region 1 (VL1); and
   d) a second light chain (LC2) comprising a light chain variable region 2 (VL2), wherein the VH1 and the VL1 pair to form a first antigen-binding site that specifically binds EGFR, the VH2 and the VL2 pair to form a second antigen-binding site that specifically binds c-Met, the HC1 comprises at least one substitution in the HC1 CH3 and the HC2 comprises at least one substitution in the HC2 CH3, and the substitution in the HC1 CH3 and the substitution in the HC2 CH3 occur at different amino acid residue positions, when residue numbering is according to the EU index.
2. The bispecific antibody of claim 1,

   wherein the antibody inhibits phosphorylation of extracellular signal-related kinases 1 and 2 (ERK1/2) in NCI-H292, NCI-H1975 or SKMES-1 cell line with an IC_{50} value that is at least about 10-fold less, at least about 20-fold less, at least about 30-fold less, at least about 40-fold less, at least about 50-fold less or at least about 60-fold less when compared to the IC_{50} value of inhibition of phosphorylation of ERK1/2 in NCI-H292, NCI-H1975 or SKMES-1 cell lines with a mixture of a control monovalent EGFR antibody comprising a heavy chain 3 (HC3) and a light chain 3 (LC3) and a control monovalent c-Met antibody comprising a heavy chain 4 (HC4) and a light chain 4 (LC4), wherein

   the HC3 and the HC1, the LC3 and the LC1, the HC4 and the HC2, and the LC4 and the LC2 have identical amino acid sequences, respectively, and

   the phosphorylation of ERK1/2 is measured in whole cell lysates by sandwich immunoassay using an anti-phosphoERK1/2 antibody as a capture antibody and an antibody binding to unphosphorylated and phosphorylated ERK1/2 conjugated with an electrochemiluminescent compound as a detection antibody.

3. The bispecific antibody of claims 1 or 2, wherein the antibody inhibits phosphorylation of ERK1/2 with an IC_{50} value of about $2x10^{-9}$ M or less, about $1x10^{-9}$ M or less, or about $1x10^{-10}$ M or less.
4. The bispecific antibody of claim 2 or 3, wherein ERK1 is phosphorylated at residues Thr202 and Tyr204, and ERK2 is phosphorylated at residues Thr185 and Tyr197.
5. The bispecific antibody of any of the claims 1-4,

wherein the antibody inhibits phosphorylation of protein kinase B (AKT) at Ser473 in NCI-H1975 cell line with an IC_{50} value that is at least about 70-fold less when compared to the IC_{50} value of inhibition of phosphorylation of AKT at Ser473 in NCI- H1975 cell line with the mixture of control monovalent EGFR antibody comprising the HC3 and the LC3 and control monovalent c-Met antibody comprising the HC4 and the LC4, wherein

the HC3 and the HC1, the LC3 and the LC1, the HC4 and the HC2, and the LC4 and the LC2 have identical amino acid sequences, respectively, and

phosphorylation of AKT at Ser473 is measured in whole cell lysates by sandwich immunoassay using an antibody binding to unphosphorylated and phosphorylated AKT as a capture antibody and an anti-phospho AKT Ser473 antibody conjugated with an electrochemiluminescent compound as a detection antibody.
6. The bispecific antibody of any of the claims 1-5,

wherein the antibody inhibits phosphorylation of AKT at Thr308 in NCI-H1975 cell line with an IC_{50} value that is at least about 100-fold less when compared to the IC_{50} value of inhibition of phosphorylation of AKT at Thr308 in NCI-H1975 cell line with the mixture of the control monovalent EGFR antibody comprising the HC3 and the LC3 and the control monovalent c-Met antibody comprising the HC4 and the LC4, wherein

the HC3 and the HC1, the LC3 and the LC1, the HC4 and the HC2, and the LC4 and the LC2 have identical amino acid sequences, respectively, and

the phosphorylation of AKT at Thr308 is measured in whole cell lysates by sandwich immunoassay using an antibody binding to unphosphorylated and phosphorylated AKT as a capture antibody and an anti-phospho AKT Thr308 antibody conjugated to an electrochemiluminescent compound as a detection antibody.
7. The bispecific antibody of claim 5 or 6, wherein the antibody inhibits phosphorylation of AKT at Ser473 or at Thr308 with an IC_{50} value of about $1x10^{-9}$ M or less.
8. The bispecific antibody of any of the claims 1-7, wherein the HC1, the LC1, the HC2 and the LC2 comprise the amino acid sequences of SEQ ID NOs: 199, 200, 201 and

202, respectively, optionally having a C-terminal lysine removed from the HC1, the HC2, or both the HC1 and the HC2.

9. The bispecific antibody any of the claims 1-8, wherein the bispecific antibody binds EGFR having the amino acid sequence shown in SEQ ID NO: 73 at EGFR residues K489, I491, K467 and S492 and c-Met at residues PEFRDSYPIKYVHAF (SEQ ID NO: 238) and FAQSKPDSAEPMDRSA (SEQ ID NO: 239).

10. The bispecific antibody of of any of the claims 1-9, wherein the antibody inhibits growth of NCI-H292 or NCI-H1975 cells with an IC_{50} value that is at least about 300-fold less, at least about 400-fold less, at least about 500-fold less, at least about 600-fold less, at least about 700-fold less or at least about 800-fold less when compared to the IC_{50} value of inhibition of growth of NCI-H292 or NCI-H1975 cells with cetuximab when NCI-H292 or NCI-H1975 cells are grown in low attachment conditions.

11. The bispecific antibody of any of the claims 1-10, wherein the antibody inhibits growth of HGF-expressing SKMES-1 cell tumor in SCID Beige mice with a percentage (%) T/C value of at least 500-fold less on day 36 when compared to cetuximab, when the bispecific antibody and cetuximab are administered at 20 mg/kg dose.

12. The bispecific antibody of any of the claims 1-11, wherein the antibody neutralizes EGFR and c-Met signaling.

13. The bispecific antibody of any of the claims 1-12, wherein the HC1 and the HC2 are of IgG1, IgG2, IgG3 or IgG4 isotype.

14. The bispecific antibody of claim 13, wherein the HC1 and the HC2 are of IgG1 isotype.

15. The bispecific antibody of claim 13 or 14, wherein the HC1 CH3 comprises at least one, two, three, four, five, six, seven or eight substitutions and the HC2 CH3 comprises at least one, two, three, four, five, six, seven or eight substitutions at residue positions 350, 366, 368, 370, 399, 405, 407 or 409, when residue numbering is according to the EU index.

16. The bispecific antibody of claim 15, wherein the HC1 CH3 comprises at least one, two, three or four substitutions and the HC2 CH3 comprises at least one, two, three or four substitutions at residue positions 350, 370, 405 or 409.

17. The bispecific antibody of claim 16, wherein the HC1 CH3 comprises at least one substitution and the HC2 CH3 comprises at least one substitution at residue positions 405 or 409.
18. The bispecific antibody of claim 17, wherein the HC1 CH3 comprises a K409R or a F405L substitution and the HC2 CH3 comprises a K409R or F405L substitution.
19. The bispecific antibody of claim 18, wherein the HC1 CH3 comprises the F405L substitution and the HC2 CH3 comprises the K409R substitution.
20. The bispecific antibody any of the claims 1-19, wherein
    a) the VH1 comprises the heavy chain complementarity determining region (HCDR) 1 (HCDR1), HCDR2 and HCDR3 amino acid sequences of SEQ ID NOs: 210, 211 and 212, respectively; and
    b) the VL1 comprises the light chain complementarity determining region (LCDR) 1 (LCDR1), LCDR2 and LCDR3 amino acid sequences of SEQ ID NOs: 213, 214 and 215, respectively.
21. The bispecific antibody of claim 20, wherein
    a) the VH2 comprises the HCDR1, the HCDR2, and the HCDR3 amino acid sequences of SEQ ID NOs: 216, 217 and 218, respectively; and
    b) the VL2 comprises the LCDR1, the LCDR2 and the LCDR3 amino acid sequences of SEQ ID NOs: 219, 220 and 221, respectively.
22. The bispecific antibody of claim 21, wherein the VH1, the VL1, the VH2 and the VL2 comprise the amino acid sequences of SEQ ID NOs: 189, 190, 193 and 194, respectively.

23. The bispecific antibody of any of the claims 1-7 or 9-18, wherein
    a) VH1 comprises the HCDR1, the HCDR2, and the HCDR3 amino acid sequences of SEQ ID NOs: 222, 223 and 224, respectively; and
    b) VL1 comprises the LCDR1, the LCDR2 and the LCDR3 amino acid sequences of SEQ ID NOs: 225, 226 and 227, respectively.
24. The bispecific antibody of claim 23, wherein
    a) VH2 comprises the HCDR1, the HCDR2, and the HCDR3 amino acid sequences of SEQ ID NOs: 228, 229 and 230, respectively; and
    b) VL2 comprises the LCDR1, the LCDR2 and the LCDR3 amino acid sequences of SEQ ID NOs: 231, 232 and 233, respectively.

25. The bispecific antibody of claim 24, wherein the VH1, the VL1, the VH2 and the VL2 comprise the amino acid sequences of SEQ ID NOs: 191, 192, 195 and 196, respectively.
26. The bispecific antibody of claim 25, wherein the HC1, the LC1, the HC2 and the LC2 comprise the amino acid sequences of SEQ ID NOs: 234, 235, 236 and 237, respectively, and the C-terminal lysine is optionally removed from the HC1, the HC2, or both the HC1 and the HC2.
27. The bispecific antibody of claim 22 or 26, further comprising 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 conservative amino acid substitutions in the HC1, the LC1, the HC2 or the LC2.
28. The bispecific antibody of claim 27, comprising a substitution M252Y/S254T/T256E in the HC1 and/or the HC2, wherein residue numbering is according to the EU index.
29. The bispecific antibody of any of the claims 1-29, wherein the antibody has a biantennary glycan structure with a fucose content of about between 1% to about 15%.
30. The bispecific antibody of claim 2, wherein HC1, LC1, HC2 and LC2 are encoded by synthetic polynucleotides comprising the sequence of SEQ ID NOs: 205, 206, 207 and 208, respectively.
31. An isolated synthetic polynucleotide encoding the HC1, the HC2, the LC1 or the LC2 of claim 8 or 26.
32. The isolated polynucleotide of claim 31 comprising the polynucleotide sequence of SEQ ID NOs: 205, 206, 207 or 208.
33. A vector comprising the polynucleotide of claim 31 or 32.
34. An isolated host cell comprising the vector of claim 33.
35. A method of producing the isolated bispecific EGFR/c-Met antibody of claim 8, comprising:
    a) combining an isolated monospecific bivalent anti-EGFR antibody comprising two heavy chains of SEQ ID NO: 199 and two light chains of SEQ ID NO: 200 and an isolated monospecific bivalent anti-c-Met antibody comprising two heavy chains of SEQ ID NO: 201 and two light chains of SEQ ID NO: 202 in a mixture of about 1:1 molar ratio;
    b) introducing a reducing agent into the mixture;
    c) incubating the mixture about ninety minutes to about six hours;
    d) removing the reducing agent; and
    e) purifying the bispecific EGFR/c-Met antibody that comprises a first heavy chain of SEQ ID NO: 199 and a second heavy chain of SEQ ID NO: 201, a first light

chain of SEQ ID NO: 200 and a second light chain of SEQ ID NO: 202, wherein the first heavy chain of SEQ ID NO: 199 pairs with the first light chain of SEQ ID NO: 200 to form the first binding domain that specifically binds EGFR, and the second heavy chain of SEQ ID NO: 201 pairs with the second light chain of SEQ ID NO: 202 to form the second binding domain that specifically binds c-Met.

36. The method of claim 35, wherein the reducing agent is 2- mercaptoethanolamine (2-MEA).
37. The method of claim 36, wherein the 2-MEA is present at a concentration of about 25 mM to about 75 mM.
38. The method of claim 37, wherein the incubating step is performed at a temperature of about 25°C to about 37°C.
39. A pharmaceutical composition comprising the bispecific antibody of any of the claims 1-30 and a pharmaceutically acceptable carrier.
40. A method of treating a subject having cancer, comprising administering a therapeutically effective amount of the bispecific EGFR/c-Met antibody of claim 2, 8 or 26 to a patient in need thereof for a time sufficient to treat the cancer.
41. The method of claim 40, wherein the cancer is associated with an EGFR activating mutation, an EGFR gene amplification, increased levels of circulating HGF, a c-Met activating mutation, a c-Met gene amplification or a mutant KRAS.
42. The method of claim 41, wherein the EGFR activating mutation is G719A, G719X (X being any amino acid), L861X (X being any amino acid), L858R, E746K, L747S, E749Q, A750P, A755V, V765M, L858P or T790M substitution, deletion of E746-A750, deletion of R748-P753, insertion of Ala (A) between M766 and A767, insertion of Ser, Val and Ala (SVA) between S768 and V769, and insertion of Asn and Ser (NS) between P772 and H773.
43. The method of claim 42, wherein the EGFR activating mutation is L858R, del(E476, A750) and/or T790M substitution.
44. The method of claim 41, wherein the mutant KRAS has a G12V or G12C substitution.
45. The method of claim 44, wherein the mutant KRAS has a G12V substitution.
46. The method of claim 41, wherein the subject is resistant or has acquired resistance to treatment with erlotinib, gefitinib, afatinib, CO-1686, AZD9192 or cetuximab.
47. The method of claim 41, wherein the cancer is an epithelial cell cancer, breast cancer, ovarian cancer, lung cancer, non-small cell lung cancer (NSCLC), lung adenocarcinoma, small cell lung cancer, colorectal cancer, anal cancer, prostate

cancer, kidney cancer, bladder cancer, head and neck cancer, pharynx cancer, cancer of the nose, pancreatic cancer, skin cancer, oral cancer, cancer of the tongue, esophageal cancer, vaginal cancer, cervical cancer, cancer of the spleen, testicular cancer, gastric cancer, cancer of the thymus, colon cancer, thyroid cancer, liver cancer, hepatocellular carcinoma (HCC) or sporadic or hereditary papillary renal cell carcinoma (PRCC).

48. The method of claim 40, wherein the subject is homozygous for phenylalanine at position 158 of CD16 or heterozygous for valine and pheynylalanine at position 158 of CD16.
49. The method of claim 47, comprising administering a second therapeutic agent.
50. The method of claim 49, wherein the second therapeutic agent is a chemotherapeutic agent or a targeted anti-cancer therapy.
51. The method of claim 50, wherein the chemotherapeutic agent is cisplatin or vinblastine.
52. The method of claim 50, wherein the chemotherapeutic agent or the targeted anti-cancer therapy is a tyrosine kinase inhibitor of EGFR, c-Met, HER2, HER3, HER4 or VEGFR.
53. The method of claim 52, wherein the tyrosine kinase inhibitor is erlotinib, gefitinib or afatinib.
54. The method of claim 49, wherein the second therapeutic agent is administered simultaneously, sequentially or separately.
55. A method of inhibiting growth or proliferation of cells that express EGFR and/or c-Met, comprising contacting the cells with the bispecific antibody of claim 2, 8 or 26.
56. A method of inhibiting growth or metastasis of EGFR and/or c-Met expressing tumor or cancer cells in a subject comprising administering to the subject an effective amount of the bispecific antibody of claim 2, 8 or 26 to inhibit the growth or metastasis of EGFR and/or c-Met expressing tumor or cancer cells.
57. The method of claim 56, wherein the EGFR and/or c-Met expressing tumor is an epithelial cell cancer, breast cancer, ovarian cancer, lung cancer, non-small cell lung cancer (NSCLC), lung adenocarcinoma, small cell lung cancer, colorectal cancer, anal cancer, prostate cancer, kidney cancer, bladder cancer, head and neck cancer, pharynx cancer, cancer of the nose, pancreatic cancer, skin cancer, oral cancer, cancer of the tongue, esophageal cancer, vaginal cancer, cervical cancer, cancer of the spleen, testicular cancer, gastric cancer, cancer of the thymus, colon cancer, thyroid cancer,

liver cancer, hepatocellular carcinoma (HCC) or sporadic or hereditary papillary renal cell carcinoma (PRCC).

58. The method of claim 57, wherein the EGFR and/or c-Met expressing tumor is associated with an EGFR activating mutation, an EGFR gene amplification, increased levels of circulating HGF, a c-Met activating mutation, a c-Met gene amplification or a mutant KRAS.
59. The method of claim 58, wherein the EGFR activating mutation is G719A, G719X (X being any amino acid), L861X (X being any amino acid), L858R, E746K, L747S, E749Q, A750P, A755V, V765M, L858P or T790M substitution, deletion of E746-A750, deletion of R748-P753, insertion of Ala (A) between M766 and A767, insertion of Ser, Val and Ala (SVA) between S768 and V769, and insertion of Asn and Ser (NS) between P772 and H773.
60. The method of claim 59, wherein the EGFR activating mutation is L858R, del(E476, A750) and/or T790M substitution.
61. The method of claim 58, wherein the mutant KRAS has a G12V or G12C substitution.
62. The method of claim 61, wherein the mutant KRAS has a G12V substitution.
63. Use of a bispecific antibody of any of the claims 1-30 for therapy.
64. A bispecific antibody according to any of the claims 1-30 for use in treatment of cancer.
65. A bispecific antibody according to any of the claims 1-30 for use according to claim 64, wherein cancer is an epithelial cell cancer, breast cancer, ovarian cancer, lung cancer, non-small cell lung cancer (NSCLC), lung adenocarcinoma, small cell lung cancer, colorectal cancer, anal cancer, prostate cancer, kidney cancer, bladder cancer, head and neck cancer, pharynx cancer, cancer of the nose, pancreatic cancer, skin cancer, oral cancer, cancer of the tongue, esophageal cancer, vaginal cancer, cervical cancer, cancer of the spleen, testicular cancer, gastric cancer, cancer of the thymus, colon cancer, thyroid cancer, liver cancer, hepatocellular carcinoma (HCC) or sporadic or hereditary papillary renal cell carcinoma (PRCC).