(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
18 December 2008 (18.12.2008)

PCT

(10) International Publication Number
WO 2008/153933 A2

(51) International Patent Classification:
A61K 38/17 (2006.01)

(21) International Application Number:
PCT/US2008/007111

(22) International Filing Date: 6 June 2008 (06.06.2008)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/942,319	6 June 2007 (06.06.2007)	US
60/956,887	20 August 2007 (20.08.2007)	US

(71) Applicant *(for all designated States except US)*: **AVI BIOPHARMA, INC.** [US/US]; 4575 S.W. Research Way, Suite 200, Vorvallis, OR 97333 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **KOLE, Ryszard** [US/US]; 4575 S.W. Research Way, Suite 200, Corvallis, OR 97333 (US). **SAZANI, Peter** [US/US]; 4575 SW Research Way, Suite 200, Corvallis, OR 97333 (US). **WAN, Jing** [CN/US]; 832 Louise Circle, Durham, NC 27705 (US).

(74) Agents: **DEHLINGER, Peter, J.** et al.; King & Spalding, P.O. Box 889, Belmont, CA 94002-0889 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, NO, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

WO 2008/153933 A2

(54) **Title:** SOLUBLE HER2 AND HER3 SPLICE VARIANT PROTEINS, SPLICE-SWITCHING OLIGONUCLEOTIDES, AND THEIR USE IN THE TREATMENT OF DISEASE

(57) **Abstract:** Soluble epidermal growth factor receptors 2 and 3 (HER2 and HER3) splice variant proteins with HER2 and HER3 antagonist activity and anti-proliferative properties, as well as the corresponding nucleic acids, are provided for treatment of proliferative diseases, in particular cancer. Also provided are compositions and methods for inducing expression of these splice variants, including splice switching oligonucleotides that modulate splicing of pre-mRNA that codes for these receptors.

SOLUBLE HER2 AND HER3 SPLICE VARIANT PROTEINS, SPLICE-SWITCHING OLIGONUCLEOTIDES, AND THEIR USE IN THE TREATMENT OF DISEASE

Field of the Invention

[0001] The present invention relates generally to the fields of protein and nucleotide chemistry and biochemistry, and to biotechnology and medicine. More specifically, it relates to epidermal growth factor receptor (EGFR) antagonists, nucleic acids derived from epidermal growth factor receptors and their use in the treatment of proliferative diseases, such as cancer.

Background of the Invention

[0002] Breast cancer is the most common cancer in women, aside from skin cancer. In 2006, according to the National Cancer Institute, approximately 41,000 women per year in the United States die from the disease. Based on current rates, 13.2% of women born today will be diagnosed with breast cancer at some time in their lives. Intensive research has led to advances in diagnosis and treatment; however, serious problems still exist, including low cure rates, substantial adverse effects and resistance to certain therapies. Given that breast cancer is a group of diseases, each having distinct molecular properties, molecularly targeted drugs have emerged as important anti-cancer therapeutics in recent years.

[0003] In 25-30% of breast cancers, amplification and overexpression of the growth factor receptor gene HER2 (human epidermal growth factor receptor-2, also known as neu/erbB2) is associated with enhanced tumor aggressiveness and a high risk of relapse and death (Slamon, D., et al., 1987, Science 235:177; Yarden, Y., 2001, Oncology 1:1). This oncogene encodes a 185 kilodalton (kDa) transmembrane receptor tyrosine kinase. As one of the four members of the human epidermal growth factor receptor (EGFR) family, HER2 distinguishes itself in several ways. First, HER2 is an orphan receptor. No high-affinity ligand has been identified. Second, HER2 is a preferred partner for other EGFR family members (HER1/EGFR, HER3, and HER4) for the formation of heterodimers, which show high ligand affinity and superior signaling activity. Third, full-length HER2 undergoes proteolytic cleavage, releasing a soluble extracellular domain (ECD). Shedding of the ECD has been shown to represent an alternative activation mechanism of full-length HER2

both *in vitro* and *in vivo*, as it leaves a membrane-anchored fragment with kinase activity. The central role of HER2 in EGFR family signaling correlates with its involvement in the oncogenesis of several types of cancers, such as breast, ovarian, colon, and gastric cancers, regardless of its expression level (Slamon, D., et al., 1989, Science 244:707; Hynes, N., et al., 1994, Biochem. Biophys. Acta. 1198:165). HER2 may also render tumor cells resistant to certain chemotherapeutics (Pegram, M., et al., 1997, Oncogene 15:537). Given its vital role in tumorigenesis, HER2 is an important target for cancer therapeutics.

[0004] As a cell membrane receptor, HER2 is composed of an extracellular domain (ECD) (632 amino acids), a transmembrane domain (22 amino acids), and an intracellular domain with tyrosine kinase activity (580 amino acids). As initially transcribed, the pre-mRNA for HER2 contains 27 exons and 26 introns. The fully spliced HER2 mRNA from which the introns have been spliced out is composed of 27 exons. Upon expression, HER2 protein is translocated to the cell surface. Activated through constitutive homo-dimerization and ligand-stimulated hetero-dimerization, HER2 protein directs subsequent steps in signal transduction, which affect cell growth, survival, and differentiation.

[0005] HER2 has been validated as a therapeutic target for several epithelial malignancies, including those originating in the breast, lung and colon. Currently there is only one FDA-approved therapeutic for HER2 positive breast cancer, Herceptin® (Colomer, R., et al., 2001, Cancer Investigation 19:49). Herceptin is a recombinant humanized monoclonal antibody that selectively binds to the HER2 extracellular domain with high affinity (K_d = 5 nM). Alone or in combination with chemotherapy, Herceptin has been shown to inhibit the proliferation of human tumor cells that overexpress HER2 (Slamon, D., et al., 2001, N. Engl. J. Med. 344:783; Baselga, J., et al., 1998, Cancer Research 58:2825).

[0006] However, this antibody-based therapeutic reagent has certain limitations. First, its inhibitory effect is restricted to the HER2 displayed on the cell surface; intracellular HER2 molecules are still available for mitogenic signaling. Second, Herceptin can be bound and thus "neutralized" by circulating ECDs that are released by proteolysis of membrane-bound HER2 (Brodowicz, T., et al., 1997, Int. J. Cancer 73:875). Finally, as with many other drugs, prolonged treatment with Herceptin leads to acquired resistance (Kute, T., et al., 2004, Cytometry Part A 57A:86). Another anti-HER2 antibody, pertuzumab, has been shown in a phase II

clinical trial to have activity in ovarian cancer (Gordon, M.S., et al., 2006, J. Clin. Oncol. 24:4324).

[0007] At least two autoinhibitors of HER2, translated from alternatively spliced HER2 mRNA species, have been reported. These are HER2-68 and HER2-100. Retention of intron 8 in the HER2 mRNA produces a variant mRNA that encodes a 68-kDa HER2 protein, HER2-68 or Herstatin. Retention of Intron 15 produces a variant mRNA that encodes a 100-kDa truncated HER2 protein, HER2-100. Both HER2 splice variants are soluble and act as dominant-negative inhibitors of HER2, most likely through interfering with receptor dimerization.

[0008] When HER2-100 is overexpressed in MCF-7 breast cancer cells, spontaneous proliferation and heregulin-mediated soft agar colony formation of MCF-7 cells decreases (Aigner, et al., 2001, Oncogene, 20(17):2101). Downstream signaling pathways are also negatively affected.

[0009] The 68-kDa variant, or Herstatin, has been characterized in more detail. Upon expression in tumor cells, Herstatin is secreted and binds to HER2-presenting cells with high affinity (K_d = 14 nM); Herstatin also binds to HER1 and HER4. Herstatin interferes with the activity of HER2 and other EGFR family members, and thus interferes with their downstream signal transduction. Herstatin has been reported to cause tumor growth arrest and inhibition of breast cancer cell growth. Herstatin overcomes tamoxifen resistance in HER2 positive breast cancer cells (Justman, Q., et al., 2003, J. Biol. Chem. 277:20618; Jhabvala-Romero, F., et al., 2003, Oncogene 22:8178). Therefore, Herstatin has been recognized as a promising anti-cancer drug candidate (Stix, G., 2006, Scientific American 294:60). With both HER2-100 and Herstatin, a progressive loss of their expression in more advanced tumors has been observed.

[0010] HER3 (human epidermal growth factor receptor-3, erbB3) is a receptor protein that plays an important role in regulating normal cell growth. HER3 lacks an intrinsic kinase activity and relies on the presence of HER2 to transduce signals across the cell membrane. As initially transcribed, the pre-mRNA for HER3 contains 28 exons and 27 introns. The fully spliced HER3 mRNA from which the introns have been spliced out is composed of 28 exons.

[0011] Two natural splice variants of HER3, p45 and p85, have been reported. Both are soluble, secreted, truncated proteins generated through alternative splicing of HER3 pre-mRNA. The mRNAs that code for each of these splice variants do not

allow translation of the full-length HER3 protein, and instead generate truncated proteins. In particular, the p85 form results from the retention of Intron 13 (Fig. **12**). These proteins block Heregulin-stimulated activation of HER3, HER2 and HER4, thereby inhibiting the growth of cells through the EGFR signaling pathway. Using a dominant negative truncated form of HER3 to inhibit HER2/HER3 signaling, it is possible to protect against pulmonary fibrosis (Nethery, D.E., et al., 2005, J. Appl. Physiol. 99:298).

Summary of the Invention

[0012] The invention includes, in one aspect, an isolated, soluble, human epidermal growth factor receptor-2 (HER2) protein lacking the region encoded by exon 15 of the full-length mRNA transcript of the HER2 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER2 transcript. The sequence of the protein may be, for example, one having at least 90%, preferably at least 95% sequence homology with SEQ ID No: **6** or amino acids 23-584 of SEQ ID No: 6, and the protein may be pegylated, that is, derivatized with polyethyleneglycol chains, to improve its pharmacokinetic properties, e.g., circulation time in the blood.

[0013] Also disclosed, as part of the invention, is a coding sequence for the above soluble HER2 protein. The coding sequence corresponds to a processed HER2 mRNA lacking exon 15, with exon 14 joined directly to exon 16, and may take the form of a processed HER2 mRNA, the corresponding cDNA, or a vector containing the coding sequence. An exemplary coding sequence is that having at least 80%, preferably at least 85% sequence homology to SEQ ID NO: SEQ ID NO: 5, or that portion of the sequence terminating at a stop codon within exon 16.

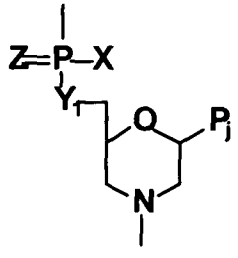
[0014] In another aspect, the invention includes a method of treating a female subject having an ovarian or breast cancer characterized by overexpression of human epidermal growth factor receptor-2 (HER2). The method includes the steps of

(i) administering to the subject, a pharmaceutically effective amount of a soluble, human epidermal growth factor receptor-2 (HER2) protein lacking the region encoded by exon 15 of the full-length mRNA transcript of the HER2 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER2 transcript, and

(ii) continuing the administering, at periodic intervals, until a defined end point in the status of the cancer is obtained. The soluble HER2 protein employed in the method are as described above. More generally, the method may be applied to the treatment of other cell-proliferative diseases or conditions.

[0015] In still another aspect, the invention provides a splice-switching oligonucleotide compound comprising an oligonucleotide containing between 12-30 bases and at least 12 contiguous bases complementary to an exon-15 acceptor or donor splice site region contained within SEQ ID. NO: 15 of the full-length mRNA transcript of human epidermal growth factor receptor-2 (HER2) protein. The oligonucleotide may contain between 12 and 25 bases and a sequence of at least 12 contiguous bases complementary to a region contained with SEQ ID NOS: 44 or 45, both of which are contained in SEQ ID NO: 15. The oligonucleotide, may be, for example, a locked nucleic acid (LNA), 2'O-methoxyethyl oligoribonucleotide, or a phosphorodiamidate mopholino oligonucleotide. The compound may further include, conjugated to the 5'- or 3'-end of the oligonucleotide, an arginine-rich polypeptide effective to promote uptake of the compound into cells. Exemplary arginine-rich peptides include those identified by SEQ ID NOS: 52-67, and preferably those identified by SEQ ID NOS: 56-60 and 62.

[0016] In one general embodiment, the compound is composed of morpholino subunits and phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit. The morpholino subunits may be joined by phosphorodiamidate linkages having the structure:



where Y_1=O, Z=O, Pj is a purine or pyrimidine base-pairing moiety effective to bind, by base-specific hydrogen bonding, to a base in a polynucleotide, and X is an amino or alkyl amino, including dialkylamino.

[0017] In still another aspect of the invention, there is provided a method of treating a female subject having an ovarian or breast cancer characterized by overexpression of human epidermal growth factor receptor-2 (HER2), by the steps of:

(i) administering to the subject, a pharmaceutically effective amount of a compound comprising an oligonucleotide containing between 12-30 bases and at least 12 contiguous bases complementary to an exon-15 acceptor or donor splice site region contained within SEQ ID. NO: 15 of the full-length mRNA transcript of human epidermal growth factor receptor-2 (HER2) protein, and

(ii) continuing the administering, at periodic intervals, until a defined end point in the status of the cancer is obtained. The oligonucleotide compound employed in the method may have the features noted above. More generally, the method may be applied to the treatment of other cell-proliferative diseases or conditions.

[0018] The method may further include administering to the subject, a pharmaceutically effective amount of a soluble, human epidermal growth factor receptor-2 (HER2) protein lacking the region encoded by exon 15 of the full-length mRNA transcript of the HER2 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER2 transcript.

[0019] In still another aspect, the invention includes an isolated, soluble, human epidermal growth factor receptor-3 (HER3) protein lacking the region encoding by one of (i) exon 13 of the full-length mRNA transcript of the HER3 gene, and truncated, at its C terminus, in the region encoded by exon 15 of the HER3 transcript, (ii) exon 14 of the full-length mRNA transcript of the HER3 gene, and truncated, at its C terminus, in the region encoded by exon 15 of the HER3 transcript, or (iii) exon 15 of the full-length mRNA transcript of the HER3 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER3 transcript. The protein may have a sequence that is at least 90%, preferably at least 95% homologous to one of (i) SEQ ID No: **8** or amino acids 20-541 of SEQ ID No:8, (ii) SEQ ID No: **10** or amino acids 20-555 of SEQ ID No:10, or (iii) SEQ ID NO: 12 or amino acids 20-569 of SEQ ID No:12. The soluble HER3 protein may be pegylated, that is, derivatized with polyethyleneglycol chains, to improve its pharmacokinetic properties, e.g., circulation time in the blood.

[0020] Also disclosed, as part of the invention, is a coding sequence for the above soluble HER3 protein. The coding sequence corresponds to a processed

HER3 mRNA (i) lacking exon 13, with exon 12 joined directly to exon 14, (ii) (i) lacking exon 14, with exon 13 joined directly to exon 15, or (iii) lacking exon 15, with exon 14 joined directly to exon 16, and may take the form of a processed HER3 mRNA, the corresponding cDNA, or a vector containing the coding sequence. Exemplary coding sequences are those having at least 80%, preferably at least 85% sequence homology to SEQ ID NOS: 7, 9, or 11, or that portion of the sequence terminating at a stop codon within exon 15 (for SEQ ID NOS: 7 and 9), or a stop codon within exon 16 (for SEQ ID NO:11.

[0021] In another aspect, the invention includes a method of treating a female subject having an ovarian or breast cancer characterized by overexpression of human epidermal growth factor receptor-2 (HER2). The method includes the steps of

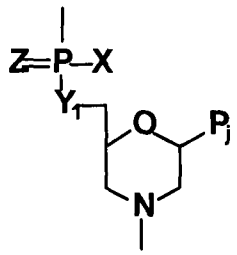
(i) administering to the subject, a pharmaceutically effective amount of soluble, human epidermal growth factor receptor-3 (HER3) protein lacking the region encoding by one of (i) exon 13 of the full-length mRNA transcript of the HER3 gene, and truncated, at its C terminus, in the region encoded by exon 15 of the HER3 transcript, (ii) exon 14 of the full-length mRNA transcript of the HER3 gene, and truncated, at its C terminus, in the region encoded by exon 15 of the HER3 transcript, or (iii) exon 15 of the full-length mRNA transcript of the HER3 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER3 transcript, and

(ii) continuing the administering, at periodic intervals, until a defined end point in the status of the cancer is obtained. The soluble HER2 protein employed in the method are as described above. More generally, the method may be applied to the treatment of other cell-proliferative diseases or conditions.

[0022] In still another aspect, the invention provides a splice-switching oligonucleotide compound comprising an oligonucleotide containing between 12-30 bases and at least 12 contiguous bases complementary to one of (i) an exon-13 acceptor or donor splice site region contained within SEQ ID. NO: 16 of the full-length mRNA transcript of human epidermal growth factor receptor-3 (HER3) protein; (ii) an exon-13 acceptor or donor splice site region contained within SEQ ID. NO: 16 of the full-length mRNA transcript of human epidermal growth factor receptor-3 (HER3) protein; or (iii) an exon-15 acceptor or donor splice site region contained within SEQ ID. NO: 16 of the full-length mRNA transcript of human epidermal growth

factor receptor-3 (HER3) protein. The oligonucleotide may contain between 12 and 25 bases and a sequence of at least 12 contiguous bases complementary to a region contained within one or SEQ ID NOS: 46-51, all of which are contained in SEQ ID NO: 16. The oligonucleotide, may be, for example, a locked nucleic acid (LNA), 2'-O-methoxyethyl oligoribonucleotide or a phosphorodiamidate mopholino oligonucleotide (PMO). The compound may further include, conjugated to the 5'- or 3'-end of the oligonucleotide, an arginine-rich polypeptide effective to promote uptake of the compound into cells. Exemplary arginine-rich peptides include those identified by SEQ ID NOS: 52-67, and preferably those identified by SEQ ID NOS: 56-60 and 62.

[0023] In one general embodiment, the compound is composed of morpholino subunits and phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit. The morpholino subunits may be joined by phosphorodiamidate linkages having the structure:



where Y_1=O, Z=O, Pj is a purine or pyrimidine base-pairing moiety effective to bind, by base-specific hydrogen bonding, to a base in a polynucleotide, and X is an amino or alkyl amino, including dialkylamino.

[0024] In still another aspect of the invention, there is provided a method of treating a female subject having an ovarian or breast cancer characterized by overexpression of human epidermal growth factor receptor-3 (HER3), by the steps of:

(i) administering to the subject, a pharmaceutically effective amount of a compound comprising an oligonucleotide containing between 12-30 bases and at least 12 contiguous bases complementary to one of (i) an exon-13 acceptor or donor splice site region contained within SEQ ID. NO: 16 of the full-length mRNA transcript of human epidermal growth factor receptor-3 (HER3) protein; (ii) an exon-13 acceptor or donor splice site region contained within SEQ ID. NO: 16 of the full-

length mRNA transcript of human epidermal growth factor receptor-3 (HER3) protein; or (iii) an exon-15 acceptor or donor splice site region contained within SEQ ID. NO: 16 of the full-length mRNA transcript of human epidermal growth factor receptor-3 (HER3) protein, and

(ii) continuing the administering, at periodic intervals, until a defined end point in the status of the cancer is obtained. The oligonucleotide compound employed in the method may have the features noted above. More generally, the method may be applied to the treatment of other cell-proliferative diseases or conditions.

[0025] The method may further include administering to the subject, a pharmaceutically effective amount of a soluble human epidermal growth factor receptor-2 (HER2) protein lacking the region encoding by exon 15 of the full-length mRNA transcript of the HER2 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER2 transcript.

[0026] These and other and features of the invention will become more fully apparent when the following detailed description of the invention is read in conjunction with the accompanying drawings.

Brief Description of the Drawings

[0027] FIG. **1**: Oligonucleotides (bars) directed toward exon 15 elicit the induction of a novel HER2 mRNA that lacks exon 15, such that downstream exons, including exon 16 which encodes the transmembrane domain, have an improper reading frame that introduces a stop codon in the exon, as indicated.

[0028] FIG. **2**: SK-BR-3 cells were transfected with the indicated concentration (50 or 150 nM) of the indicated oligonucleotide. Twenty-four hours later total RNA was isolated and RT-PCR was used to amplify a fragment of HER2 mRNA. Full length Her2 transcripts are represented by a 307 bp band (mHER2), and transcripts lacking exon 15 are represented by a 246 bp band (sHER2). LF, Lipofectamine™ 2000 only; U, untreated cells.

[0029] FIG. **3**: SK-BR-3 cells were transfected with the indicated concentration (10, 20, 40, 80, 100, 150 nM) of either oligonucleotide 111, M111 or L111 as described in Figure 2.

[0030] FIG. **4**: SK-BR-3 cells were transfected with the indicated concentration (25, 50, 100 nM) of SSO111 as described in Figure 2. After 48 hours, lysates were

analyzed by western blot for A) poly(ADP ribose) polymerase (PARP) cleavage and B) mHER2 protein expression. LF, Lipofectamine™ 2000 only; U, untreated cells.

[0031] FIG. **5**: MCF-7 cells were transfected with mammalian expression plasmids containing Δ15HER2 (sHER2) cDNA. After 48 hours, cell lysates and extracellular media were analyzed by western blot. Unglycosylated (~64kD) and glycosylated (~80kD) sHER2 protein was detected in the lysate (Lysate) and extracellular media (Media), respectively.

[0032] FIG. **6**: MCF-7 cells were transfected with the sHER2 plasmid, or a control plasmid expressing β-galactosidase. The extracellular media was then transferred to the extracellular media of cultured SK-BR-3 cells and incubated for 48 hours. The SK-BR-3 cells were then analyzed for A) PARP cleavage (Fig. 6A) and B) mHER2 expression as in previous figures (Fig. 6B). SK-BR-3 cells were treated with purified Δ15HER2-His protein at designated concentrations and analyzed for HER2, HER3, and their phoshorylation status (Fig. 6C). Fig. 6D shows growth inhibition of SK-BR-3 cells by Δ15HER2-His protein treatment after 72 hours

incubation analyzed by an MTS assay. Shown are the mean ± standard deviation of triplicates.

[0033] FIG. **7**: Oligonucleotides directed toward splicing elements (Arrows) elicit the induction of the indicated novel HER3 mRNAs, such that downstream exons have an improper reading frame, leading to soluble truncated HER3 splice variants that are terminated, as indicated by the arrows over the downstream ends of the soluble receptors.

[0034] FIG. **8**: MCF-7 cells were transfected with 100 nM of the indicated SSO. After 24 hours, total RNA was isolated and RT-PCR was used to amplify a fragment of HER3 mRNA. Full length HER3 transcripts are represented by a 619 bp band (HER3), and transcripts lacking exon 13 are represented by a 486 bp band (Δ13HER3).

[0035] FIG. **9**: MCF-7 cells were transfected with the indicated SSO as in Figure 8. Full length HER3 transcripts are represented by a 353 bp band, and transcripts lacking exon 14 (Δ14HER3) or exon 15 (Δ15HER3) are represented by 262 bp and 198 bp bands, respectively.

[0036] FIG. **10**: SK-BR-3 cells were transfected with 100 nM of the indicated SSO as described in the previous figures. After 48 hours, cell viability was measured and expressed as percent of untreated cells.

[0037] FIG. **11**: The sequence of a portion of the human HER2 gene is presented. The sequence shown is from the middle of intron 14 through a portion of exon 16. Exon sequences are underlined and in bold. The stop codon in exon 16 for the Δ15HER2 protein is boxed.

[0038] FIG. **12**: The sequence of a portion of the human HER3 gene is presented. The sequence shown is from the middle of intron 12 through a portion of exon 16. Exon sequences are underlined and in bold.

[0039] FIG. **13A-C**: Exemplary structures of a phosphorodiamidate-linked morpholino oligomer (PMO) (Fig. 13A), a peptide-conjugated PMO (PPMO) (Fig. 13B), and a peptide-conjugated PMO having cationic intersubunit linkages (PPMO+) (Fig. 13C). Though multiple cationic linkage types are illustrated in Fig. 13C, a PMO+ or PPMO+ oligomer will typically include just one type of cationic linkage.

[0040] FIG **13D-G**: Repeating subunit segment of four exemplary morpholino oligonucleotides, designated D through G.

[0041] FIG **14A-B**: Splice-correction activity in organs from EGFP-654 transgenic mice treated with various EGFP-654-targeted carrier peptide-PMOs as measured in mammalian gland (FIG. 14A) and ovary and prostate (FIG. 14B).

Detailed Description of the Drawings

I Definitions:

[0042] As used herein, the terms "epidermal growth factor receptor", "EGF receptor", and "EGFR" refer to proteins having amino acid sequences of or which are substantially similar to native mammalian epidermal growth factor receptor family sequences, preferably HER1, HER2, HER3 and HER4. In this context, a "native" receptor or gene for such a receptor, means a full-length receptor or gene that occurs in nature, as well as the naturally-occurring allelic variations of such receptors and genes.

[0043] As used herein, the terms "soluble epidermal growth factor receptor", "soluble EGF receptor", and "sEGFR" refer to soluble proteins whose sequences are or are substantially similar to those encoded by an mRNA derived from a native

EGFR mRNA where a single exon has been skipped or a single intron has been retained during splicing.

[0044] The term "mature" as used in connection with a protein means a protein expressed in a form lacking a leader or signal sequence as may be encoded in full-length transcripts of a native gene.

[0045] The terms "secreted" and "soluble" are used interchangeably herein and mean that the protein is soluble, i.e., that it is not bound to the cell membrane. In this context, a form will be soluble if, using conventional assays known to one of skill in the art, most of this form can be detected in fractions that are not associated with the membrane, e.g., in cellular supernatants from lysed or intact cells or in serum.

[0046] The term "stable" means that the sEGFR is detectable using conventional assays known to one of skill in the art, such as for example, western blots or ELISA assays of harvested cells, cellular supernatants, or serum.

[0047] As used herein, the term "a cell-proliferative disease or condition" refers to a disease, disorder, or other medical condition that, at least in part, results from or is aggravated by either an increase in cell division or cell survival or a decrease in apoptosis. Such diseases or conditions include, but are not limited to, those associated with increased levels of EGFR ligands, increased levels of EGF receptors, or increased sensitization or deregulation of an EGFR signaling pathway, and in particular, increased levels of HER2 and/or HER3. The term also encompasses diseases and conditions for which known EGFR antagonists have been shown useful. Examples of proliferative diseases or conditions include, but are not limited to, cancer and pulmonary fibrosis. Psoriasis (Wierzbicka, E., et al., 2006, Brit. J. of Dermatol., 155: 207-229) and diabetic retinopathy (Xu, K.P., 2007, Investig. Ophthal. and Visual Sci., 48: 2242-2248) can also be treated with HER2 antagonists.

[0048] As used herein, the term "HER2 antagonist" means that the protein is capable of causing a measurable increase in cytotoxicity in HER2 expressing cells, either by directly antagonizing HER2 function or by binding and inactivating EGFR ligands such as heregulin, using standard assays as are well known in the art. (*See, e.g.*, the cell viability assay in the examples herein).

[0049] As used herein, the term "induce apoptosis" means to cause cell death by apoptosis. Induction of apoptosis can be measured using conventional assays know to one of skill in the art. These assays include but are not limited to: i) Annexin

V-FITC staining (Invitrogen) and FACS, which can detect phosphatidylserine displayed on the surface of cells undergoing apoptotic death; ii) ApoAlert® CPP32 colorimetric assay (Clontech), which detects CPP32 protease activity, a key early event in apoptosis; and iii) Western blot for specific intracellular proteins, such as poly(ADP ribose) polymerase (PARP) and cyclin B, which are degraded by caspases during apoptosis (*See, e.g.*, the PARP cleavage assay in the examples herein).

[0050] As used herein, the terms "transformation" or "transfection" refer to the insertion of an exogenous nucleic acid into a cell, irrespective of the method used for the insertion, for example, lipofection, transduction, infection or electroporation. The exogenous nucleic acid can be maintained as a non-integrated vector, for example, a plasmid, or alternatively, can be integrated into the cell's genome.

[0051] As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting into a cell another nucleic acid to which it has been linked

[0052] As used herein, the term "isolated protein" refers to a protein or polypeptide that is not naturally-occurring and is separated from one or more components that are associated with it at its synthesis or is naturally-occurring and is separated from one or more components that are naturally associated with it.

[0053] As used herein, the term "isolated nucleic acid" refers to a nucleic acid that is in the form of a separate fragment or as a component of a larger construct, which has been derived from a nucleic acid isolated at least once in substantially pure form, i.e., free of contaminating endogenous materials, and in a quantity or concentration enabling identification and manipulation by standard biochemical methods, for example, using a cloning vector.

[0054] As used herein the term "purified protein" refers to a protein that is present in the substantial absence of other proteins. However, such purified proteins can contain other proteins added as stabilizers, carriers, excipients, or co-therapeutics. The term "purified" as used herein preferably means at least 80% by dry weight, more preferably in the range of 95-99% by weight, and most preferably at least 99.8% by weight, of protein present, excluding proteins added as stabilizers, carriers, excipients, or co-therapeutics.

[0055] As used herein, the term "altering the splicing of a pre-mRNA" refers to altering the splicing of a cellular pre-mRNA target resulting in an altered ratio of spliced products. Such an alteration of splicing can be detected by a variety of techniques well known to one of skill in the art. For example, RT-PCR can be used

on total cellular RNA to detect the ratio of splice products in the presence and the absence of an SSO.

[0056] As used herein, the term "complementary" is used to indicate a sufficient degree of complementarity or precise pairing such that stable and specific binding occurs between an oligonucleotide and a DNA or RNA containing the target sequence. It is understood in the art that the sequence of an oligonucleotide need not be 100% complementary to that of its target. For example, for an SSO there is a sufficient degree of complementarity when, under conditions which permit splicing, binding to the target will occur and non-specific binding will be substantially avoided.

[0057] As used here, a protein or nucleic acid has at least a specified percentage of sequence homology with a given SEQ ID NO, if the protein or nucleic acid in question has the same amino acid residues or bases, in the same sequence, in at least the specified percentage of residues or bases of the identified SEQ ID NO. In making nucleic acids with at least a given degree of sequence homology to a specified coding sequence, one skilled in the art, with the aid of a computer, could readily generate all nucleic acid sequences that would encode a given protein sequence. In making proteins with at least a given degree of sequence homology to specified protein sequence, one skilled in the art, guided by a knowledge of the physicochemical properties of amino acids, the position of a given residue within a protein, the known effects of certain amino acids on the conformation of proteins, and with the aid of a computer, could readily select certain amino acid substitutions at certain residue positions that would, with reasonable predictability, preserve the functional properties of the protein.

IIA. Splice Variant Her2 and Her3 Proteins:

[0058] One embodiment of the present invention is a protein, either full length or mature, which is encoded by a cDNA derived from a native epidermal growth factor receptor (EGFR) gene, particularly either HER2 or HER3, where a single exon in the cDNA is skipped resulting in a soluble protein (sEGFR). Furthermore the sEGFR can act as an EGFR, preferably HER2, antagonist. "Mammalian sEGFR", according to the present invention, includes but is not limited to soluble human, primate, murine, canine, feline, bovine, ovine, equine, and porcine EGFR. Furthermore, mammalian sEGFR according to the present invention includes, but is not limited to, a protein sequence that results from one or more single nucleotide

polymorphisms, as long as the protein retains a comparable biological activity to the reference sEGFR with which it is being compared.

[0059] In one embodiment, the soluble mammalian EGFR is a mammalian HER2, preferably a human HER2. In particular, in the cDNA for this protein exon 14 is followed directly by exon 16 and as a result exon 15 is skipped (Fig. **11**). For soluble human HER2, two non-limiting examples of this embodiment are given by Δ15HER2 that includes the signal sequence as shown in SEQ ID No: 6 and mature Δ15HER2 (amino acids 23-584 of SEQ ID No: 6) that lacks the signal sequence.

[0060] In another embodiment, the soluble mammalian EGFR is a mammalian HER3, preferably a human HER3. In one aspect of this embodiment, exon 12 is followed directly by exon 14 and as a result exon 13 is skipped (Fig. **12**). For soluble human HER3, two non-limiting examples of this embodiment are given by Δ13HER3 that includes the signal sequence as shown in SEQ ID No: 8 and mature Δ13HER3 (amino acids 20-541 of SEQ ID No: 8) that lacks the signal sequence. In another aspect, exon 13 is followed directly by exon 15 and as a result exon 14 is skipped (Fig. **12**). For soluble human HER3, two non-limiting examples of this embodiment are given by Δ14HER3 that includes the signal sequence as shown in SEQ ID No: 10 and mature Δ14HER3 (amino acids 20-555 of SEQ ID No: 10) that lacks the signal sequence. In yet another aspect, exon 14 is followed directly by exon 16 and as a result exon 15 is skipped (Fig. **12**). For soluble human HER3, two non-limiting examples of this embodiment are given by Δ15HER3 that includes the signal sequence as shown in SEQ ID No: 12 and mature Δ15HER3 (amino acids 20-569 of SEQ ID No: 12) that lacks the signal sequence.

[0061] The proteins of the present invention also include those proteins that are chemically modified. Chemical modification of a protein refers to a protein where at least one of its amino acid residues is modified by either natural processes, such as processing or other post-translational modifications, or by chemical modification techniques known in the art. Such modifications include, but are not limited to, acetylation, acylation, amidation, ADP-ribosylation, glycosylation, methylation, pegylation, prenylation, phosphorylation, or cholesterol conjugation.

IIB. Protein Expression and Purification:

[0062] When mammalian or insect cells are used, properly expressed sEGFR will be secreted into the extracellular media. The protein is recovered from the media, and is concentrated and purified using standard biochemical techniques.

After expression in mammalian cells by lentiviral or AAV transduction, plasmid transfection, or any similar procedure, or in insect cells after baculoviral transduction, the extracellular media of these cells is concentrated using concentration filters with an appropriate molecular weight cutoff, such as Amicon® filtration units.

[0063] When sEGFR is expressed in bacterial culture it can be purified by standard biochemical techniques. Bacteria are lysed, and the cellular extract containing the sEGFR is desalted and concentrated.

[0064] In either case, the sEGFR can be purified by affinity chromatography. The use of column chromatography with an affinity matrix comprising an EGFR ligand can be used to purify HER3 splice variants. Alternatively, an affinity purification tag can be added to either the N- or the C-terminus of the sEGFR. For example, a polyhistidine-tag (His-tag), which is an amino acid motif with at least six histidines, can be used for this purpose (Hengen, P., 1995, Trends Biochem. Sci. 20:285-86). The addition of a His-tag can be achieved by the in-frame addition of a nucleotide sequence encoding the His-tag directly to either the 5' or 3' end of the sEGFR open reading frame in an expression vector. When a His-tag is incorporated into the protein, a nickel or cobalt affinity column is employed to purify the tagged sEGFR, and the His-tag can optionally then be cleaved. Other suitable affinity purification tags and methods of purification of proteins with those tags are well known in the art.

[0065] Alternatively, a non-affinity based purification scheme can be used, involving fractionation of the sEGFR extracts on a series of columns that separate the proteins based on size (size exclusion chromatography), charge (anion and cation exchange chromatography) and hydrophobicity (reverse phase chromatography). High performance liquid chromatography can be used to facilitate these steps.

IIC. Use of proteins for the treatment of proliferative diseases:

[0066] For therapeutic use, sEGFR of the present invention is administered to a patient, preferably a human, for treating HER2-dependent proliferative diseases, such as cancer. In the treatment of humans, the use of soluble human EGFR is preferred. The sEGFR of the present invention can be administered by bolus injection, continuous infusion, sustained release from implants, or other suitable techniques. Typically, therapeutic sEGFR will be administered in the form of a composition comprising purified protein in conjunction with physiologically

acceptable carriers, excipients or diluents. Such carriers will be nontoxic to recipients at the dosages and concentrations employed. Ordinarily, the preparation of such compositions entails combining the sEGFR with buffers, antioxidants such as ascorbic acid, polypeptides, proteins, amino acids, carbohydrates including glucose, sucrose or dextrins, chelating agents such as EDTA, glutathione and other stabilizers and excipients. Neutral buffered saline or saline mixed with nonspecific serum albumin are exemplary appropriate diluents. Preferably, product is formulated as a lyophilizate using appropriate excipient solutions, for example, sucrose, as diluents. Preservatives, such as benzyl alcohol can also be added. The amount and frequency of administration will depend of course, on such factors as the nature and the severity of the indication being treated, the desired response, the condition of the patient and so forth.

[0067] sEGFR of the present invention is administered systemically in therapeutically effective amounts preferably ranging from about 0.1 mg/kg/week to about 100 mg/kg/week. In preferred embodiments, sEGFR is administered in amounts ranging from about 0.5 mg/kg/week to about 50 mg/kg/week. For local administration, dosages preferably range from about 0.01 mg/kg to about 1.0 mg/kg per injection.

IID. Treatment Methods using the splice variant proteins

[0068] The present invention provides for the use of proteins as set forth above for the preparation of a medicament for treating a patient afflicted with a proliferative disorder involving excessive EGFR, preferably HER2, activity, as discussed below. In the manufacture of a medicament according to the present invention, the proteins of the present invention are typically admixed with, inter alia, an acceptable carrier. The carrier must, of course, be acceptable in the sense of being compatible with other ingredients in the formulation and must not be deleterious to the patient. The carrier can be a solid or liquid. The proteins of the present invention are incorporated in formulations, which can be prepared by any of the well known techniques of pharmacy consisting essentially of admixing the components, optionally including one or more accessory therapeutic ingredients.

[0069] Formulations of the present invention can comprise sterile aqueous and non-aqueous injection solutions of the active compounds, which preparations are preferably isotonic with the blood of the intended recipient and essentially pyrogen free. These preparations can contain anti-oxidants, buffers, bacteriostats,

and solutes which render the formulation isotonic with the blood of the intended recipient. Aqueous and non-aqueous sterile suspensions can include, but are not limited to, suspending agents and thickening agents. The formulations can be presented in unit dose or multi-dose containers, for example, sealed ampoules and vials, and can be stored in freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carrier, for example, saline or water-for-injection immediately prior to use.

[0070] In the formulations, the nucleic acids and proteins of the present invention can be contained within a particle or vesicle, such as a liposome or microcrystal, which can be suitable for parenteral administration. The particles can be of any suitable structure, such as dendritic, hyper-branched, unilamellar or plurilameller, so long as the nucleic acids and proteins of the present invention are contained therein. Positively charged lipids such as N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethyl-ammoniummethylsulfate, or "DOTAP," are particularly preferred for such particles and vesicles. The preparation of such lipid particles is well known (See references in U.S. Pat. No. 5,976,879 col. 6).

IIIA. Splice Variant Nucleic Acids:

[0071] One embodiment of the present invention is a nucleic acid that encodes a protein, either full length or mature, which is encoded by a cDNA derived from an epidermal growth factor receptor (EGFR) gene, particularly either HER2 or HER3, where a single exon in the cDNA is skipped resulting in a soluble protein. Furthermore the encoded protein can act as an HER2 antagonist.

[0072] Such sequences are preferably provided in the form of an open reading frame uninterrupted by internal nontranslated sequences, or introns, which are typically present in eukaryotic genes. Genomic DNA containing the relevant sequences can also be used. In one embodiment, the nucleic acid is either an mRNA or a cDNA. In another embodiment, it is genomic DNA.

[0073] In one embodiment, the soluble mammalian EGFR is a mammalian HER2, preferably a human HER2. For soluble human HER2, two non-limiting examples of this embodiment are nucleic acids that encode the Δ15HER2 that includes the signal sequence as shown in SEQ ID No: 6 and mature Δ15HER2 (amino acids 23-584 of SEQ ID No: 6) that lacks the signal sequence. Examples of the sequences of these Δ15HER2 nucleic acids are, without limitation, nucleotides 1-

1752 of SEQ ID No: 5, which includes the signal sequence and nucleotides 67-1752 of SEQ ID No: 5, which lacks the signal sequence.

[0074] In another embodiment, the soluble mammalian EGFR is a mammalian HER3, preferably a human HER3. For soluble human HER3, two non-limiting examples of this embodiment are nucleic acids that encode the Δ13HER3 that includes the signal sequence as shown in SEQ ID No: 8 or mature Δ13HER3 (amino acids 20-541 of SEQ ID No: 8) that lacks the signal sequence. Examples of the sequences of these Δ13HER3 nucleic acids are, without limitation, nucleotides 1-1623 of SEQ ID No: 7, which includes the signal sequence and nucleotides 58-1623 of SEQ ID No: 7, which lacks the signal sequence.

[0075] For soluble human HER3, two further non-limiting examples of this embodiment are nucleic acids that encode the Δ14HER3 that includes the signal sequence as shown in SEQ ID No: 10 or mature Δ14HER3 (amino acids 20-555 of SEQ ID No: 10) that lacks the signal sequence. Examples of the sequences of these Δ14HER3 nucleic acids are, without limitation, nucleotides 1-1665 of SEQ ID No: 9, which includes the signal sequence and nucleotides 58-1665 of SEQ ID No: 9, which lacks the signal sequence.

[0076] For soluble human HER3, two other non-limiting examples of this embodiment are nucleic acids that encode the Δ15HER3 that includes the signal sequence as shown in SEQ ID No: 12 or mature Δ15HER3 (amino acids 20-569 of SEQ ID No: 12) that lacks the signal sequence. Examples of the sequences of these Δ15HER3 nucleic acids are, without limitation, nucleotides 1-1707 of SEQ ID No: 11, which includes the signal sequence and nucleotides 58-1707 of SEQ ID No: 11, which lacks the signal sequence.

[0077] The bases of the nucleic acids of the present invention can be the conventional bases cytosine, guanine, adenine and uracil or thymidine. Optionally, modified bases can be used.

[0078] Suitable nucleic acids of the present invention include numerous alternative chemistries. For example, suitable nucleic acids of the present invention include, but are not limited to, those wherein at least one of the internucleotide bridging phosphate residues is a modified phosphate, such as phosphorothioate, methyl phosphonate, methyl phosphonothioate, phosphoromorpholidate, phosphoropiperazidate, and phosphoroamidate.

[0079] Nucleic acids of the present invention also include, but are not limited to, those wherein at least one, of the nucleotides is a nucleic acid analogue.

[0080] Nucleic acids of the present invention include, but are not limited to, modifications of the nucleic acids involving chemically linking to the nucleic acids one or more moieties or conjugates. Such moieties include, but are not limited to, lipid moieties such as a cholesterol moiety, cholic acid, a thioether, e.g. hexyl-S-tritylthiol, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipids, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, an adamantane acetic acid, a palmityl moiety, an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety.

IIIB. Expression and Gene-therapy Vectors

[0081] The present invention also provides expression vectors to amplify or express DNA encoding the foregoing proteins of the current invention, as well as host cells transformed with the foregoing expression vectors. Expression vectors are replicable DNA constructs which have synthetic or cDNA-derived DNA fragments encoding soluble mammalian EGFR, particularly HER2 or HER3, or bioequivalent analogues operably linked to suitable transcriptional or translational regulatory elements derived from mammalian, microbial, viral, or insect genes. A transcriptional unit generally comprises an assembly of (a) a genetic element or elements having a regulatory role in gene expression, such as, transcriptional promoters or enhancers, (b) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (c) appropriate transcription and translation initiation and termination sequences. Such regulatory elements can include an operator sequence to control transcription, and a sequence encoding suitable mRNA ribosomal binding sites. The ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants, can additionally be incorporated.

[0082] DNA regions are operably linked when they are functionally related to each other. For example, DNA for a signal peptide (secretory leader) is operably linked to DNA for a polypeptide if it is expressed as part of a precursor which participates in the secretion of the polypeptide; a promoter is operably linked to a coding sequence if it controls the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit

translation. Generally, operably linked means contiguous and, in the case of secretory leaders, contiguous and in reading frame. Structural elements intended for use in yeast expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it can include an N-terminal methionine residue. This residue can optionally be subsequently cleaved from the expressed protein to provide a final product.

[0083] Soluble mammalian EGFR DNA is expressed or amplified in a recombinant expression system comprising a substantially homogeneous monoculture of suitable host microorganisms, for example, bacteria such as E. coli or yeast such as S. cerevisiae, which have stably integrated (by transformation or transfection) a recombinant transcriptional unit into chromosomal DNA or which carry the recombinant transcriptional unit as a component of a resident plasmid. Recombinant expression systems as defined herein will express heterologous protein either constitutively or upon induction of the regulatory elements linked to the DNA sequence or synthetic gene to be expressed.

[0084] Transformed host cells are cells which have been transformed or transfected with soluble mammalian EGFR vectors constructed using recombinant DNA techniques. Transformed host cells ordinarily express sEGFR, but host cells transformed for purposes of cloning or amplifying sEGFR DNA do not need to express sEGFR. Suitable host cells for expression of soluble mammalian EGFR include prokaryotes, yeast, fungi, or higher eukaryotic cells. Prokaryotes include gram negative or gram positive organisms, for example E. coli or bacilli. Higher eukaryotic cells include, but are not limited to, established insect and mammalian cell lines. Cell-free translation systems can also be employed to produce soluble mammalian EGFR using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are well known in the art.

[0085] Prokaryotic expression hosts can be useful for expression of sEGFR that does not undergo extensive posttranslational processing. Prokaryotic expression vectors generally comprise one or more phenotypic selectable markers, for example a gene encoding proteins conferring antibiotic resistance or supplying an autotrophic requirement, and an origin of replication recognized by the host to ensure amplification within the host. Suitable prokaryotic hosts for transformation

include E. coli, Bacillus subtilis, Salmonella typhimurium, and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others can also be employed as a matter of choice.

[0086] Useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells. Such commercial vectors include, for example, the series of Novagen® pET vectors (EMD Biosciences, Inc., Madison, Wis.).

[0087] Promoters commonly used in recombinant microbial expression vectors include the lactose promoter system, and the λ P_L promoter, the T7 promoter, and the T7 lac promoter. A particularly useful bacterial expression system, Novagen® pET system (EMD Biosciences, Inc., Madison, Wis.) employs a T7 or T7 lac promoter and E. coli strain, such as BL21(DE3) which contain a chromosomal copy of the T7 RNA polymerase gene.

[0088] sEGFR proteins can also be expressed in yeast and fungal hosts, preferably from the genus Saccharomyces, such as S. cerevisiae. Yeast of other genera, such as Pichia or Kluyveromyces can also be employed. Yeast vectors will generally contain an origin of replication from the 2μ yeast plasmid or an autonomously replicating sequence (ARS), promoter, DNA encoding sEGFR, sequences for polyadenylation and transcription termination and a selection gene. Preferably, yeast vectors will include an origin of replication and selectable marker permitting transformation of both yeast and E. coli, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 or URA3 gene, which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan or uracil, respectively, and a promoter derived from a highly expressed yeast gene to induce transcription of a structural sequence downstream. The presence of the TRP1 or URA3 lesion in the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan or uracil, respectively.

[0089] Suitable promoter sequences in yeast vectors include the promoters for metallothionein, 3-phosphoglycerate kinase or other glycolytic enzymes , such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Suitable vectors and promoters for use in yeast expression are well known in the art.

[0090] Preferred yeast vectors can be assembled using DNA sequences from pUC18 for selection and replication in E. coli (Amp^r gene and origin of replication) and yeast DNA sequences including a glucose-repressible ADH2 promoter and α-factor secretion leader. The yeast α-factor leader, which directs secretion of heterologous proteins, can be inserted between the promoter and the structural gene to be expressed. The leader sequence can be modified to contain, near its 3' end, one or more useful restriction sites to facilitate fusion of the leader sequence to foreign genes. Suitable yeast transformation protocols are known to those of skill in the art.

[0091] Host strains transformed by vectors comprising the ADH2 promoter can be grown for expression in a rich medium consisting of 1% yeast extract, 2% peptone, and 1% or 4% glucose supplemented with 80 □g/ml adenine and 80 □g/ml uracil. Derepression of the ADH2 promoter occurs upon exhaustion of medium glucose. Crude yeast supernatants are harvested by filtration and held at 4°C prior to further purification.

[0092] Various mammalian or insect cell culture systems are also advantageously employed to express sEGFR protein. Expression of recombinant proteins in mammalian cells is particularly preferred because such proteins are generally correctly folded, appropriately modified and completely functional. Examples of suitable mammalian host cell lines include the COS-7 lines of monkey kidney cells, and other cell lines capable of expressing an appropriate vector including, for example, L cells, such as L929, C127, 3T3, Chinese hamster ovary (CHO), HeLa and BHK cell lines. Mammalian expression vectors can comprise nontranscribed elements such as an origin of replication, a suitable promoter, for example, the CMVie promoter, the chicken beta-actin promoter, or the composite hEF1-HTLV promoter, and enhancer linked to the gene to be expressed, and other 5' or 3' flanking nontranscribed sequences, and 5' or 3' nontranslated sequences,

such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and transcriptional termination sequences. Baculovirus systems for production of heterologous proteins in insect cells are known to those of skill in the art.

[0093] The transcriptional and translational control sequences in expression vectors to be used in transforming vertebrate cells can be provided by viral sources. For example, commonly used promoters and enhancers are derived from Polyoma, Adenovirus 2, Simian Virus 40 (SV40), human cytomegalovirus, such as the CMVie promoter, HTLV, such as the composite hEF1-HTLV promoter. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites can be used to provide the other genetic elements required for expression of a heterologous DNA sequence.

[0094] Further, mammalian genomic EGFR promoters, such as control and/or signal sequences can be utilized, provided such control sequences are compatible with the host cell chosen.

[0095] In preferred aspects of the present invention, recombinant expression vectors comprising sEGFR cDNAs are stably integrated into a host cell's DNA.

[0096] One embodiment is a method of treating a proliferative disease or condition by administering sEGFR to a subject, thereby decreasing HER2 activity. Another embodiment is a method of treating a proliferative disease or condition by administering to a subject an expression vector that encodes sEGFR, thereby decreasing HER2 activity. Another embodiment is a method of producing sEGFR.

[0097] The following aspects of the present invention apply to the foregoing embodiments.

[0098] The methods, nucleic acids, proteins, and formulations of the present invention are also useful as *in vitro* or *in vivo* tools.

[0099] In further embodiments, apoptosis in mammalian cells can be induced by administering to the mammalian cells, in an amount and under conditions sufficient to induce apoptosis, nucleic acids, proteins, and formulations of the present invention.

[00100] Embodiments of the invention can be used to treat any condition in which the medical practitioner intends to limit the effect of a signaling pathway involving EGFR. In particular, the formulations of the present invention can be used to treat a proliferative disease. Such diseases include, but are not limited to cancer

and pulmonary fibrosis. In one embodiment, the condition is a cancer selected from the group consisting of breast, lung, ovarian, gastric and colon cancer. In one embodiment, the condition is a cancer which is resistant to chemotherapy. The uses of the present invention include, but are not limited to, treatment of diseases for which known HER2 antagonists, such as Herceptin, Herstatin and pertuzumab, have been shown useful.

IIIC. Use of expression vectors to increase the levels of an HER2 antagonist in a mammal:

[00101] The present invention provides a process of increasing the levels of an HER2 antagonist in a mammal. The process includes the step of transforming cells of the mammal with an expression vector described herein, which drives expression of sEGFR as described herein.

[00102] The process is particularly useful in large mammals such as domestic pets, those used for food production, and primates. Exemplary large mammals are dogs, cats, horses cows, sheep, deer, and pigs. Exemplary primates are monkeys, apes, and humans.

[00103] The mammalian cells can be transformed either *in vivo* or *ex vivo*. When transformed *in vivo*, the expression vector is administered directly to the mammal, such as by injection. Means for transforming cells *in vivo* are well known in the art. When transformed *ex vivo*, cells are removed from the mammal, transformed *ex vivo*, and the transformed cells are reimplanted into the mammal.

IV. Pharmaceutical Compositions and Preparations:

[00104] Other embodiments of the present invention are pharmaceutical compositions comprising the foregoing proteins or nucleic acids.

[00105] The nucleic acids or proteins of the present invention can be admixed, encapsulated, conjugated, or otherwise associated with other molecules, molecule structures, or mixtures of compounds, as for example liposomes, and receptor targeted molecules, in oral, rectal, topical or other formulations, for assisting in uptake, distribution, and/or absorption.

[00106] Formulations of the present invention comprise nucleic acids or proteins in a physiologically or pharmaceutically acceptable carrier, such as an aqueous carrier. Thus formulations for use according to the present invention include, but are not limited to, those suitable for parenteral administration including

intraperitoneal, intravenous, intraarterial, subcutaneous, intraarticular, or intramuscular injection or infusion, as well as those suitable for topical, ophthalmic, vaginal, oral, rectal or pulmonary administration (including inhalation or insufflation of powders or aerosols, including by nebulizer, intratracheal, and intranasal delivery). The formulations can conveniently be presented in unit dosage form and can be prepared by any of the methods well known in the art. The most suitable route of administration in any given case can depend upon the subject, the nature and severity of the condition being treated, and the particular active compound which is being used.

[00107] Pharmaceutical compositions of the present invention include, but are not limited to, physiologically and pharmaceutically acceptable salts, i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological properties. Examples of such salts are (a) salts formed with cations such as sodium, potassium, NH_4^+, magnesium, calcium, polyamines such as spermine and spermidine; (b) acid addition salts formed with inorganic acids, for example, hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid and the like; and (c) salts formed with organic acids such as, for example, acetic acid, oxalic acid, tartaric acid, succinic acid, maleic acid, fumaric acid, gluconic acid, citric acid, malic acid, ascorbic acid, benzoic acid, palmitic acid, alginic acid, polyglutamic acid, napthalenesulfonic acid, methanesulfonic acid, p-toluenesulfonic acid, napthalenedisulfonic acid, polygalacturonic acid, and the like.

V. Splice-switching oligomers (SSOs):

[00108] In another aspect, the present invention employs splice switching oligonucleotides or splice switching oligomers (SSOs) to control the alternative splicing of either HER2 or HER3 so that the amount of a soluble form is increased, and optionally the amount of the integral membrane form is decreased. The methods and compositions of the present invention can be used in the treatment of diseases associated with excessive HER2 activity.

[00109] Accordingly, one embodiment of the present invention is a method of treating a proliferative disease or condition by administering SSOs to a patient. The SSOs that are administered alter the splicing of a pre-mRNA to produce a soluble form of either HER2 or HER3. In one embodiment, the soluble form is

Δ15HER2. In another embodiment, the soluble form is Δ13HER3. In yet another embodiment, the soluble form is Δ14HER3. In yet a further embodiment, the soluble form is Δ15HER3. In another embodiment, the soluble form is the p85 form of HER3.

[00110] In another embodiment, a method of producing a soluble form of either HER2 or HER3 in a cell by administering SSOs to the cell is disclosed. In yet another embodiment, a method of inducing apoptosis in mammalian cells by administering SSOs to the mammalian cell is disclosed.

The length of the SSO (i.e., the number of monomers in the oligomer) is similar to an antisense oligonucleotide (ASON), typically between about 8 and 30 nucleotides. In preferred embodiments, the SSO will be between about 10 to 30, more preferably 15 to 25, nucleotides. In this aspect, the invention can be practiced with SSOs comprised of several chemistries that hybridize to RNA, but that do not activate the destruction of the target RNA by RNase H, as do conventional antisense 2'-deoxy oligonucleotides. The invention can be practiced using 2'O modified nucleic acid oligomers, such as where the 2'O is replaced with $-O-CH_3$, $-O-CH_2-CH_2-O-CH_3$, $-O-CH_2-CH_2-CH_2-NH_2$, $-O-CH_2-CH_2-CH_2-OH$ or –F, where 2'O-methyl (2'-OMe) or 2'O-methyloxyethyl (MOE) is preferred. The nucleobases do not need to be linked to sugars. So-called peptide nucleic acid oligomers or morpholine-based oligomers can be used. A comparison of these different linking chemistries is found in Sazani, P. et al., 2001, Nucleic Acids Res. 29:3695 and in Crooke, S. T. (2008) Antisense Drug Technology, Boca Raton, CRC PressThe term splice-switching oligonucleotide (SSO) is intended to cover the above forms. The SSO described in the examples of the present invention include 2'-OMe and MOE oligomers. It will be obvious to one skilled in the art that additional oligomer chemistries can be used to practice the invention including phosphorodiamidate-linked morpholino oligomers (PMO) or locked nucleic acid (LNA) oligomers as described below.

[00111] The SSOs of this invention can be made through the well-known technique of solid phase synthesis. Any other means for such synthesis known in the art can additionally or alternatively be used. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives.

[00112] The bases of the SSO can be the conventional cytosine, guanine, adenine and uracil or thymidine bases. Alternatively, modified bases can be used. Of particular interest are modified bases that increase binding affinity. One non-limiting example of preferred modified bases are the so-called G-clamp or 9-(aminoethoxy)phenoxazine nucleotides, cytosine analogues that form 4 hydrogen bonds with guanosine. (Flanagan, W.M., et al., 1999, Proc. Natl. Acad. Sci. 96:3513; Holmes, S.C., 2003, Nucleic Acids Res. 31:2759). Specific examples of other bases include, but are not limited to, 5-methylcytosine (^{Me}C), isocytosine, pseudoisocytosine. 5-(1-propynyl)-cytosine, 5-bromouracil, 5-(1-propynyl)-uracil, 5-propyny-6, 5-methylthiazoleuracil, 6-aminopurine, 2-aminopurine, inosine, 2,6-diaminopurine, 7-propyne-7-deazaadenine, 7-propyne-7-deazaguanine and 2-chloro-6-aminopurine.

[00113] Those skilled in the art will appreciate the relationship between antisense oligonucleotide gapmers and SSOs. Gapmers are ASON that contain an RNase H activating region (typically a 2'-deoxyribonucleoside phosphorothioate) which is flanked by non-activating nuclease resistant oligomers. In general, any chemistry suitable for the flanking sequences in a gapmer ASON can be used in an SSO. For similar reasons, ASON chemistries that induce RNase H activity and do not contain flanking nuclease resistant oligomers are also not appropriate as SSOs.

VA. Phosphorodiamidate Morpholino Oligomers as SSOs

[00114] An example of a preferred SSO chemistry includes morpholino oligonucleotides having phosphorus-containing backbone linkages as illustrated in Figs. 13A-13G. Also preferred is a phosphorodiamidate-linked morpholino oligonucleotide (PMO) such as shown in Fig. 13C, which is modified, in accordance with one aspect of the present invention, to contain positively charged groups at preferably 10%-50% of its backbone linkages. Morpholino oligonucleotides with uncharged backbone linkages, including antisense oligonucleotides, are detailed, for example, in (Summerton, J. and D. Weller (1997) Antisense Nucleic Acid Drug Dev 7(3): 187-95) and in co-owned U.S. Patent Nos. 5,698,685, 5,217,866, 5,142,047, 5,034,506, 5,166,315, 5,185, 444, 5,521,063, and 5,506,337, all of which are expressly incorporated by reference herein.

[00115] Important properties of the morpholino-based subunits include: 1) the ability to be linked in a oligomeric form by stable, uncharged or positively charged backbone linkages; 2) the ability to support a nucleotide base (*e.g.* adenine,

cytosine, guanine, thymidine, uracil and inosine) such that the polymer formed can hybridize with a complementary-base target nucleic acid, including target RNA, Tm values above about 45°C in relatively short oligonucleotides (*e.g.*, 10-15 bases); 3) the ability of the oligonucleotide to be actively or passively transported into mammalian cells; and 4) the ability of the antisense oligonucleotide:RNA heteroduplex to resist RNAse and RNaseH degradation, respectively.

[00116] Exemplary backbone structures for antisense oligonucleotides of the claimed subject matter include the morpholino subunit types shown in Figs. 13D-G, each linked by an uncharged or positively charged, phosphorus-containing subunit linkage. Fig. 13D shows a phosphorus-containing linkage which forms the five atom repeating-unit backbone, where the morpholino rings are linked by a 1-atom phosphoamide linkage. Fig. 13E shows a linkage which produces a 6-atom repeating-unit backbone. In this structure, the atom Y linking the 5' morpholino carbon to the phosphorus group may be sulfur, nitrogen, carbon or, preferably, oxygen. The X moiety pendant from the phosphorus may be fluorine, an alkyl or substituted alkyl, an alkoxy or substituted alkoxy, a thioalkoxy or substituted thioalkoxy, or unsubstituted, monosubstituted, or disubstituted nitrogen, including cyclic structures, such as morpholines or piperidines. Alkyl, alkoxy and thioalkoxy preferably include 1-6 carbon atoms. The Z moieties are sulfur or oxygen, and are preferably oxygen.

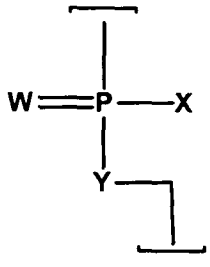
[00117] The linkages shown in Figs. 13F and 13G are designed for 7-atom unit-length bacbones. In structure 13F, the X moiety is as in Structure 13E, and the Y moiety may be methylene, sulfur, or, preferably, oxygen. In Structure 13G, the X and Y moieties are as in Structure 13E. Particularly preferred morpholino oligonucleotides include those composed of morpholino subunit structures of the form shown in Fig. 13E, where X=NH_2, $N(CH_3)_2$, or 1-piperazine or other charged group, Y=O, and Z=O.

[00118] As noted above, the substantially uncharged oligonucleotide may be modified, in accordance with an aspect of the invention, to include charged linkages, *e.g.* up to about 1 per every 2-5 uncharged linkages, such as about 4-5 per every 10 uncharged linkages. Optimal improvement in antisense activity may be seen when about 25% of the backbone linkages are cationic. Suboptimal enhancement is typically seen with a small number e.g., 10-20% cationic linkages,

and where the number of cationic linkages are in the range 50-80%, and typically above about 60%, the sequence specificity of the antisense binding to its target may be compromised or lost.

[00119] The antisense compounds can be prepared by stepwise solid-phase synthesis, employing methods detailed in the references cited above, and below with respect to the synthesis of oligonucleotides having a mixture or uncharged and cationic backbone linkages. In some cases, it may be desirable to add additional chemical moieties to the antisense compound, *e.g.* to enhance pharmacokinetics or to facilitate capture or detection of the compound. Such a moiety may be covalently attached, typically to a terminus of the oligomer, according to standard synthetic methods. For example, addition of a polyethyleneglycol moiety or other hydrophilic polymer, *e.g.*, one having 10-100 monomeric subunits, may be useful in enhancing solubility. One or more charged groups, *e.g.*, anionic charged groups such as an organic acid, may enhance cell uptake. A reporter moiety, such as fluorescein or a radiolabeled group, may be attached for purposes of detection. Alternatively, the reporter label attached to the oligomer may be a ligand, such as an antigen or biotin, capable of binding a labeled antibody or streptavidin. In selecting a moiety for attachment or modification of an antisense compound, it is generally of course desirable to select chemical compounds of groups that are biocompatible and likely to be tolerated by a subject without undesirable side effects.

[00120] As noted above, the antisense compound can be optionally constructed to contain a selected number of cationic linkages interspersed with uncharged linkages of the type described above. The intersubunit linkages, both uncharged and cationic, preferably are phosphorus-containing linkages, having the structure:



where

W is S or O, and is preferably O,

X = NR^1R^2 or OR^6,

Y = O or NR^7,

and each said linkage in the oligomer is selected from:

(a) uncharged linkage (a), where each of R^1, R^2, R^6 and R^7 is independently selected from hydrogen and lower alkyl;

(b1) cationic linkage (b1), where X = NR^1R^2 and Y = O, and NR^1R^2 represents an optionally substituted piperazino group, such that R^1R^2 = -CHRCHRN(R^3)(R^4)CHRCHR-, where

each R is independently H or CH_3,

R^4 is H, CH_3, or an electron pair, and

R^3 is selected from H, lower alkyl, e.g. CH_3, C(=NH)NH_2, Z-L-NHC(=NH)NH_2, and $[C(O)CHR'NH]_mH$, where: Z is C(O) or a direct bond, L is an optional linker up to 18 atoms in length, preferably upt to 12 atoms, and more preferably up to 8 atoms in length, having bonds selected from alkyl, alkoxy, and alkylamino, R' is a side chain of a naturally occurring amino acid or a one- or two-carbon homolog thereof, and m is 1 to 6, preferably 1 to 4;

(b2) cationic linkage (b2), where X = NR^1R^2 and Y = O, R^1 = H or CH_3, and R^2 = $LNR^3R^4R^5$, where L, R^3, and R^4 are as defined above, and R^5 is H, lower alkyl, or lower (alkoxy)alkyl; and

(b3) cationic linkage (b3), where Y = NR^7 and X = OR^6, and R^7 = $LNR^3R^4R^5$, where L, R^3, R^4 and R^5 are as defined above, and R^6 is H or lower alkyl;

and at least one said linkage is selected from cationic linkages (b1), (b2), and (b3).

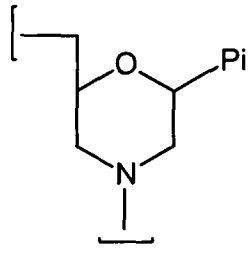
[00121] Preferably, the oligomer includes at least two consecutive linkages of type (a) (i.e. uncharged linkages). In further embodiments, at least 5% of the linkages in the oligomer are cationic linkages (i.e. type (b1), (b2), or (b3)); for example, 10% to 60%, and preferably 20-50% linkages may be cationic linkages.

[00122] In one embodiment, at least one linkage is of type (b1), where, preferably, each R is H, R^4 is H, CH_3, or an electron pair, and R^3 is selected from H, lower alkyl, e.g. CH_3, C(=NH)NH_2, and C(O)-L-NHC(=NH)NH_2. The latter two embodiments of R^3 provide a guanidino moiety, either attached directly to the piperazine ring, or pendant to a linker group L, respectively. For ease of synthesis, the variable Z in R^3 is preferably C(O) (carbonyl), as shown.

[00123] The linker group L, as noted above, contains bonds in its backbone selected from alkyl (e.g. -CH_2-CH_2-), alkoxy (-C-O-), and alkylamino (e.g. -

CH_2-NH-), with the proviso that the terminal atoms in L (e.g., those adjacent to carbonyl or nitrogen) are carbon atoms. Although branched linkages (e.g. -CH_2-$CHCH_3$-) are possible, the linker is preferably unbranched. In one embodiment, the linker is a hydrocarbon linker. Such a linker may have the structure -$(CH_2)_n$-, where n is 1-12, preferably 2-8, and more preferably 2-6.

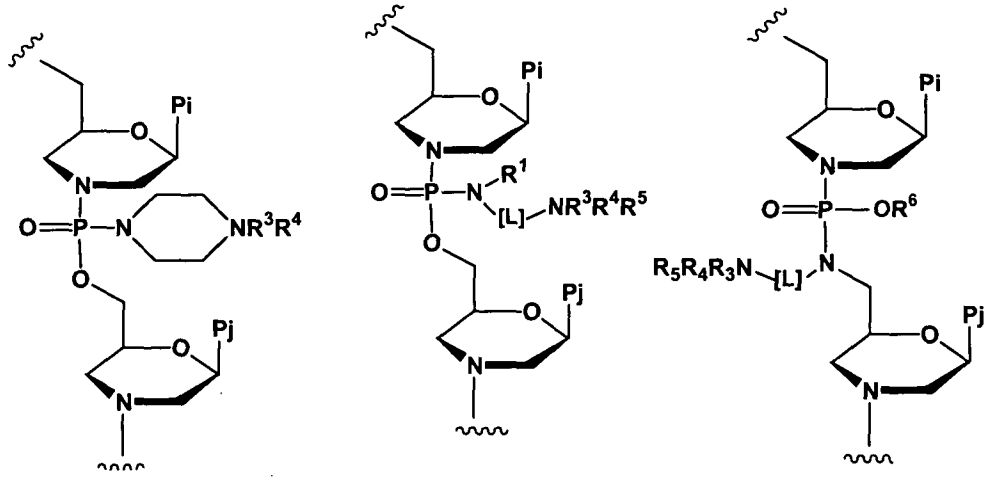
[00124] The morpholino subunits have the structure:



(i)

where Pi is a base-pairing moiety, and the linkages depicted above connect the nitrogen atom of (i) to the 5' carbon of an adjacent subunit. The base-pairing moieties Pi may be the same or different, and are generally designed to provide a sequence which binds to a target nucleic acid.

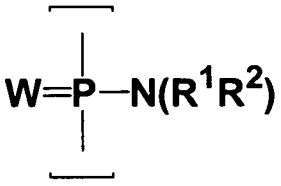
[00125] The use of embodiments of linkage types (b1), (b2) and (b3) above to link morpholino subunits may be illustrated graphically as follows:



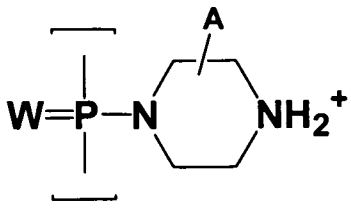
(b1) (b2) (b3)

[00126] Preferably, all cationic linkages in the oligomer are of the same type; i.e. all of type (b1), all of type (b2), or all of type (b3).

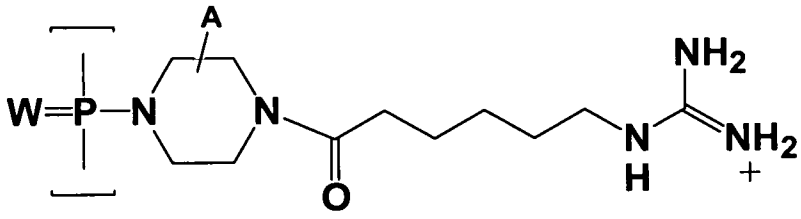
[00127] In further embodiments, the cationic linkages are selected from linkages (b1') and (b1") as shown below, where (b1") is referred to herein as a "Pip" linkage and (b1") is referred to herein as a "GuX" linkage:



(a)



(b1')



(b1")

[00128] In the structures above, W is S or O, and is preferably O; each of R^1 and R^2 is independently selected from hydrogen and lower alkyl, and is preferably methyl; and A represents hydrogen or a non-interfering substituent on one or more carbon atoms in (b1') and (b1"). Preferably, the ring carbons in the piperazine ring are unsubstituted; however, they may include non-interfering substituents, such as methyl or fluorine. Preferably, at most one or two carbon atoms is so substituted.

[00129] In further embodiments, at least 10% of the linkages are of type (b1') or (b1"); for example, 10%-60% and preferably 20% to 50%, of the linkages may be of type (b1') or (b1").

[00130] In other embodiments, the oligomer contains no linkages of the type (b1') above. Alternatively, the oligomer contains no linkages of type (b1) where each R is H, R^3 is H or CH_3, and R^4 is H, CH_3, or an electron pair.

[00131] The morpholino subunits may also be linked by non-phosphorus-based intersubunit linkages, as described further below, where at least one linkage is modified with a pendant cationic group as described above.

[00132] Other oligonucleotide analog linkages which are uncharged in their unmodified state but which could also bear a pendant amine substituent could be used. For example, a 5'nitrogen atom on a morpholino ring could be employed in a sulfamide linkage or a urea linkage (where phosphorus is replaced with carbon or sulfur, respectively) and modified in a manner analogous to the 5'-nitrogen atom in structure (b3) above.

[00133] Oligomers having any number of cationic linkages are provided, including fully cationic-linked oligomers. Preferably, however, the oligomers are uncharged or partially charged, having, for example, 10%-80%. In preferred embodiments, about 10% to 60%, and preferably 20% to 50% of the linkages are cationic.

[00134] In one embodiment, the cationic linkages are interspersed along the backbone. The partially charged oligomers preferably contain at least two consecutive uncharged linkages; that is, the oligomer preferably does not have a strictly alternating pattern along its entire length.

[00135] Also considered are oligomers having blocks of cationic linkages and blocks of uncharged linkages; for example, a central block of uncharged linkages may be flanked by blocks of cationic linkages, or vice versa. In one embodiment, the oligomer has approximately equal-length 5', 3' and center regions, and the percentage of cationic linkages in the center region is greater than about 50%, preferably greater than about 70%.

[00136] Oligomers for use in antisense applications generally range in length from about 10 to about 40 subunits, more preferably about 10 to 30 subunits, and typically 15-25 bases. For example, an oligomer of the invention having 19-20 subunits, a useful length for an antisense compound, may ideally have two to ten, e.g. four to eight, cationic linkages, and the remainder uncharged linkages. An oligomer having 14-15 subunits may ideally have two to five, e.g. 3 or 7, cationic linkages and the remainder uncharged linkages.

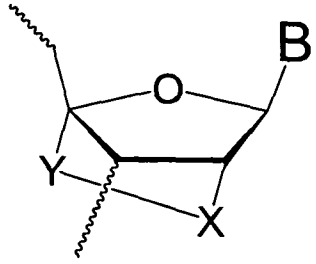
[00137] Each morpholino ring structure supports a base pairing moiety, to form a sequence of base pairing moieties which is typically designed to hybridize to a selected antisense target in a cell or in a subject being treated. The base pairing moiety may be a purine or pyrimidine found in native DNA or RNA (A, G, C, T, or U) or an analog, such as hypoxanthine (the base component of the nucleoside inosine) or 5-methyl cytosine.

VB. Locked Nucleic Acids as SSOs

[00138] Another preferred chemistry appropriate for SSOs is provided by locked nucleic acids (LNA) (Koshkin, A.A., et al., 1998, Tetrahedron 54:3607; Obika, S., et al., 1998, Tetrahedron Lett. 39:5401). As used herein, the terms "LNA unit", "LNA monomer", "LNA residue", "locked nucleic acid unit", "locked nucleic acid monomer" or "locked nucleic acid residue", refer to a bicyclic nucleoside analogue.

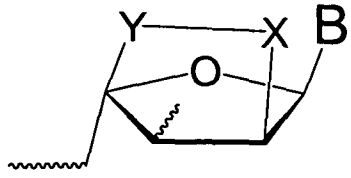
LNA units and methods of their synthesis are described in *inter alia* WO 99/14226, WO 00/56746, WO 00/56748, WO 01/25248, WO 02/28875, WO 03/006475 and WO 03/095467. The LNA unit can also be defined with respect to its chemical formula. Thus, an "LNA unit", as used herein, has the chemical structure shown in Formula 1 below:

Formula 1



1A

or



1B

wherein,

X is selected from the group consisting of O, S and NRH, where R is H or C_1-C_4-alkyl;

Y is $(-CH_2)_r$, where r is an integer of 1-4; and

B is a base of natural or non-natural origin as described above.

[00139] In a preferred embodiment, r is 1 or 2, and in a more preferred embodiment r is 1.

[00140] When LNA nucleotides are employed in an SSO it is preferred that non-LNA nucleotides also be present. LNA nucleotides have such high affinities of hybridization that there can be significant non-specific binding, which may reduce the effective concentration of the free-SSO. When LNA nucleotides are used they can be alternated conveniently with 2'-deoxynucleotides. The pattern of alternation is not critical. Alternating nucleotides, alternating dinucleotides or mixed patterns, e.g., LDLDLD or LLDLLD or LDDLDD can be used. For example, one embodiment contains a sequence of nucleotides selected from the group consisting of: LdLddLLddLdLdLL, LdLdLLLddLLLdLL, LMLMMLLMMLMLMLL, LMLMLLLMMLLLMLL, LFLFFLLFFLFLFLL, LFLFLLLFFLLLFLL, LddLddLddL, dLddLddLdd, ddLddLddLd, LMMLMMLMML, MLMMLMMLMM, MMLMMLMMLM, LFFLFFLFFL, FLFFLFFLFF, FFLFFLFFLF, dLdLdLdLdL, LdLdLdLdL, MLMLMLMLML, LMLMLMLML, FLFLFLFLFL, LFLFLFLFL, where L is a LNA unit, d is a DNA unit, M is 2'MOE, F is 2'fluoro.

[00141] When 2'-deoxynucleotides or 2'-deoxynucleoside phosphorothioates are mixed with LNA nucleotides it is important to avoid RNase H activation. It is expected that between about one third and two thirds of the LNA nucleotides of an SSO will be suitable to avoid RNase H activation. When affinity-enhancing modifications are used, including but not limited to LNA or G-clamp nucleotides, the skilled person will recognize that it can be necessary to increase the proportion of such affinity-enhancing modifications.

[00142] Numerous additional examples of alternative chemistries which do not activate RNase H are available. For example, suitable SSOs can be oligonucleotides wherein at least one of the internucleotide bridging phosphate residues is a modified phosphate, such as methyl phosphonate, methyl phosphonothioate, phosphoromorpholidate, phosphoropiperazidate, and phosphoroamidate. For example, every other one of the internucleotide bridging phosphate residues can be modified as described. In another non-limiting example, such SSOs are oligonucleotides wherein at least one of the nucleotides contains a 2' lower alkyl moiety (e.g., C_1-C_4, linear or branched, saturated or unsaturated alkyl, such as methyl, ethyl, ethenyl, propyl, 1-propenyl, 2-propenyl, and isopropyl). For example, every other one of the nucleotides can be modified as described. (See references in U.S. Pat. 5,976,879 col. 4). For *in vivo* use, phosphorothioate linkages are preferred.

[00143] The length of the SSO will be from about 8 to about 30 bases in length. Those skilled in the art appreciate that when affinity-increasing chemical modifications are used, the SSO can be shorter and still retain specificity. Those skilled in the art will further appreciate that an upper limit on the size of the SSO is imposed by the need to maintain specific recognition of the target sequence, and to avoid secondary-structure forming self-hybridization of the SSO and by the need to enter the cell. These limitations imply that an SSO of increasing length (above and beyond a certain length which will depend on the affinity of the SSO) will be more frequently found to be less specific, inactive or poorly active.

VC. Chemical modifications and conjugates of SSOs

[00144] SSOs of the invention include, but are not limited to, modifications of the SSO involving chemically linking to the SSO one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the SSO. Such moieties include, but are not limited to, peptides, lipid

moieties such as a cholesterol moiety, cholic acid, a thioether, e.g. hexyl-S-tritylthiol, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipids, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, an adamantane acetic acid, a palmityl moiety, an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety.

[00145] A preferred chemical modification of SSO includes an oligonucleotide moiety conjugated to an arginine-rich peptide transport moiety effective to enhance transport of the compound into cells. The transport moiety is preferably attached to a terminus of the oligomer, as shown, for example, in Figures 13B and 13C. The peptide transport moiety preferably comprises 6 to 16 subunits selected from X' subunits, Y' subunits, and Z' subunits,

where

(a) each X' subunit independently represents lysine, arginine or an arginine analog, said analog being a cationic α-amino acid comprising a side chain of the structure $R^1N=C(NH_2)R^2$, where R^1 is H or R; R^2 is R, NH_2, NHR, or NR_2, where R is lower alkyl or lower alkenyl and may further include oxygen or nitrogen; R^1 and R^2 may together form a ring; and the side chain is linked to said amino acid via R^1 or R^2;

(b) each Y' subunit independently represents a neutral amino acid -C(O)-$(CHR)_n$-NH-, where n is 2 to 7 and each R is independently H or methyl; and

(c) each Z' subunit independently represents an α-amino acid having a neutral aralkyl side chain;

wherein the peptide comprises a sequence represented by one of $(X'Y'X')_p$, $(X'Y')_m$, and $(X'Z'Z')_p$, where p is 2 to 5 and m is 2 to 8.

[00146] In selected embodiments, for each X', the side chain moiety is guanidyl, as in the amino acid subunit arginine (Arg). In further embodiments, each Y' is -CO-$(CH_2)_n$-CHR-NH-, where n is 2 to 7 and R is H. For example, when n is 5 and R is H, Y' is a 6-aminohexanoic acid subunit, abbreviated herein as Ahx; when n is 2 and R is H, Y' is a β-alanine subunit, abbreviated herein as B.

[00147] Preferred peptides of this type include those comprising arginine dimers alternating with single Y' subunits, where Y' is preferably Ahx. Examples include peptides having the formula $(RY'R)_p$ or the formula $(RRY')_p$, where Y' is

preferably Ahx. In one embodiment, Y' is a 6-aminohexanoic acid subunit, R is arginine and p is 4.

[00148] In a further embodiment, each Z' is phenylalanine, and m is 3 or 4.

[00149] The conjugated peptide is preferably linked to a terminus of the oligomer via a linker Ahx-B, where Ahx is a 6-aminohexanoic acid subunit and B is a β-alanine subunit, as shown, for example, in Figs. 13B and 13C.

[00150] In selected embodiments, for each X', the side chain moiety is independently selected from the group consisting of guanidyl ($HN=C(NH_2)NH$-), amidinyl ($HN=C(NH_2)C<$), 2-aminodihydropyrimidyl, 2-aminotetrahydropyrimidyl, 2-aminopyridinyl, and 2-aminopyrimidonyl, and it is preferably selected from guanidyl and amidinyl . In one embodiment, the side chain moiety is guanidyl, as in the amino acid subunit arginine (Arg).

[00151] The Y' subunits are either contiguous, in that no X' subunits intervene between Y' subunits, or interspersed singly between X' subunits. However, the linking subunit may be between Y' subunits. In one embodiment, the Y' subunits are at a terminus of the transporter; in other embodiments, they are flanked by X' subunits. In further preferred embodiments, each Y' is $-CO-(CH_2)_n-CHR-NH-$, where n is 2 to 7 and R is H. For example, when n is 5 and R is H, Y' is a 6-aminohexanoic acid subunit, abbreviated herein as Ahx. In selected embodiments of this group, each X' comprises a guanidyl side chain moiety, as in an arginine subunit. Preferred peptides of this type include those comprising arginine dimers alternating with single Y' subunits, where Y' is preferably Ahx. Examples include peptides having the formula $(RY'R)_4$ or the formula $(RRY')_4$, where Y' is preferably Ahx. In the latter case, the nucleic acid analog is preferably linked to a terminal Y' subunit, preferably at the C-terminus, as shown, for example, in Figs. 13B and 13C. The preferred linker is of the structure AhxB, where Ahx is a 6-aminohexanoic acid subunit and B is a β-alanine subunit.

[00152] The transport moieties as described above have been shown to greatly enhance cell entry of attached oligomers, relative to uptake of the oligomer in the absence of the attached transport moiety, and relative to uptake by an attached transport moiety lacking the hydrophobic subunits Y'. Such enhanced uptake is preferably evidenced by at least a two-fold increase, and preferably a four-fold

increase, in the uptake of the compound into mammalian cells relative to uptake of the agent by an attached transport moiety lacking the hydrophobic subunits Y'. Uptake is preferably enhanced at least twenty fold, and more preferably forty fold, relative to the unconjugated compound.

[00153] A further benefit of the transport moiety is its expected ability to stabilize a duplex between an antisense compound and its target nucleic acid sequence, presumably by virtue of electrostatic interaction between the positively charged transport moiety and the negatively charged nucleic acid. The number of charged subunits in the transporter is less than 14, as noted above, and preferably between 8 and 11, since too high a number of charged subunits may lead to a reduction in sequence specificity.

[00154] The use of arginine-rich peptide transporters (i.e., cell-penetrating peptides) are particulary useful in practicing the present invention. Certain peptide transporters have been shown to be highly effective at delivery of antisense compounds into primary leukocytes (Marshall, N. B., S. K. Oda, et al. (2007) J. Immunological Methods 325(1-2): 114-126). Furthermore, compared to other known peptide transporters such as Penetratin, the peptide transporters described herein, when conjugated to an antisense PMO, demonstrate an enhanced ability to alter splicing of several gene transcripts (Marshall, N. B., S. K. Oda, et al. (2007) J. Immunological Methods 325(1-2): 114-126). Especially preferred are the P007 and CPO6062 transport peptides listed below in Table 3 (SEQ ID NOS: 62 and 53, respectively).

[00155] Exemplary peptide transporters, including linkers (B or AhxB) are given below in Table 1. Preferred sequences are those designated P007 (SEQ ID NO: 62) and CPO6020 (SEQ ID NO: 53). Also preferred, in the present invention, are the peptide transporters identified as SEQ ID NOS: 48-50. As described in Example 4, these peptides showed superior delivery to mammary (SEQ ID NOS:56-58) and ovary (SEQ ID NO:58) tissues and may prove valuable when cancerous tissues derived from those tissues are targeted with the SSO of the present invention.

Table 1. Exemplary Peptide Transporters for Intracellular Delivery of PMO

Peptide	Sequence (N-terminal to C-terminal)	SEQ ID
R_8XB	RRRRRRRR-XB	52
$(RXRRBR)_2XB$	RXRRBRRXRRBR-XB	53
$(RXR)_3RBR$-XB	RXRRXRRXRRBR-XB	54
$(RB)_5RXRBRX$-B	RBRBRBRBRBRXRBRX-B	55
$(RBRBRBRX)_2X$	RBRBRBRXRBRBRBRX-X	56
X-$(RB)_3RX(RB)_3RX$	XRBRBRBRXRBRBRBR-X	57
$(RBRX)_4B$	RBRXRBRXRBRXRBRX-B	58
$(RB)_4(RX)_4B$	RBRBRBRBRXRXRXRX-B	59
$RX(RB)_2RX(RB)_3RX$-X	RXRBRBRXRBRBRBRX	60
$(rXr)_4$	rXrrXrrXrrXr-XB	61
$(RAhxR)_4AhxB$	RAhxRRAhxRRAhxRRAhxRAhxB	62
$(RRAhx)_4B$	RRAhxRRAhxRRAhxRRAhxB	63
$(AhxRR)_4AhxB$	AhxRRAhxRRAhxRRAhxRRAhxB	64
$(RAhx)_6B$	RAhxRAhxRAhxRAhxRAhxRAhxB	65
$(RAhx)_8B$	RAhxRAhxRAhxRAhxRAhxRAhxRAhxB	66
$(RAhxR)_3AhxB$	RAhxRRAhxRRAhxR AhxB	67

[00156] It is not necessary for all positions in a given SSO to be uniformly modified, and in fact more than one of the aforementioned modifications can be incorporated in a single compound or even at a single nucleoside within an SSO.

[00157] The SSOs can be admixed, encapsulated, conjugated, or otherwise associated with other molecules, molecule structures, or mixtures of compounds, as for example liposomes, receptor targeted molecules, oral, rectal, topical or other formulation, for assisting in uptake, distribution, and/or absorption.

[00158] Those skilled in the art appreciate that cellular differentiation includes, but is not limited to, differentiation of the spliceosome. Accordingly, the activity of any particular SSO can depend upon the cell type into which they are introduced. For example, SSOs which are effective in one cell type can be ineffective in another cell type.

VD. Methods and Applications of the SSOs

[00159] The methods, oligonucleotides, and formulations of the present invention are also useful as *in vitro* or *in vivo* tools to examine splicing in human or animal genes. Such methods can be carried out by the procedures described herein, or modifications thereof which will be apparent to skilled persons.

[00160] The SSOs disclosed herein can be used to treat any condition in which the medical practitioner intends to induce apoptosis in cells, or inhibit the proliferation of cells, or inhibit the signaling pathway activated by an EGFR, particularly HER2. In particular, the invention can be used to treat a proliferative disease or condition. In one embodiment, the condition is a cancer. In another embodiment, the disease is pulmonary fibrosis. In one embodiment, the condition is a cancer selected from the group consisting of breast, lung, ovarian, gastric and colon cancer. In one embodiment, the condition is a cancer which is resistant to chemotherapy.

[00161] The uses of the present invention include, but are not limited to, treatment of diseases for which known HER2 antagonists such as Herceptin, Herstatin and pertuzumab, have been shown useful.

[00162] The administration of the SSO to subjects can be accomplished using procedures developed for the administration of ASONs. ASONs have been successfully administered to experimental animals and human subjects by intravenous administration in saline in doses as high as 6 mg/kg three times a week (Yacysyhn, B.R., et al., 2002, Gut 51:30 (anti-ICAM-1 ASON for treatment of Crohn's disease); Stevenson, J., et al., 1999, J. Clinical Oncology 17:2227 (anti-RAF-1 ASON targeted to PBMC)). The pharmacokinetics of 2'O-MOE phosphorothioate ASON, directed towards TNF-α has been reported (Geary, R.S., et al., 2003, Drug Metabolism and Disposition 31:1419). The systemic efficacy of mixed LNA/DNA molecules has also been reported (Fluiter, K., et al., 2003, Nucleic Acids Res. 31:953).

[00163] The systemic activity of SSOs in a mouse model system was investigated using 2'O-MOE phosphorothioates, PMO and PNA chemistries. Significant activity was observed in all tissues investigated except brain, stomach and dermis (Sazani, P., et al., 2002, Nature Biotechnology 20, 1228).

[00164] In general any method of administration that is useful in conventional antisense treatments can be used to administer the SSOs of the

invention. For testing of the SSO in cultured cells, any of the techniques that have been developed to test ASONs or SSOs can be used.

[00165] Formulations of the present invention comprise SSOs in a physiologically or pharmaceutically acceptable carrier, such as an aqueous carrier. Thus formulations for use in the present invention include, but are not limited to, those suitable for parenteral administration including intraperitoneal, intraarticular, intravenous, intraarterial, subcutaneous, or intramuscular injection or infusion, as well as those suitable for topical, ophthalmic, vaginal, oral, rectal or pulmonary (including inhalation or insufflation of powders or aerosols, including by nebulizer, intratracheal, intranasal delivery) administration. The formulations can conveniently be presented in unit dosage form and can be prepared by any of the methods well known in the art. The most suitable route of administration in any given case can depend upon the subject, the nature and severity of the condition being treated, and the particular active compound which is being used.

[00166] Pharmaceutical compositions of the present invention include, but are not limited to, physiologically and pharmaceutically acceptable salts, i.e, salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological properties. Examples of such salts are (a) salts formed with cations such as sodium, potassium, NH_4^+, magnesium, calcium, polyamines such as spermine and spermidine; (b) acid addition salts formed with inorganic acids, for example, hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid and the like; and (c) salts formed with organic acids such as, for example, acetic acid, oxalic acid, tartaric acid, succinic acid, maleic acid, fumaric acid, gluconic acid, citric acid, malic acid, ascorbic acid, benzoic acid, palmitic acid, alginic acid, polyglutamic acid, napthalenesulfonic acid, methanesulfonic acid, p-toluenesulfonic acid, napthalenedisulfonic acid, polygalacturonic acid, and the like.

[00167] The present invention provides for the use of SSOs having the characteristics set forth above for the preparation of a medicament for increasing the ratio of a mammalian soluble form of either HER-2 or HER-3 to its corresponding membrane bound form, in a patient afflicted with a proliferative disorder, as discussed above. In the manufacture of a medicament according to the invention, the SSOs are typically admixed with, inter alia, an acceptable carrier. The carrier must, of course, be acceptable in the sense of being compatible with any other ingredients in the formulation and must not be deleterious to the patient. The carrier

can be a solid or liquid. SSOs are incorporated in the formulations of the invention, which can be prepared by any of the well known techniques of pharmacy consisting essentially of admixing the components, optionally including one or more accessory therapeutic ingredients.

[00168] Formulations of the present invention can comprise sterile aqueous and non-aqueous injection solutions of the active compounds, which preparations are preferably isotonic with the blood of the intended recipient and essentially pyrogen free. These preparations can contain anti-oxidants, buffers, bacteriostats, and solutes which render the formulation isotonic with the blood of the intended recipient. Aqueous and non-aqueous sterile suspensions can include, but are not limited to, suspending agents and thickening agents. The formulations can be presented in unit dose or multi-dose containers, for example, sealed ampoules and vials, and can be stored in freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carrier, for example, saline or water-for-injection immediately prior to use.

[00169] In the formulation the SSOs can be contained within a particle or vesicle, such as a liposome, or microcrystal, which can be suitable for parenteral administration. The particles can be of any suitable structure, such as unilamellar or plurilameller, so long as the SSOs are contained therein. Positively charged lipids such as N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethyl-ammoniummethylsulfate, or "DOTAP," are particularly preferred for such particles and vesicles. The preparation of such lipid particles is well known. [See references in U.S. Pat. 5,976,879 col. 6]

[00170] The SSO can be targeted to any element or combination of elements that regulate splicing, including the 3' splice site, the 5' splice site, the branch point, the polypyrimidine tract, exonic splicing enhancers, exonic splicing silencers, intronic splicing enhancers, and intronic splicing silencers.

[00171] Those skilled in the art can appreciate that the invention as directed toward human HER2 can be practiced using SSOs having a sequence that is complementary to at least 8, to at least 9, to at least 10, to at least 11, to at least 12, to at least 13, to at least 14, to at least 15, preferably between 10 and 20 nucleotides of the portions of the human HER2 gene comprising exon 15 and its adjacent introns. SEQ ID No: 15 contains the sequence of exon 15 of human HER2 and 50 adjacent nucleotides of the flanking introns. For example, SSOs targeted to human HER2 can have a sequence selected from the sequences with splice-

switching activity listed in Table 2. SSO that target (i.e., are complementary to) exon and adjacent intron regions of Exon 15 in the HER2 pre-mRNA (SEQ ID NO: 15) are useful in practicing the invention. More preferred are SSOs that target the HER2 pre-mRNA in the vicinity of the Exon 15 splice donor and splice acceptor junctions. These target sequence regions are defined as 50 nucleotides upstream (i.e., 5') and downstream (i.e., 3') of the splice acceptor and splice donor junctions (SEQ ID NOS: 44 and 45, respectively).

[00172] Those skilled in the art can appreciate that the invention as directed toward human HER3 can be practiced using SSOs having a sequence that is complementary to at least 8, to at least 9, to at least 10, to at least 11, to at least 12, to at least 13, to at least 14, to at least 15, preferably between 10 and 20 nucleotides of the portions of the human HER3 gene comprising exons 13, 14 and 15 and its adjacent introns, as well as the region containing the polyadenylation signal in exon 28. SEQ ID No: 16 contains the human HER3 sequence of exons13 through 15 including the intervening introns and 50 adjacent nucleotides of the flanking introns. SEQ ID No: 17 contains the sequence of the region containing the polyadenylation signal in exon 28 of human HER3. For example, SSOs targeted to human HER3 can have a sequence selected from the sequences with splice-switching activity listed in Table 3. SSO that target (i.e., are complementary to) exon and adjacent intron regions of HER3 pre-mRNA in the vicinity of Exons 13, 14 and 15 (SEQ ID NO: 16) are useful in practicing the invention. More preferred are SSOs that target the HER3 pre-mRNA in the vicinity of the Exon 13, 14 and 15 splice donor and splice acceptor junctions. These preferred target sequence regions are defined as 50 nucleotides upstream (i.e., 5') and downstream (i.e., 3') of the splice acceptor and splice donor junctions (SEQ ID NOS: 46 to 51, respectively).

[00173] When affinity-enhancing modifications are used, including but not limited to LNA or G-clamp nucleotides, the skilled person recognizes the length of the SSO can be correspondingly reduced. The pattern of alternation of LNA and conventional nucleotides is not important.

[00174] Those skilled in the art will also recognize that the selection of SSO sequences must be made with care to avoid a self-complementary SSO, which may lead to the formation of partial "hairpin" duplex structures. In addition, high GC content should be avoided to minimize the possibility of non-specific base pairing.

Furthermore, SSOs matching off-target genes, as revealed for example by BLAST, should also be avoided.

[00175] In some situations, it can be preferred to select an SSO sequence that can target a human and at least one other species. These SSOs can be used to test and to optimize them in the other species before being used in humans, thereby being useful for regulatory approval and drug development purposes.

[00176] It will be appreciated by those skilled in the art that various omissions, additions and modifications may be made to the invention described above without departing from the scope of the invention, and all such modifications and changes are intended to fall within the scope of the invention, as defined by the appended claims. All references, sequence citations, patents, patent applications or other documents cited are herein incorporated by reference.

Example 1

Materials and Methods

[00177] *Cell culture and transfections*: SK-BR-3 cells were maintained in McCoy's 5A media supplemented with 10% fetal bovine serum. MCF-7 cells were maintained in modified essential media supplemented with 10% fetal bovine serum, 1 mM sodium pyruvate, and 0.1 mM nonessential amino acids. For transfection, treatment, the cells were plated either in 2 mL of media in 6-well plates at a density of 2×10^5 cells/well, or in 1 mL of media in 24-well plates at a density of 1×10^5 cells/well and transfected 24 hours later. Oligonucleotides were complexed, at the indicated concentrations, with Lipofectamine™ 2000 (Invitrogen), and the cationic lipid complexes were applied to the cells according to the manufacturer's directions.

[00178] *RT-PCR*: Total RNA was isolated 24 hours after transfection, by harvesting the cells in 800 μL of TRI-reagent (Molecular Research Center, Inc.). Approximately 200 ng of RNA was used per reaction with r*Tth* enzyme (PerkinElmer Life Sciences) in the presence of 0.02mM Cy5-AP3-dCTP (GE Healthcare) and forward and reverse primers flanking the targeted mRNA region. The reaction mixture was incubated at 70°C, 15min for the RT step followed by PCR: 95°C, 3 min, 1 cycle; 22 cycles of 95°C for 30 sec, 56 °C for 30 sec, 72°C for 1 min; and final extension at 72°C for 7 min. The PCR products were separated on a 10% pre-cast TBE-Urea polyacrylamide gel (Invitrogen), and bands were visualized on Typhoon™

Variable Mode Imager (GE Healthcare). The density of the bands was quantified with ImageQuant™ software (GE Healthcare).

[00179] *Cell viability assay*: Cell viability post oligo treatment was measured by CellTiter 96® AQ_{ueous} One Solution Cell Proliferation Assay (Promega). Cells (~2×10^4/well) were plated in 96-well plates. On the next day, cells were transfected with 100 nM of the indicated SSOs. After 48 hours, CellTiter 96® AQ_{ueous} One Solution reagent was added into each well of the 96-well plate. The plate was incubated at 37°C for 1-4 hours. The absorbance was recorded at 490nm using a 96-well plate reader. Cell viability was normalized to untreated cells.

[00180] *PARP cleavage assay*: Cells were plated in 6-well lates and transfected with the designated SSOs. After 48 hours, cells were harvested in RIPA buffer (radioimmune precipitation assay buffer; 50 mM Tris-HCl, 150 mM NaCl, 5mM EDTA, 1% Triton X-100, 0.1% SDS, and 1% sodium deoxycholate) (Sigma) and a mixture of protease inhibitors (Sigma). Total protein (20 μg) was electrophoresed on a 4-12% NuPAGE Novex Bis-Tris gel (Invitrogen) and electrotransferred to polyvinylidene difluoride (PVDF) membranes (Invitrogen). Membranes were blocked for 30 min with StartingBlock (PBS) blocking buffer (Pierce) and incubated overnight at 4°C with mouse PARP monoclonal antibody (1:10,000 dilution; Invitrogen), followed by 2-hour incubation with horseradish peroxidase-conjugated anti-mouse (1:100,000; Invitrogen) secondary antibodies. Blots were developed with ECL Plus™ reagents (GE Healthcare) and exposed to Kodak film. Full-length and cleaved PARP proteins migrated at ~116 and 85 kDa, respectively.

[00181] *Plasmid constructs and purification of Δ15HER2-His protein*: The Δ15HER2 sequence was reverse-transcribed and amplified from the total RNA isolated from SK-BR-3 cells treated with SSO111. The forward and reverse primers used were CACCATGGAGCTGGCGGCCT (SEQ ID NO: 68) and TCCAGGTCCACACAGCGGTCC (SEQ ID NO: 69), respectively. The Δ15HER2 sequence was cloned into the pcDNA™3.1, a directional TOPO expression vector (Invitrogen), which encodes six histidine residues at the carboxy terminus of the expressed protein. The Δ15HER2-His expression plasmid was transfected into MCF-7 cells with Lipofectamine™ 2000 (Invitrogen) in serum-free medium. After 48 hours, the medium was collected, concentrated, purified with HisPur™ Cobalt spin

columns (Pierce), and desalted using Zeba™ Desalt spin columns to yield the soluble Δ15HER2-His protein. Purity of the protein was confirmed by SDS-PAGE, and the yield was determined by Bradford Assay. Inhibition of SK-BR-3 cell growth by the Δ15HER2-His protein was evaluated by plating cells at ~$2X10^4$ cells/well in 96 well plates for 24 hours, and then treated with 60, 120 or 240 nM Δ15HER2-His protein for 72 hours. Cell viability was normalized to mock-treated cells and analyzed using CellTiter 96® Aqueous Solution reagent (Promega).

[00182] *Western blots*: Transfected cells were harvested 48 hours post transfection (or at the indicated time points) in RIPA buffer (radioimmune precipitation assay buffer 50mM Tris-HCl, 150mM NaCl, 5 mM EDTA, 1% Triton X-100, 0.1% SDS, and 1% sodium deoxycholate) (Sigma) and a mixture of protease inhibitors (Sigma). Total protein (20 μg for PARP, β-actin, HER2, p-HER2, HER3 and p-HER3) from the cells was electrophoresed on a 4-10% pre-cast Bis-Tris gel (Invitrogen) and electrotransferred to polyvinylidene difluoride membranes. Membranes were blocked for 30 min in StartingBlock (PBS) blocking buffer (Pierce) and incubated overnight at 4°C with rabbit anti-erbB2 polyclonal antibody (1:1000 dilution; Abcam), rabbit anti-erbB3 polyclonal antibody (1:1000 dilution; Abcam), rabbit phospho-HER2/erbB2 (Tyr877) polyclonal antibody (1:4000 dilution; Cell Signaling), rabbit phospho-HER3/erbB3 (Tyr1289) monoclonal antibody (1:4000 dilution; Cell Signaling), or mouse anti-PARP monoclonal antibody (1:1000 dilution; Invitrogen), followed by 1-hour incubation with horseradish peroxidase-conjugated anti-rabbit (1:100,000 dilution; Abcam) or anti-mouse (1:100,000 dilution; Invitrogen) secondary antibodies. Blots were developed with ECL™ Plus reagents (GE Healthcare) and exposed to Kodak film. HER2, HER3, full-length PARP, cleaved PARP, and β-actin migrated at ~180, 185, 116, 85, 42 kDa, respectively. β-actin was used as a loading control.

Example 2

HER2 Splice Variants

[00183] Exemplary splice switching oligonucleotides (SSOs) containing phosphorothioate internucleotide bonds and targeted to regions of human HER2 pre-mRNA (**Fig. 1**, Table 2) were synthesized.

Table 2: Splice switching Oligonucleotides Targeted to HER2

SEQ ID.	Name	Sequence (5'-3')	Modification	Activity
18	106	ggg cag aaa aga ttt gtg gg	2'-OMe, PS	+
19	107	cac act ggt cag cct cct gg	2'-OMe, PS	+
20	108	gcc aca cac tgg tca gcc tc	2'-OMe, PS	+
21	109	ctc acg agt ggg tgc agt tg	2'-OMe, PS	+
22	110	gtt gga ctc acg agt ggg tg	2'-OMe, PS	+
23	111	gac cgt tgg act cac gag tg	2'-OMe, PS	+
24	M111	gac cgt tgg act cac gag tg	MOE, PS	+
25	L111	CgTtGgAcTcAcGaGt	Upper case: LNA; lower case: deoxyribose, PS	+

2'-OMe, 2'-O-methyl oligoribonucleotide; MOE, 2'-O-methoxyethyl oligoribonucleotide; LNA, locked nucleic acid oligonucleotide; PS, phosphorothioate internucleotide linkage.

[00184] These oligonucleotides were transfected into SK-BR-3 human breast cancer cells with the cationic transfection reagent Lipofectamine™ 2000 (Invitrogen) as per the manufacturer's directions. After 24 hours, the total RNA was collected and RT-PCR was used to determine the ratio of HER2 lacking exon 15 (sHER2) and full length HER2 (mHER2) mRNA.

[00185] As shown in **Fig. 2** and **Fig. 3** these SSOs, especially SSO111, (SEQ ID NO. 23) caused skipping of exon 15, leading to reduced levels of mHER2 mRNA and increased levels of sHER2 mRNA. This same sequence was also effective at skipping exon 15 in a dose dependant manner, when synthesized as a 2'-OMe (SEQ ID NO. 23), an MOE (SEQ ID NO. 24) or an LNA (SEQ ID NO. 25) oligomer (**Fig. 3**).

[00186] SSO111 (SEQ ID NO. 23) was transfected into SK-BR-3 human breast cancer cells with the cationic transfection reagent Lipofectamine™ 2000 (Invitrogen) as per the manufacturer's directions. After 48 hours, cells were collected in RIPA lysis buffer (Sigma) and the lysates were analyzed by western blot for poly (ADP ribose) polymerase (PARP) cleavage and mHER2 protein expression (**Fig. 4**). PARP is involved with DNA repair and is cleaved by caspases early in apoptosis. Therefore, PARP cleavage is indicative of apoptosis. The SSO111-induced upregulation of sHER2 protein caused the induction of poly(ADP ribose) polymerase (PARP) cleavage, an apoptotic marker, in transfected SK-BR-3 cells (**Fig. 4A**), and a simultaneous downregulation of mHER2 protein (**Fig. 4B**).

[00187] The cDNA encoding Δ15HER2 (sHER2) was cloned into a mammalian expression vector, which was then transfected into and expressed in MCF-7 cells. After 48 hours, cell lysates and concentrated extracellular media were

collected and analyzed by western blot for the presence of HER2 isoforms. Unglycosylated (~64 kDa) and glycosylated (~80 kDa) sHER2 protein was detected only in sHER2 plasmid transfected cells, in the lysate (Lysate) and extracellular media (Media), respectively (**Fig. 5**). As shown in **Fig. 5**, the sHER2 protein was produced, processed and secreted from cells.

[00188] The extracellular media from the MCF-7 cells expressing sHER2 was transferred to the media of SK-BR-3 cells. After 48 hours, cells were collected in RIPA lysis buffer (Sigma) and the lysates were analyzed by western blot for PARP cleavage and mHER2 protein expression (**Fig. 6**). Incubation with sHER2 resulted in the induction of apoptosis in those cells, as shown by PARP cleavage assays (**Fig. 6A**). The application of exogenous sHER2 protein to cultured SK-BR-3 cells also caused a reduction in HER2 expression levels (**Fig. 6B**). Relative to the intensity of the mHER2 band for untreated SK cells, the band intensities for β-gal, control (C), and sHER2 were 82%, 92%, and 73%, respectively.

[00189] A cloned and purified C-terminal 6-His tag bearing version of the sHER2 protein (*Δ15*HER2-His) was applied at concentrations of 60, 120, or 240 nM to the culture media of
SK-BR-3 cells, and after 48 hours incubation, cells were analyzed by Western blot for HER2, HER3, and their phosphorylation status. Increasing concentrations of *Δ15*HER2-His protein decreased total HER2 protein in the cells by up to 80% while phosphorylated HER2 (p-HER2) decreased up to 80% by 240 nM *Δ15*HER2-His. In agreement with established importance of HER2 in HER3 phosphorylation in SK-BR-3 cells, phosphorylated HER3 (p-HER3) also decreased in a dose-dependent manner in parallel with HER2 protein while the affect on HER3 was minimal **(Fig. 6C)**. The densities of the bands shown in the gels in **Fig. 6** were quantified with ImageQuant™ (GE Healthcare) software. Growth inhibition of SK-BR-3 cells by *Δ15*HER2-His protein treatment after 72 hours incubation was analyzed by MTS assay. Inhibition was evaluated by plating cells at ~$2X10^4$ cells/well in 96 well plates for 24 hours, and then treated with 60, 120 or 240 nM Δ15HER2-His protein for 72 hours. Cell viability was normalized to mock-treated cells and analyzed using CellTiter 96® Aqueous Solution reagent (Promega). Shown in Fig 6D are the mean ± standard deviation of triplicates (Fig. 6D). The Δ15HER2-His protein treatment decreased viability of SK-BR-3 cells in a dose-dependent manner.

Example 3

HER3 Splice Variants

[00190] Exemplary plice switching oligonucleotides (SSOs) containing phosphorothioate internucleotide bonds and targeted to regions of human HER3 pre-mRNA (**Fig. 7**, Table 3) were synthesized.

Table 3. Splice switching Oligonucleotides Targeted to HER3

SEQ ID.	Name	Sequence (5'-3')	HER3 Target Site	Modification
26	1	GGGTCACTTCCAAGTCCTGA	Putative branch site	2'-OMe, PS
27	2	GTCACTTCCAAGTCCTGACC	Putative branch site	2'-OMe, PS
28	3	CACTTCCAAGTCCTGACCTT	Putative branch site	2'-OMe, PS
29	4	CTTCCAAGTCCTGACCTTCA	Putative branch site	2'-OMe, PS
30	5	CCCTTACTGTACCCATTCAG	5' splice site of intron 13	2'-OMe, PS
31	6	CTCCCCTTACTGTACCCATT	5' splice site of intron 13	2'-OMe, PS
32	7	TGGCTCCCCTTACTGTACCC	5' splice site of intron 13	2'-OMe, PS
33	8	CTCGAGGCTCCCTGTAGTGG	3' splice site of intron 13	2'-OMe, PS
34	9	ATTCTCGAGGCTCCCTGTAG	3' splice site of intron 13	2'-OMe, PS
35	10	CAAATTCTCGAGGCTCCCTG	3' splice site of intron 13	2'-OMe, PS
36	11	CTAGTATACCGAGCCATTGC	5' splice site of intron 14	2'-OMe, PS
37	12	GTGCTACTAGTATACCGAGC	5' splice site of intron 14	2'-OMe, PS
38	13	CAAGTATCAGAGCCCTGAGT	3' splice site of intron 14	2'-OMe, PS
39	14	TTATCCCATCACTGACCCCT	5' splice site of intron 15	2'-OMe, PS
40	15	TATTATCCCATCACTGACCC	5' splice site of intron 15	2'-OMe, PS
41	16	ATTTCATCTCTTTAAGGCTC	PolyA signal site	2'-OMe, PS
42	17	CTGGATCTACTGCTTAATTT	PolyA signal site	2'-OMe, PS

2'-OMe, 2'-O-methyl oligoribonucleotide; PS, phosphorothioate internucleotide linkage.

[00191] These oligonucleotides were transfected into MCF-7 human breast cancer cells with the cationic transfection reagent Lipofectamine™ 2000 (Invitrogen) as per the manufacturer's directions. After 24 hours, the total RNA was collected and RT-PCR was used to determine the ratio of splice variants and full length HER3 mRNA. As shown in **Fig. 8** certain SSOs caused skipping of exon 13 (e.g., SSO 5 (SEQ ID NO. 30) and 6 (SEQ ID NO. 31)), leading to reduced levels of HER3 mRNA and increased levels of Δ13HER3 mRNA. As shown in **Fig. 9**, SSOs 8, 9 and 10 (SEQ ID NOs. 33 thru 35, respectively) all induced Δ14HER3 mRNA, while SSO 13 (SEQ ID NO. 38) induced Δ15HER3 mRNA.

[00192] SK-BR-3 cells were transfected with 100 nM of SSOs 1 thru 17 (SEQ ID NOs. 26 thru 42). After 48 hours, cell viability was measured by the addition of MTS reagent (Promega) (**Fig. 10**). As shown in **Fig. 10**, the induction of HER3 splice variants in SK-BR-3 cells by the SSOs, including SSOs 8, 9 and 10 (SEQ ID NOs. 33 thru 35, respectively), all of which induce Δ14HER3 mRNA, caused reduced cell viability compared to mock or untransfected cells.

Example 4

Evaluation of Carrier Peptide Conjugated PMOs in the EGFP-654 Transgenic Mouse

[00193] A PMO (654;5'-GCT ATT ACC TTA ACC CAG-3'; SEQ ID NO: 43) designed to restore correct splicing in the enhanced green fluorescent protein (EGFP) gene was conjugated to various carrier peptides (SEQ ID NOS:44-54) to produce peptide-conjugated PMOs (P-PMOs) and evaluated *in vivo* for their splice-correction activity and toxicity in the EGFP-654 transgenic mouse model (Sazani, P., F. Gemignani, et al. (2002) Nat Biotechnol 20(12): 1228-33). In this model, the EGFP-654 gene encoding for functional EGFP is interrupted by an aberrantly-spliced mutated intron, and cellular uptake of EGFP-654 targeted P-PMOs can be evaluated by RT-PCR detection of the restored EGFP-654 splice product in tissues.

[00194] Female EGFP-654 transgenic mice were injected intraperitoneally once daily for 4 consecutive days with saline or a 12.5 mg/kg dose of P-PMO. Post treatment on day 4, the heart, muscles, liver, kidney, lungs, small intestine, colon, stomach, mammary gland, thymus, spleen, ovary, skin, bone marrow, and brain were harvested, and extracted RNA was evaluated by RT-PCR and densitometry of PCR products for percentage of corrected splice products of the

EGFP-654 gene in tissues versus 100% EGFP-654 splice-corrected diaphragm controls.

[00195] Restoration of functional EGFP splice products post-treatment with various P-PMOs based on RT-PCR analysis of selected tissues including mammary and ovary tissues is shown in Figures 14A and 14B. Optimal carrier peptide uptake for mammary (SEQ ID NOS:56-58) and ovary (SEQ ID NO: 58) tissues based on these and similar results is summarized in Table 4 below (indicated by a *). Further examples of tissue-specific peptide delivery of antisense oligonucleotides is described in Sazani, et al, Mol Therapy (2008), in press)

Table 4: Carrier Peptide Uptake in Tissues

Tissue (%)	Optimal Tissue Targeting Peptides: SEQ ID NO.										
	52	53	54	55	56	57	58	59	60	61	62
Mammary Gland (≥60%)					*	*	*				
Ovary (>60%)							*				

Sequence Listing

SEQ ID NO: 1 (human HER2 Full Length DNA)

atggagctggcggccttgtgccgctgggggctcctcctcgccctcttgccccccggagccgcgagcaccca
agtgtgcaccggcacagacatgaagctgcggctccctgccagtcccgagacccacctggacatgctccgccacctc
taccagggctgccaggtggtgcagggaaacctggaactcacctacctgcccaccaatgccagcctgtccttcctgca
ggatatccaggaggtgcagggctacgtgctcatcgctcacaaccaagtgaggcaggtcccactgcagaggctgcg
gattgtgcgaggcacccagctctttgaggacaactatgccctggccgtgctagacaatggagacccgctgaacaata
ccacccctgtcacaggggcctccccaggaggcctgcgggagctgcagcttcgaagcctcacagagatcttgaaag
gaggggtcttgatccagcggaacccccagctctgctaccaggacacgattttgtggaaggacatcttccacaagaac
aaccagctggctctcacactgatagacaccaaccgctctcgggcctgccacccctgttctccgatgtgtaagggctcc
cgctgctggggagagagttctgaggattgtcagagcctgacgcgcactgtctgtgccggtggctgtgcccgctgcaag
gggccactgcccactgactgctgccatgagcagtgtgctgccggctgcacgggccccaagcactctgactgcctggc
ctgcctccacttcaaccacagtggcatctgtgagctgcactgcccagccctggtcacctacaacacagacacgtttga
gtccatgcccaatcccgagggccggtatacattcggcgccagctgtgtgactgcctgtccctacaactacctttctacg
gacgtgggatcctgcaccctcgtctgccccctgcacaaccaagaggtgacagcagaggatggaacacagcggtgt
gagaagtgcagcaagccctgtgcccgagtgtgctatggtctgggcatggagcacttgcgagaggtgagggcagtta
ccagtgccaatatccaggagtttgctggctgcaagaagatctttgggagcctggcatttctgccggagagctttgatgg
ggacccagcctccaacactgccccgctccagccagagcagctccaagtgtttgagactctggaagagatcacaggt
tacctatacatctcagcatggccggacagcctgcctgacctcagcgtcttccagaacctgcaagtaatccggggacg
aattctgcacaatggcgcctactcgctgaccctgcaagggctgggcatcagctggctggggctgcgctcactgaggg
aactgggcagtggactggccctcatccaccataacacccacctctgcttcgtgcacacggtgccctgggaccagctct
ttcggaacccgcaccaagctctgctccacactgccaaccggccagaggacgagtgtgtgggcgagggcctggcct
gccaccagctgtgcgcccgagggcactgctggggtccagggcccacccagtgtgtcaactgcagccagttccttcg
gggccaggagtgcgtggaggaatgccgagtactgcaggggctccccagggagtatgtgaatgccaggcactgtttg
ccgtgccaccctgagtgtcagccccagaatggctcagtgacctgttttggaccggaggctgaccagtgtgtggcctgt
gcccactataaggaccctcccttctgcgtggcccgctgccccagcggtgtgaaacctgacctctcctacatgcccatct
ggaagtttccagatgaggagggcgcatgccagccttgccccatcaactgcacccactcctgtgtggacctggatgac
aagggctgccccgccgagcagagagccagccctctgacgtccatcatctctgcggtggttggcattctgctggtcgtg
gtcttgggggtggtctttgggatcctcatcaagcgacggcagcagaagatccggaagtacacgatgcggagactgct
gcaggaaacggagctggtggagccgctgacacctagcggagcgatgcccaaccaggcgcagatgcggatcctg
aaagagacggagctgaggaaggtgaaggtgcttggatctggcgcttttggcacagtctacaagggcatctggatccc
tgatggggagaatgtgaaaattccagtggccatcaaagtgttgagggaaaacacatcccccaaagccaacaaaga
aatcttagacgaagcatacgtgatggctggtgtgggctccccatatgtctcccgccttctgggcatctgcctgacatcca
cggtgcagctggtgacacagcttatgccctatggctgcctcttagaccatgtccgggaaaaccgcggacgcctgggct
cccaggacctgctgaactggtgtatgcagattgccaaggggatgagctacctggaggatgtgcggctcgtacacag
ggacttggccgctcggaacgtgctggtcaagagtcccaaccatgtcaaaattacagacttcgggctggctcggctgct
ggacattgacgagacagagtaccatgcagatgggggcaaggtgcccatcaagtggatggcgctggagtccattctc
cgccggcggttcacccaccagagtgatgtgtggagttatggtgtgactgtgtgggagctgatgacttttggggccaaac
cttacgatgggatcccagcccgggagatccctgacctgctggaaaaggggagcggctgccccagcccccatct
gcaccattgatgtctacatgatcatggtcaaatgttggatgattgactctgaatgtcggccaagattccgggagttggtgt
ctgaattctcccgcatggccagggacccccagcgctttgtggtcatccagaatgaggacttgggcccagccagtccct
tggacagcaccttctaccgctcactgctggaggacgatgacatgggggacctggtggatgctgaggagtatctggta
ccccagcagggcttcttctgtccagaccctgccccgggcgctgggggcatggtccaccacaggcaccgcagctcat
ctaccaggagtggcggtggggacctgacactagggctggagccctctgaagaggaggcccccaggtctccactgg
caccctccgaaggggctggctccgatgtatttgatggtgacctgggaatgggggcagccaaggggctgcaaagcct
ccccacacatgaccccagccctctacagcggtacagtgaggaccccacagtaccctgccctctgagactgatggc
tacgttgcccccctgacctgcagcccccagcctgaatatgtgaaccagccagatgttcggccccagcccccttcgccc
cgagagggccctctgcctgctgcccgacctgctggtgccactctggaaaggcccaagactctctccccagggaaga
atggggtcgtcaaagacgtttttgcctttgggggtgccgtggagaaccccgagtacttgacaccccagggaggagct

gcccctcagccccaccctcctcctgccttcagcccagccttcgacaacctctattactgggaccaggacccaccaga
gcgggggctccacccagcaccttcaaagggacacctacggcagagaacccagagtacctgggtctggacgtgc
cagtgtga

SEQ ID NO: 2 (human HER2 Full Length Protein)

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQ
GCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLF
EDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQ
DTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC
AGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYN
TDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQR
CEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPA
SNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLT
LQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRP
EDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPRE
YVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPD
LSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVGILLV
VVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELR
KVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVG
SPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM
SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA
LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPIC
TIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDST
FYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGG
DLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRY
SEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATL
ERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY
WDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV

SEQ ID NO: 3 (human HER3 Full Length DNA)

atgagggcgaacgacgctctgcaggtgctgggcttgcttttcagcctggcccggggctccgaggtgggcaa
ctctcaggcagtgtgtcctgggactctgaatggcctgagtgtgaccggcgatgctgagaaccaataccagacactgta
caagctctacgagaggtgtgaggtggtgatggggaaccttgagattgtgctcacgggacacaatgccgacctctcctt
cctgcagtggattcgagaagtgacaggctatgtcctcgtggccatgaatgaattctctactctaccattgcccaacctcc
gcgtggtgcgagggacccaggtctacgatgggaagtttgccatcttcgtcatgttgaactataacaccaactccagcc
acgctctgcgccagctccgcttgactcagctcaccgagattctgtcaggggtgtttatattgagaagaacgataagctt
tgtcacatggacacaattgactggagggacatcgtgagggaccgagatgctgagatagtggtgaaggacaatggc
agaagctgtccccctgtcatgaggtttgcaaggggcgatgctggggtcctggatcagaagactgccagacattgac
caagaccatctgtgctcctcagtgtaatggtcactgctttgggcccaaccccaaccagtgctgccatgatgagtgtgcc
gggggctgctcaggccctcaggacacagactgctttgcctgccggcacttcaatgacagtggagcctgtgtacctcgc
tgtccacagcctcttgtctacaacaagctaactttccagctggaacccaatccccacaccaagtatcagtatggagga
gtttgtgtagccagctgtccccataactttgtggtggatcaaacatcctgtgtcagggcctgtcctcctgacaagatggaa
gtagataaaaatgggctcaagatgtgtgagccttgtgggggactatgtcccaaagcctgtgagggaacaggctctgg
gagccgcttccagactgtggactcgagcaacattgatggatttgtgaactgcaccaagatcctgggcaacctggacttt
ctgatcaccggcctcaatggagacccctggcacaagatccctgccctggacccagagaagctcaatgtcttccgga
cagtacgggagatcacaggttacctgaacatccagtcctggccgccccacatgcacaacttcagtgtttttccaatttg
acaaccattggaggcagaagcctctacaaccggggcttctcattgttgatcatgaagaacttgaatgtcacatctctgg
gcttccgatccctgaaggaaattagtgctgggcgtatctatataagtgccaataggcagctctgctaccaccactctttg
aactggaccaaggtgcttcgggggcctacggaagagcgactagacatcaagcataatcggccgcgcagagactg
cgtggcagagggcaaagtgtgtgacccactgtgctcctctgggggatgctggggcccaggccctggtcagtgcttgtc

ctgtcgaaattatagccgaggaggtgtctgtgtgacccactgcaactttctgaatggggagcctcgagaatttgcccat
gaggccgaatgcttctcctgccacccggaatgccaacccatggagggcactgccacatgcaatggctcgggctctg
atacttgtgctcaatgtgcccattttcgagatgggccccactgtgtgagcagctgcccccatggagtcctaggtgccaa
gggcccaatctacaagtacccagatgttcagaatgaatgtcggccctgccatgagaactgcacccaggggtgtaaa
ggaccagagcttcaagactgtttaggacaaacactggtgctgatcggcaaaacccatctgacaatggctttgacagt
gatagcaggattggtagtgattttcatgatgctgggcggcacttttctctactggcgtgggcgccggattcagaataaaa
gggctatgaggcgatacttggaacggggtgagagcatagagcctctggaccccagtgagaaggctaacaaagtctt
ggccagaatcttcaaagagacagagctaaggaagcttaaagtgcttggctcgggtgtctttggaactgtgcacaaag
gagtgtggatccctgagggtgaatcaatcaagattccagtctgcattaaagtcattgaggacaagagtggacggcag
agttttcaagctgtgacagatcatatgctggccattggcagcctggaccatgcccacattgtaaggctgctgggactatg
cccagggtcatctctgcagcttgtcactcaatatttgcctctgggttctctgctggatcatgtgagacaacaccgggggg
cactggggccacagctgctgctcaactggggagtacaaattgccaagggaatgtactaccttgaggaacatggtatg
gtgcatagaaacctggctgcccgaaacgtgctactcaagtcacccagtcaggttcaggtggcagattttggtgtggctg
acctgctgcctcctgatgataagcagctgctatacagtgaggccaagactccaattaagtggatggcccttgagagtat
ccactttgggaaatacacacaccagagtgatgtctggagctatggtgtgacagtttgggagttgatgaccttcggggca
gagccctatgcagggctacgattggctgaagtaccagacctgctagagaaggggagcggttggcacagccccag
atctgcacaattgatgtctacatggtgatggtcaagtgttggatgattgatgagaacattcgcccaacctttaaagaacta
gccaatgagttcaccaggatggcccgagacccaccacggtatctggtcataaagagagagagtgggcctggaata
gcccctgggccagagccccatggtctgacaaacaagaagctagaggaagtagagctggagccagaactagacct
agacctagacttggaagcagaggaggacaacctggcaaccaccacactgggctccgccctcagcctaccagttgg
aacacttaatcggccacgtgggagccagagccttttaagtccatcatctggatacatgcccatgaaccagggtaatctt
ggggagtcttgccaggagtctgcagtttctgggagcagtgaacggtgcccccgtccagtctctctacacccaatgcca
cggggatgcctggcatcagagtcatcagaggggcatgtaacaggctctgaggctgagctccaggagaaagtgtca
atgtgtaggagccggagcaggagccggagcccacggccacgcggagatagcgcctaccattcccagcgccaca
gtctgctgactcctgttaccccactctccccacccgggttagaggaagaggatgtcaacggttatgtcatgccagatac
acacctcaaaggtactccctcctcccgggaaggcacccttttcttcagtgggtctcagttctgtcctgggtactgaagaag
aagatgaagatgaggagtatgaatacatgaaccggaggagaaggcacagtccacctcatccccctaggccaagtt
cccttgaggagctgggttatgagtacatggatgtggggtcagacctcagtgcctctctgggcagcacacagagttgcc
cactccaccctgtacccatcatgcccactgcaggcacaactccagatgaagactatgaatatatgaatcggcaacga
gatggaggtggtcctgggggtgattatgcagccatgggggcctgcccagcatctgagcaagggtatgaagagatga
gagcttttcaggggcctggacatcaggccccccatgtccattatgcccgcctaaaaactctacgtagcttagaggctac
agactctgcctttgataaccctgattactggcatagcaggcttttccccaaggctaatgcccagagaacgtaa

SEQ ID NO: 4 (human HER3 Full Length Protein)

MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLY
KLYERCEVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVR
GTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDW
RDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQCNGHC
FGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQL
EPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCGGL
CPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEK
LNVFRTVREITGYLNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSL
GFRSLKEISAGRIYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCVAEGK
VCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEPREFAHEAECFS
CHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCPHGVLGAKGPIYKYPD
VQNECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLTMALTVIAGLVVIFMMLGG
TFLYWRGRRIQNKRAMRRYLERGESIEPLDPSEKANKVLARIFKETELRKLKVLGSG
VFGTVHKGVWIPEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIGSLDHAHIVRLLG
LCPGSSLQLVTQYLPLGSLLDHVRQHRGALGPQLLLNWGVQIAKGMYYLEEHGMV
HRNLAARNVLLKSPSQVQVADFGVADLLPPDDKQLLYSEAKTPIKWMALESIHFGK

YTHQSDVWSYGVTVWELMTFGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYM
VMVKCWMIDENIRPTFKELANEFTRMARDPPRYLVIKRESGPGIAPGPEPHGLTNK
KLEEVELEPELDLDLDLEAEEDNLATTTLGSALSLPVGTLNRPRGSQSLLSPSSGYM
PMNQGNLGESCQESAVSGSSERCPRPVSLHPMPRGCLASESSEGHVTGSEAELQ
EKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVMPDT
HLKGTPSSREGTLSSVGLSSVLGTEEEDEDEEYEYMNRRRRHSPPHPPRPSSLEE
LGYEYMDVGSDLSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYMNRQRDGGGPG
GDYAAMGACPASEQGYEEMRAFQGPGHQAPHVHYARLKTLRSLEATDSAFDNPD
YWHSRLFPKANAQRT

SEQ ID NO: 5 (human Δ15HER2 DNA)

atggagctggcggccttgtgccgctgggggctcctcctcgccctcttgccccccggagccgcgagcaccca
agtgtgcaccggcacagacatgaagctgcggctccctgccagtcccgagacccacctggacatgctccgccacctc
taccagggctgccaggtggtgcagggaaacctggaactcacctacctgcccaccaatgccagcctgtccttcctgca
ggatatccaggaggtgcagggctacgtgctcatcgctcacaaccaagtgaggcaggtcccactgcagaggctgcg
gattgtgcgaggcacccagctctttgaggacaactatgccctggccgtgctagacaatggagacccgctgaacaata
ccacccctgtcacaggggcctccccaggaggcctgcgggagctgcagcttcgaagcctcacagagatcttgaaag
gaggggtcttgatccagcggaacccccagctctgctaccaggacacgattttgtggaaggacatcttccacaagaac
aaccagctggctctcacactgatagacaccaaccgctctcgggcctgccacccctgttctccgatgtgtaagggctcc
cgctgctggggagagagttctgaggattgtcagagcctgacgcgcactgtctgtgccggtggctgtgcccgctgcaag
gggccactgcccactgactgctgccatgagcagtgtgctgccggctgcacgggccccaagcactctgactgcctggc
ctgcctccacttcaaccacagtggcatctgtgagctgcactgcccagccctggtcacctacaacacagacacgtttga
gtccatgcccaatcccgagggccggtatacattcggcgccagctgtgtgactgcctgtccctacaactacctttctacg
gacgtgggatcctgcaccctcgtctgccccctgcacaaccaagaggtgacagcagaggatggaacacagcggtgt
gagaagtgcagcaagccctgtgcccgagtgtgctatggtctgggcatggagcacttgcgagaggtgagggcagtta
ccagtgccaatatccaggagtttgctggctgcaagaagatctttgggagcctggcatttctgccggagagctttgatgg
ggacccagcctccaacactgccccgctccagccagagcagctccaagtgtttgagactctggaagagatcacaggt
tacctatacatctcagcatggccggacagcctgcctgacctcagcgtcttccagaacctgcaagtaatccggggacg
aattctgcacaatggcgcctactcgctgaccctgcaagggctgggcatcagctggctggggctgcgctcactgaggg
aactgggcagtggactggccctcatccaccataacacccacctctgcttcgtgcacacggtgccctgggaccagctct
ttcggaacccgcaccaagctctgctccacactgccaaccggccagaggacgagtgtgtgggcgagggcctggcct
gccaccagctgtgcgcccgagggcactgctggggtccagggcccacccagtgtgtcaactgcagccagttccttcg
gggccaggagtgcgtggaggaatgccgagtactgcaggggctccccagggagtatgtgaatgccaggcactgtttg
ccgtgccaccctgagtgtcagccccagaatggctcagtgacctgttttggaccgctgtgtggacctggatga

SEQ ID NO: 6 (human Δ15HER2 Protein)

MELAALCRWGLLLALLPPGAAST+QVCTGTDMKLRLPASPETHLDMLRHLY
QGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQ
LFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCY
QDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTV
CAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTY
NTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQ
RCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDP
ASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSL
TLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANR
PEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPR
EYVNARHCLPCHPECQPQNGSVTCFGPLCGPG

SEQ ID NO: 7 (human Δ13HER3 DNA)

atgagggcgaacgacgctctgcaggtgctgggcttgcttttcagcctggcccggggctccgaggtgggcaa
ctctcaggcagtgtgtcctgggactctgaatggcctgagtgtgaccggcgatgctgagaaccaataccagacactgta
caagctctacgagaggtgtgaggtggtgatggggaaccttgagattgtgctcacgggacacaatgccgacctctcctt
cctgcagtggattcgagaagtgacaggctatgtcctcgtggccatgaatgaattctctactctaccattgcccaacctcc
gcgtggtgcgagggacccaggtctacgatgggaagtttgccatcttcgtcatgttgaactataacaccaactccagcc
acgctctgcgccagctccgcttgactcagctcaccgagattctgtcaggggtgtttatattgagaagaacgataagctt
tgtcacatggacacaattgactggagggacatcgtgagggaccgagatgctgagatagtggtgaaggacaatggc
agaagctgtccccctgtcatgaggtttgcaaggggcgatgctggggtcctggatcagaagactgccagacattgac
caagaccatctgtgctcctcagtgtaatggtcactgctttgggcccaaccccaaccagtgctgccatgatgagtgtgcc
gggggctgctcaggccctcaggacacagactgctttgcctgccggcacttcaatgacagtggagcctgtgtacctcgc
tgtccacagcctcttgtctacaacaagctaactttccagctggaacccaatccccacaccaagtatcagtatggagga
gtttgtgtagccagctgtccccataactttgtggtggatcaaacatcctgtgtcagggcctgtcctcctgacaagatggaa
gtagataaaaatgggctcaagatgtgtgagccttgtgggggactatgtcccaaagcctgtgagggaacaggctctgg
gagccgcttccagactgtggactcgagcaacattgatggatttgtgaactgcaccaagatcctgggcaacctggacttt
ctgatcaccggcctcaatggagacccctggcacaagatccctgccctggacccagagaagctcaatgtcttccgga
cagtacgggagatcacaggttacctgaacatccagtcctggccgccccacatgcacaacttcagtgtttttccaatttg
acaaccattggaggcagaagcctctacaaccggggcttctcattgttgatcatgaagaacttgaatgtcacatctctgg
gcttccgatccctgaaggaaattagtgctgggcgtatctatataagtgccaataggcagctctgctaccaccactctttg
aactggaccaaggtgcttcgggggcctacggaagagcgactagacatcaagcataatcggccgcgcagagactg
cgggagcctcgagaatttgcccatgaggccgaatgcttctcctgccacccggaatgccaacccatggagggcactg
ccacatgcaatggctcgggctctgatacttgtgctcaatgtgcccattttcgagatgggccccactgtgtga

SEQ ID NO: 8 (human Δ13HER3 Protein)

MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLY
KLYERCEVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVR
GTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDW
RDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQCNGHC
FGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQL
EPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCGGL
CPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEK
LNVFRTVREITGYLNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSL
GFRSLKEISAGRIYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCGSLEN
LPMRPNASPATRNANPWRALPHAMARALILVLNVPIFEMGPTV

SEQ ID NO: 9 (human Δ14HER3 DNA)

atgagggcgaacgacgctctgcaggtgctgggcttgcttttcagcctggcccggggctccgaggtgggcaa
ctctcaggcagtgtgtcctgggactctgaatggcctgagtgtgaccggcgatgctgagaaccaataccagacactgta
caagctctacgagaggtgtgaggtggtgatggggaaccttgagattgtgctcacgggacacaatgccgacctctcctt
cctgcagtggattcgagaagtgacaggctatgtcctcgtggccatgaatgaattctctactctaccattgcccaacctcc
gcgtggtgcgagggacccaggtctacgatgggaagtttgccatcttcgtcatgttgaactataacaccaactccagcc
acgctctgcgccagctccgcttgactcagctcaccgagattctgtcaggggtgtttatattgagaagaacgataagctt
tgtcacatggacacaattgactggagggacatcgtgagggaccgagatgctgagatagtggtgaaggacaatggc
agaagctgtccccctgtcatgaggtttgcaaggggcgatgctggggtcctggatcagaagactgccagacattgac
caagaccatctgtgctcctcagtgtaatggtcactgctttgggcccaaccccaaccagtgctgccatgatgagtgtgcc
gggggctgctcaggccctcaggacacagactgctttgcctgccggcacttcaatgacagtggagcctgtgtacctcgc
tgtccacagcctcttgtctacaacaagctaactttccagctggaacccaatccccacaccaagtatcagtatggagga
gtttgtgtagccagctgtccccataactttgtggtggatcaaacatcctgtgtcagggcctgtcctcctgacaagatggaa
gtagataaaaatgggctcaagatgtgtgagccttgtgggggactatgtcccaaagcctgtgagggaacaggctctgg
gagccgcttccagactgtggactcgagcaacattgatggatttgtgaactgcaccaagatcctgggcaacctggacttt

ctgatcaccggcctcaatggagacccctggcacaagatccctgccctggacccagagaagctcaatgtcttccgga
cagtacgggagatcacaggttacctgaacatccagtcctggccgccccacatgcacaacttcagtgttttttccaatttg
acaaccattggaggcagaagcctctacaaccggggcttctcattgttgatcatgaagaacttgaatgtcacatctctgg
gcttccgatccctgaaggaaattagtgctgggcgtatctatataagtgccaataggcagctctgctaccaccactctttg
aactggaccaaggtgcttcgggggcctacggaagagcgactagacatcaagcataatcggccgcgcagagactg
cgtggcagagggcaaagtgtgtgacccactgtgctcctctgggggatgctggggcccaggccctggtcagtgcttgtc
ctgtcgaaattatagccgaggaggtgtctgtgtgacccactgcaactttctgaatggggctctgatacttgtgctcaatgt
gcccattttcgagatgggccccactgtgtga

SEQ ID NO: 10 (human Δ14HER3 Protein)

MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLY
KLYERCEVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVR
GTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDW
RDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQCNGHC
FGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQL
EPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCGGL
CPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEK
LNVFRTVREITGYLNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSL
GFRSLKEISAGRIYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCVAEGK
VCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGALILVLNVPIFEMGP
TV

SEQ ID NO: 11 (human Δ15HER3 DNA)

atgagggcgaacgacgctctgcaggtgctgggcttgcttttcagcctggcccggggctccgaggtgggcaa
ctctcaggcagtgtgtcctgggactctgaatggcctgagtgtgaccggcgatgctgagaaccaataccagacactgta
caagctctacgagaggtgtgaggtggtgatggggaaccttgagattgtgctcacgggacacaatgccgacctctcctt
cctgcagtggattcgagaagtgacaggctatgtcctcgtggccatgaatgaattctctactctaccattgcccaacctcc
gcgtggtgcgagggacccaggtctacgatgggaagtttgccatcttcgtcatgttgaactataacaccaactccagcc
acgctctgcgccagctccgcttgactcagctcaccgagattctgtcaggggtgtttatattgagaagaacgataagctt
tgtcacatggacacaattgactggagggacatcgtgagggaccgagatgctgagatagtggtgaaggacaatggc
agaagctgtccccctgtcatgaggtttgcaaggggcgatgctggggtcctggatcagaagactgccagacattgac
caagaccatctgtgctcctcagtgtaatggtcactgctttgggcccaaccccaaccagtgctgccatgatgagtgtgcc
gggggctgctcaggccctcaggacacagactgctttgcctgccggcacttcaatgacagtggagcctgtgtacctcgc
tgtccacagcctcttgtctacaacaagctaactttccagctggaacccaatccccacaccaagtatcagtatggagga
gtttgtgtagccagctgtccccataactttgtggtggatcaaacatcctgtgtcagggcctgtcctcctgacaagatggaa
gtagataaaaatgggctcaagatgtgtgagccttgtgggggactatgtcccaaagcctgtgagggaacaggctctgg
gagccgcttccagactgtggactcgagcaacattgatggatttgtgaactgcaccaagatcctgggcaacctggacttt
ctgatcaccggcctcaatggagacccctggcacaagatccctgccctggacccagagaagctcaatgtcttccgga
cagtacgggagatcacaggttacctgaacatccagtcctggccgccccacatgcacaacttcagtgttttttccaatttg
acaaccattggaggcagaagcctctacaaccggggcttctcattgttgatcatgaagaacttgaatgtcacatctctgg
gcttccgatccctgaaggaaattagtgctgggcgtatctatataagtgccaataggcagctctgctaccaccactctttg
aactggaccaaggtgcttcgggggcctacggaagagcgactagacatcaagcataatcggccgcgcagagactg
cgtggcagagggcaaagtgtgtgacccactgtgctcctctgggggatgctggggcccaggccctggtcagtgcttgtc
ctgtcgaaattatagccgaggaggtgtctgtgtgacccactgcaactttctgaatggggagcctcgagaatttgcccat
gaggccgaatgcttctcctgccacccggaatgccaacccatggagggcactgccacatgcaatggctcggtgtaa

SEQ ID NO: 12 (human Δ15HER3 Protein)

MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLY
KLYERCEVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVR
GTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDW

RDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQCNGHC
FGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQL
EPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCGGL
CPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEK
LNVFRTVREITGYLNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSL
GFRSLKEISAGRIYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCVAEGK
VCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEPREFAHEAECFS
CHPECQPMEGTATCNGSV

SEQ ID NO: 13 (human p85-HER3 DNA)

atgagggcgaacgacgctctgcaggtgctgggcttgcttttcagcctggcccggggctccgaggtgggcaa
ctctcaggcagtgtgtcctgggactctgaatggcctgagtgtgaccggcgatgctgagaaccaataccagacactgta
caagctctacgagaggtgtgaggtggtgatggggaaccttgagattgtgctcacgggacacaatgccgacctctcctt
cctgcagtggattcgagaagtgacaggctatgtcctcgtggccatgaatgaattctctactctaccattgcccaacctcc
gcgtggtgcgagggacccaggtctacgatgggaagtttgccatcttcgtcatgttgaactataacaccaactccagcc
acgctctgcgccagctccgcttgactcagctcaccgagattctgtcaggggtgtttatattgagaagaacgataagctt
tgtcacatggacacaattgactggagggacatcgtgagggaccgagatgctgagatagtggtgaaggacaatggc
agaagctgtccccctgtcatgaggtttgcaaggggcgatgctggggtcctggatcagaagactgccagacattgac
caagaccatctgtgctcctcagtgtaatggtcactgctttgggcccaaccccaaccagtgctgccatgatgagtgtgcc
gggggctgctcaggccctcaggacacagactgctttgcctgccggcacttcaatgacagtggagcctgtgtacctcgc
tgtccacagcctcttgtctacaacaagctaactttccagctggaacccaatccccacaccaagtatcagtatggagga
gtttgtgtagccagctgtccccataactttgtggtggatcaaacatcctgtgtcagggcctgtcctcctgacaagatggaa
gtagataaaaatgggctcaagatgtgtgagccttgtgggggactatgtcccaaagcctgtgagggaacaggctctgg
gagccgcttccagactgtggactcgagcaacattgatggatttgtgaactgcaccaagatcctgggcaacctggacttt
ctgatcaccggcctcaatggagacccctggcacaagatccctgccctggacccagagaagctcaatgtcttccgga
cagtacgggagatcacaggttacctgaacatccagtcctggccgccccacatgcacaacttcagtgttttttccaatttg
acaaccattggaggcagaagcctctacaaccggggcttctcattgttgatcatgaagaacttgaatgtcacatctctgg
gcttccgatccctgaaggaaattagtgctgggcgtatctatataagtgccaataggcagctctgctaccaccactctttg
aactggaccaaggtgcttcgggggcctacggaagagcgactagacatcaagcataatcggccgcgcagagactg
cgtggcagagggcaaagtgtgtgacccactgtgctcctctgggggatgctggggcccaggccctggtcagtgcttgtc
ctgtcgaaattatagccgaggaggtgtctgtgtgacccactgcaactttctgaatgggtacagtaaggggagccagtc
aaggatgggtgggggtggggccctgcaatggaactgttcaggtggcatacaataa

SEQ ID NO: 14 (human p85-HER3 Protein)

MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLY
KLYERCEVVMGNLEIVLTGHNADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVR
GTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDW
RDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQCNGHC
FGPNPNQCCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQL
EPNPHTKYQYGGVCVASCPHNFVVDQTSCVRACPPDKMEVDKNGLKMCEPCGGL
CPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHKIPALDPEK
LNVFRTVREITGYLNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSL
GFRSLKEISAGRIYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCVAEGK
VCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGYSKGSQSRMGGG
GALQWNCSGGIQ

SEQ ID NO: 15 (human HER2 gene from part of intron 14 through part of intron 15; the exon is underlined)

cctgggggtgtcagtgccagccccccacaaatcttttctgccccccccag**gaggctgaccagtgtgtggc**
ctgtgcccactataaggaccctcccttctgcgtggcccgctgccccagcggtgtgaaacctgacctctccta

catgcccatctggaagtttccagatgaggagggcgcatgccagccttgccccatcaactgcacccactcgt
gagtccaacggtcttttctgcagaaaggaggactttcctttcaggggt

SEQ ID NO: 16 (human HER3 gene from part of intron 12 through part of intron 15; the exons are underlined)

cttgctgggagtcctcagactcctctcctaacccacccttcctttccag**tggcagagggcaaagtgtgtga**
cccactgtgctcctctgggggatgctggggcccaggccctggtcagtgcttgtcctgtcgaaattatagccg
aggaggtgtctgtgtgacccactgcaactttctgaatgggtacagtaaggggagccagtcaaggatgggtggg
ggtggggccctgcaatggaactgttcaggtggcatacaataaaagtctttagacagctttctgcatgtgccttggtggga
ttgaggtaggagacctgtggttgtgagatcggagcatgaaggtcaggacttggaagtgacccccccctccctttattcc
ccactacag**ggagcctcgagaatttgcccatgaggccgaatgcttctcctgccacccggaatgccaaccca**
tggagggcactgccacatgcaatggctcggtatactagtagcaccaggatctccaagggagacagagaaggg
gcaatacttggagcatctggggaatgatatggctaaggatagcacagagaggccagataatgctagggcctgcag
atagaagatcctgaatgtctgggttggtctttgctgggaggtatggaattgaccttgggatctgattcttcctgaccttctctc
ttccactcag**ggctctgatacttgtgctcaatgtgcccattttcgagatgggccccactgtgtgagcagctgccc**
ccatggagtcctaggtgccaagggcccaatctacaagtacccagatgttcagaatgaatgtcggccctgcc
atgagaactgcacccaggggtcagtgatgggataataaggagaggggtcaggtggaagggtaggagca

SEQ ID NO: 17 (human HER3 from part of exon 28)

Gccagcactttgggaggctgagatgggaagatcacttgagcccagaattagagataagcctatggaaac
atagcaagacactgtctctacaggggaaaaaaaaaaaagaaactgagccttaaagagatgaaataaattaagca
gtagatccaggatgcaaaatcctcccaattcctgtgc

Antisense Oligonucleotides		
SEQ ID.	Name	Sequence (5'-3')
18	106	ggg cag aaa aga ttt gtg gg
19	107	cac act ggt cag cct cct gg
20	108	gcc aca cac tgg tca gcc tc
21	109	ctc acg agt ggg tgc agt tg
22	110	gtt gga ctc acg agt ggg tg
23	111	gac cgt tgg act cac gag tg
24	M111	gac cgt tgg act cac gag tg
25	L111	CgTtGgAcTcAcGaGt
26	1	GGGTCACTTCCAAGTCCTGA
27	2	GTCACTTCCAAGTCCTGACC
28	3	CACTTCCAAGTCCTGACCTT
29	4	CTTCCAAGTCCTGACCTTCA
30	5	CCCTTACTGTACCCATTCAG
31	6	CTCCCCTTACTGTACCCATT
32	7	TGGCTCCCCTTACTGTACCC
33	8	CTCGAGGCTCCCTGTAGTGG
34	9	ATTCTCGAGGCTCCCTGTAG
35	10	CAAATTCTCGAGGCTCCCTG
36	11	CTAGTATACCGAGCCATTGC
37	12	GTGCTACTAGTATACCGAGC
38	13	CAAGTATCAGAGCCCTGAGT
39	14	TTATCCCATCACTGACCCCT
40	15	TATTATCCCATCACTGACCC
41	16	ATTTCATCTCTTTAAGGCTC
42	17	CTGGATCTACTGCTTAATTT
43	654	GCTATTACCTTAACCCAG
Splice Junction Targets		
44	HER2-Ex15SA	cctgggggtgtcagtgccagccccccacaaatcttt tctgccccccccag**gaggctgaccagtgtgtggc ctgtgcccactataaggaccctcccttctg**
45	HER2-Ex15SD	**ccagatgaggagggcgcatgccagccttgcc ccatcaactgcacccactc**gtgagtccaacggtctt ttctgcagaaaggaggactttcctttcaggggt
46	HER3-Ex13SA	cttgctgggagtcctcagactcctctcctaacccac cccttcctttccag**tggcagagggcaaagtgtgtga cccactgtgctcctctgggggatgctgg**
47	HER3-Ex13SD	**aattatagccgaggaggtgtctgtgtgacccac tgcaactttctgaatgg**gtacagtaaggggagcca gtcaaggatgggtgggggtggggccctgcaat
48	HER3-Ex14SA	aaggtcaggacttggaagtgacccccccctcccttt attccccactacag**ggagcctcgagaatttgccca tgaggccgaatgcttctcctgccacccgg**
49	HER3-Ex14SD	**gccacccggaatgccaacccatggagggca ctgccacatgcaatggctcg**gtatactagtagcac caggatctccaagggagacagagaaggggcaata c
50	HER3-	ggaattgaccttgggatctgattcttcctgaccttctct

	Ex15SA	cttccactcag**ggctctgatacttgtgctcaatgtgc ccattttcgagatgggccccactg**
51	HER3-Ex15SD	**ccagatgttcagaatgaatgtcggccctgccat gagaactgcacccaggg**gtcagtgatgggataat aaggagaggggtcaggtggaagggtaggagca

Exemplary Peptide Transporters for Intracellular Delivery of PMO

Peptide	Sequence (N-terminal to C-terminal)	SEQ ID
R_8	RRRRRRRR-XB	52
$(RXRRBR)_2$-XB (CPO6062)	RXRRBRRXRRBR-XB	53
$(RXR)_3RBR$-XB	RXRRXRRXRRBR-XB	54
$(RB)_5RXRBRX$-B	RBRBRBRBRBRXRBRX-B	55
$(RBRBRBRX)_2$-X	RBRBRBRXRBRBRBRX-X	56
X-$(RB)_3RX(RB)_3RX$	XRBRBRBRXRBRBRBR-X	57
$(RBRX)_4B$	RBRXRBRXRBRXRBRX-B	58
$(RB)_4(RX)_4B$	RBRBRBRBRXRXRXRX-B	59
$RX(RB)_2RX(RB)_3RX$-X	RXRBRBRXRBRBRBRX	60
$(rXr)_4$	rXrrXrrXrrXr-XB	61
$(RXR)_4XB$ (P007)	RXRRXRRXRRXRXB	62
$(RRX)_4B$	RRXRRXRRXRRXB	63
$(XRR)_4XB$	XRRXRRXRRXRRXB	64
$(RX)_6B$	RXRXRXRXRXRXB	65
$(RX)_8B$	RXRXRXRXRXRXRXB	66
$(RXR)_3XB$	RXRRXRRXR XB	67

X refers to 6-aminohexanoic acid

Claims:

IT IS CLAIMED:

1. An isolated, soluble, human epidermal growth factor receptor-2 (HER2) protein lacking the region encoded by exon 15 of the full-length mRNA transcript of the HER2 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER2 transcript.

2. The protein of claim 1, wherein the sequence of said protein comprises a sequence having at least 95% sequence homology to the sequence identified by SEQ ID No: 6 or amino acids 23-584 of SEQ ID No: 6.

3. The protein of claim 1, which is modified by protein pegylation.

4. An isolated nucleic acid encoding human epidermal growth factor receptor-2 (HER2) protein, but lacking exon 15 of the normal (HER2) transcript, with exon 14 joined directly to exon 16, and containing a stop codon within exon 16.

5. The nucleic acid of claim 4, having at least 85% sequence homology to the sequence identified by SEQ ID NO: 5 or that portion of the sequence terminating at a stop codon within exon 16.

6. A method of treating a female subject having an ovarian or breast cancer characterized by overexpression of human epidermal growth factor receptor-2 (HER2), comprising

administering to the subject, a pharmaceutically effective amount of a soluble, human epidermal growth factor receptor-2 (HER2) protein lacking the region encoded by exon 15 of the full-length mRNA transcript of the HER2 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER2 transcript, and

continuing said administering, at periodic intervals, until a defined end point in the status of the cancer is obtained.

7. The method of claim 6, wherein the sequence of said protein comprises a sequence having at least 95% sequence homology to SEQ ID No: **6** or to amino acids 23-584 of SEQ ID No: **6**.

8. The method of claim 7, in which the protein is modified by pegylation.

9. A splice-switching oligonucleotide compound comprising

an oligonucleotide containing between 12-30 bases and at least 12 contiguous bases complementary to an exon-15 acceptor or donor splice site region contained within SEQ ID. NO: 15 of the full-length mRNA transcript of human epidermal growth factor receptor-2 (HER2) protein.

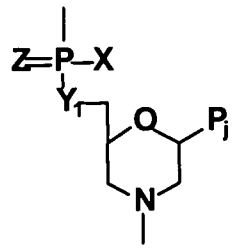
10. The compound of claim 9, wherein the oligonucleotide contains between 12 and 25 bases and a sequence of at least 12 contiguous bases complementary to a region contained with SEQ ID NOS: 44 or 45.

11. The compound of claim 9, wherein the oligonucleotide is selected from the group consisting of a locked nucleic acid, 2'-O-methoxyethyloligoribonucleotide, and a phosphorodiamidate morpholino oligonucleotide.

12. The compound of claim 9, which further includes, conjugated to the 5'- or 3'-end of the oligonucleotide, an arginine-rich polypeptide effective to promote uptake of the compound into cells.

13. The compound of claim 12, wherein the oligonucleotide is composed of morpholino subunits and phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit.

14. The compound of claim 13, wherein the morpholino subunits in the oligonucleotide compound to which the cells are exposed is administered to the subject are joined by phosphorodiamidate linkages having the structure:



where Y_1=O, Z=O, Pj is a purine or pyrimidine base-pairing moiety effective to bind, by base-specific hydrogen bonding, to a base in a polynucleotide, and X is an amino or alkyl amino, including dialkylamino.

15. A method of treating a female subject having an ovarian or breast cancer characterized by overexpression of human epidermal growth factor receptor-2 (HER2), comprising

administering to the subject, a pharmaceutically effective amount of a compound comprising an oligonucleotide containing between 12-30 bases and at least 12 contiguous bases complementary to an exon-14 acceptor or donor splice site region contained within SEQ ID. NO: 15 of the full-length mRNA transcript of human epidermal growth factor receptor-2 (HER2) protein, and

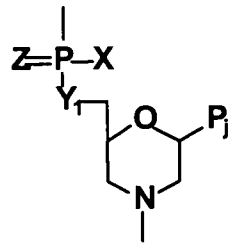
continuing said administering, at periodic intervals, until a defined end point in the status of the cancer is obtained.

16. The method of claim 15, wherein the oligonucleotide in the compound administered to the subject is selected from the group consisting of a locked nucleic acid, 2'-O-methoxyethyloligoribonucleotide, and a phosphorodiamidate morpholino oligonucleotide.

17. The method of claim 15, wherein the compound administered to the subject further includes, conjugated to the 5'- or 3'-end of the oligonucleotide, an arginine-rich polypeptide effective to promote uptake of the compound into infected host cells.

18. The method of claim 15, wherein the oligonucleotide in the compound administered to the subject is composed of morpholino subunits and phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit.

19. The method of claim 18, wherein the morpholino subunits in the compound to which the host cells are exposed are joined by phosphorodiamidate linkages having the structure:



where Y_1=O, Z=O, Pj is a purine or pyrimidine base-pairing moiety effective to bind, by base-specific hydrogen bonding, to a base in a polynucleotide, and X is an amino or alkyl amino, including dialkylamino.

20. The method of claim 15, which further includes administering to the subject, a pharmaceutically effective amount of a soluble, human epidermal growth factor receptor-2 (HER2) protein lacking the region encoded by exon 15 of the full-length mRNA transcript of the HER2 gene, and truncated, at its C terminus, in the region encoded by exon 16 of the HER2 transcript.

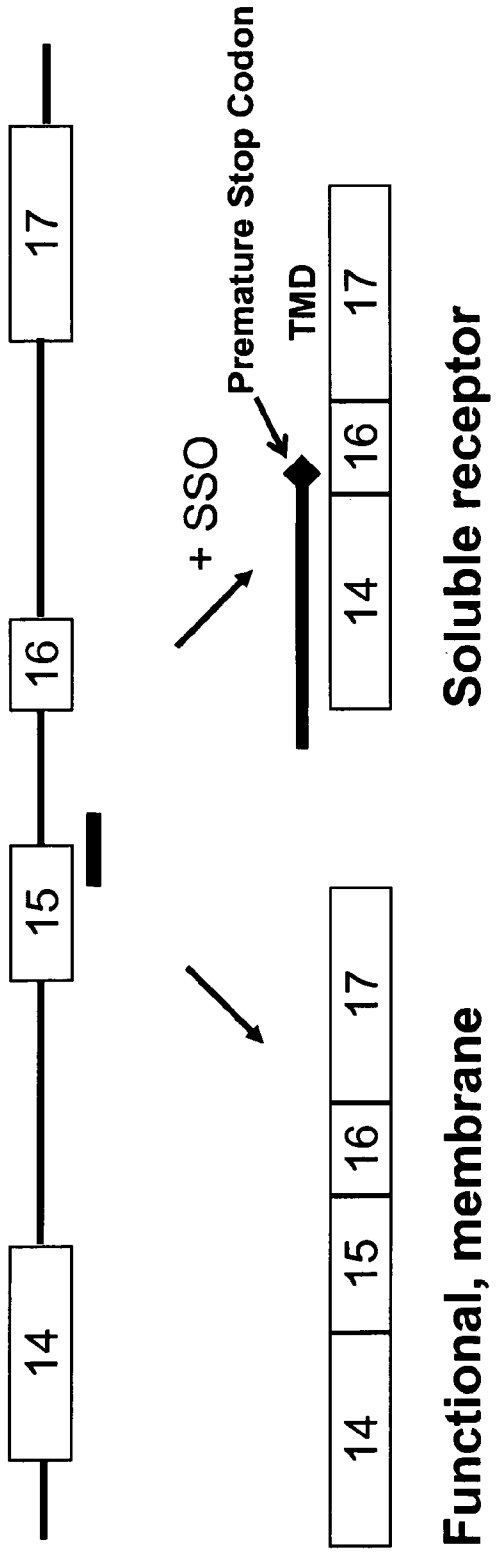

17
16
15
14
+ SSO
Premature Stop Codon
TMD
17
16
14
Soluble receptor
17
16
15
14
Functional, membrane bound receptor

Fig. 1

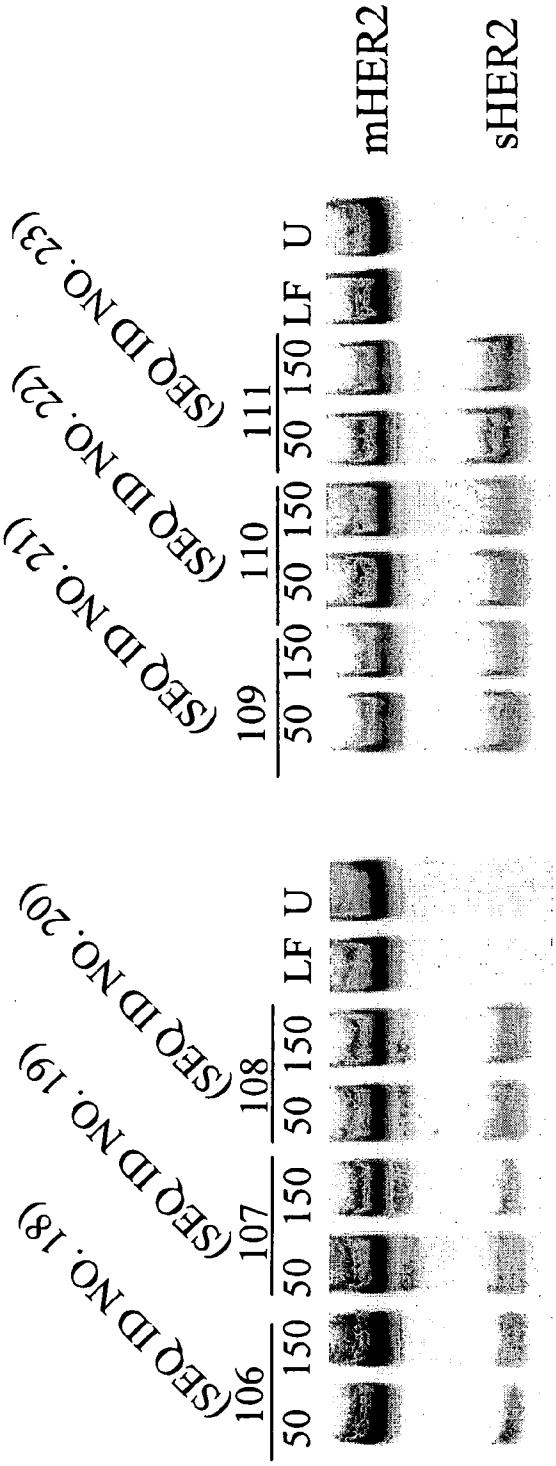

mHER2
sHER2
50 150 106 50 150 107 50 150 108 LF U
50 150 109 50 150 110 50 150 111 LF U
(SEQ ID NO. 18)
(SEQ ID NO. 19)
(SEQ ID NO. 20)
(SEQ ID NO. 21)
(SEQ ID NO. 22)
(SEQ ID NO. 23)

Fig. 2

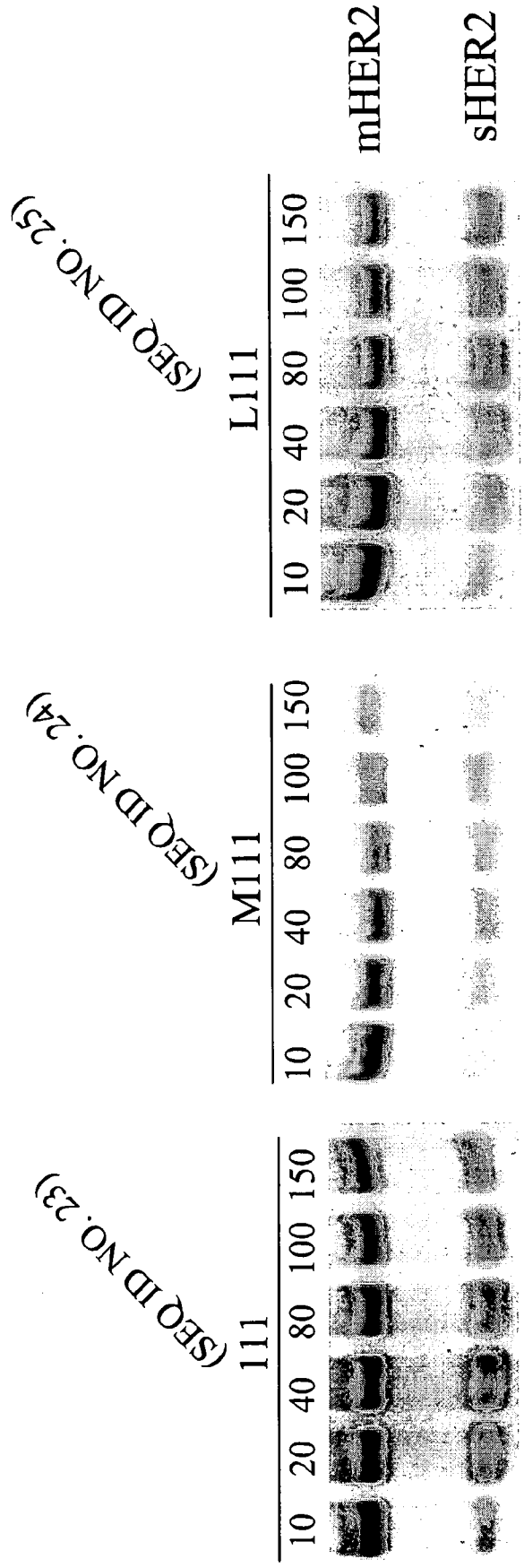

mHER2
sHER2
L111
(SEQ ID NO. 25)
M111
(SEQ ID NO. 24)
111
(SEQ ID NO. 23)
10
20
40
80
100
150

Fig. 3

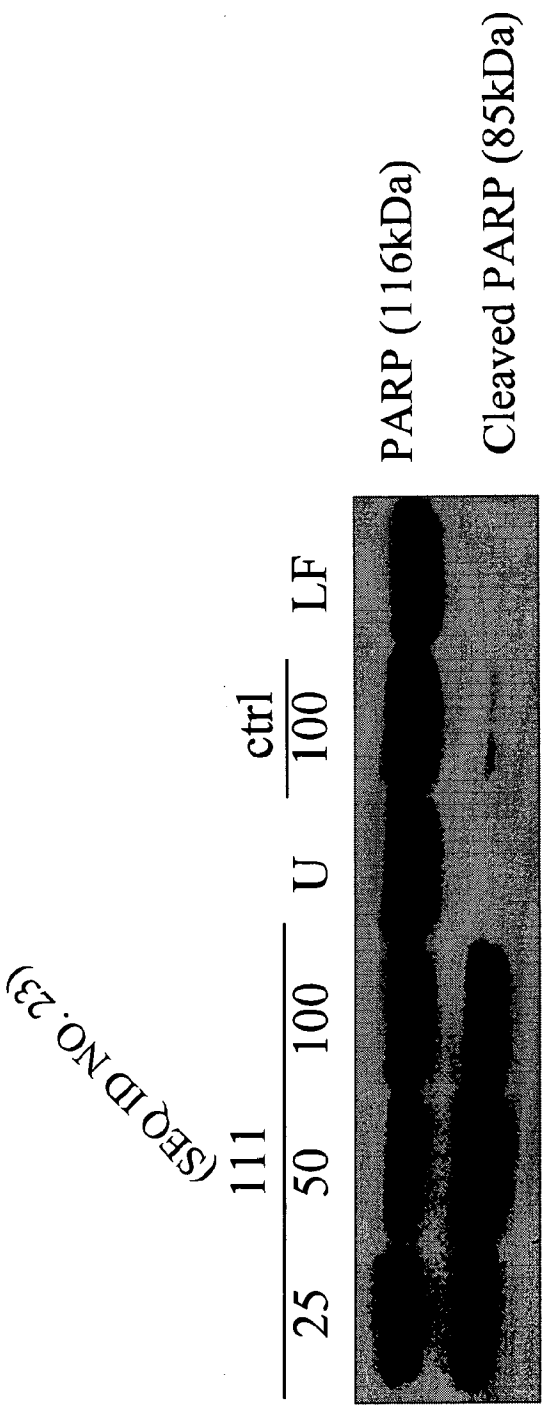

(SEQ ID NO. 23)
111
25 50 100
U
ctrl
100
LF
PARP (116kDa)
Cleaved PARP (85kDa)

Fig. 4A

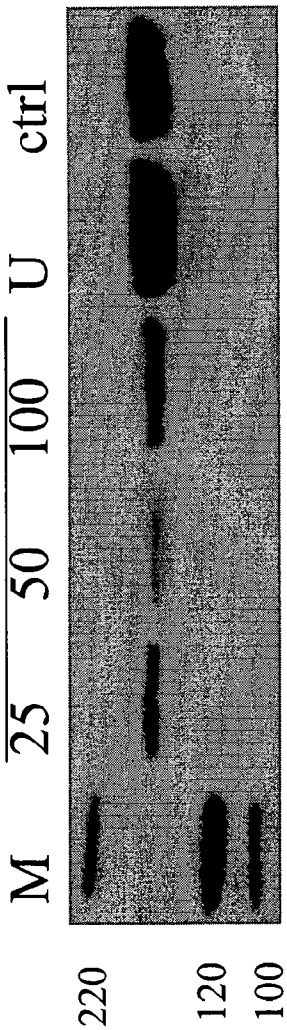

111
M 25 50 100
U
ctrl
mHER2
220
120
100

Fig. 4B

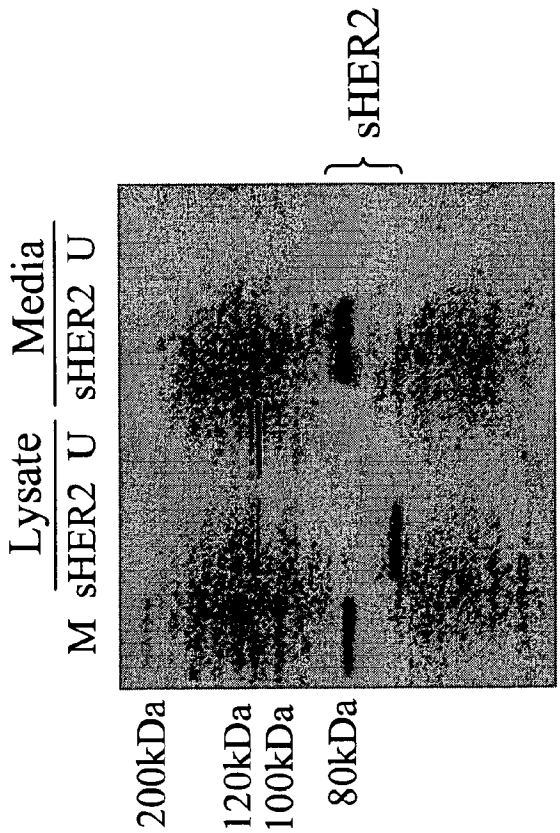

Lysate
Media
M
sHER2 U
sHER2 U
sHER2
200kDa
120kDa
100kDa
80kDa

Fig. 5

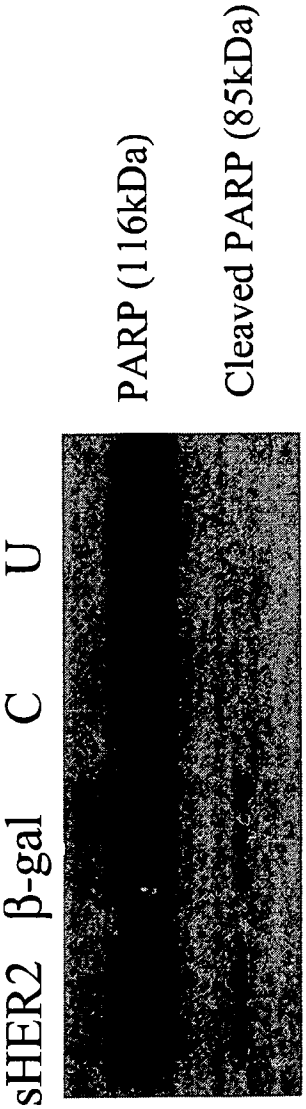

sHER2 β-gal C U
PARP (116kDa)
Cleaved PARP (85kDa)

Fig. 6A

β-gal C sHER2 U
mHER2
220 kDa
120 kDa

Fig. 6B

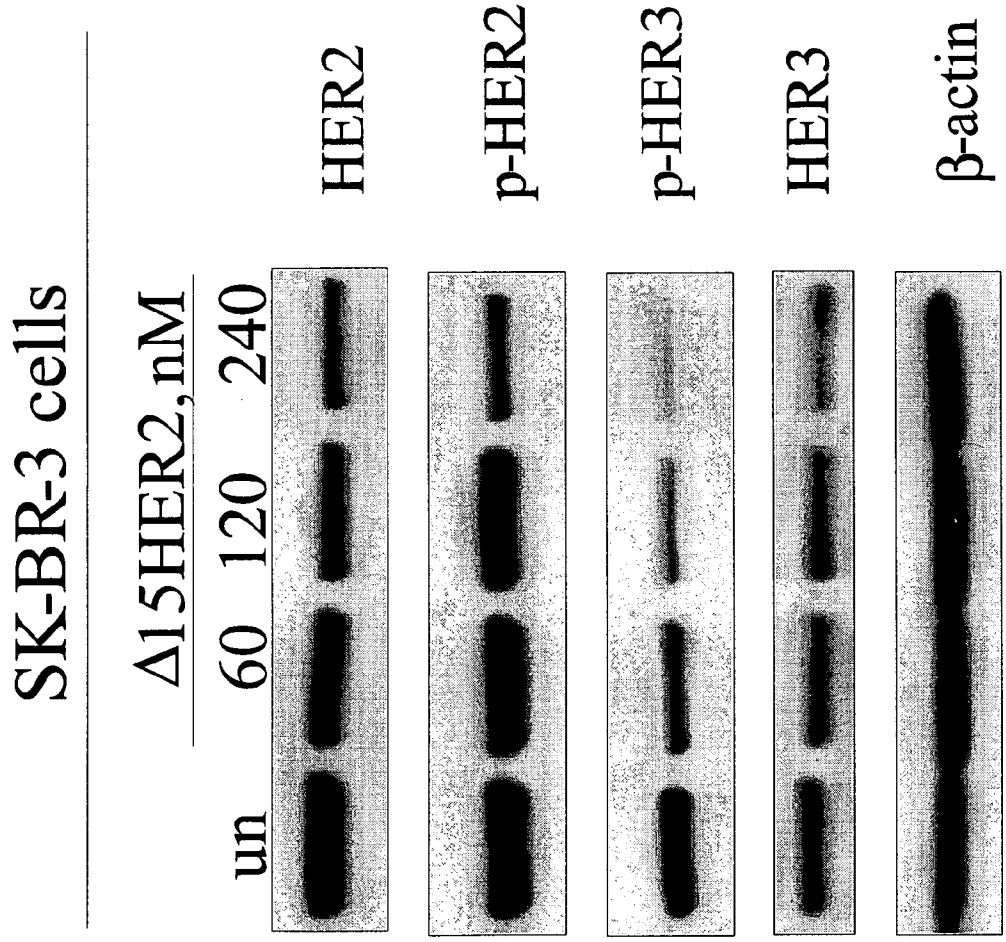

SK-BR-3 cells
Δ15HER2, nM
un
60
120
240
HER2
p-HER2
p-HER3
HER3
β-actin

Fig. 6C

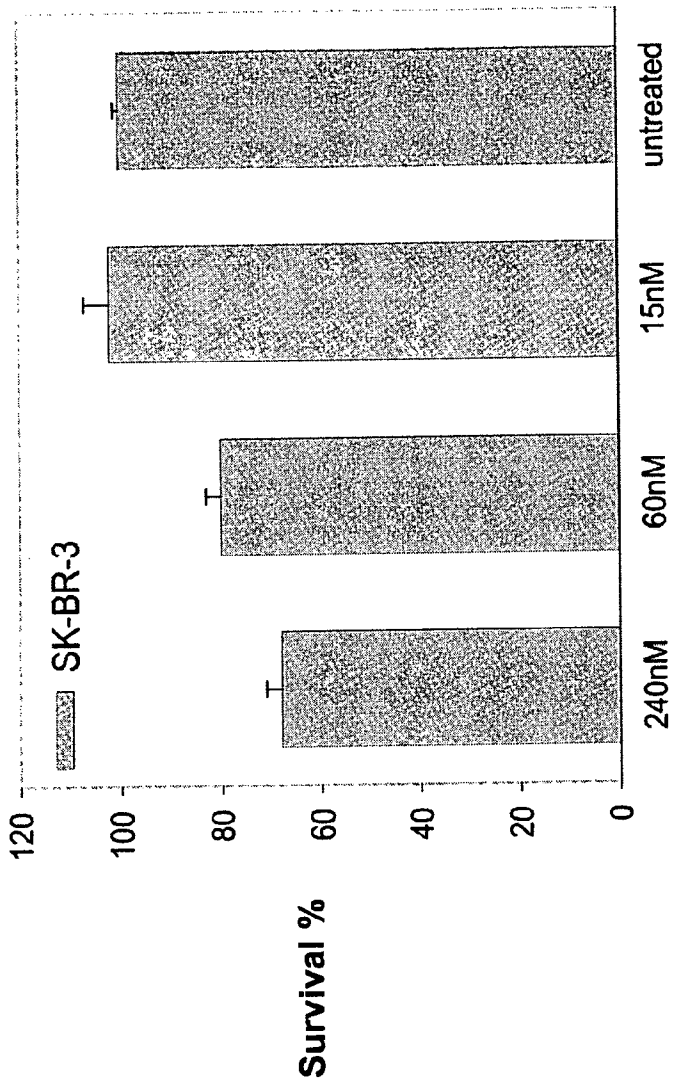

SK-BR-3
Survival %
120
100
80
60
40
20
0
240nM
60nM
15nM
untreated
d15HER2 protein concentration

Fig. 6D

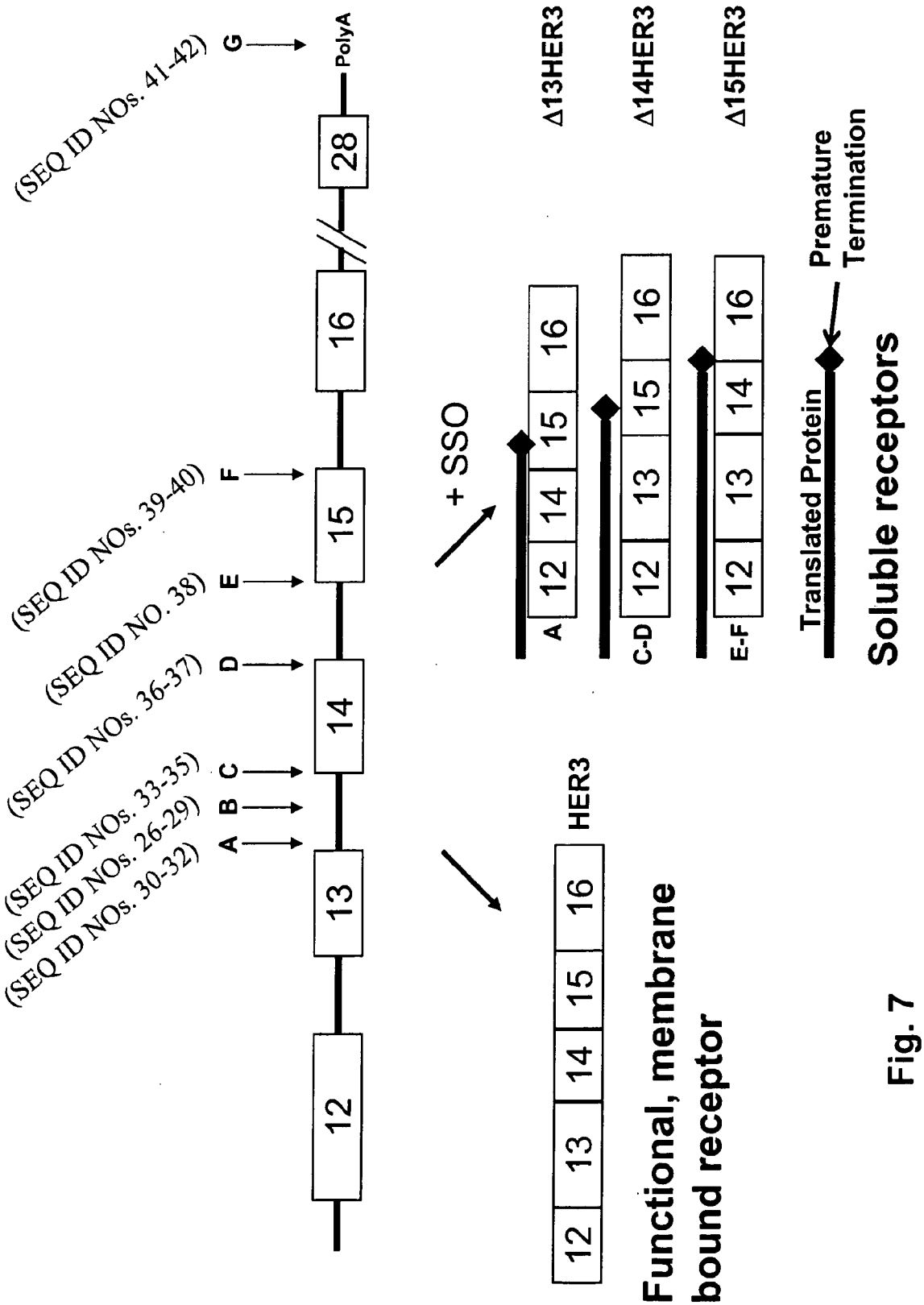

(SEQ ID NOs. 41-42)
G
PolyA
28
16
(SEQ ID NOs. 39-40)
F
(SEQ ID NO. 38)
E
15
(SEQ ID NOs. 36-37)
D
14
(SEQ ID NOs. 33-35)
C
(SEQ ID NOs. 26-29)
B
(SEQ ID NOs. 30-32)
A
13
12
HER3
12 13 14 15 16
Functional, membrane bound receptor
+ SSO
Δ13HER3
Δ14HER3
Δ15HER3
A
C-D
E-F
12 13 14 15 16
Translated Protein
Premature Termination
Soluble receptors

Fig. 7

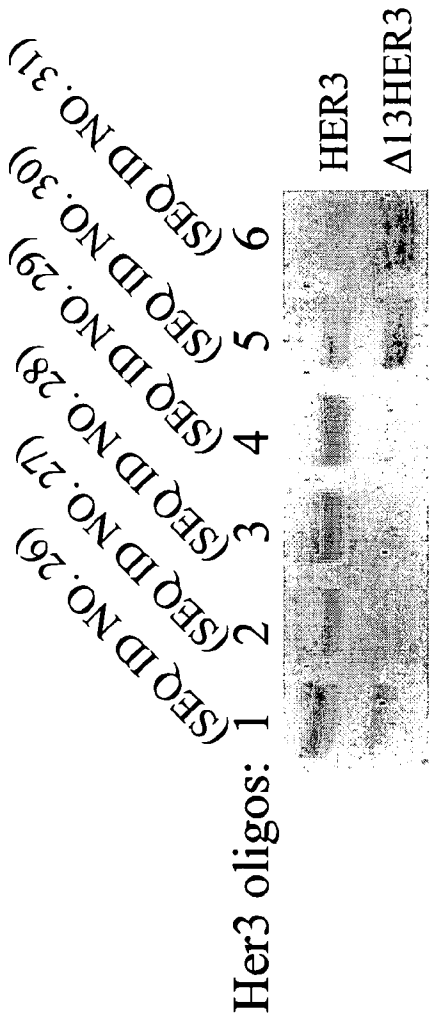

HER3
Δ13HER3
Her3 oligos:
1 (SEQ ID NO. 26)
2 (SEQ ID NO. 27)
3 (SEQ ID NO. 28)
4 (SEQ ID NO. 29)
5 (SEQ ID NO. 30)
6 (SEQ ID NO. 31)

Fig. 8

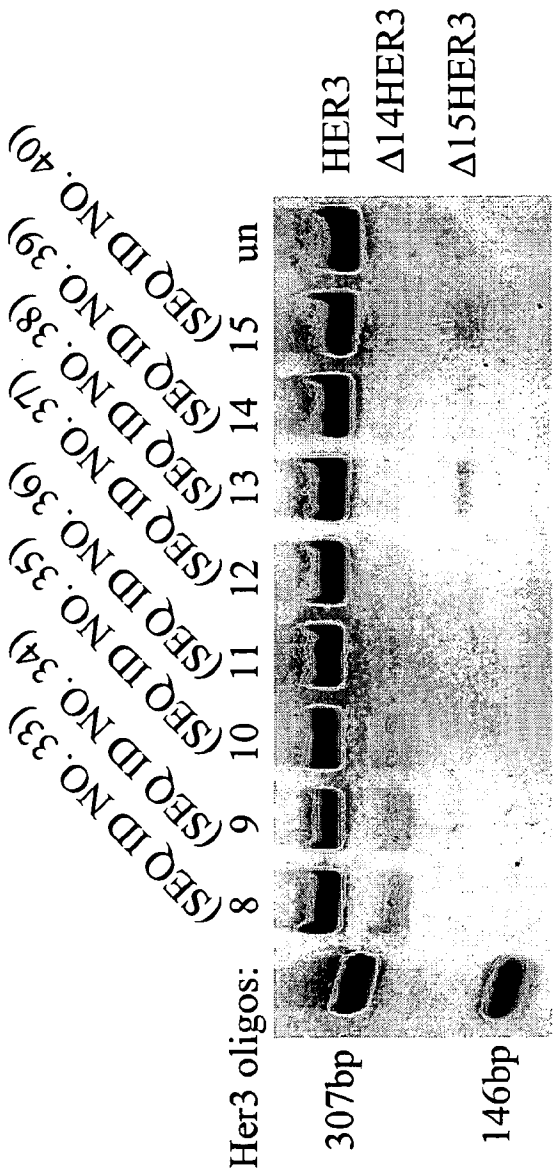

HER3
Δ14HER3
Δ15HER3
307bp
146bp
Her3 oligos:
8
9
10
11
12
13
14
15
un
(SEQ ID NO. 33)
(SEQ ID NO. 34)
(SEQ ID NO. 35)
(SEQ ID NO. 36)
(SEQ ID NO. 37)
(SEQ ID NO. 38)
(SEQ ID NO. 39)
(SEQ ID NO. 40)

Fig. 9

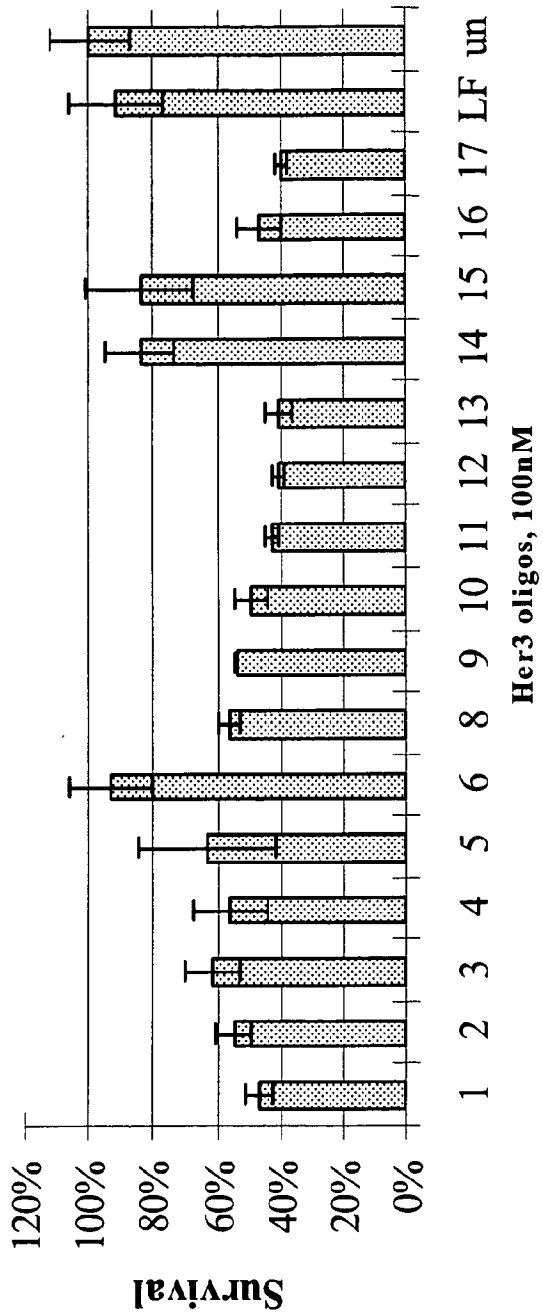

Survival
120%
100%
80%
60%
40%
20%
0%
1 2 3 4 5 6 8 9 10 11 12 13 14 15 16 17 LF un
Her3 oligos, 100nM

Fig. 10

cctgggggtgtcagtgccagccccccacaaatctttctgccccccccaggaggctgaccagtgtgt

ggcctgtgcccactataaggaccctccttctgcgtggcccgctgccccagcggtgtgaaacctgac

EXON 15

ctctcctacatgcccatctggaagtttccagatgagggcgcatgccagccttgccccatcaact

gcacccactcgtgagtccaacggtctttttctgcagaaaggaggacttttccttttcagggggt ...

INTRON 15 ... tcccaagagggtggttcccagaattgttgatgagactgtttctcctgcag

ctgtgtggacctggatgacaaggctgccccgccgagcagagccag

Δ15

EXON 16

Fig. 11

ttgctgtgggagtcctcagactccctcctaacccaccccttcctttccagtggcagagggcaaagtgtgt

gacccactgtgctcctctgtgggggatgctgtggcccaggccctggtcagtgcttgtcctgtcgaaattata

EXON 13

gccgaggaggtgtctgtgtgacccactgcaactttctgaatgggtacagtaagggagccagtcaaggat

gggtgggggtgggggccctgcaatggaactgttcaggtggcatacaataaaagtctttagacagctttctg

p85

catgtgccttgtgggattgaggtaggagacctgtggttgtgagatcggagcatgaaggtcaggacttga

INTRON 13

agtgaccccccccctcccctttatttccccactacag**ggagcctcgagaatttgcccatgaggccgaatgctt**

ctcctgccacccggaatgccaacccatggagggcactgccacatgcaatggctcggtatactagtagcac

EXON 14

caggatctccaagggagacagagaagggggcaatacttgggagcatctgggggaatgatatggctaaggatag

cacagagaggccagataatgctagggccctgcagatagaagatccctgaatgtctgggttggtctttgctggg

INTRON 14

gaggtatggaattgaccttgggatctgattctttccctgaccttctcttctccactcag**ggctctgatactt**

gtgctcaatgtgccatttttcgagatgggccccccactgtgtgaagcagctgccccccatggagtcctaggtgc

Δ13, Δ14

caagggcccaatctacaagtacccagatgttcagaatgaatgtcggcccctgccatgagaactgcacccag

EXON 15

gggtcagtgatgggataataaggagagggggtcaggtgggaagggtaggagca ... **INTRON 15**

... gagcctctgctgtccaagctctcatttaaggtggtgacttttcttccctag**gtgtaa**a**ggaccagag**

Δ15

cttcaagactgtttaggacaaacactggtgctgatcgg

EXON 16

Fig. 12

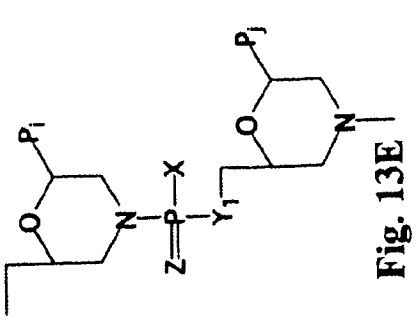


Fig. 13E

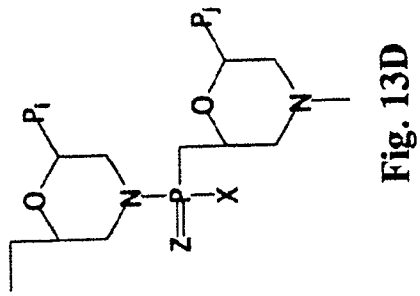


Fig. 13D

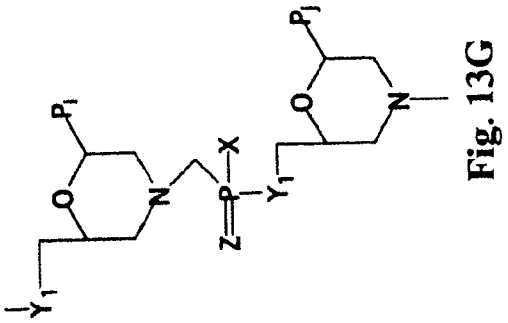


Fig. 13G

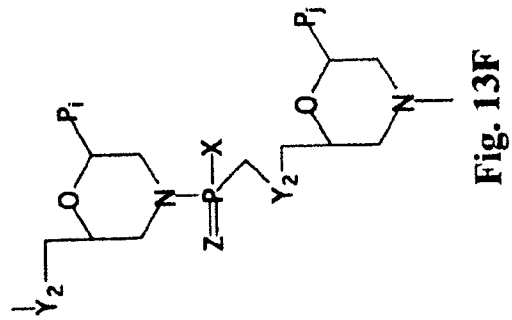


Fig. 13F

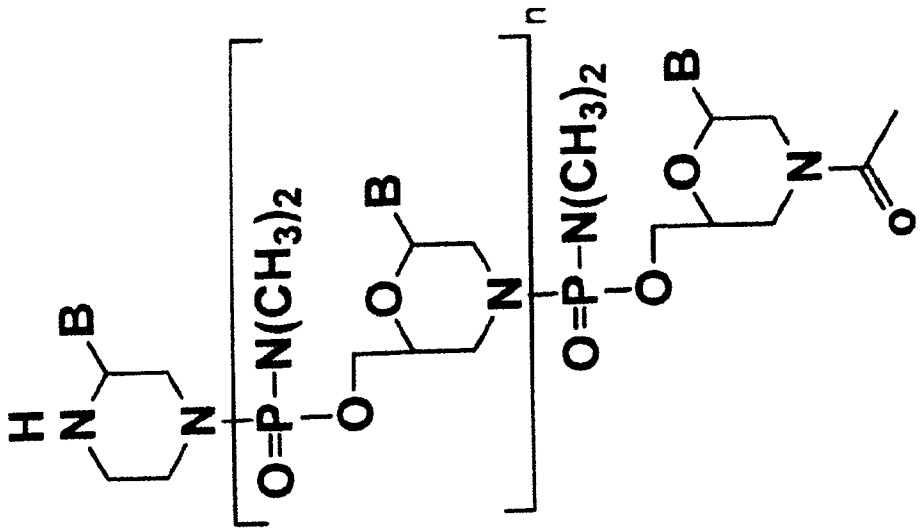


Fig. 13A

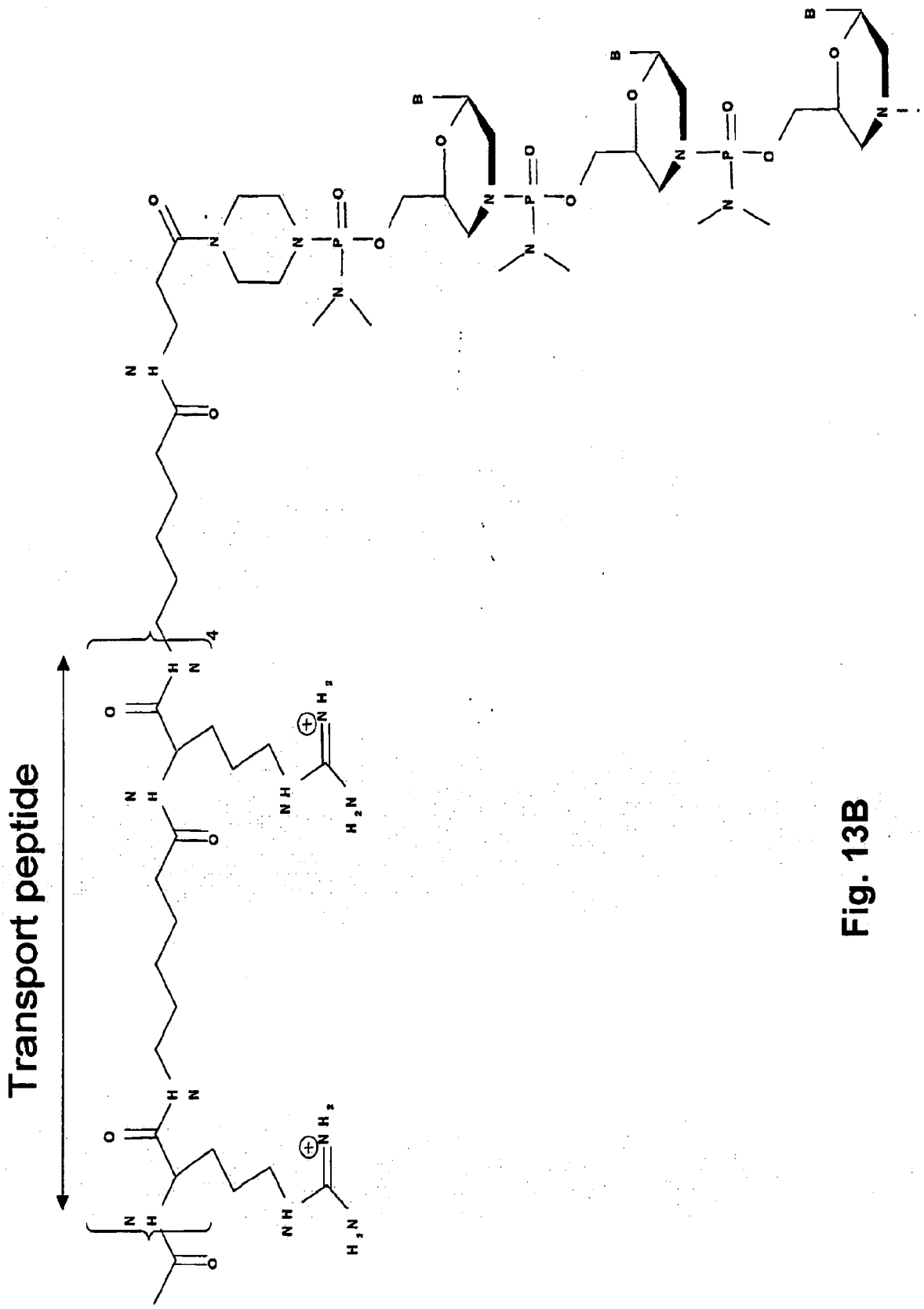


Fig. 13B

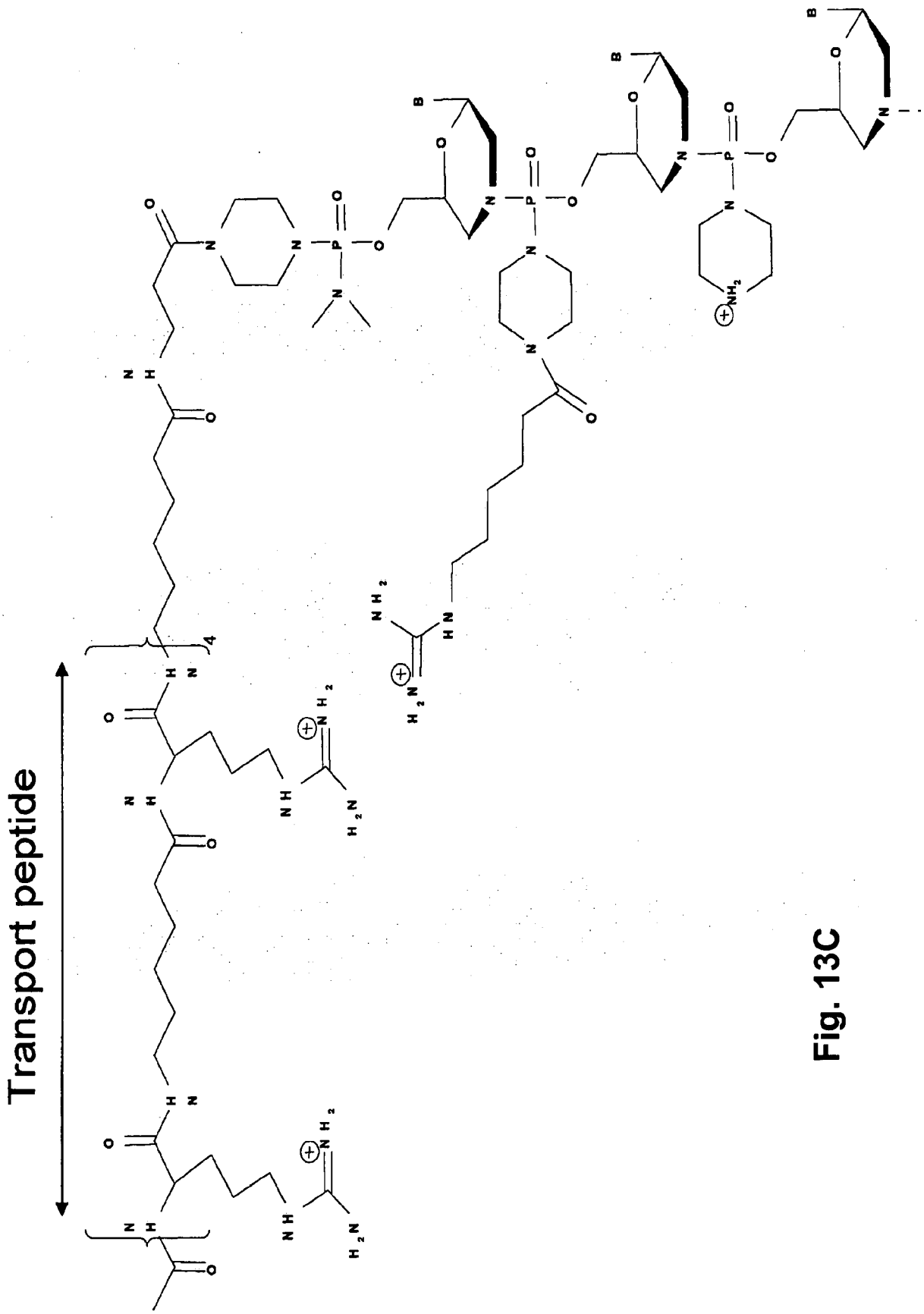


Fig. 13C

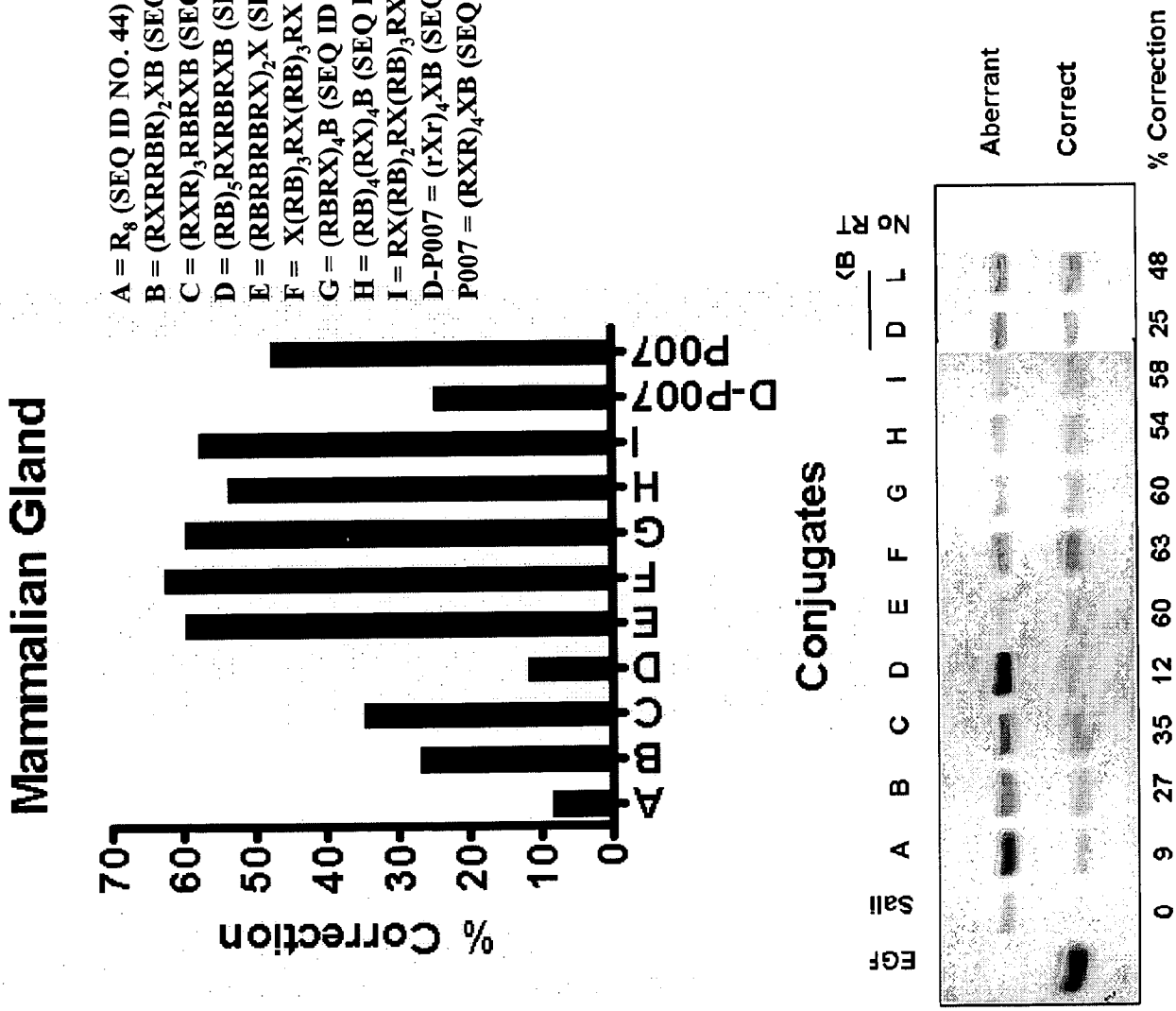

Mammalian Gland
A = R_8 (SEQ ID NO. 44)
B = $(RXRRBR)_2XB$ (SEQ ID NO. 45)
C = $(RXR)_3RBRXB$ (SEQ ID NO. 46)
D = $(RB)_5RXRBRXB$ (SEQ ID NO. 47)
E = $(RBRBRBRX)_2X$ (SEQ ID NO. 48)
F = $X(RB)_3RX(RB)_3RX$ (SEQ ID NO. 49)
G = $(RBRX)_4B$ (SEQ ID NO. 50)
H = $(RB)_4(RX)_4B$ (SEQ ID NO. 51)
I = $RX(RB)_2RX(RB)_3RX$ (SEQ ID NO. 52)
D-P007 = $(rXr)_4XB$ (SEQ ID NO. 53)
P007 = $(RXR)_4XB$ (SEQ ID NO. 54)
% Correction
70
60
50
40
30
20
10
0
A
B
C
D
E
F
G
H
I
D-P007
P007
Conjugates
EGF
Sali
A
B
C
D
E
F
G
H
I
D
L
No RT
0
9
27
35
12
60
63
60
54
58
25
48
Aberrant
Correct
% Correction

Fig. 14A

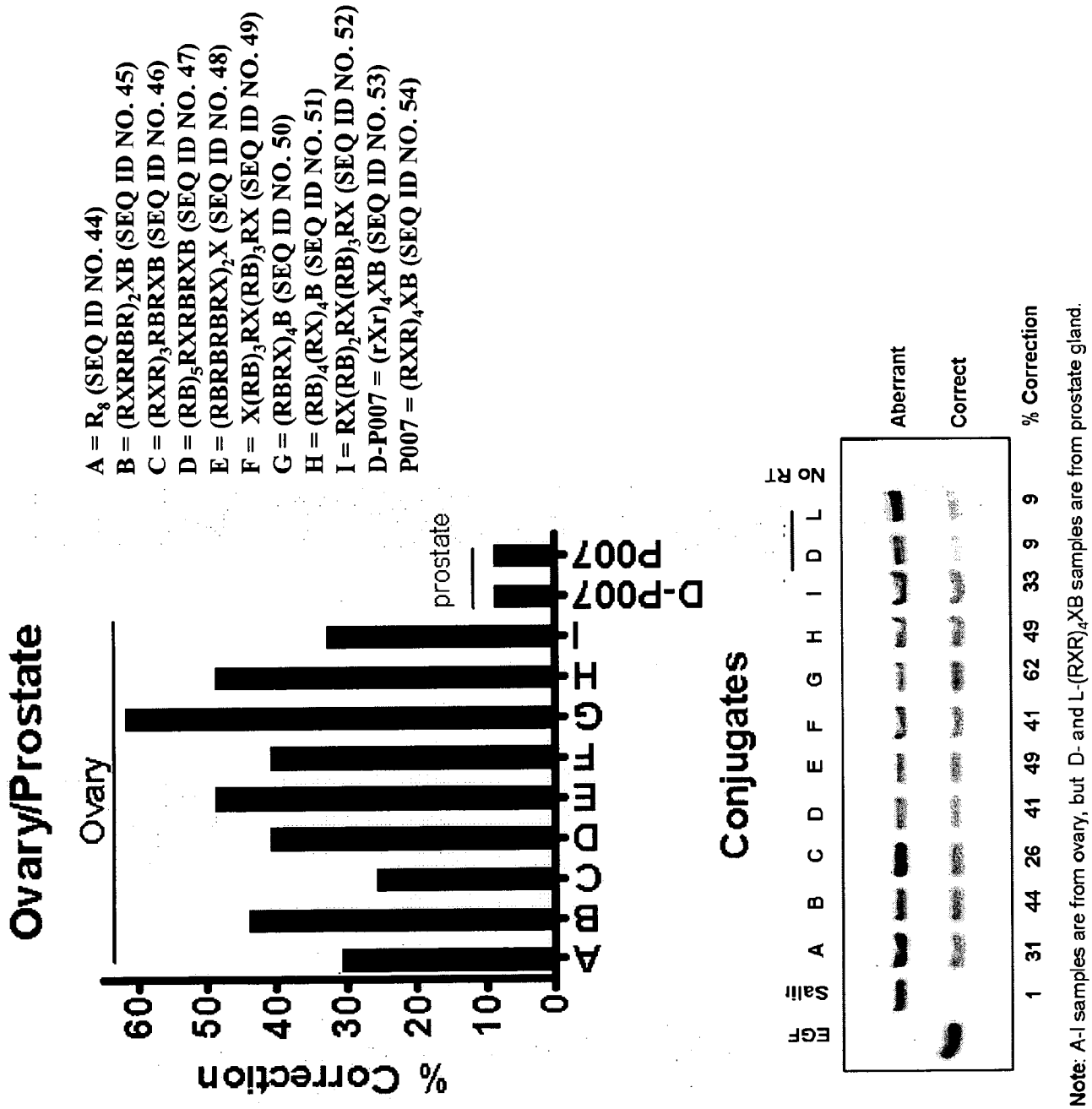

Ovary/Prostate
Ovary
prostate
% Correction
60
50
40
30
20
10
0
A
B
C
D
E
F
G
H
D-P007
P007
A = R8 (SEQ ID NO. 44)
B = (RXRRBR)2XB (SEQ ID NO. 45)
C = (RXR)3RBRXB (SEQ ID NO. 46)
D = (RB)5RXRBRXB (SEQ ID NO. 47)
E = (RBRBRBRX)2X (SEQ ID NO. 48)
F = X(RB)3RX(RB)3RX (SEQ ID NO. 49)
G = (RBRX)4B (SEQ ID NO. 50)
H = (RB)4(RX)4B (SEQ ID NO. 51)
I = RX(RB)2RX(RB)3RX (SEQ ID NO. 52)
D-P007 = (rXr)4XB (SEQ ID NO. 53)
P007 = (RXR)4XB (SEQ ID NO. 54)
Conjugates
EGF
Saline
A B C D E F G H I D L
No RT
1 31 44 26 41 49 41 62 49 33 9 9
% Correction
Aberrant
Correct
Note: A-I samples are from ovary, but D- and L-(RXR)4XB samples are from prostate gland.

Fig. 14B