



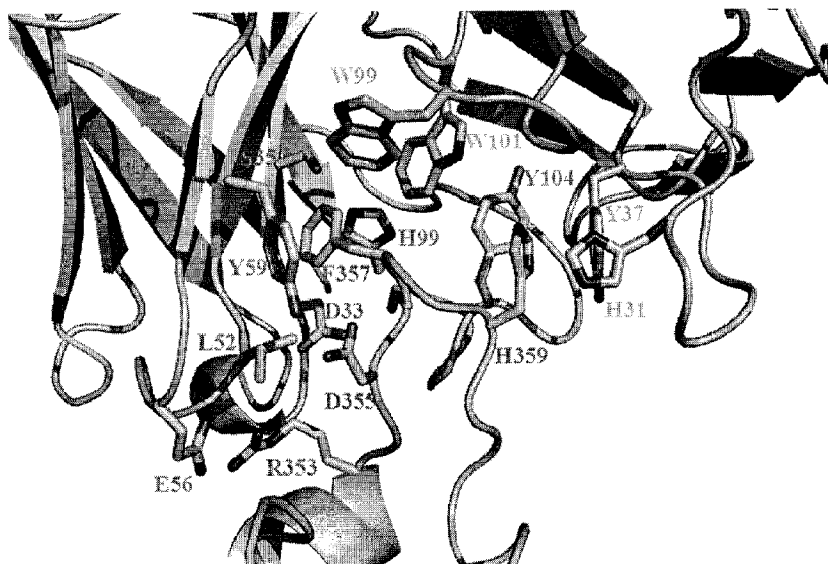
(86) Date de dépôt PCT/PCT Filing Date: 2013/03/27
 (87) Date publication PCT/PCT Publication Date: 2013/10/03
 (45) Date de délivrance/Issue Date: 2022/06/28
 (85) Entrée phase nationale/National Entry: 2014/10/21
 (86) N° demande PCT/PCT Application No.: KR 2013/002550
 (87) N° publication PCT/PCT Publication No.: 2013/147509
 (30) Priorité/Priority: 2012/03/27 (US61/616,073)

(51) Cl.Int./Int.Cl. *A61K 38/17* (2006.01),
A61K 38/16 (2006.01), *A61K 39/395* (2006.01),
A61K 48/00 (2006.01), *A61P 35/00* (2006.01)

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(54) Titre : EPITOPES D'UN ANTIGENE DE SURFACE DE RECEPTEUR DE FACTEUR DE CROISSANCE
 EPIDERMIQUE ET LEUR UTILISATION
 (54) Title: EPITOPES OF EPIDERMAL GROWTH FACTOR RECEPTOR SURFACE ANTIGEN AND USE THEREOF



(57) Abrégé/Abstract:

The present invention relates to epitopes of the epidermal growth factor receptor (EGFR) and the use thereof. The epitopes provided by the present invention are highly preserved, and located in the domain closely related to binding with an epidermal

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(57) **Abrégé(suite)/Abstract(continued):**

growth factor (EGF). Therefore, vaccine compositions comprising the epitopes or compositions comprising antibodies to the epitopes may efficiently block a signal transduction caused by binding of EGF and EGRF, and thus can be highly valuably used in treating various diseases such as cancer. An antibody bound to the epitopes of the present invention may efficiently inhibit binding of various EGFR ligands such as not only EGF but also TGF- α , AR, BTC, EPR and HB-EGF, with EGFR, and therefore can be used in treating various diseases resulting from an activation of EGFR caused by binding not only with EGF but also with other EGFR ligands.

ABSTRACT

The present invention relates to epitopes of the epidermal growth factor receptor (EGFR) and the use thereof. The epitopes provided by the present invention
5 are highly preserved, and located in the domain closely related to binding with an
epidermal growth factor (EGF). Therefore, vaccine compositions comprising the
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EPITOPES OF EPIDERMAL GROWTH FACTOR RECEPTOR SURFACE
ANTIGEN AND USE THEREOF

FIELD OF THE INVENTION

The present invention relates to epitopes on an epidermal growth factor
5 receptor (hereinafter referred to as 'EGFR') and the use thereof. The epitopes
provided according to one exemplary embodiment of the present invention are highly
conserved, and located in a domain closely associated with binding to an epidermal
growth factor (hereinafter referred to as 'EGF'). Therefore, vaccine compositions
including the epitopes, antibodies against the epitopes, or compositions including the
10 antibodies may efficiently block a signal transduction caused by binding of EGFR to
EGF, and thus can be highly valuable and useful in treating various diseases such as
cancer. Further, antibodies binding to the epitopes may efficiently inhibit binding of
various EGFR ligands such as not only EGF but also transforming growth factor- α
(TGF- α), amphiregulin (AR), betacellulin (BTC), epiregulin (EPR) and a heparin-
15 binding EGF-like growth factor (HB-EGF) to EGFR, and thus can be used to treat
various diseases caused by activation of EGFR.

Also, the present invention relates to a method of producing an antibody
specific to the epitopes.

BACKGROUND OF THE INVENTION

20 Immunotherapeutic methods of treating cancer have advantages in that
specificity to target diseases in patients is enhanced compared to surgeries, radiation
therapies and chemotherapies, thereby enhancing anti-cancer effects and reducing side
effects. Tumor-specific monoclonal antibodies have been used as a therapeutic agent
which is very useful in treating tumors by targeting certain proteins specifically
25 overexpressed according to various types of cancer to acquire anti-cancer effects.

An epidermal growth factor receptor (EGFR) is a type I membrane protein having a molecular weight of 170 kDa, and is known to be overexpressed in various types of tumors. The EGFR has been studied for a long period of time, and current crystallographic studies of a cellular domain (Garrett TP *et al.*, *Cell*, 2002, 110: 763-773) and an intracellular kinase domain (Stamos J *et al.*, *J. Biol. Chem.*, 2002, 277: 46265-46272) have been successfully conducted. These studies presented crucial information on the behavior of receptors and ligands thereof. EGFR is a cell surface-associated molecule that is activated through binding of EGF ligands and transforming growth factor- α (TGF- α) thereto. After the binding of the ligands, receptors are dimerized to phosphorylate an intracellular tyrosine kinase domain. As a result, the subsequent signal cascade reactions are activated to induce the growth and proliferation of normal cells and the growth of tumor cells. In particular, since the functions of the tumor cells depend mainly on the EGFR, the receptor has been recognized as a common target for treatment due to the extent of probability of inhibiting the regulatory functions of the EGFR.

The overexpression of the EGFR is, for example, observed in certain types of cancer, such as lung cancer, breast cancer, colon cancer, gastric cancer, brain cancer, bladder cancer, head and neck cancer, ovarian cancer, and prostate cancer. When the binding of EGF to the EGFR is inhibited using antibodies against the EGFR, the growth of cancer cells may be inhibited to treat cancer, which was already experimentally proven using a monoclonal antibody against the EGFR.

Meanwhile, although there have been attempts conducted to elucidate the positions of respective domains of EGFR binding to EGF (S. Yokoyama *et al.*, *Cell*, 2002, 110: 775-787), it has to be further studied whether an antibody where such EGFR domain is used as an epitope inhibits the activation of an EGFR signal transduction pathway by EGF.

In recent years, cetuximab (C225 antibody, Product name: Erbitux; ImClone, US) used to treat metastatic colorectal cancer in the clinical field is a chimeric antibody which is obtained by binding of a variable region of a mouse antibody to an IgG1 constant region of a human antibody (having approximately 30% of a mouse amino acid sequence), and thus inhibits the growth of tumor cells and phosphorylation of EGFR by EGF *in vitro*, and suppresses the formation of human tumors in a nude mouse. Also, the antibody was found to have synergism with a certain chemotherapeutic agent to eradicate the human tumors in a xenograft mouse model. However, cetuximab has a problem in that it causes an immune response in patients (approximately 10%), and can only be used as a combination therapy with a chemotherapeutic agent since it does not have a satisfactory therapeutic effect using the stand-alone therapy.

Panitumumab (Product name: Vectibix; Amgen Inc. US) that is another antibody used to treat metastatic colorectal cancer is a fully human antibody which inhibits the growth of tumor cells and phosphorylation of EGFR by EGF *in vitro*, and suppresses the formation of human tumors in a nude mouse. Also, the antibody was found to have synergism with a certain chemotherapeutic agent to eradicate the human tumors in a xenograft mouse model. Panitumumab is different from cetuximab in that it is a fully human antibody, has an antigen binding ability 10 times of cetuximab, reduces the probability of inducing an immune response like cetuximab as an IgG2-type antibody, and exhibits only an inhibitory effect of signal transduction by binding of EGFR to EGF due to limitations of IgG2 although the binding ability was enhanced to reduce the side effects and improve effectiveness. Therefore, it was reported that panitumumab has overall clinical effects similar to cetuximab because it has no antibody-dependent cell cytotoxicity (ADCC) activities among the inhibitory effect of signal transduction and ADCC activities of cetuximab known in the related art.

Also, matuzumab (mAb425) which is being jointly developed by Merck Serono and Takeda Pharmaceuticals does not have a satisfactory therapeutic effect in the stand-alone therapy so far.

Above all, all the conventional antibody therapeutic agents targeting the EGFR are not allowed to be prescribed to treat K-ras mutant colorectal cancer. The data reported in 2009 confirmed that a percentage of patients in which the two antibodies show a therapeutic effect amounts to approximately 21%, and the antibodies show no therapeutic effect in the remaining 79 % of the patients. 43% of the patients group in which the antibodies show no therapeutic effect, i.e., approximately 30% of the overall number of patients, have a K-ras mutant, which belongs to this group of K-ras mutant colorectal cancer. The conventional antibody therapeutic agents, cetuximab and panitumumab, show a therapeutic effect only in approximately 1.5% of K-ras mutant.

Therefore, the demands for novel anti-EGFR antibodies having differentiation and superiority with which the problems and limits of the conventional EGFR antibodies can be overcome by inhibiting the binding of EGFR to EGF more efficiently tend to continuously increase.

SUMMARY OF THE INVENTION

Therefore, it is an objective of the present invention to provide an amino acid sequence of RGDSFTH (SEQ ID NO: 2), or an epitope on EGFR including the same, and particularly, an epitope having an amino acid sequence of RGDSFTHTP (SEQ ID NO: 3).

It is another objective of the present invention to provide a method of producing the epitope, a composition for cancer vaccines or a cancer vaccine including the epitope, a method of producing an antibody, which has the ability to

specifically bind to the epitope, using the epitope, and a composition or a therapeutic agent for preventing and/or treating cancer including the antibody produced by the method.

It is a further objective of the present invention to provide the epitope or a polynucleotide sequence encoding the epitope, and a composition and a kit for diagnosing cancer including the polynucleotide sequence.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a diagram showing the binding characteristics of EGFR to a GC1118 antibody in a 3D manner.

FIG. 2 is a diagram showing the binding characteristics of EGFR to EGF in a 3D manner.

FIG. 3 is a diagram showing the binding characteristics of the GC1118 antibody to EGFR to which EGF is bound when the GC1118 antibody overlaps the EGFR.

FIG. 4 is a diagram showing the binding characteristics of EGFR to cetuximab and matuzumab in a 3D manner.

FIG. 5 is a diagram showing a procedure of synthesizing an EGFR variant gene and a procedure of transforming yeast cells.

FIG. 6 is a diagram showing that respective EGFR variants are properly synthesized by identifying the amino acid sequence determined from a DNA base sequence.

FIG. 7 is a diagram showing the expression rates of the respective EGFR variants.

FIG. 8 is a diagram showing the binding abilities of antibodies against the respective EGFR mutants: (A) GC1118, and (B) cetuximab (control).

FIG. 9 is a diagram showing the competitive binding abilities of EGFR ligands to GC1118: (A) GC1118, and (B) cetuximab (control).

5 **FIG. 10** is a diagram showing the inhibitory activities of GC1118 on the induction of cell proliferation.

DETAILED DESCRIPTION OF THE INVENTION

Hereinafter, the present invention will be described in detail.

The present inventors have elucidated that an amino acid sequence of
10 RGDSFTH (SEQ ID NO: 2) or an amino acid sequence including the same, especially
an amino acid sequence represented by RGDSFTHTP (SEQ ID NO: 3), essentially
functions in binding to EGF among amino acid sequences of EGFR, and found that
antibodies having the amino acid sequence as an epitope very efficiently inhibit the
binding of EGFR to EGF, and thus shows superior effects in treating cancer by
15 blocking the signal transduction from the binding. Therefore, the present invention
has been completed based on these facts.

The amino acid sequence of RGDSFTH set forth in SEQ ID NO: 2
corresponds to 353rd to 359th amino acid residues of an amino acid sequence of an
extracellular domain of EGFR set forth in SEQ ID NO: 1, and the amino acid
20 sequence of RGDSFTHTP set forth in SEQ ID NO: 3 corresponds to 353rd to 361st
amino acid residues of the extracellular domain of EGFR set forth in SEQ ID NO: 1.

The amino acid residues present in the amino acid sequence provided in the
present invention are represented by their three- or one-letter abbreviations known in
the related art. Also, in the present invention, the term “xA” refers to an Ath amino

acid x of an EGFR sequence set forth in SEQ ID NO: 1, and the term “xAz” means that an Ath amino acid x is substituted with z. For example, the term “R353” refers to arginine (Arg) that is the 353rd amino acid residue of the amino acid sequence set forth in SEQ ID NO: 1, and the term “R353G” means that arginine (Arg) that is the
5 353rd amino acid residue of the amino acid sequence set forth in SEQ ID NO: 1 is substituted with glycine (Gly).

An epitope having the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence set forth in SEQ ID NO: 3 may be used in combination with a
10 carrier in order to maintain its own 3D structure or provide efficiency in use as a composition such as a cancer vaccine. The carrier according to one exemplary embodiment of the present invention is biocompatible, and all types of carriers may be used herein as long as they can achieve desired effects. In this case, the carrier may be selected from the group consisting of a peptide, serum albumin, an
15 immunoglobulin, hemocyanin, and a polysaccharide, but the present invention is not limited thereto.

An epitope having the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence set forth in SEQ ID NO: 3 may be used per se, or used as a
20 complex in combination with a carrier. In this case, the epitope or the complex may be used in a cancer vaccine composition. Here, the vaccine composition may further include a pharmaceutically acceptable adjuvant or excipient. Any type of adjuvant may be used as long as they can serve to enhance antibody formation when injected into the body, thereby achieving the objectives of the present invention. In particular,
25 the adjuvant may be at least one selected from the group consisting of an aluminum salt (Al(OH)₃, or AlPO₄), squalene, sorbitane, polysorbate 80, CpG, a liposome,

cholesterol, monophosphoryl lipid A (MPL), and glucopyranosyl lipid A (GLA), but the present invention is not limited thereto.

A polynucleotide encoding the epitope having the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3 provided in the present invention may be used in the form of a genetic cancer vaccine per se. In this case, the polynucleotide itself may be used without using a delivery system, or may be delivered into the body contained in a viral or non-viral delivery system. Any type of viral or non-viral delivery system may be used as long as they are known to be conventionally available in the art. Specifically, the viral delivery system preferably includes an adenovirus, an adeno-associated virus, a lentivirus, a retrovirus, and the like, and the non-viral vector that may be used herein includes at least one selected from the group consisting of a cationic polymer, a non-ionic polymer, a liposome, a lipid, phospholipid, a hydrophilic polymer, a hydrophobic polymer, and a complex thereof, but the present invention is not limited thereto.

The present invention provides a recombinant vector including the polynucleotide encoding the epitope having the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence set forth in SEQ ID NO: 3, a host cell including the recombinant vector, and a method of preparing the epitope, which has the amino acid sequence of SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence of SEQ ID NO: 3, using the recombinant vector or the host cell according to the present invention.

In the present invention, the term "recombinant vector" refers to an expression vector capable of expressing a target protein in a proper host cell, that is, a gene construct including an essential regulatory element operably linked to express a

gene insert. In the present invention, the term “operably linked” means that a nucleic acid sequence encoding a desired protein is functionally linked with a nucleic acid expression control sequence to execute general functions. The operable linkage with the recombinant vector may be performed using genetic recombination techniques widely known in the art, and the site-specific DNA cleavage and ligation may be readily performed using enzymes widely known in the art.

A proper expression vector that can be used in the present invention may include signal sequences for membrane targeting or secretion in addition to expression control elements such as a promoter, an initiation codon, a stop codon, a polyadenylation signal, and an enhancer. The initiation codon and the stop codon are generally considered to be a portion of a nucleotide sequence encoding an immunogenic target protein, and thus should be essentially operated in an individual when a gene construct is administered into the individual, and inserted in-frame with a coding sequence. A common promoter may be constitutive or inducible. There are Lac, Tac, T3, and T7 promoters present in prokaryotic cells, but not limited thereto. There are a β -actin promoter and promoters derived from human hemoglobin, human muscle creatine, and human metallothionein, as well as promoters derived from a simian virus 40(SV40), a mouse mammary tumor virus (MMTV), a human immunodeficiency virus (HIV) (for example, a long terminal repeat (LTR) promoter from HIV), a Moloney virus, a cytomegalovirus (CMV), an Epstein-Barr virus (EBV), and a Rous sarcoma virus (RSV) present in eukaryotic cells, but not limited thereto.

The expression vector may include a selection marker for selecting a host cell containing the vector. The selection marker is used to select cells transformed with the vector. Here, markers giving selectable phenotypes such as drug tolerance, auxotrophy, tolerance to cytotoxic agents, or expression of surface proteins may be used as the selection marker. Since only the cells expressing the selection marker survive in an environment treated with a selective agent, it is possible to select the

transformed cells. Also, when the vector is a replicable expression vector, the vector may include a replication origin that is a certain nucleic acid sequence from which a replication is initiated. Various types of vectors such as a plasmid, a virus, and a cosmid may be used as the recombinant expression vector. Any type of the recombinant vector may be used without particular limitation as long as they can function to express a desired gene in various host cells such as prokaryotic cells and eukaryotic cells, and produce a desired protein. However, a vector, which includes a promoter having strong activities and can mass-produce a foreign protein having a similar shape to the wild type while retaining strong expression intensity, may be preferably used as the recombinant vector.

In particular, various combinations of expression hosts/vectors may be employed to express the epitope according to one exemplary embodiment of the present invention, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3. The expression vector suitable for eukaryotic hosts may contain regulatory sequence for expression, including without limitation, derived from SV40, a bovine papilloma virus, an adenovirus, an adeno-associated virus, a cytomegalovirus, a lentivirus and a retrovirus. The expression vector that may be used in a bacterial host includes bacterial plasmids obtained from *Escherichia coli*, such as pET, pRSET, pBluescript, pGEX2T, pUC vector, col E1, pCR1, pBR322, pMB9 and derivatives thereof; plasmids having a wide host range such as RP4; phage DNAs including various phage lambda derivatives such as λ gt10, λ gt11 and NM989; and other DNA phages such as M13 and filamentous single-stranded DNA phages. A vector useful for insect cells is pVL941.

The recombinant vector is introduced into host cells to form transformants. The suitable host cells may include prokaryotes such as *E. coli*, *Bacillus subtilis*, *Streptomyces* sp., *Pseudomonas* sp., *Proteus mirabilis*, or *Staphylococcus* sp.; fungi

such as *Aspergillus* sp.; yeast cells such as *Pichia pastoris*, *Saccharomyces cerevisiae*, *Schizosaccharomyces* sp., and *Neurospora crassa*; and other lower eukaryotes, and higher eukaryotic cells such as insect cells. Further, the host cells may be preferably derived from plants, and mammals such as monkey kidney cells (COS7), NSO cells, 5 SP2/0, Chinese hamster ovary (CHO) cells, W138, baby hamster kidney (BHK) cells, MDCK, a myeloma cell line, HuT 78 cells, and HEK293 cells, without limitation. The CHO cells are particularly preferred.

In the present invention, the term “transformation” into the host cells encompasses any method of introducing a nucleic acid sequence into an organism, a cell, a tissue, or an organ, and may be performed using standard techniques suitable for the host cell as known in the art. Such methods include, without limitation, such as electroporation, protoplast fusion, calcium phosphate (CaPO₄) precipitation, calcium chloride (CaCl₂) precipitation, agitation using silicon carbide fibers, *Agrobacteria*-mediated transformation, a PEG method, a dextran sulfate method, 15 lipofectamine method, and drying/suppression-mediated transformation. The epitope according to one exemplary embodiment of the present invention, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, may be subjected to large-scale production by culturing the transformants expressing the recombinant vector in a nutrient medium. The medium 20 and culture conditions may be properly selected depending upon the host cell. The conditions such as temperature, pH of a medium, and a culture time may be properly adjusted to enable the efficient growth of cells and mass-production of a protein. As described above, the epitope having the amino acid sequence set forth in SEQ ID NO: 25 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3 may be recovered recombinantly from a medium, or a cell lysate, and may be separated and purified using conventional

biochemical separation techniques (Sambrook et al., Molecular Cloning: A laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press(1989); Deucher, M., Guide to Protein Purification Methods Enzymology, Vol. 182. Academic Press. Inc., San Diego, CA (1990)). The biochemical separation techniques that may be used herein
5 may include, without limitation, electrophoresis, centrifugation, gel filtration, precipitation, dialysis, chromatography (ion exchange chromatography, affinity chromatography, immunoabsorbent chromatography, or size exclusion chromatography), isoelectric focusing, and various modified and combined methods thereof.

10 The present invention provides a method of expressing an epitope, which has an amino acid sequence set forth in SEQ ID NO: 2, an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence set forth in SEQ ID NO: 3, on the surface of microorganisms or viruses. In this method, a recombinant vector characterized in that it comprises a sequence encoding an
15 inducible promoter or a signal protein, and various microorganisms or viruses comprising the recombinant vector may be used. The particularly proper microorganisms or viruses include, without limitation, recombinant *E. coli*, recombinant yeasts, and recombinant bacteriophages. Display techniques widely known in the art may be used to express the epitope having an amino acid sequence as
20 set forth in SEQ ID NO: 2 or SEQ ID NO: 3 on the surface of the microorganism or virus. Particularly, a method of binding a polynucleotide sequence encoding the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, to a sequence encoding a promoter or a
25 signal protein to induce the expression of the epitope on the surface of microbial or viral cells, or a method of deleting a portion of a gene encoding a protein originally expressed on the surface of the microbial or viral cells and inserting a polynucleotide

sequence encoding the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, into the partially deleted gene, may be used herein, but not limited thereto. The epitope expressed on the surfaces of the microorganisms or viruses, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, may be separated and purified per se, and may be used for the purpose of specific use according to one exemplary embodiment of the present invention, and may be used for panning an antibody specifically binding to the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, when expressed on the surface of the microorganisms or viruses, to obtain the antibody.

Also, the present invention provides an epitope having an amino acid sequence set forth in SEQ ID NO: 2, an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence set forth in SEQ ID NO: 3, an antibody specifically binding to the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, using a complex including the epitope or a polynucleotide encoding the epitope, or a method of producing a fragment of such an antibody. Such an antibody may be a polyclonal antibody, or a monoclonal antibody, and the fragment of the antibody falls within the scope of the present invention as long as it retains characteristics to bind to the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence comprising the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3. In particular, the antibody or its fragment

according to one exemplary embodiment of the present invention includes, without limitation, single-chain antibodies, diabodies, triabodies, tetrabodies, Fab fragments, F(ab')₂ fragments, Fd, scFv, domain antibodies, bispecific antibodies, minibodies, scAb, IgD antibodies, IgE antibodies, IgM antibodies, IgG1 antibodies, IgG2 antibodies, IgG3 antibodies, IgG4 antibodies, derivatives of constant regions of the antibodies, and artificial antibodies based on protein scaffolds, as long as they have a binding activity to the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3. Also, antibodies having mutations in variable regions thereof are encompassed within the scope of the present invention as long as they retain their characteristics according to one exemplary embodiment of the present invention. By way of example, the mutations may include conservative substitutions of amino acids in the variable regions. The conservative substitution refers to a substitution of an original amino acid sequence with another amino acid residue having a similar characteristic. For example, lysine, arginine, and histidine residues are similar in terms of having a basic side chain. Also, aspartic acid and glutamic acid residues are similar in terms of having an acidic side chain. Also, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, and tryptophan residues are similar in terms of having a non-charged, polar side chain, and alanine, valine, leucine, threonine, isoleucine, proline, phenylalanine, and methionine residues are similar in terms of having a non-polar side chain. Further, tyrosine, phenylalanine, tryptophan, and histidine residues are similar in terms of having an aromatic side chain. Therefore, it is apparent to those skilled in the art that the amino acid substitutions among the group of the amino acids having the similar characteristics as described above will not cause any change in the characteristics. As a result, a method of producing an antibody having mutations by conservative substitutions in a variable region thereof falls within the scope of the present invention as long as it retains its characteristics.

The antibody binding to the epitope according to the present invention, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, may be obtained using methods widely known in the art to which the present invention belongs. Specifically, the antibody may be prepared by inoculating an animal with an epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, a complex including the epitope, or a polynucleotide encoding the epitope and producing and panning an antibody specifically binding to the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, from the inoculated animal.

In this case, the animal is preferably an animal transformed to produce an antibody having the same sequence as a human-derived sequence, especially a transformed rat. Here, a fully human antibody having reduced immunogenicity may be prepared using the transformed rat in accordance with methods disclosed in US Patent Nos. 5,569,825; 5,633,425; and 7,501,552. When the animal is not transformed to produce the antibody having the same sequence as the human-derived sequence, a humanization or deimmunization step may be further performed on the antibody obtained from the animal so that the antibody becomes suitable for a treatment use in the body, as described in the methods disclosed in US Patent Nos. 5,225,539; 5,859,205; 6,632,927; 5,693,762; 6,054,297; and 6,407,213; and WO 1998/52976. Specifically, the humanization or deimmunization step may include a CDR grafting step of engrafting a CDR sequence of the antibody produced from the animal into the framework (FR) of a human antibody, and a CDR-walking step of

substituting, inserting or deleting at least one amino acid sequence in order to further enhance affinity or reduce immunogenicity.

When a full-length EGFR rather than the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, the complex including the epitope, or the polynucleotide encoding the epitope, is used as an immunogen, a method of panning an antibody, which includes primarily panning antibodies having binding capacity to the EGFR and panning the antibody specifically recognizing the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, among the primarily panned antibodies, may also be used. In this case, a method of panning an antibody, which include inducing mutations in a crucial binding site of the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, and panning the antibodies having lost or reduced binding capacity to the EGFR due to the mutations in the crucial binding site of the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, among the primarily panned antibodies binding to the EGFR, may also be used herein.

Also, a human antibody binding to the epitope set forth in SEQ ID NO: 2 or SEQ ID NO: 3 may be produced and panned using a display technique widely known in the art to which the present invention belongs. The display technique is preferably at least one selected from the group consisting of phage display, yeast display, bacteria display, and ribosome display techniques, but the present invention is not limited thereto. The preparation and display of a library may be easily

performed as disclosed in US Patent Nos. 5,733,743; 7063943; 6172197; 6,348,315; and 6,589,741. Particularly, the library used in the display is preferably designed to have a sequence of the human-derived antibody. Specifically, the method is characterized in that it includes panning only antibodies specifically binding to the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, using the epitope, which has the amino acid sequence set forth in SEQ ID NO: 2, the amino acid sequence including the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence set forth in SEQ ID NO: 3, or the complex including the epitope.

Finally, the present invention provides an epitope having an amino acid sequence set forth in SEQ ID NO: 2, an amino acid sequence including the amino acid sequence of SEQ ID NO: 2, or an amino acid sequence set forth in SEQ ID NO: 3, a complex including the epitope, or a composition for cancer vaccines including a polynucleotide encoding the epitope.

The present invention will be described in further detail through the exemplary embodiments below. However, it should be understood that the detailed description and specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the scope of the invention will become apparent to those skilled in the art from this detailed description.

Example 1: Identification of binding structure of EGFR to Fab of GC1118

To identify a binding structure of EGFR to an fragment antigen-binding (Fab) of GC1118 (see KR 10-2011-0034914 A) developed by a group of researchers of the present invention, the X-ray diffraction data of a crystal structure of an EGFR/GC1118 Fab composite was obtained using the BL26B2 beamline (Spring-8

Institution, Japan), and indexed and scaled using HKL2000 software (HKL Research Inc., US), and an early electron density map of the EGFR/GC1118 composite was then obtained using a molecular replacement (MR) method. To employ the MR method, the data on a 3D structure of a protein having a structure similar to that of the

5 EGFR/target antibody composite was needed. In this case, a structure of an EGFR/cetuximab composite (PDB ID: 1YY9) was used as the structure for the EGFR/GC1118 composite. The information on an early phase of the EGFR/GC1118 composite was obtained using Molrepprogram, and model building task was performed using a free crystallographic object-oriented toolkit COOT based on the obtained information on the early phase. Then, a refinement task was completed using Refmac5 software distributed by CCP4 and python-based hierarchical environment for integrated xtallography PHENIX software.

As a result, it was revealed that the epitope on EGFR of GC1118 was positioned in a 3rd domain of EGFR, and particularly the epitope was a short loop region of the 3rd domain, which consists of 9 amino acid residues spanning from the 353rd to 361st amino acid residues of the amino acid sequence (see SEQ ID NO: 1 and

20 FIG. 1). This loop region protrudes outwards, and is surrounded by CDR of the antibody. In particular, the amino acid residues playing a crucial role in binding between GC1118 and EGFR are F357 and H359 of the EGFR. The two amino acid residues are surrounded by amino acid residues of a CDR region of the GC1118 antibody, and function to form hydrophobic bonds and hydrogen bonds with the
25 amino acid residues of the CDR region in order to firmly maintain the binding between EGFR and GC1118. Also, R353 contributes to further binding to the

antibody via ionic bonds to a variable region (VH) of a heavy chain of the GC1118 antibody (see FIG. 1).

Meanwhile, a region to which EGF binds is positioned between 1st and 3rd domains of EGFR. In this case, EGF first binds to the 1st domain of EGFR (see FIG. 2) to induce a structural change of the EGFR domain, and then binds to the 3rd domain (see FIG. 3). In this case, the important EGFR amino acid residue participating in the binding to EGF is D355 of the 3rd domain (Ferguson et al., Molecular Cell, 2003, 11:507-517). Here, the amino acid residue is present in a loop containing R353, F357 and H359 which are the epitopes of GC1118. That is, since the epitopes on EGFR to which GC1118 binds are present in the same region as the region to which EGF binds, the antibody binding to the epitopes of GC1118 may directly inhibit the binding of EGF to the 3rd domain of EGFR. This is further confirmed by comparison with the structure of EGFR bound to EGF. Accordingly, when the structure of EGFR activated through the binding of EGF overlaps that of GC1118, it could be seen that the VH region of GC1118 and EGF overlapped each other (see FIG. 3).

On comparison with the binding of currently used cetuximab to EGFR, cetuximab had epitopes positioned in the 3rd domain of EGFR, but the binding sites of cetuximab were widely dispersed on a surface of the 3rd domain. Therefore, some of the epitopes had an indirect influence on the binding of EGF (see FIG. 4A). Matuzumab which was another antibody also had epitopes positioned in the 3rd domain of EGFR, but the epitopes of matuzumab were present at different positions than the epitopes according to one exemplary embodiment of the present invention, and positioned in a region other than the region to which EGF was bound so that the epitopes of matuzumab were not able to directly hinder the binding of EGF (see FIG. 4B).

Example 2: Verification of epitopes on EGFR of GC1118 using yeast cell surface expression method

To verify the epitopes (R353, F357, and H359 amino acid residues) of EGFR against GC1118 found through a structure model, the corresponding amino acid residues were substituted with glycine having no binding reactivity to produce the variants, and then expressed on surfaces of yeast cells. Thereafter, the binding of GC1118 to EGFR variants in which the epitopes were expressed on the surfaces of the yeast cells was confirmed using flow cytometry (BD FACSCalibur™, US). As a result, it was confirmed that the binding affinity to GC1118 was reduced in all of the EGFR variants.

2.1 Construction of EGFR variants

EGFR variants were constructed by substituting one or more of R353, F357 and H359 of the amino acid sequence of EGFR (see SEQ ID NO: 1) with glycine using an overlapping PCR method in which a gene sequence encoding an extracellular domain of human EGFR was used as a template. The results are listed in the following Table 1.

Table 1

EGFR variants substituted with glycine (Gly)				
EGFR variants	Amino acid substitution	Details		
		Position	Before substitution	After substitution
Variant 1	R353G	353	Arg	Gly
Variant 2	F357G	357	Phe	Gly
Variant 3	H359G	359	His	Gly
Variant 4	R353G + F357G	353	Arg	Gly
		357	Phe	Gly
Variant 5	F357G + H359G	357	Phe	Gly
		359	His	Gly
Variant 6	R353G + H359G	353	Arg	Gly
		359	His	Gly
Variant 7	R353G + F357G + H359G	353	Arg	Gly
		357	Phe	Gly
		359	His	Gly

2.1.1 PCR reaction for synthesis of EGFR variants

Two gene fragments (approximately 1,150 bp and 720 bp) commonly including each of the EGFR variants were synthesized by performing a PCR reaction

using AccuPower™ TLA PCR PreMix (Bioneer, Korea) including a gene sequence of the human EGFR as the template, and a set of primers (see Table 2) designed to induce mutation of an EGFR gene. The two synthesized gene fragments were electrophoresed in 1% agarose gel, and the DNA of each of the gene fragments was purified using a Qiagen kit (Qiagen 28706, Germany). Subsequently, an overlapping PCR reaction was performed using the DNA of the set of the two purified gene fragments as one template and primers having amino acid sequences set forth in SEQ ID NOS: 4 to 19 (see Table 2), thereby synthesizing final EGFR variant genes (see FIG. 5). The synthesized genes were cleaved using restriction enzymes NheI/MluI (New England BioLabs, US). The term “For” following the primer names as listed in Table 2 represents a forward primer, and the term “Rev” represents a reverse primer.

Table 2

Primers used in PCR reaction to construct EGFR variants			
Primer name	Target variants	Sequence	SEQ ID NO
pCTCON-For	Control	5'-CGGCTAGCCTGGAGGAAAAGAAAGTTTGC-3'	4
pCTCON-Rev		5'-CGACGCGTTGGACGGGATCTTAGGCC-3'	5
R353G-For	Variant 1	5'-CTGCCGGTGGCATTGCGGTGACTCCTCACA-3'	6
R353G-Rev		5'-TGTGAAGGAGTCACCGCAAATGCCACCGGCAG-3'	7
F357G-For	Variant 2	5'-TTTAGGGGTGACTCCGGCACACATACTCCTCCT-3'	8
F357G-Rev		5'-AGGAGGAGTATGTGTGCCGGAGTACCCCTAAA-3'	9

H359G-For	Variant 3	5'-GGTGACTCCTTCACAGGCACTCCTCCTCTGGAC-3'	10
H359G-Rev		5'-GTCCAGAGGAGGAGTGCCTGTGAAGGAGTCACC-3'	11
R353G,F357G-For	Variant 4	5'-CTGCCGGTGGCATTGCGGTGACTCCGGGACACAT ACTCCTCCT-3'	12
R353G,F357G-Rev		5'-AGGAGGAGTATGTGTCCCGGAGTCACCGCCAAATGC CACCGGCAG-3'	13
F357G,H359G-For	Variant 5	5'-TTAGGGGTGACTCCGGCACAGGGACTCCTCCTCTG GAC-3'	14
F357G,H359G-Rev		5'-GTCCAGAGGAGGAGTCCCTGTGCCGGAGTCACCCCT AAA-3'	15
R353G,H359G-For	Variant 6	5'-CTGCCGGTGGCATTGCGGTGACTCCT TCACAGGTACTCCTCCTCTGGAC-3'	16
R353G,H359G-Rev		5'-GTCCAGAGGAGGAGTACCTGTGAAGGAG TCACCGCCAAATGCCACCGGCAG-3'	17
R353G,F357G, H359G-For	Variant 7	5'-CTGCCGGTGGCATTGCGGTGACTCCG GAACAGGTACTCCTCCTCTGGAC-3'	18
R353G,F357G, H359G-Rev		5'-GTCCAGAGGAGGAGTACCTGTTCCGGAGT CACCGCCAAATGCCACCGGCAG-3'	19

2.1.2 Ligation and transformation of EGFR variants

A yeast surface expression vector pCTCON (Boder, E.T. et al., Nat Biotechnol. 1997, 15(6):553-7) was cleaved using restriction enzymes NheI/MluI, electrophoresed in 1% agarose gel, and purified using a Qiagen kit. The EGFR
5 variant DNAs prepared in Example 2.1.1 were mixed with pCTCON, and a T4 DNA ligase (New England BioLabs, US) was added thereto, and reacted at 25 °C for 2 hours. The ligation mixture was transformed with *E. coli* XL1-blue cells (Stratagene, US) through electroporation using Gene Pulser (Bio-Rad Laboratories, Inc., US), and incubated for an hour in a total of 2 mL of a medium. Thereafter, the transformed
10 cells were spread on an LB-agar plate supplemented with carbenicillin (Sigma, US). Subsequently, the cells were incubated overnight at 37 °C.

2.1.3 Base sequencing of EGFR variants

Colonies on the plate cultured in Example 2.1.2 were incubated overnight in 2 mL of an LB medium supplemented with 50 µg/mL of carbenicillin, and a
15 recombinant plasmid was then separated using a Qiagen plasmid minikit (Qiagen 27106, Germany) to determine DNA base sequences of the EGFR variants inserted into the plasmid. Primers having sequences set forth in SEQ ID NOS: 20 to 22 were used as the sequencing primers used for the base sequencing (see Table 3), and the base sequencing was performed and analyzed by Genotech Corporation (Daejeon,
20 Republic of Korea) according to a known method. The base sequence of human EGFR was used as the control. After the DNA base sequences of the EGFR variants were determined, the determined DNA base sequences were translated into amino acid sequences using a web-based program available from ExpASy. which translates a base sequence into an amino acid sequence. The
25 translation results are shown in FIG. 6. Then, it was confirmed that all the EGFR variant genes listed in Table 1 were correctly inserted into the pCTCON vectors.

Table 3

Primers used in sequencing reaction		
Types of primers	Sequence	SEQ ID NO
seq-F1	5'- ATGAAGGTTTTGATTGTCTTGTTGG	20
seq-F1	5'- CCAGTGACTGCTGCCACAACCAAGTG	21
seq-F1	5'- CGTCGGCCTGAACATAACATCCTTG	22

2.2 Analysis of expression of EGFR variants on yeast cell surfaces and binding to the antibody

2.2.1 Procedure of expressing EGFR variants on surfaces of yeast cells

A EBY100 (*S. cerevisiae*) yeast strain was transformed with the pCTCON-EGFR verified in Example 2.1 using Gene Pulser from Bio-Rad Laboratories, Inc. (FIG. 1). The transformed colonies were incubated at 30 °C for 20 hours in a selective medium, an SD-CAA liquid medium (20 g/L glucose, 6.7 g/L yeast nitrogen base without amino acids, 5.4 g/L Na₂HPO₄, 8.6 g/L NaH₂PO₄H₂O, and 5 g/L casamino acids). Thereafter, the expression of the EGFR variant on surfaces of yeast cells was induced by incubating the transformed colonies at 30 °C for 20 hours in a selective medium, an SD-CAA liquid medium (20 g/L galactose, 6.7 g/L yeast nitrogen base without amino acids, 5.4 g/L Na₂HPO₄, 8.6 g/L NaH₂PO₄H₂O, and 5 g/L casamino acids).

2.2.2 Determination of expression of EGFR variants on surfaces of yeast cells

The expression of the EGFR variants on the surfaces of the yeast cells was confirmed using BD FACS Calibur™ (Becton Dickinson). The yeast cells expressed at a density of approximately 1×10^7 cells/ml were reacted with anti-c-myc 9E10 mAb (dilution of 1:100) in 0.1 ml of phosphate buffered saline (PBSB including 1 mg/ml BSA; pH 7.4) (at 25 °C for 30 minutes), and washed with PBSB. The yeast cells were secondarily reacted with R-phycoerythrin conjugated goat anti-mouse IgG (dilution of 1:25) on ice for 15 minutes, washed with PBSB, and then analyzed using BD FACS Calibur™. From the analysis results, it was revealed that the EGFR variants were well expressed on the surfaces of the yeast cells (see FIG. 7).

2.2.3 Analysis of binding between EGFR variants and GC1118 using flow cytometry

The binding between GC1118 and the EGFR variants expressed on the surfaces of the yeast cells was confirmed using BD FACS Calibur™ (Becton Dickinson). Cetuximab was used as a control antibody. The yeast cells expressed at a density of approximately 1×10^7 cells/ml were reacted with 1 µg of each of the antibodies in 0.1 ml of PBSB (including 1 mg/ml BSA; pH 7.4) (at 25 °C for 30 minutes), and washed with PBSB. The yeast cells were secondarily reacted with FITC conjugated anti-human IgG (dilution of 1:50) on ice for 15 minutes, washed with PBSB, and then measured for mean fluorescence intensity using BD FACS Calibur™. The measurement results are listed in Table 4 and shown in FIG. 8. As seen from Table 4, it was proven that the binding of GC1118 was inhibited in the EGFR variants in which the epitopes(R353, F357 and H359 according to one exemplary embodiment of the present invention through the structural analysis) were substituted with glycine, and thus the substituted amino acid residues were the epitopes of GC1118.

Table 4

Binding of antagonist to EGFR variants			
EGFR	Expression	Antagonist binding activity (%)	
Variants	Level (%)	GC1118	Cetuximab
EGFR (wild type)	100	100	100
Variant 1 (R353G)	66.5	30.4	23.8
Variant 2 (F357G)	91.3	26.1	88.3
Variant 3 (H359G)	89.3	34.1	82.9
Variant 4 (R353G+F357G)	71.4	14.1	34.8
Variant 5 (F357G+H359G)	74.4	15	77.3
Variant 6 (R353G+H359G)	68	13.7	35.2
Variant 7 (R353G+F357G+H359G)	69.2	13.61	42.6

Example 3: Analysis of competitive binding of GC1118 and ligands to EGFR

To determine whether GC1118 and six ligands listed in Table 5 had identical or similar binding sites for EGFR, a competitive binding test was performed. Cetuximab was used as a control antibody. First, a predetermined concentration of an antibody (1.5 nM) and various concentrations of a ligand were reacted together on a plate coated with 2 µg/ml of EGFR. In this case, the ligand was present at a concentration so that the molar ratio of the antibody and the ligand amounted to 1:1, 1:10, 1:10², 1:10³, 1:10⁴, and 1:10⁵. The resulting mixture was reacted at room

temperature for 30 minutes, and then washed five times with PBST (including 0.05% Tween20; pH 7.4). Then, the mixture was secondarily reacted with anti-human IgG (Fc specific) Peroxidase conjugated (Sigma A0170, US) at room temperature for 30 minutes, and washed five times with PBST. Subsequently, 100 μ L of a 3,3',5,5'-
 5 tetramethylbenzidine (TMB) Microwell Peroxidase Substrate (KPL 50-76-03, US) solution was added to each well, and then measured for O.D values at 405 nm. It was noticed that two reactants (the antibody and the ligand) competed against each other when the binding affinity of GC1118 to EGFR was reduced with an increasing concentration of the ligand, indicating that the two reactants had the identical epitopes
 10 to the EGFR, or were a very close match. The competition between the antibody and the ligands is shown in FIG. 9 and listed in Table 6. As a result, it could be seen that GC1118 has superior ability to inhibit the binding of EGF, TGF- α , BTC, EPR, and HB-EGF, compared to cetuximab.

Table 5

EGFR ligands used	
Human EGFR ligands	Details
EGF	Epidermal growth factor
TGF- α	Transforming growth factor- α
AR	Amphiregulin
BTC	β -Cellulin
EPR	Epiregulin
HB-EGF	Heparin-binding EGF-like growth factor

15

Table 6

Competitive binding capacities of EGFR ligands to GC1118				
	Antibody binding (%)			
	GC1118		Cetuximab	
Antibody : ligand (molar ratio)	1:10 ⁴	1:10 ⁵	1:10 ⁴	1:10 ⁵
EGF	30.2	15.2	61.8	22.5
TGF- α	94.1	61.1	96.5	92.4
AR	99.6	99.9	96.6	99.9
BTC	40.4	18.9	80.2	51.1
EPR	90.0	54.4	99.9	91.5
HB-EGF	65.1	31.2	96.2	76.1

Example 4: Inhibitory effect on cell proliferation induced by EGFR ligands

To compare an inhibitory effect on GC1118 of the present invention and cetuximab on cancer cell proliferation induced by EGFR ligands, a colorectal cancer cell line, LS174T (ATCC, CL-188), was spread on a 96-well microplate (Nunc) so that the number of cells amounted to 3,000 cells/ml. After one day, a culture medium was removed, and culture media including no bovine serum albumin were treated with GC1118 and the control antibody, cetuximab, at concentrations of 0.1, 1, and 10 μ g/ml. At the same time as the antibody treatment, the culture media were treated with EGFR ligands by type at concentrations (EGF; 50 ng/ml, TGF- α ; 100

ng/ml, amphiregulin; 100 ng/ml, epiregulin; 300 ng/ml, HB-EGF; 50 ng/ml, and β -cellulin; 100 ng/ml), and then incubated at 37 °C for 3 days in a CO₂ incubator. To measure a proliferation level of cancer cells after 3 days, 40 μ l of an MTS solution (CellTiter 96 Aqueous One solution Reagent, Promega) was added to the cancer cells
5 incubated in the 96-well plate, reacted at 37 °C for 3 hours in a CO₂ incubator, and then measured for O.D values at 490 nm.

As a result, it could be seen that GC1118 much more efficiently inhibited the proliferation of the cancer cells induced by the EGF, TGF- α , HB-EGF, and BTC ligands, compared to cetuximab, which indicated that these results corresponded to
10 those of Example 3.

From the above results, it was revealed that the antibodies having the epitopes according to one exemplary embodiment of the present invention showed superior inhibitory effect on the cell proliferation since the antibodies had different epitopes than cetuximab, and thus had an ability to inhibit the ligand binding (see FIG.
15 10). In particular, the antibodies binding to the epitopes according to one exemplary embodiment of the present invention are able to be used to treat various diseases such as cancer developed by the activation of EGFR due to the binding of not only EGF but also the other EGFR ligands since the antibodies efficiently inhibits the binding of the various EGFR ligands such as not only EGF but also TGF- α , AR, BTC, EPR and
20 HB-EGF to EGFR.

INDUSTRIAL APPLICABILITY

The epitopes on EGFR provided according to one exemplary embodiment of the present invention are highly conserved, and located in a domain closely associated with binding to EGF. Therefore, the compositions including antibodies against the
25 epitopes, or the vaccine compositions including the epitopes can efficiently block a

signal transduction caused by binding of EGR to EGFR, and thus can be highly valuable and useful in treating various diseases such as cancer.

WE CLAIM:

1. An epitope of an epidermal growth factor receptor (EGFR) consisting of an amino acid sequence of RGDSFTH (SEQ ID NO: 2).
2. An epitope of an epidermal growth factor receptor (EGFR) consisting of an amino acid sequence of RGDSFTHTP (SEQ ID NO: 3).
3. A complex in which the epitope of claim 1 or 2 is bound to a carrier.
4. The complex of claim 3, wherein the carrier is at least one selected from the group consisting of a peptide, serum albumin, immunoglobulin, hemocyanin and polysaccharide.
5. A polynucleotide encoding the epitope of claim 1 or 2.
6. A recombinant vector comprising the polynucleotide of claim 5.
7. The recombinant vector of claim 6, which comprises a promoter inducing an expression of the epitope on the surface of a microorganism cell or virus, or a nucleotide sequence encoding a signal protein.
8. A recombinant microorganism or virus transformed with the recombinant vector of claim 6 or 7.
9. The recombinant microorganism or virus of claim 8, which is selected from the group consisting of a recombinant E. coli, a recombinant yeast and a recombinant bacteriophage.
10. A method of preparing the epitope consisting of the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence of SEQ ID NO: 3, comprising culturing the recombinant microorganism or virus of any one of claims 8 to 9.
11. A vaccine compound for treating cancer, which comprises the epitope of any one of claims 1 or 2, the complex of claim 3, or the polynucleotide of claim 5, wherein the cancer is a cancer associated with EGFR activation.
12. The vaccine compound for treating cancer of claim 11, which further comprises

a pharmaceutically acceptable adjuvant improving the formation of an antibody when injected into a body.

13. The vaccine compound for treating cancer of claim 12, wherein the adjuvant is at least one selected from the group consisting of aluminum salts, squalene, sorbitane, polysorbate 80, CpG, liposome, cholesterol, MPL (monophosphoryl lipid A) and GLA (glucopyranosyl lipid A).
14. The vaccine compound for treating cancer of claim 13, wherein the aluminum salts are selected from the group consisting of $AL(OH)_3$ and $ALPO_4$.
15. The vaccine compound for treating cancer of claim 11, wherein the polynucleotide is included in a pharmaceutically acceptable carrier.
16. The vaccine compound for treating cancer of claim 15, wherein the pharmaceutically acceptable carrier is a viral or a non-viral carrier.
17. A method of producing an antibody or a fragment thereof specifically binding to an epitope consisting of an amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 3, said method comprising

producing an antibody using the epitope consisting of the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence of SEQ ID NO: 3; the complex of claim 3; or the polynucleotide of claim 5.
18. The method of claim 17, wherein the antibody is a polyclonal or monoclonal antibody.
19. The method of claim 17, which comprises the steps of:

administering to an animal the epitope consisting of the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence of SEQ ID NO: 3; the complex of claim 3; or the polynucleotide of claim 5; and

panning the antibody specifically binding to the epitope consisting of the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence of SEQ ID NO: 3,

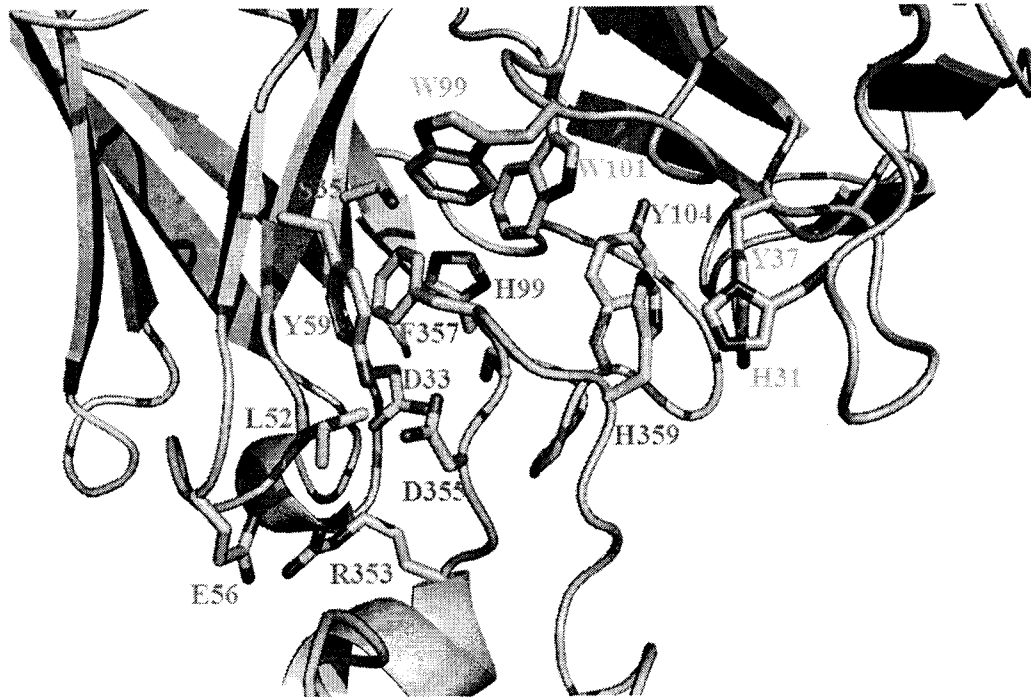
from the animal.

21. The method of claim 19, which further comprises the step of performing humanization or deimmunization.
22. The method of claim 20, wherein the humanization comprises grafting CDR sequence of the antibody produced from the animal to framework (FR) of a human antibody.
23. The method of claim 21, which further comprises the step of performing substitution, insertion or deletion of at least one amino acid for improving affinity or reducing immunogenicity.
24. The method of claim 19, wherein the animal is a transgenic animal which can produce an antibody having an identical amino acid sequence to that of human antibody.
25. The method of claim 23, wherein the transgenic animal is a transgenic mouse. The method of claim 17, which employs a display technique.
26. The method of claim 25, wherein the display technique is at least one selected from the group consisting of phage display, bacteria display, and ribosome display.
27. The method of claim 25 or 26, wherein the display employs a library designed to comprise a sequence of human-originated antibody.
28. The method of any one of claims 25 to 27, which comprises panning the antibody specifically binding to the epitope consisting of the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence of SEQ ID NO: 3, by using the epitope consisting of the amino acid sequence of SEQ ID NO: 2, or the amino acid sequence of SEQ ID NO: 3, or the complex of claim 3.
29. A compound for diagnosing cancer comprising the epitope of any one of claims 1 or 2, the complex of claim 3, or the polynucleotide of claim 5, wherein the cancer is

a cancer associated with EGFR activation.

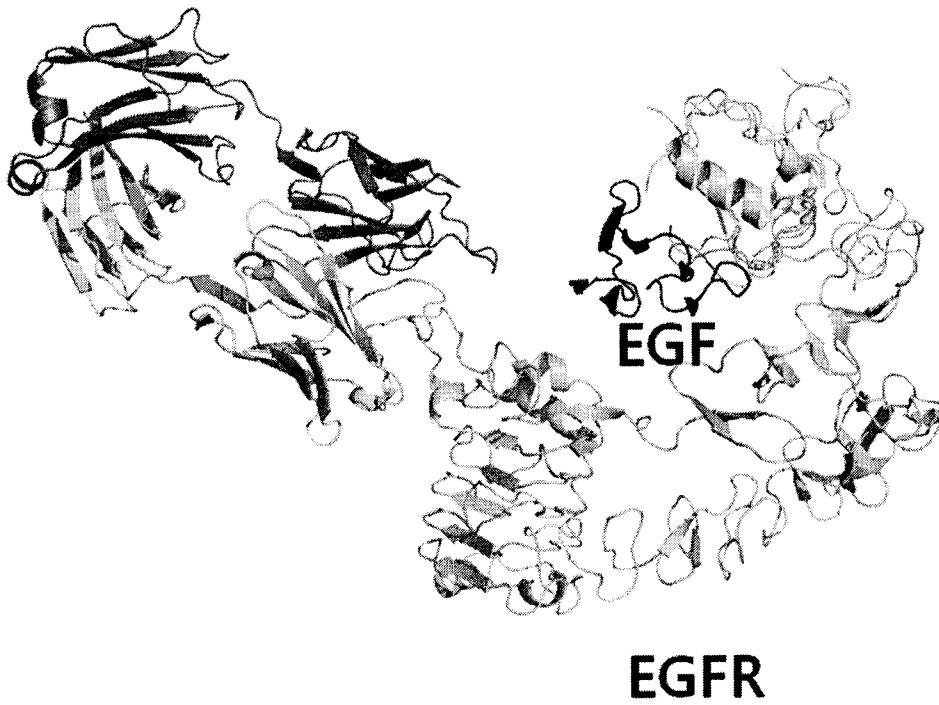
30. A kit for diagnosing cancer comprising the epitope of any one of claims 1 or 2, the complex of claim 3, or the polynucleotide of claim 5, wherein the cancer is a cancer associated with EGFR activation.

[Fig. 1]



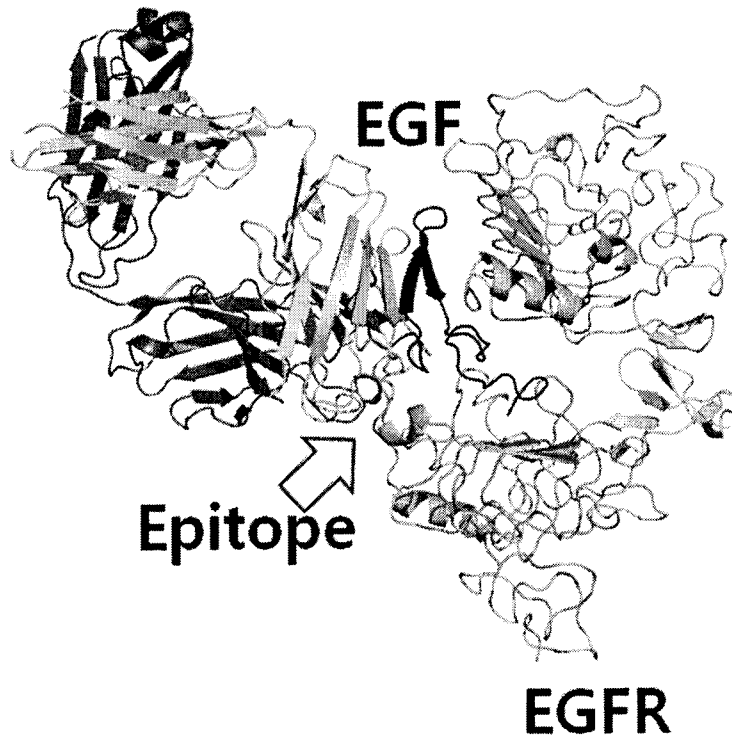
[Fig. 2]

GC1118 Fab



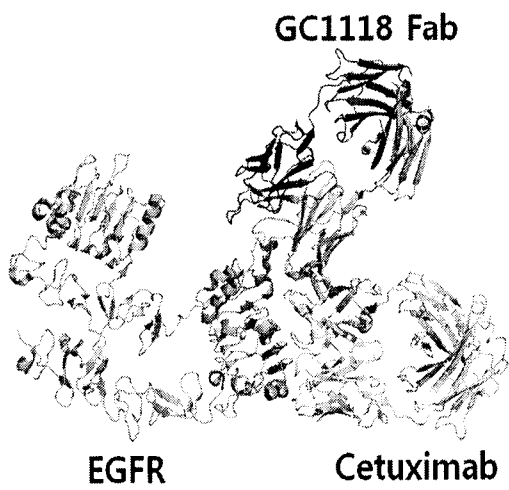
[Fig. 3]

GC1118 Fab

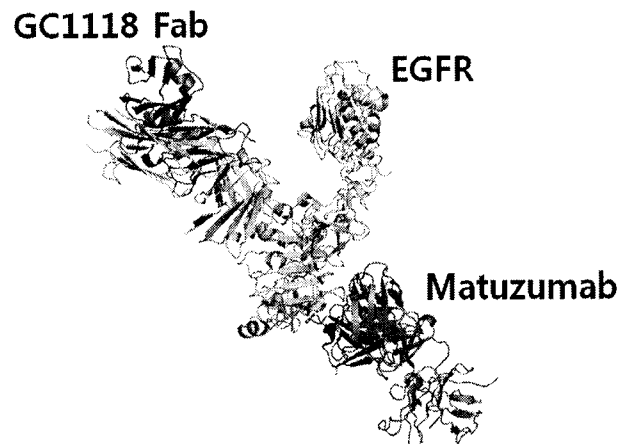


[Fig. 4]

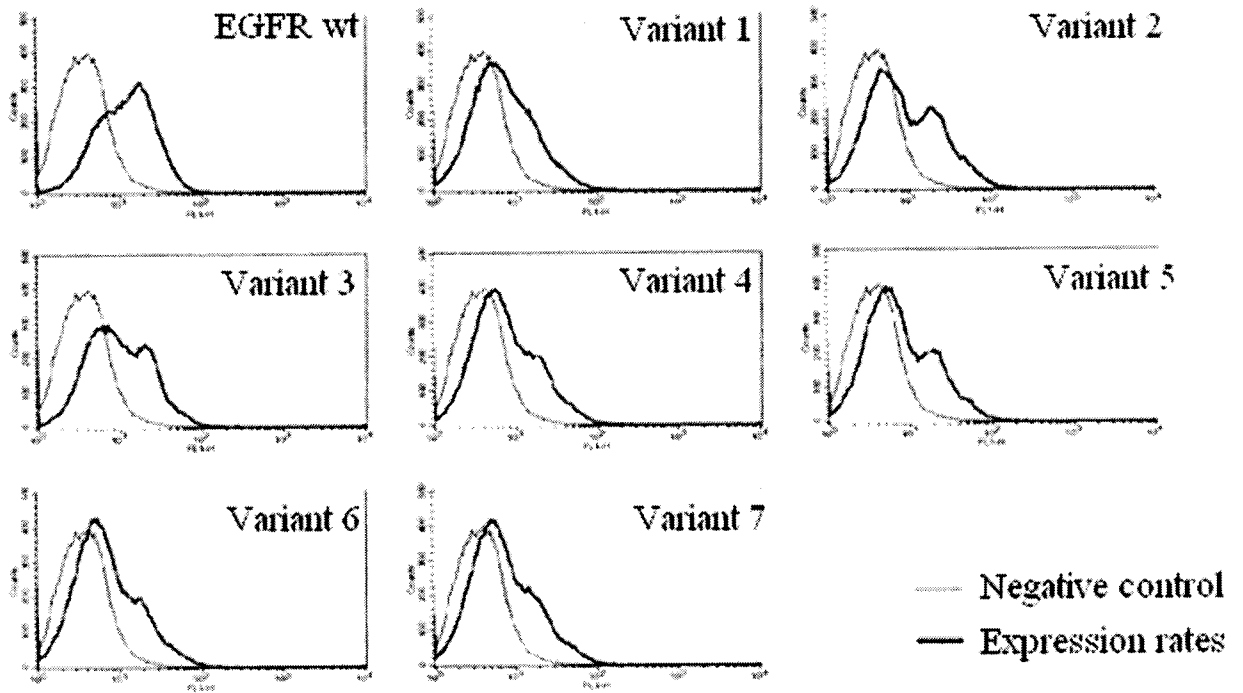
(A)



(B)

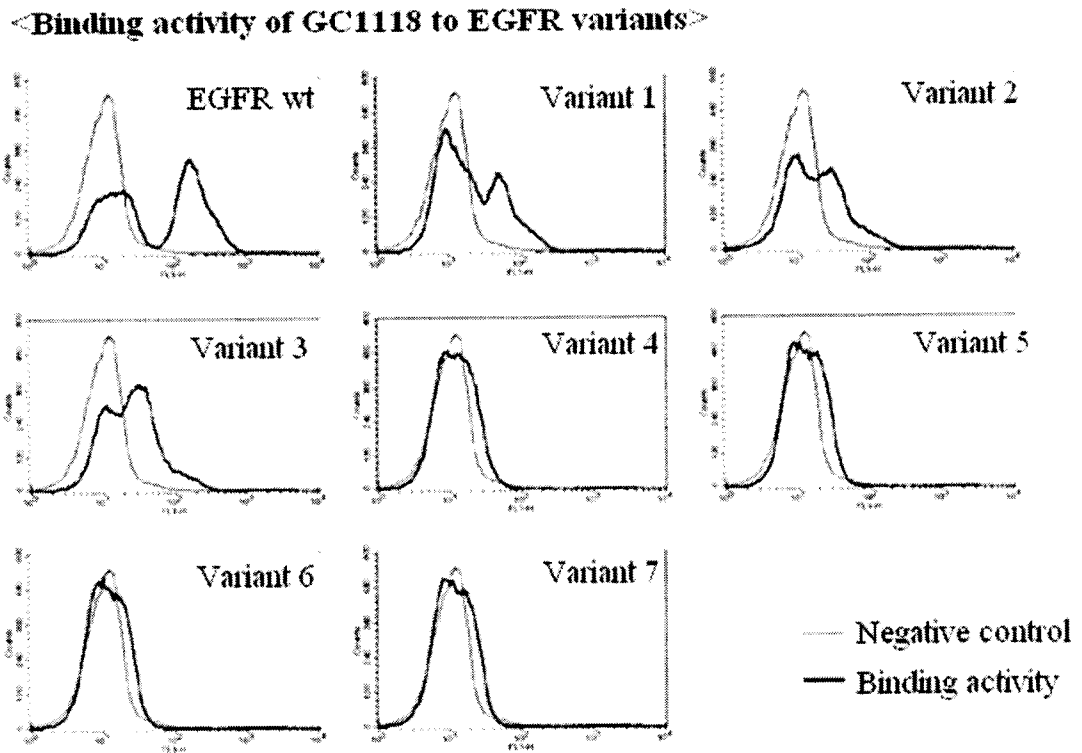


[Fig. 7]

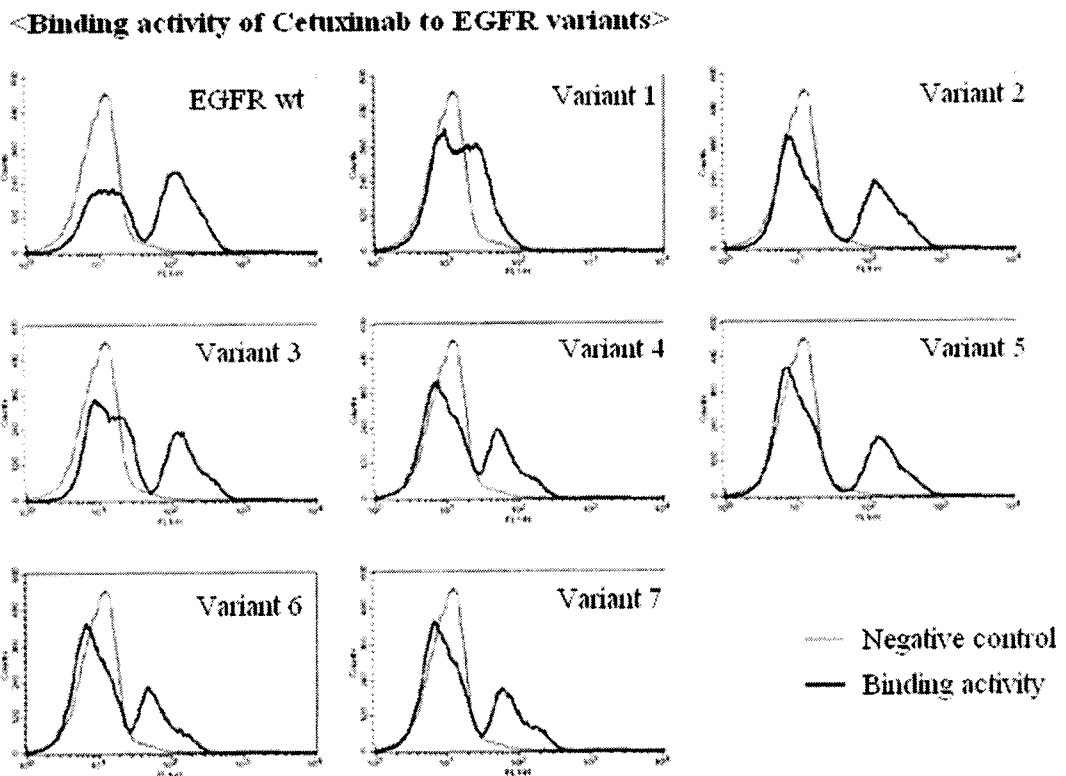
<Expression rates of EGFR variants>

[Fig. 8]

(A)

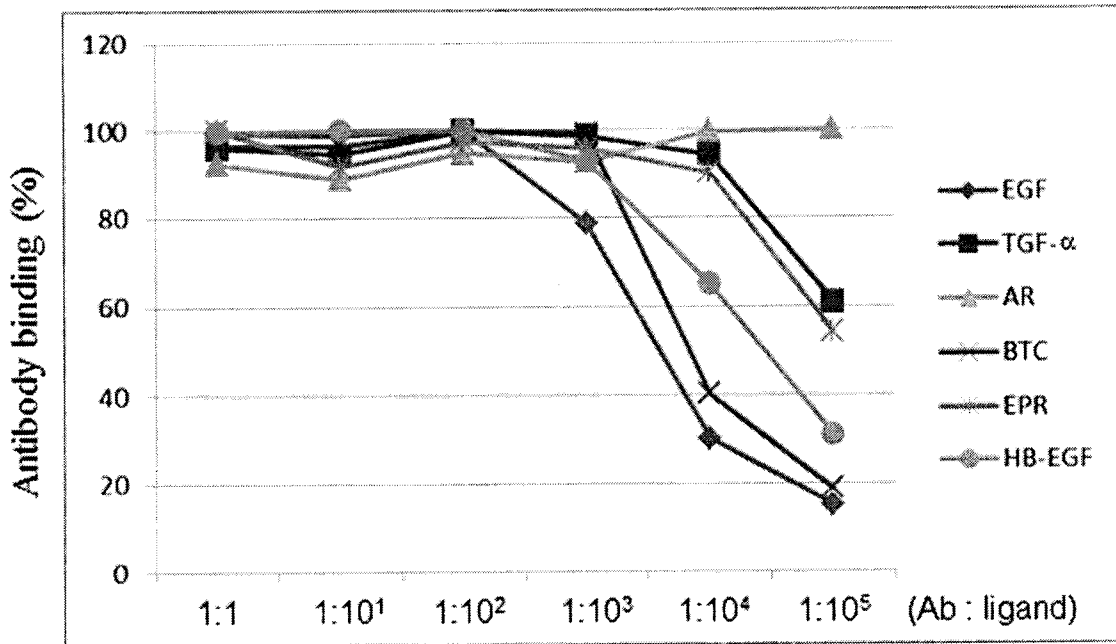


(B)

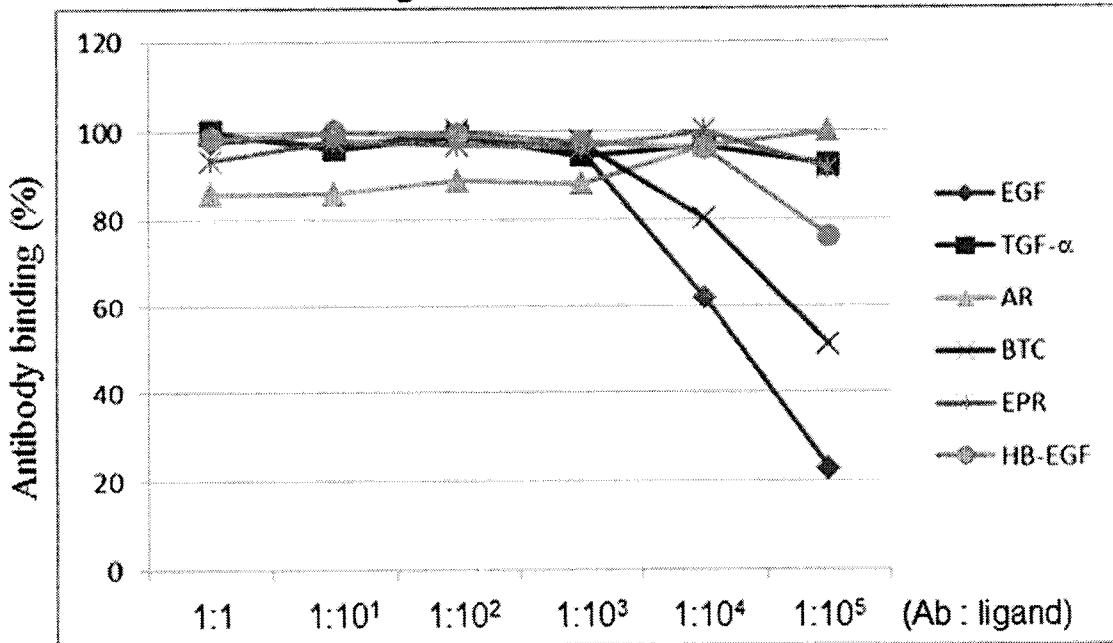


[Fig. 9]

A. GC1118 vs Ligands



B. Cetuximab vs Ligands



[Fig. 10]

