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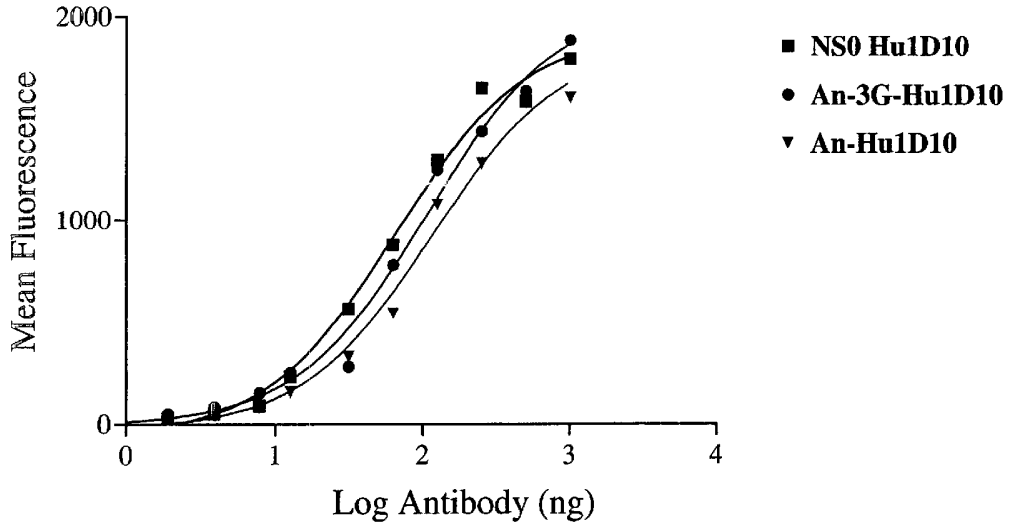
(54) Title: PRODUCTION OF FUNCTIONAL ANTIBODIES IN FILAMENTOUS FUNGI



(57) Abstract: Described herein are methods for the production of monoclonal antibodies in filamentous fungi host cells. The monoclonal antibodies are expressed as full-length fusion proteins that retain functional antigen binding and antibody-dependent cellular cytotoxicity capabilities. Improvements in the cleavage of the glucoamylase-light chainfusion protein to yield a mature antibody are also provided. The antibodies produced in filamentous fungi show equivalent pharmacokinetic disposition to antibodies produced in mammalian cells.

WO 03/089614 A2

PRODUCTION OF FUNCTIONAL ANTIBODIES IN FILAMENTOUS FUNGI

FIELD OF THE INVENTION

The present invention is directed to increased secretion of immunoglobulins from filamentous fungi. The invention discloses fusion nucleic acids, vectors, fusion polypeptides, and processes for obtaining the immunoglobulins.

BACKGROUND OF THE INVENTION

Production of fusion polypeptides has been reported in a number of organisms, including *E. coli,* yeast, and filamentous fungi. For example, bovine chymosin and porcine pancreatic prophospholipase A_2 have both been produced in *Aspergillus niger* or *Aspergillus niger* var. *awamori* (previously known as *Aspergillus awamori*) as fusions to full-length glucoamylase (GAI) (US Pat. No. 5,679,543; Ward et al., Bio/technology 8:435-440,1990; Roberts et al.,Gene 122:155-161, 1992). Human interleukin 6 (hIL6) has been produced in *A. nidulans* as a fusion to full-length *A. niger* GAI (Contreras et al., Biotechnology 9:378-381, 1991). Hen egg white lysozyme (Jeenes et al., FEMS Microbiol. Lett. 107:267-272, 1993) and human lactoferrin (Ward et al., Bio/technology 13:498-503, 1995) have been produced in *A. niger* as fusions to residues 1-498 of glucoamylase and hIL6 has been produced in *A. niger* as a fusion to glucoamylase residues 1-514 (Broekhuijsen et al., J. Biotechnol. 31:135-145, 1993). In some of the above experiments (Contreras et al., 1991; Broekhuijsen et al., 1993; Ward et al., 1995) a KEX2 protease recognition site (Lys, Arg) has been inserted between glucoamylase and the desired polypeptide to allow in vivo release of the desired polypeptide from the fusion protein as a result of the action of a native *Aspergillus* KEX2-like protease (the *Aspergillus* KEX2-like protease is now designated KEXB).

Additionally, bovine chymosin has been produced in *A. niger* var. *awamori* as a fusion with full-length native alpha-amylase (Korman et al., Curr. Genet. 17:203-212, 1990) and in *A. oryzae* as a fusion with truncated forms of *A. oryzae* glucoamylase (either residues 1-603 or 1-511; Tsuchiya et al., Biosci. Biotech. Biochem. 58:895-899, 1994). A small protein (epidermal growth hormone; 53 amino acids) has been produced in *Aspergillus* as a tandem fusion of three copies of the protein (US Patent 5,218,093). The trimer of EGF was secreted as a result of the inclusion of an N-terminal secretion signal

sequence. However, the EGF molecules were not additionally fused to a protein efficiently secreted by filamentous fungi and no method for subsequent separation of monomeric EGF proteins was provided.

The *glaA* gene encodes glucoamylase which is highly expressed in many strains of *Aspergillus niger* and *Aspergillus niger* var. *awamori*. The promoter and secretion signal sequence of the gene have been used to express heterologous genes in *Aspergilli* including bovine chymosin in *Aspergillus nidulans* and *A. niger* var. *awamori* as previously described (Cullen, D. *et al.* (1987) Bio/Technology 5, 713-719 and EPO Publication No. 0 215 594). In the latter experiments, a variety of constructs were made, incorporating prochymosin cDNA, either the glucoamylase or the chymosin secretion signal and, in one case, the first 11 codons of mature glucoamylase. Maximum yields of secreted chymosin obtained from *A. awamori* were below 15 mg/l in 50 ml shake flask cultures and were obtained using the chymosin signal sequence encoded by pGRG3. These previous studies indicated that integrated plasmid copy number did not correlate with chymosin yields. Abundant polyadenylated chymosin mRNA was produced, and intracellular levels of chymosin were high in some transformants regardless of the source of secretion signal. It was inferred that transcription was not a limiting factor in chymosin production but that secretion may have been inefficient. It was also evident that the addition of a small amino terminal segment (11 amino acids) of glucoamylase to the propeptide of prochymosin did not prevent activation to mature chymosin. The amount of extracellular chymosin obtained with the first eleven codons of glucoamylase, however, was substantially less than that obtained when the glucoamylase signal was used alone. Subsequently, it was demonstrated that chymosin production could be greatly increased when a fusion protein consisting of full-length glucoamylase and prochymosin was produced (USSN 08/318,494; Ward et al. Bio/technology 8:435-440, 1990).

Aspergillus niger and *Aspergillus niger* var. *awamori* (*A. awamori*) glucoamylases have identical amino acid sequences. The glucoamylase is initially synthesized as preproglucoamylase. The pre and pro regions are removed during the secretion process so that mature glucoamylase is released to the external medium. Two forms of mature glucoamylase are recognized in culture supernatants: GAI is the full-length form (amino acid residues 1-616) and GAII is a natural proteolytic fragment comprising amino acid residues 1-512. GAI is known to fold as two separate domains joined by an extended linker region. The two domains are the 471 residue catalytic domain (amino acids 1-471) and the 108 residue starch binding domain (amino acids 509-616), the linker region being 36 residues in length (amino acids 472-508). GAII lacks the starch binding domain. These

details of glucoamylase structure are reviewed by Libby et al. (Protein Engineering 7:1109-1114, 1994) and are shown diagrammatically in Fig. 2.

Trichoderma reesei produces several cellulase enzymes, including cellobiohydrolase I (CBHI), which are folded into two separate domains (catalytic and binding domains) separated by an extended linker region. Foreign polypeptides have been secreted in *T. reesei* as fusions with the catalytic domain plus linker region of CBHI (Nyyssonen et al., Bio/technology 11:591-595, 1993).

Antibody production has been, to date, preferably performed in transgenic animals, mammalian cell culture or plants. Each of these methods suffers from one or more drawbacks. For example, transgenic animals and mammalian cell cultures each have a risk of being contaminated by viral or other adventitious agents, e.g., prions. In addition, the ability to scale up any one of these production systems is limited. Recombinant plants may take approximately ten months to produce a recombinant protein, while mammalian cells may take about three months. Thus, there remains a need for alternative methods for antibody production.

SUMMARY OF THE INVENTION

Provided herein are nucleic acids, cells and methods for the production of immunoglobulins.

In a first embodiment, nucleic acids encoding a functional monoclonal immunoglobulin are provided. In one aspect, a nucleic acid comprising regulatory sequences operatively linked to a first, second, third and fourth nucleic acid sequences are provided. Terminator sequences are optionally provided following the fourth nucleic acid sequence. In a second aspect, the first nucleic acid sequence encodes a signal polypeptide functional as a secretory sequence in a first filamentous fungus, the second nucleic acid encodes a secreted polypeptide or functional portion thereof normally secreted from said first or a second filamentous fungus, the third nucleic acid encodes a cleavable linker and the fourth nucleic acid encodes an immunoglobulin chain or fragment thereof.

In a third aspect, an expression cassette comprising nucleic acid sequences encoding an immunoglobulin chain is provided.

In a second embodiment, methods of expressing a functional monoclonal antibody are provided. In one aspect, a host cell is (i) transformed with a first expression cassette comprising a nucleic acid sequence encoding a first immunoglobulin chain, (ii) transformed with a second expression cassette comprising a nucleic acid sequence encoding a second immunoglobulin chain, and (iii) cultured under appropriate conditions to express the immunoglobulin chains. Optionally, the immunoglobulin chains may be recovered. In one

aspect, the immunoglobulin chains are expressed as a fusion protein. The expressed fusion immunoglobulin chains are subsequently assembled as functional antibodies and secreted.

In a third embodiment, cells capable of expressing an immunoglobulin are provided. Host cells are transformed with two expression cassettes, a first expression cassette encoding a first immunoglobulin chain type (e.g., either a heavy or light chain) and a second expression cassette encoding a second immunoglobulin chain type (e.g., either light or heavy chain, respectively). The heavy chain may be of any immunoglobulin class.

In a fourth embodiment, a functional monoclonal immunoglobulin is provided. In one aspect, the functional monoclonal antibody chains are expressed as fusion proteins consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 502 of mature glucoamylase, followed by amino acids YKR and then by the mature immunoglobulin chain. One chain may be either the heavy or light chain.

In a second aspect, the fully assembled antibodies are treated with a protease to liberate an immunoglobulin from the fusion protein. In a third aspect, the antibodies may be treated with a deglycosylating enzyme.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the scope and spirit of the invention will become apparent to one skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows a schematic representation of an antibody. Indicated on the drawing are the various regions of the antibody and the names of various antibody fragments.

Figure 2 is a diagram depicting the two forms of glucoamylase from *Aspergillus niger* or *Aspergillus niger* var. *awamori*.

Figure 3 is a diagram of plasmid pQ83.

Figure 4 is a diagram of plasmid pCL1.

Figure 5 is a diagram of pCL5, a second trastuzumab heavy chain expression plasmid.

Figure 6 is a diagram of plasmid pCL2.

Figure 7 is a diagram of plasmid pCL3.

Figure 8 shows the results of SDS-PAGE under reducing conditions and with Coomassie Brilliant Blue staining of samples which had been purified by protein A chromatography. The bands observed for transformant 1-LC/HC-3 (lane 3) were identified as the light chain (25 kDa), non-glycosylated and glycosylated forms of the heavy chain (50 and 53 kDa), glucoamylase-light chain fusion protein (85 kDa) and glucoamylase-heavy chain fusion (116 kDa). The bands observed for transformant 1-HCΔ-4 (lane 2) were identified as the light chain (25 kDa), non-glycosylated form of the heavy chain (50 kDa), glucoamylase-light chain fusion protein (85 kDa) and glucoamylase-heavy chain fusion (116 kDa). The bands observed for transformant 1-Fab-1 (lane 1) were identified as the light chain and Fd' chain (both 25 kDa) and the glucoamylase-light chain and glucoamylase-Fd' fusion proteins (both 85 kDa).

Figure 9 shows the results of SDS-PAGE (NuPAGE Tris-Acetate Electrophoresis System from Invitrogen Corporation, Carlsbad, CA) under non- reducing conditions and with Coomassie Brilliant Blue staining of samples which had been purified by protein A chromatography. The major bands observed for transformant 1-LC/HC-3 (lane 4) were identified as assembled IgG1 (150 kDa), assembled IgG1 with one molecule of glucoamylase attached (~200 kDa) and assembled IgG1 with two molecules of glucoamylase attached (~250 kDa). The major bands observed for transformant 1-HCΔ-4 (lane 3) were identified as assembled IgG1 (150 kDa), assembled IgG1 with one molecule of glucoamylase attached (~200 kDa) and assembled IgG1 with two molecules of glucoamylase attached (~250 kDa). The major bands observed for transformant 1-Fab-1 (lane 2) were identified as assembled Fab' (50 kDa) and assembled Fab' with one molecule of glucoamylase attached (~100 kDa).

Figure 10 shows the results of SDS-PAGE under reducing and non-reducing conditions of samples of Fab' and F(ab')2 purified from supernatant of transformant 1-Fab-12 by hydrophobic charge induction chromatography followed by size exclusion chromatography. A5, B11, B7 and B3 represent different fractions collected from the size exclusion chromatography column.

Figure 11 is a graph showing the anti-proliferative effect of the HER2 antibodies on human breast adenocarcinoma cell line, SK-BR-3 (ATCC number: HTB-30). Commercial Herceptin antibodies are indicated by diamonds (♦) and triangles (▲). *Aspergillus* transformant 1LC/HC-3 antibodies are indicated by circles (●) and squares (■). Control cells were A-431, a human epidermoid carcinoma that expresses high levels of the EGF receptor and low levels of HER2.

Figure 12 is a graph showing the binding of Hu1D10 antibody derived from NS0 mouse myeloma cell line (squares; ■), and two Aspergillus produced antibodies (designated

as An-3G-Hu1D10 [circles; •] and An-Hu1D10 [inverted triangles; ▼]) to Raji cells. No significant difference in binding was observed.

Figure 13 is a graph showing the competitive binding of FITC-labeled antibody with Hu1D10 antibody derived from NS0 mouse myeloma cell line (squares; ■), and two Aspergillus produced antibodies (An-3G-Hu1D10 [circles; •] and An-Hu1D10 [inverted triangles; ▼]) to Raji cells. No significant difference in binding was observed.

Figure 14 is a bar graph indicating the percentage of cells in which apoptosis has been induced by Hu1D10, An-3G-Hu1D10 and An-Hu1D10 at 5 hours or 24 hours. No significant difference in inducing apoptosis was observed.

Figures 15 A and B are graphs depicting the levels of Antibody-Dependent Cellular Cytotoxicity reached by each of the three antibodies tested, i.e., Hu1D10, An-3G-Hu1D10 and An-Hu1D10, in two different donors. Clear indication of ADCC activity by Aspergillus-derived antibodies is exhibited.

Figure 16 is a graph of the *in vivo* pharmacokinetics of CHO-derived and Aspergillus-derived trastuzumab. No significant difference in pharmacokinetic disposition was observed for the fungal-derived antibody.

DETAILED DESCRIPTION OF THE INVENTION

The inventors have discovered that desired antibodies can be expressed and secreted in filamentous fungi at levels higher than that previously obtained using other expression systems.

The invention will now be described in detail by way of reference only using the following definitions and examples. All patents and publications, including all sequences disclosed within such patents and publications, referred to herein are expressly incorporated by reference.

Unless defined otherwise herein, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton, *et al.*, DICTIONARY OF MICROBIOLOGY AND MOLECULAR BIOLOGY, 2D ED., John Wiley and Sons, New York (1994), and Hale & Marham, THE HARPER COLLINS DICTIONARY OF BIOLOGY, Harper Perennial, NY (1991) provide one of skill with a general dictionary of many of the terms used in this invention. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are described. Numeric ranges are inclusive of the numbers defining the range. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively. Practitioners are

particularly directed to Sambrook *et al.,* 1989, and Ausubel FM *et al.,* 1993, for definitions and terms of the art. It is to be understood that this invention is not limited to the particular methodology, protocols, and reagents described, as these may vary.

The headings provided herein are not limitations of the various aspects or embodiments of the invention which can be had by reference to the specification as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the specification as a whole.

Definitions

The terms "isolated" or "purified" as used herein refer to a nucleic acid or amino acid or polypeptide that is removed from at least one component with which it is naturally associated.

An "expression cassette" or "expression vector" is a nucleic acid construct generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a target cell. The recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression cassette portion of an expression vector includes, among other sequences, a nucleic acid sequence to be transcribed and a promoter. Expression cassette may be used interchangeably with DNA construct and its grammatical equivalents.

As used herein, the term "vector" refers to a nucleic acid construct designed for transfer nucleic acid sequences into cells. An "expression vector" refers to a vector that has the ability to incorporate and express heterologous DNA fragments in a foreign cell. Many prokaryotic and eukaryotic expression vectors are commercially available. Selection of appropriate expression vectors is within the knowledge of those having skill in the art.

As used herein, the term "plasmid" refers to a circular double-stranded (ds) DNA construct used as a cloning vector, and which forms an extrachromosomal self-replicating genetic element in some eukaryotes.

The term "nucleic acid molecule" or "nucleic acid sequence" includes RNA, DNA and cDNA molecules. It will be understood that, as a result of the degeneracy of the genetic code, a multitude of nucleotide sequences encoding a given protein may be produced.

As used herein, a "fusion DNA sequence" comprises from 5' to 3' first, second, third and fourth DNA sequences.

As used herein, "a first nucleic acid sequence" or "first DNA sequence" encodes a signal peptide functional as a secretory sequence in a first filamentous fungus. Such signal

sequences include those from glucoamylase, α-amylase and aspartyl proteases from *Aspergillus niger* var. *awamori, Aspergillus niger, Aspergillus oryzae*, signal sequences from cellobiohydrolase I, cellobiohydrolase II, endoglucanase I, endoglucanase III from *Trichoderma*, signal sequences from glucoamylase from *Neurospora* and *Humicola* as well as signal sequences from eukaryotes including the signal sequence from bovine chymosin, human tissue plasminogen activator, human interferon and synthetic consensus eukaryotic signal sequences such as that described by Gwynne *et al.* (1987) Bio/Technology 5, 713-719. Particularly preferred signal sequences are those derived from polypeptides secreted by the expression host used to express and secrete the fusion polypeptide. For example, the signal sequence from glucoamylase from *Aspergillus niger* is preferred when expressing and secreting a fusion polypeptide from *Aspergillus niger*. As used herein, first amino acid sequences correspond to secretory sequences which are functional in a filamentous fungus. Such amino acid sequences are encoded by first DNA sequences as defined.

As used herein, "second DNA sequences" encode "secreted polypeptides" normally expressed from filamentous fungi. Such secreted polypeptides include glucoamylase, α-amylase and aspartyl proteases from *Aspergillus niger* var. *awamori*, *Aspergillus niger*, and *Aspergillus oryzae*, cellobiohydrolase I, cellobiohydrolase II, endoglucanase I and endoglucanase III from *Trichoderma* and glucoamylase from *Neurospora* species and *Humicola* species. As with the first DNA sequences, preferred secreted polypeptides are those which are naturally secreted by the filamentous fungal expression host. Thus, for example when using *Aspergillus niger*, preferred secreted polypeptides are glucoamylase and α-amylase from *Aspergillus niger*, most preferably glucoamylase. In one aspect the glucoamylase is greater than 95%, 96%, 97%, 98% or 99% homologous with an *Aspergillus* glucoamylase.

When *Aspergillus* glucoamylase is the secreted polypeptide encoded by the second DNA sequence, the whole protein or a portion thereof may be used, optionally including a prosequence. Thus, the cleavable linker polypeptide may be fused to glucoamylase at any amino acid residue from position 468 – 509. Other amino acid residues may be the fusion site but utilizing the above residues is particularly advantageous.

A "functional portion of a secreted polypeptide" or grammatical equivalents means a truncated secreted polypeptide that retains its ability to fold into a normal, albeit truncated, configuration. For example, in the case of bovine chymosin production by *A. niger* var. *awamori* it has been shown that fusion of prochymosin following the 11th amino acid of mature glucoamylase provided no benefit compared to production of preprochymosin (US patent 5,364,770). In USSN 08/318,494, it was shown that fusion of prochymosin onto the

C-terminus of preproglucoamylase up to the 297th amino acid of mature glucoamylase plus a repeat of amino acids 1-11 of mature glucoamylase yielded no secreted chymosin in *A. niger* var. *awamori*. In the latter case it is unlikely that the portion (approximately 63%) of the glucoamylase catalytic domain present in the fusion protein was able to fold correctly so that an aberrant, mis-folded and/or unstable fusion protein may have been produced which could not be secreted by the cell. The inability of the partial catalytic domain to fold correctly may have interfered with the folding of the attached chymosin. Thus, it is likely that sufficient residues of a domain of the naturally secreted polypeptide must be present to allow it to fold in its normal configuration independently of the desired polypeptide to which it is attached.

In most cases, the portion of the secreted polypeptide will be both correctly folded and result in increased secretion as compared to its absence.

Similarly, in most cases, the truncation of the secreted polypeptide means that the functional portion retains a biological function. In a preferred embodiment, the catalytic domain of a secreted polypeptide is used, although other functional domains may be used, for example, the substrate binding domains. In the case of *Aspergillus niger* and *Aspergillus niger* var. *awamori* glucoamylase, preferred functional portions retain the catalytic domain of the enzyme, and include amino acids 1-471. Additionally preferred embodiments utilize the catalytic domain and all or part of the linker region. Alternatively, the starch binding domain of glucoamylase may be used, which comprises amino acids 509-616 of *Aspergillus niger* and *Aspergillus niger* var. *awamori* glucoamylase.

As used herein, "third DNA sequences" comprise DNA sequences encoding a cleavable linker polypeptide. Such sequences include those which encode the prosequence of bovine chymosin, the prosequence of subtilisin, prosequences of retroviral proteases including human immunodeficiency virus protease and DNA sequences encoding amino acid sequences recognized and cleaved by trypsin, factor X_a collagenase, clostripin, subtilisin, chymosin, yeast KEX2 protease, *Aspergillus* KEXB and the like. See e.g. Marston, F.A.O. (1986) Biol. Chem J. 240, 1-12. Such third DNA sequences may also encode the amino acid methionine that may be selectively cleaved by cyanogen bromide. It should be understood that the third DNA sequence need only encode that amino acid sequence which is necessary to be recognized by a particular enzyme or chemical agent to bring about cleavage of the fusion polypeptide. Thus, the entire prosequence of, for example, chymosin or subtilisin need not be used. Rather, only that portion of the prosequence which is necessary for recognition and cleavage by the appropriate enzyme is required.

It should be understood that the third nucleic acid need only encode that amino acid sequence which is necessary to be recognized by a particular enzyme or chemical agent to bring about cleavage of the fusion polypeptide.

Particularly preferred cleavable linkers are the KEX2 protease recognition site (Lys-Arg), which can be cleaved by a native *Aspergillus* KEX2-like (KEXB) protease, trypsin protease recognition sites of Lys and Arg, and the cleavage recognition site for endoproteinase-Lys-C.

As used herein, "fourth DNA sequences" encode "desired polypeptides." Such desired polypeptides include mammalian immunoglobulin chains. Immunoglobulins include, but are not limited to, antibodies from any species from which it is desirable to produce large quantities. It is especially preferred that the antibodies are human antibodies. Immunoglobulins may be from any class, i.e., G, A, M, E or D. In another aspect the antibodies are monoclonal. The antibody chains may be either the heavy or light chain. The terms "immunoglobulin" and "antibody" are used interchangeably herein.

The above-defined four DNA sequences encoding the corresponding four amino acid sequences are combined to form a "fusion DNA sequence." Such fusion DNA sequences are assembled in proper reading frame from the 5' terminus to 3' terminus in the order of first, second, third and fourth DNA sequences. As so assembled, the DNA sequence will encode a "fusion polypeptide" or "fusion protein" encoding from its amino-terminus a signal peptide functional as a secretory sequence in a filamentous fungus, a secreted polypeptide or portion thereof normally secreted from a filamentous fungus, a cleavable linker polypeptide and a desired polypeptide.

As used herein, a "promotor sequence" is a DNA sequence which is recognized by the particular filamentous fungus for expression purposes. It is operably linked to a DNA sequence encoding the above defined fusion polypeptide. Such linkage comprises positioning of the promoter with respect to the translation initiation codon of the DNA sequence encoding the fusion DNA sequence. The promoter sequence contains transcription and translation control sequences which mediate the expression of the fusion DNA sequence. Examples include the promoter from the *A. niger* var. *awamori* or *A. niger* glucoamylase genes (Nunberg, J.H. et al. (1984) Mol. Cell. Biol. 4, 2306-2315; Boel, E. et al. (1984) EMB0 J. 3, 1581-1585), the *A. oryzae, A. niger* var. *awamori* or *A. niger* or alpha-amylase genes, the *Rhizomucor miehei* carboxyl protease gene, the *Trichoderma reesei* cellobiohydrolase I gene (Shoemaker, S.P. et al. (1984) European Patent Application No. EPO0137280A1), the *A. nidulans trpC* gene (Yelton, M. et al. (1984) Proc. Natl. Acad. Sci. USA 81, 1470-1474; Mullaney, E.J. et al. (1985) Mol. Gen. Genet. 199, 37-45) the *A. nidulans alcA* gene (Lockington, R.A. et al. (1986) Gene 33 137-149), the *A. nidulans amdS*

gene (McKnight, G.L. et al. (1986) Cell 46, 143-147), the *A. nidulans amdS* gene (Hynes, M.J. et al. (1983) Mol. Cell Biol. 3, 1430-1439), and higher eukaryotic promoters such as the SV40 early promoter (Barclay, S.L. and E. Meller (1983) Molecular and Cellular Biology 3, 2117-2130).

Likewise a "terminator sequence" is a DNA sequence which is recognized by the expression host to terminate transcription. It is operably linked to the 3' end of the fusion DNA encoding the fusion polypeptide to be expressed. Examples include the terminator from the *A. nidulans trpC* gene (Yelton, M. et al. (1984) Proc. Natl. Acad. Sci. USA 81, 1470-1474; Mullaney, E.J. et al. (1985) Mol. Gen. Genet. 199, 37-45), the *A. niger* var. *awamori* or *A. niger* glucoamylase genes (Nunberg, J.H. et al. (1984) Mol. Cell. Biol. 4, 2306-253; Boel, E. et al. (1984) EMBO J. 3, 1581-1585), the *A. oryzae, A. niger* var. *awamori* or *A. niger* or alpha-amylase genes and the *Rhizomucor miehei* carboxyl protease gene (EPO Publication No. 0 215 594), although any fungal terminator is likely to be functional in the present invention.

A "polyadenylation sequence" is a DNA sequence which when transcribed is recognized by the expression host to add polyadenosine residues to transcribed mRNA. It is operably linked to the 3' end of the fusion DNA encoding the fusion polypeptide to be expressed. Examples include polyadenylation sequences from the *A. nidulans trpC* gene (Yelton, M. et al. (1984) Proc. Natl. Acad. Sci. USA 81, 1470-1474; Mullaney, E.J. et al. (1985) Mol. Gen. Genet. 199, 37-45), the *A. niger* var. *awamori* or *A. niger* glucoamylase genes (Nunberg, J.H. et al. (1984) Mol. Cell. Biol. 4, 2306-2315) (Boel, E. et al. (1984) EMBO J. 3, 1581-1585), the *A. oryzae, A. niger* var. *awamori* or *A. niger* or alpha-amylase genes and the *Rhizomucor miehei* carboxyl protease gene described above. Any fungal polyadenylation sequence, however, is likely to be functional in the present invention.

As used herein, the term "selectable marker-encoding nucleotide sequence" refers to a nucleotide sequence which is capable of expression in fungal cells and where expression of the selectable marker confers to cells containing the expressed gene the ability to grow in the presence of a corresponding selective condition.

A nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA encoding a secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However,

enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

As used herein, "recombinant" includes reference to a cell or vector, that has been modified by the introduction of a heterologous nucleic acid sequence or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all as a result of deliberate human intervention.

As used herein, the term "expression" refers to the process by which a polypeptide is produced based on the nucleic acid sequence of a gene. The process includes both transcription and translation. It follows that the term "Ig chain expression" refers to transcription and translation of the specific Ig chain gene to be expressed, the products of which include precursor RNA, mRNA, polypeptide, post-translation processed polypeptide, and derivatives thereof. Similarly, "Ig expression" refers to the transcription, translation and assembly of the Ig chains into a form exemplified by Figure 1. By way of example, assays for immunoglobulin expression include examination of fungal colonies when exposed to the appropriate conditions, western blot for Ig protein, as well as northern blot analysis and reverse transcriptase polymerase chain reaction (RT-PCR) assays for immunoglobulin mRNA.

As used herein the term "glycosylated" means that oligosaccharide molecules have been added to particular amino acid residues on a protein. A "de-glycosylated" protein is a protein that has been treated to partially or completely remove the oligosaccharide molecules from the protein. An "aglycosylated" protein is a protein that has not had the oligosaccharide molecules added to the protein. This may be due to a mutation in the protein that prevents the addition of the oligosaccharide.

A "non-glycosylated" protein is a protein that does not have the oligosaccharide attached to the protein. This may be due to various reasons, including but not limited to, the absence of enzymes responsible for the addition of the oligosaccharides to proteins. The term "non-glycosylated" encompasses both proteins that have not had the oligosaccharide added to the protein and those in which the oligosaccharides have been added but were subsequently removed. An "aglycosylated" protein may be a "non-glycosylated" protein. A "non-glycosylated" protein may be either an "aglycosylated" protein or a "deglycosylated" protein.

Fusion Proteins

The above-defined four DNA sequences encoding the corresponding four amino acid sequences are combined to form a "fusion DNA sequence." Such fusion DNA sequences are assembled in proper reading frame from the 5' terminus to 3' terminus in the order of first, second, third and fourth DNA sequences. As so assembled, the DNA sequence will encode a "fusion polypeptide" encoding from its amino-terminus a signal peptide functional as a secretory sequence in a filamentous fungus, a secreted polypeptide or portion thereof normally secreted from a filamentous fungus, a cleavable linker polypeptide and a desired polypeptide, e.g., an immunglobulin chain.

Antibodies are comprised of two chain types, one light and one heavy. The basic structure of an antibody is the same regardless of the specificity for a particular antigen. Each antibody comprises four polypeptide chains of two different types. The chains are called the heavy chain (50-70 kDa in size) and the light chain (25 kDa). Two identical heavy chains and two identical light chains are linked together via interchain disulphide bonds to create the antibody monomer (Fig.1). In addition to the interchain disulphide bonds there are also intrachain disulphide bonds in both the heavy and light chains. Different types of heavy and light chains are recognized. Heavy chains may be of the γ, μ, α, δ or ε class and this defines the class of immunoglobulin, i.e., IgG, IgM, IgA, IgD or IgE respectively. There are sub-classes within these classes, e.g., in humans there are four subclasses of the γ heavy chain, γ1, γ2, γ3 and γ4 to produce IgG1, IgG2, IgG3 and IgG4 respectively. Light chains may be of the λ or κ type but this does not affect the class or subclass definition of the immunoglobulin. Thus, a human IgG1 molecule will contain two identical γ1 heavy chains linked to two identical light chains which may be of the λ or κ type (i.e., IgG1λ or IgG1κ).

A heavy chain is divided into distinct structural domains. For example, a γ heavy chain comprises, from the amino terminus, a variable region (VH), a constant region (CH1) a hinge region, a second constant region (CH2) and a third constant region (CH3). Light chains are structurally divided into two domains, a variable region (VL) and a constant region (CL). Antibody forms in which the heavy chain has been truncated to remove some of the constant region can be generated by protease digestion or by recombinant DNA methodology. For example, Fab fragments (Fig 1) of an IgG have a form of the heavy chain (Fd) lacking the hinge region and the CH2 and CH3 domains whereas Fab' fragments (Fig 1) of an IgG have a form of the heavy chain (Fd') which includes the hinge region but lacks the CH2 and CH3 domains.

Each chain will be expressed as a fusion protein by the host fungal cell. The chains are assembled into a complete antibody comprising the two heavy and two light chains.

Although cleavage of the fusion polypeptide to release the desired antibody will often be useful, it is not necessary. Antibodies expressed and secreted as fusion proteins surprisingly assemble and retain their antigen binding function.

Expression Of Recombinant Immunoglobulin and Immunoglobulin Fragments

This invention provides filamentous fungal host cells which have been transduced, transformed or transfected with an expression vector comprising a Ig-encoding nucleic acid sequence. The culture conditions, such as temperature, pH and the like, are those previously used for the parental host cell prior to transduction, transformation or transfection and will be apparent to those skilled in the art.

In one approach, a filamentous fungal cell line is transfected with an expression vector having a promoter or biologically active promoter fragment or one or more (e.g., a series) of enhancers which functions in the host cell line, operably linked to a nucleic acid sequence encoding Ig chain(s), such that the Ig chain(s) and fully assembled Ig is expressed in the cell line. In a preferred embodiment, the DNA sequences encode an Ig coding sequence. In another preferred embodiment, the promoter is a regulatable one.

A. Nucleic Acid Constructs/Expression Vectors.

Natural or synthetic polynucleotide fragments encoding immunoglobulin ("immunoglobulin-encoding nucleic acid sequences") may be incorporated into heterologous nucleic acid constructs or vectors, capable of introduction into, and replication in, a filamentous fungal cell. The vectors and methods disclosed herein are suitable for use in host cells for the expression of immunoglobulin chain(s) and fully assembled immunoglobulin molecules. Any vector may be used as long as it is replicable and viable in the cells into which it is introduced. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. Appropriate cloning and expression vectors for use in filamentous fungal cells are also described in Sambrook *et al.*, 1989, and Ausubel FM *et al.*, 1989, expressly incorporated by reference herein. The appropriate DNA sequence may be inserted into a plasmid or vector (collectively referred to herein as "vectors") by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by standard procedures. Such procedures and related sub-cloning procedures are deemed to be within the scope of knowledge of those skilled in the art.

Appropriate vectors are typically equipped with a selectable marker-encoding nucleic acid sequence, insertion sites, and suitable control elements, such as termination sequences. The vector may comprise regulatory sequences, including, for example, non-

coding sequences, such as introns and control elements, *i.e.*, promoter and terminator elements or 5' and/or 3' untranslated regions, effective for expression of the coding sequence in host cells (and/or in a vector or host cell environment in which a modified soluble protein antigen coding sequence is not normally expressed), operably linked to the coding sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, many of which are commercially available and/or are described in Sambrook, *et al.*, (*supra*).

Exemplary promoters include both constitutive promoters and inducible promoters, examples of which include a CMV promoter, an SV40 early promoter, an RSV promoter, an EF-1α promoter, a promoter containing the tet responsive element (TRE) in the tet-on or tet-off system as described (ClonTech and BASF), the beta actin promoter and the metallothionein promoter that can upregulated by addition of certain metal salts. In one embodiment of this invention, *glaA* promoter is used. This promoter is induced in the presence of maltose. Such promoters are well known to those of skill in the art.

The choice of the proper selectable marker will depend on the host cell, and appropriate markers for different hosts are well known in the art. Typical selectable marker genes encode proteins that (a) confer resistance to antibiotics or other toxins, *for example*, ampicillin, methotrexate, tetracycline, neomycin (Southern and Berg, J., 1982), mycophenolic acid (Mulligan and Berg, 1980), puromycin, zeomycin, or hygromycin (Sugden et al., 1985) or (b) compliment an auxotrophic mutation or a naturally occuring nutritional deficiency in the host strain. In a preferred embodiment, a fungal *pyrG* gene is used as a selectable marker (Ballance, D.J. et al., 1983, Biochem. Biophys. Res. Commun. 112:284-289). In another preferred embodiment, a fungal *amdS* gene is used as a selectable marker (Tilburn, J. et al., 1983, Gene 26:205-221).

A selected immunoglobulin coding sequence may be inserted into a suitable vector according to well-known recombinant techniques and used to transform a cell line capable of immunoglobulin expression. Due to the inherent degeneracy of the genetic code, other nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used to clone and express a specific immunoglobulin, as further detailed above. Therefore it is appreciated that such substitutions in the coding region fall within the sequence variants covered by the present invention. Any and all of these sequence variants can be utilized in the same way as described herein for a parent immunoglobulin-encoding nucleic acid sequence. One skilled in the art will recognize that differing immunoglobulins will be encoded by differing nucleic acid sequences.

Once the desired form of an immunoglobulin nucleic acid sequence, homologue, variant or fragment thereof, is obtained, it may be modified in a variety of ways. Where the

sequence involves non-coding flanking regions, the flanking regions may be subjected to resection, mutagenesis, etc. Thus, transitions, transversions, deletions, and insertions may be performed on the naturally occurring sequence.

Heterologous nucleic acid constructs may include the coding sequence for an immunoglobulin, or a variant, fragment or splice variant thereof: (i) in isolation; (ii) in combination with additional coding sequences; such as fusion protein or signal peptide coding sequences, where the immunoglobulin coding sequence is the dominant coding sequence; (iii) in combination with non-coding sequences, such as introns and control elements, such as promoter and terminator elements or 5' and/or 3' untranslated regions, effective for expression of the coding sequence in a suitable host; and/or (iv) in a vector or host environment in which the immunoglobulin coding sequence is a heterologous gene.

A heterologous nucleic acid containing the appropriate nucleic acid coding sequence, as described above, together with appropriate promoter and control sequences, may be employed to transform filamentous fungal cells to permit the cells to express immunoglobulin chains and fully assembled immunoglobulins.

In one aspect of the present invention, a heterologous nucleic acid construct is employed to transfer an immunoglobulin-encoding nucleic acid sequence into a cell *in vitro*, with established cell lines preferred. Preferably, cell lines that are to be used as production hosts have the nucleic acid sequences of this invention stably integrated. It follows that any method effective to generate stable transformants may be used in practicing the invention.

In one aspect of the present invention, the first and second expression cassettes may be present on a single vector or on separate vectors.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, "Molecular Cloning: A Laboratory Manual", Second Edition (Sambrook, Fritsch & Maniatis, 1989), "Animal Cell Culture" (R. I. Freshney, ed., 1987); "Current Protocols in Molecular Biology" (F. M. Ausubel *et al.*, eds., 1987); and "Current Protocols in Immunology" (J. E. Coligan *et al.*, eds., 1991). All patents, patent applications, articles and publications mentioned herein, both *supra* and *infra*, are hereby expressly incorporated herein by reference.

B. Host Cells and Culture Conditions.

The present invention provides cell lines comprising cells which have been modified, selected and cultured in a manner effective to result in expression of immunoglobulin chain(s) and fully assembled immunoglobulin molecules.

Examples of parental cell lines which may be treated and/or modified for immunoglobulin expression include, but are not limited to, filamentous fungal cells. Examples of appropriate primary cell types for use in practicing the invention include, but are not limited to, *Aspergillus* and *Trichoderma*.

Immunoglobulin expressing cells are cultured under conditions typically employed to culture the parental cell line. Generally, cells are cultured in a standard medium containing physiological salts and nutrients, such as standard RPMI, MEM, IMEM or DMEM, typically supplemented with 5-10% serum, such as fetal bovine serum. Culture conditions are also standard, *e.g.*, cultures are incubated at 37°C in stationary or roller cultures until desired levels of immunoglobulin expression are achieved.

Preferred culture conditions for a given cell line may be found in the scientific literature and/or from the source of the cell line such as the American Type Culture Collection (ATCC; "http://www.atcc.org/"). Typically, after cell growth has been established, the cells are exposed to conditions effective to cause or inhibit the expression of immunoglobulin chain(s) and fully assembled immunoglobulin molecules.

In the preferred embodiments, where a immunoglobulin coding sequence is under the control of an inducible promoter, the inducing agent, *e.g.*, a carbohydrate, metal salt or antibiotics, is added to the medium at a concentration effective to induce immunoglobulin expression.

C. Introduction Of An Immunoglobulin-Encoding Nucleic Acid Sequence Into Host Cells.

The invention further provides cells and cell compositions which have been genetically modified to comprise an exogenously provided immunoglobulin-encoding nucleic acid sequence. A parental cell or cell line may be genetically modified (*i.e.*, transduced, transformed or transfected) with a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc, as further described above. In a preferred embodiment, a plasmid is used to transfect a filamentous fungal cell. The transformations may be sequential or by co-transformation.

Various methods may be employed for delivering an expression vector into cells *in vitro*. Methods of introducing nucleic acids into cells for expression of heterologous nucleic acid sequences are also known to the ordinarily skilled artisan, including, but not limited to electroporation; nuclear microinjection or direct microinjection into single cells; bacterial protoplast fusion with intact cells; use of polycations, *e.g.*, polybrene or polyornithine; membrane fusion with liposomes, lipofectamine or lipofection-mediated transfection; high velocity bombardment with DNA-coated microprojectiles; incubation with calcium phosphate-DNA precipitate; DEAE-Dextran mediated transfection; infection with modified

viral nucleic acids; *Agrobacterium*-mediated transfer of DNA; and the like. In addition, heterologous nucleic acid constructs comprising a immunoglobulin-encoding nucleic acid sequence can be transcribed *in vitro*, and the resulting RNA introduced into the host cell by well-known methods, *e.g.*, by injection.

Following introduction of a heterologous nucleic acid construct comprising the coding sequence for immunoglobulin chain(s), the genetically modified cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying expression of a immunoglobulin-encoding nucleic acid sequence. The culture conditions, such as temperature, pH and the like, are those previously used for the host cell selected for expression, and will be apparent to those skilled in the art.

The progeny of cells into which such heterologous nucleic acid constructs have been introduced are generally considered to comprise the immunoglobulin-encoding nucleic acid sequence found in the heterologous nucleic acid construct.

Fungal Expression

Appropriate host cells include filamentous fungal cells. The "filamentous fungi" of the present invention, which serve both as the expression hosts and the source of the first and second nucleic acids, are eukaryotic microorganisms and include all filamentous forms of the subdivision Eumycotina, Alexopoulos, C.J. (1962), Introductory Mycology, New York: Wiley. These fungi are characterized by a vegetative mycelium with a cell wall composed of chitin, glucans, and other complex polysaccharides. The filamentous fungi of the present invention are morphologically, physiologically, and genetically distinct from yeasts. Vegetative growth by filamentous fungi is by hyphal elongation. In contrast, vegetative growth by yeasts such as *S. cerevisiae* is by budding of a unicellular thallus. Illustrations of differences between *S. cerevisiae* and filamentous fungi include the inability of *S. cerevisiae* to process *Aspergillus* and *Trichoderma* introns and the inability to recognize many transcriptional regulators of filamentous fungi (Innis, M.A. *et al.* (1985) Science, 228, 21-26).

Various species of filamentous fungi may be used as expression hosts including the following genera: *Aspergillus, Trichoderma, Neurospora, Penicillium, Cephalosporium, Achlya, Phanerochaete, Podospora, Endothia, Mucor, Fusarium, Humicola,* and *Chrysosporium*. Specific expression hosts include *A. nidulans*, (Yelton, M., *et al.* (1984) Proc. Natl. Acad. Sci. USA, 81, 1470-1474; Mullaney, E.J. *et al.* (1985) Mol. Gen. Genet. 199, 37-45; John, M.A. and J.F. Peberdy (1984) Enzyme Microb. Technol. 6, 386-389; Tilburn, *et al.* (1982) Gene 26, 205-221; Ballance, D.J. et al., (1983) Biochem. Biophys. Res. Comm. 112, 284-289; Johnston, I.L. *et al.* (1985) EMBO J. 4, 1307-1311) *A. niger*, (Kelly, J.M. and M. Hynes (1985) EMBO 4, 475-479) *A. niger* var. *awamori*, e.g., NRRL

3112, ATCC 22342, ATCC 44733, ATCC 14331 and strain UVK 143f, *A. oryzae*, e.g., ATCC 11490, *N. crassa* (Case, M.E. *et al.* (1979) Proc. Natl. Acad. Scie. USA 76, 5259-5263; Lambowitz U.S. Patent No. 4,486,553; Kinsey, J.A. and J.A. Rambosek (1984) *Molecular and Cellular Biology 4*, 117-122; Bull, J.H. and J.C. Wooton (1984) Nature 310, 701-704), *Trichoderma reesei*, e.g. NRRL 15709, ATCC 13631, 56764, 56765, 56466, 56767, and *Trichoderma viride*, e.g., ATCC 32098 and 32086. A preferred expression host is *A. niger* var. *awamori* in which the gene encoding the major secreted aspartyl protease has been deleted. The production of this preferred expression host is described in United States Patent Application Serial No. 214,237 filed July 1, 1988, expressly incorporated herein by reference.

During the secretion process in fungi, which are eukaryotes, the secreted protein crosses the membrane from the cytoplasm into the lumen of the endoplasmic reticulum (ER). It is here that the protein folds and disulphide bonds are formed. Chaperone proteins such as BiP and proteins like protein disulphide isomerase assist in this process. It is also at this stage where sugar chains are attached to the protein to produce a glycosylated protein. Sugars are typically added to asparagine residues as N-linked glycosylation or to serine or threonine residues as O-linked glycosylation. Antibodies are known to assemble in the ER. In mammalian cells the heavy chains become associated with BiP immediately on entry into the ER and are not released until they have associated with the light chain. Correctly folded and glycosylated proteins pass from the ER to the Golgi apparatus where the sugar chains are modified and where the KEX2 or KEXB protease of yeast and fungi resides. The N-linked glycosylation added to secreted proteins produced in fungi differs from that added by mammalian cells.

Antibodies produced by the filamentous fungal host cells may be either glycosylated or non-glycosylated (i.e., aglycosylated or deglycosylated). Because the fungal glycosylation pattern differs from that produced by mammalian cells, the antibodies may be treated with an enzyme to deglycosylate the antibody. Enzymes useful for such deglycosylation are endoglycosidase H, endoglycosidase F1, endoglycosidase F2, endoglycosidase A, PNGase F, PNGase A, and PNGase At.

We have surprisingly found that high levels of full-length assembled antibody can be made in fungi when both the heavy and light chains are fused to a native secreted protein. From the information provided above it is clear that the antibody would be expected to assemble in the ER when glucoamylase was still attached to the N-termini of each of the four chains. This would produce a very large and complicated assembled protein of greater than 350 kD. The glucoamylase would not be expected to be cleaved from the antibody until the assembled complex passed through the Golgi apparatus.

Using the present inventive methods and host cells, we have attained surprisingly high levels of expression. The vast majority of reports of antibody production in microbial systems, e.g., *Escherichia coli* or yeasts such as *Saccharomyces cerevisiae* or *Pichia pastoris* have involved the production of antibody fragments (e.g., Fab fragments) or single-chain antibody forms (e.g., ScFv) (Verma, R. et al., 1998, J. Immunological Methods 216:165-181; Pennell, C.A. and Eldin, P., 1998, Res. Immunol. 149:599-603;). A low level of full-length antibody has been produced and secreted in *Saccharomyces cerevisiae*. In one study, 100 ng/ml of light chain and 50-80 ng/ml of heavy chain were detected in the culture supernatant and approximately 50-70% of the heavy chains were associated with light chain (Horwitz, A.H. et al., 1988, Proc. Natl. Acad. Sci USA). Full-length antibody in a correctly assembled form has been produced in the yeast *Pichia pastoris* (WO 00/23579). However, the highest yields reported were 36 mg/l.

In contrast, the system utilized herein has achieved levels of expression and secretion of greater than 0.5 g/l of full-length antibody. It is routinely found that greater than 1 g/l of the antibody may be recovered from the fermentation broth. Reproducible levels of 1.5 g/l have been achieved. Expression and/or secretion levels as high as 2 to 3 g/l of full length antibody may be attained once the optimal conditions are in place. Although the antibody is secreted as a fusion protein the antibody levels given herein have been corrected for glucoamylase. Thus, the absolute protein produced comprising an antibody is greater than those stated; the amount produced has had the contribution of glucoamylase subtracted to give the stated amounts.

Utility

For some applications of immunoglobulins it is of high important that the immunoglobulins are extremely pure, e.g. having a purity of more than 99%. This is particularly true whenever the immunoglobulin is to be used as a therapeutic, but is also necessary for other applications.

Therapeutic and prophylactic vaccine compositions are contemplated, which generally comprise mixtures of one or more of the above-described monoclonal antibodies, including fragments thereof and combinations thereof. Passive immunization by intramuscularly injection of immunoglobulin concentrates is a well-known application for temporary protection against infectious diseases, which is typically applied when people are traveling from one part of the world to the other.

A more sophisticated application of antibodies for therapeutic use is based on so called "drug-targeting" where very potent drugs are covalently linked to antibodies with specific binding affinities towards specific cells in the human organism, e.g. cancer cells.

The above-described recombinant monoclonal antibodies, including Fab molecules, Fv fragments as well as Fab' and $F(ab')_2$, which are capable of reacting immunologically with samples containing antigen particles are also used herein to detect the presence of antigens in specific binding assays of biological samples. In particular, the novel monoclonal antibodies of the present invention can be used in highly sensitive methods of screening for the presence of an antigen.

The format of specific binding assays will be subject to a great deal of variation in accordance with procedures that are well known in the art. For example, specific binding assays can be formatted to utilize one, or a mixture of several, of the recombinant monoclonal antibodies, (including Fab molecules, Fv fragments as well as Fab' and $F(ab')_2$) that have been prepared according to the present invention. The assay format can be generally based, for example, upon competition, direct binding reaction or sandwich-type assay techniques. Furthermore, the present assays can be conducted using immunoprecipitation or other techniques to separate assay reagents during, or after commencement of, the assay. Other assays can be conducted using monoclonal antibodies that have been insolubilized prior to commencement of the assay. In this regard, a number of insolubilization techniques are well known in the art, including, without limitation, insolubilization by adsorption to an immunosorbent or the like, absorption by contact with the wall of a reaction vessel, covalent crosslinking to insoluble matrices or "solid phase" substrates, noncovalent attachment to solid phase substrates using ionic or hydrophobic interactions, or by aggregation using precipitants such as polyethylene glycol or cross-linking agents such as glutaraldehyde.

There are a large number of solid phase substrates which can be selected for use in the present assays by those skilled in the art. For example, latex particles, microparticles, magnetic-, para-magnetic- or nonmagnetic-beads, membranes, plastic tubes, walls of microtitre wells, glass or silicon particles and sheep red blood cells all are suitable for use herein.

In general, most of the present assays involve the use of a labeled binding complex formed from the combination of a monoclonal antibody (including fragments thereof) with a detectable label moiety. A number of such labels are known in the art and can be readily attached (either using covalent or non-covalent association techniques) to the monoclonal antibodies of the present invention to provide a binding complex for use in the above-noted assay formats. Suitable detectable moieties include, but are not limited to, radioactive isotopes, fluorescers, luminescent compounds (e.g., fluorescein and rhodamine), chemiluminescers (e.g., acridinium, phenanthridinium and dioxetane compounds), enzymes (e.g., alkaline phosphatase, horseradish peroxidase and beta-galactosidase), enzyme

substrates, enzyme cofactors, enzyme inhibitors, dyes, and metal ions. These labels can be associated with the antibodies using attachment techniques that are known in the art.

Exemplary assay methods generally involve the steps of: (1) preparing the detectably labeled binding complexes as above; (2) obtaining a sample suspected of containing antigen; (3) incubating the sample with the labeled complexes under conditions which allow for the formation of an antibody-antigen complex; and (4) detecting the presence or absence of labeled antibody-antigen complexes. As will be appreciated by those skilled in the art upon the reading of this specification, such assays can be used to screen for the presence of antigens in human donor blood and serum products. When the assays are used in the clinical setting samples can be obtained from human and animal body fluids, such as whole blood, serum, plasma, cerebrospinal fluid, urine and the like. Furthermore, the assays can be readily used to provide quantitative information using reference to standards or calibrants as known in the art.

In one particular assay method of the invention, an enzyme-linked immunosorbent assay (ELISA) can be used to quantify an antigen concentration in a sample. In the method, the specific binding molecules of the present invention are conjugated to an enzyme to provide a labeled binding complex, wherein the assay uses the bound enzyme as a quantitative label. In order to measure antigen, a binding molecule capable of specifically binding the selected antigen (e.g., an antibody molecule) is immobilized to a solid phase substrate (e.g., a microtitre plate or plastic cup), incubated with test sample dilutions, washed and incubated with the binding molecule-enzyme complexes of the invention, and then washed again. In this regard, suitable enzyme labels are generally known, including, for example, horseradish peroxidase. Enzyme activity bound to the solid phase is measured by adding the specific enzyme substrate, and determining product formation or substrate utilization colorimetrically. The enzyme activity bound to the solid phase substrate is a direct function of the amount of antigen present in the sample.

In another particular assay method of the invention, the presence of antigen in a biological sample (e.g., as an indicator of infection) can be detected using strip immunoblot assay (SIA) techniques, such as those known in the art which combine traditional Western and dot blotting techniques, e.g., the RIBA.RTM. (Chiron Corp., Emeryville, Calif.) test. In these assays, one or more of the specific binding molecules (the recombinant monoclonal antibodies, including Fab molecules) are immobilized as individual, discrete bands on a membranous support test strip. Visualization of reactivity with antigens present in the biological sample is accomplished using sandwich binding techniques with labeled antibody-conjugates in conjunction with a colorimetric enzyme substrate. Internal controls

can also be present on the strip. The assay can be performed manually or used in an automated format.

Furthermore, the recombinant human monoclonal antibodies, (including Fab molecules, Fv fragments as well as Fab' and $F(ab')_2$ molecules) that have been prepared according to the present invention can be used in affinity chromatography techniques in order to detect the presence of antigen in a biological sample or to purify the antigen from the other components of the biological sample. Such methods are well known in the art.

Kits suitable for use in conducting any of the above-described assays and affinity chromatography techniques, and containing appropriate labeled binding molecule complex reagents can also be provided in accordance with the practice of the invention. Assay kits are assembled by packaging the appropriate materials, including all reagents and materials necessary for conducting the assay in a suitable container, along with an appropriate set of assay instructions.

EXAMPLES

The following preparations and examples are given to enable those skilled in the art to more clearly understand and practice the present invention. They should not be considered as limiting the scope and/or spirit of the invention, but merely as being illustrative and representative thereof.

In the experimental disclosure which follows, the following abbreviations apply: eq (equivalents); M (Molar); μM (micromolar); N (Normal); mol (moles); mmol (millimoles); μmol (micromoles); nmol (nanomoles); g (grams); mg (milligrams); kg (kilograms); μg (micrograms); L (liters); ml (milliliters); μl (microliters); cm (centimeters); mm (millimeters); μm (micrometers); nm (nanometers); °C. (degrees Centigrade); h (hours); min (minutes); sec (seconds); msec (milliseconds); Ci (Curies) mCi (milliCuries); μCi (microCuries); TLC (thin layer achromatography); Ts (tosyl); Bn (benzyl); Ph (phenyl); Ms (mesyl); Et (ethyl), Me (methyl), SDS (sodium dodecyl sulfate), PAGE (polyacrylamide gel electrophoresis), kDa (kiloDaltons), bp (base pairs).

Example 1
Cloning DNA encoding the human Ig κ light chain constant region

The human Ig κ light chain constant region was PCR amplified from human leukocyte cDNA (QUICK-Clone cDNA, Clontech Laboratories, Palo Alto, CA). The primers used were:

BPF001: 5'- CCGTGGCGGCGCCATCTGTCTTCATCTTCCCGCCATCTG-3' (SEQ ID NO: 1)

BPF002: 5'- CAGTTCTAGAGGATCAACACTCTCCCCTGTTGAAGCTCTTTG-3' (SEQ ID NO: 2)

BPF001 includes two silent mutations to introduce a *Nar*I restriction site (GGCGCC) for cloning purposes. BPF002 introduces an *Xba*I restriction site (TCTAGA) following the translation termination signal for cloning purposes. The PCR product was cloned into pCR2.1 TOPO (Invitrogen Corporation, Carlsbad, CA) using the TOPO TA cloning kit and protocol supplied by the manufacturer to create K1-pCR2.1TOPO. DNA from clone K1-pCR2.1TOPO was sequenced. The sequence is shown below.

GAATTCGCCCTTCCGTGGCGGCGCCATCTGTCTTCATCTTCCCGCCATCTGATGAGC
AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGA
GGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCT
GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGG
CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGATCCTCTAGAAC
TGAAGGGCGAATTC (SEQ ID NO: 3)

The sequence obtained matches GenBank (<www.ncbi.nlm.nih.gov/>) accession number J00241; human Ig germline κ L chain, C region (inv3 allele).

Example 2
Cloning DNA encoding the human γ1 heavy chain constant region

The human γ 1 heavy chain constant region was PCR amplified from human leukocyte cDNA (QUICK-Clone cDNA, Clontech Laboratories, Palo Alto, CA). The primers used were:

BPF006: 5'- GGGCCCATCGGTCTTCCCCCTGGCA-3' (SEQ ID NO: 4) and
BPF004: 5'- CAGTTCTAGAGGATCATTTACCCGGAGACAGGGAGAGGCTC-3' (SEQ ID NO: 5)

BPF006 takes advantage of the naturally occurring *Apa*I restriction site (GGGCCC) at the 5' end of the human γ 1 CH1 region. BPF004 introduces an *Xba*I restriction site (TCTAGA) following the translation termination codon for cloning purposes. The PCR product was cloned into pCR2.1 TOPO (Invitrogen Corporation, Carlsbad, CA) using the TOPO TA cloning kit and protocol supplied by the manufacturer to create BG13-pCR2.1-TOPO. DNA from clone BG13-pCR2.1-TOPO was sequenced. The sequence is shown below.

GGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG

CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGG
AACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG
ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC
TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT
CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG
CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC
CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA
GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTG
TACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGC
CTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG
CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC
CTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
TCTCCGGGTAAATGATCCTCTAGA (SEQ ID NO: 6)

The sequence obtained matches the exon sequences of GenBank (<www.ncbi.nlm.nih.gov>) accession number Z17370; human germline immunoglobulin γ1 chain constant region gene, except for the following:

1) A change from an A to a G at nucleotide number 500 in Z17370 which represents a Lysine to an Arginine change in the protein corresponding to the G1m(3) allotype.

2) Changes from a T to a G and from a C to an A at nucleotide numbers 1533 and 1537 respectively in Z17370 representing Aspartate to Glutamate and Leucine to Methionine changes respectively. These changes correspond to the non(1) allotype.

3) a silent mutation of C to T corresponding to base 1686 of Z17370.

Example 3
Synthesis of DNA encoding Trastuzumab light chain variable region

DNA encoding the amino acid sequence of the trastuzumab light chain variable region (As given in Carter et al., 1992, Proc. Natl. Acad. Sci. USA 89:4285-4289 except that tyrosine replaced glutamic acid at amino acid position 55) was synthesized by Aptagen, Inc., Herndon, VA, using their Gene Forge custom gene synthesis technology. The sequence is shown below.

TACGTATAAGCGCGATATCCAGATGACCCAGTCCCCGAGCTCCCTGTCCGCCTCTGT
GGGCGATAGGGTCACTATCACCTGCCGTGCCAGTCAGGATGTGAATACTGCTGTAGC
CTGGTATCAACAGAAACCCGGAAAGGCCCCGAAACTGCTGATTTACTCGGCATCCTTC
CTCTACTCTGGAGTCCCTTCTCGCTTCTCTGGTTCCCGCTCTGGGACGGATTTCACTC
TGACCATCAGCTCCCTGCAGCCGGAAGACTTCGCAACTTATTACTGTCAGCAACACTA
TACTACTCCTCCGACGTTCGGACAGGGTACCAAGGTGGAGATCAAACGTACCGTGGC
GGCGCC (SEQ ID NO: 7)

This DNA sequence includes a 5' *Sna*B1 restriction site (TACGTA) to allow digestion and ligation to the *A. niger* glucoamylase coding region followed by codons for the amino acids Lysine and Arginine (AAG CGC) representing a KEX2 protease cleavage site. At the 3' end there is a *Nar*I restriction site to allow digestion and ligation to the light chain constant region. The codon usage in this DNA reflects the frequency of codon usage observed in *Aspergillus* genes.

Example 4
Synthesis of DNA encoding Trastuzumab heavy chain variable region

DNA encoding the amino acid sequence of the trastuzumab heavy chain variable region (As given in Carter et al., 1992, Proc. Natl. Acad. Sci. USA 89:4285-4289 except that tyrosine replaced valine at amino acid position 105) was synthesized by Aptagen, Inc., Herndon, VA, using their Gene Forge custom gene synthesis technology. The sequence is shown below.

TACGTATAAGCGCGAGGTTCAGCTGGTGGAGTCTGGCGGTGGCCTGGTGCAGCCCG
GGGGCTCTCTCCGTTTGTCCTGTGCAGCTTCTGGCTTCAACATTAAAGACACCTATAT
CCACTGGGTGCGTCAGGCTCCGGGTAAGGGCCTGGAGTGGGTTGCAAGGATTTATC
CTACGAATGGTTATACTCGTTATGCCGATAGCGTCAAGGGCCGTTTCACTATAAGCGC
AGACACTTCGAAAAACACAGCCTACCTCCAGATGAACAGCCTGCGTGCTGAGGACAC
TGCCGTCTATTATTGTAGCAGATGGGGTGGGGACGGCTTCTATGCTATGGACTACTG
GGGTCAAGGTACACTAGTCACCGTCAGCAGCGCTAGCACCAAGGGCCC (SEQ ID NO: 8)

This DNA sequence includes a 5' *Sna*B1 restriction site (TACGTA) to allow digestion and ligation to the *A. niger* glucoamylase coding region followed by codons for the amino acids Lysine and Arginine (AAG CGC) representing a KEX2 protease cleavage site. At the 3' end there is an *Apa*I restriction site to allow digestion and ligation to the heavy

chain constant region. The codon usage in this DNA reflects the frequency of codon usage observed in *Aspergillus* genes.

Example 5
Construction of a trastuzumab light chain expression plasmid containing the *pyrG* marker

The expression plasmid used for light chain expression in *Aspergillus* was based on pGAMpR, a glucoamylase-prochymosin expression vector which is described in detail in US 5,679,543. This plasmid was digested with the restriction endonucleases *Sna*BI and *Xba*I, each of which cuts only once in pGAMpR. *Sna*BI cuts the plasmid within the coding region for the glucoamylase linker region and *Xba*I cuts pGAMpR just after the 3' end of the chymosin coding region. Using techniques known in the art the DNA sequences encoding the light chain variable and constant regions were assembled and inserted into pGAMpR replacing the chymosin encoding region. The final plasmid was named pQ83 (Fig.3). This plasmid contains the *Neurospora crassa pyr4* gene as a selectable marker for transformation into *Aspergillus* or other fungi. The *Aspergillus awamori glaA* (glucoamylase) promoter and *A. niger glaA* terminator are included to control expression of the open reading frame which includes the light chain encoding DNA. This plasmid was designed for the expression of a fusion protein consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 502 of mature glucoamylase (Nunberg, J.H. et al., 1984, Mol. Cell. Biol. 4:2306-2315), followed by amino acids YKR and then by the mature light chain. Free light chain can be obtained after cleavage of this fusion protein immediately after the KR residues placed at the end of the glucoamylase linker region by Aspergillus KEX2 proteinase. The complete amino acid sequence of the fusion protein is given here. The YKR sequence between the end of the glucoamylase linker region and the start of the light chain sequence is underlined.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIV
VASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNPSGDLS
SGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTATDIVWPL
VRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCSWCDSQ
APEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCSPRALAN
HKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDALYQWDK
QGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHAASNGSM
SEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCAATSAIGT
YSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASKTSTYKRDIQMTQSPSSLSA
SVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTL

TISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL
LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC
EVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 9)

Example 6
Construction of trastuzumab heavy chain expression plasmids

The *Aspergillus* expression vector pGAMpR was modified by methods known in the art to replace the *N. crassa pyr4* gene with the *Aspergillus nidulans amdS* gene as a selectable marker for transformation into *Aspergillus* or other fungi (Kelly J.M. and Hynes, M.J., 1985, EMBO J. 4:475-479; Corrick,C.M. et al., 1987, Gene 53:63-71). Using techniques known in the art the DNA sequences encoding the heavy chain variable and constant regions were assembled and inserted into the version of the *Aspergillus* expression vector pGAMpR with the *amdS* selectable marker. The final plasmid was named pCL1 (Fig.4). The *Aspergillus awamori glaA* (glucoamylase) promoter and *A. niger glaA* terminator are included to control expression of the open reading frame which includes the heavy chain encoding DNA. This plasmid was designed for the expression of a fusion protein consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 502 of mature glucoamylase, followed by amino acids YKR and then by the mature heavy chain. Free heavy chain can be obtained after cleavage of this fusion protein immediately after the KR residues placed at the end of the glucoamylase linker region by Aspergillus KEX2 proteinase. The complete amino acid sequence of the fusion protein is given here. The YKR sequence between the end of the glucoamylase linker region and the start of the heavy chain sequence is underlined.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIV
VASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNPSGDLS
SGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTATDIVWPL
VRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCSWCDSQ
APEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCSPRALAN
HKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDALYQWDK
QGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHAASNGSM
SEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCAATSAIGT
YSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASKTSTYKREVQLVESGGGLV
QPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISA
DTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP

KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC
LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 10)

A second trastuzumab heavy chain expression plasmid (pCL5; Fig. 5) was constructed which contained exactly the same expression cassette as pCL1 (i.e., the *Aspergillus niger* var. *awamori glaA* promoter and *A. niger glaA* terminator controlling expression of the open reading frame encoding a fusion protein consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 502 of mature glucoamylase, followed by amino acids YKR and then by the mature heavy chain). The only differences between pCL1 and pCL5 were that the latter plasmid lacked the *A. nidulans amdS* gene and, therefore, lacked a fungal transformation marker and that pBR322 instead of pUC100 was used as the bacterial plasmid backbone.

Example 7
Construction of an expression plasmid for the Fd' fragment of the trastuzumab heavy chain

PCR was used to generate a DNA fragment encoding the Fd' portion of the heavy chain (heavy chain truncated after the antibody hinge region) using the assembled heavy chain variable and constant region DNA as template. The following two primers were used: oligo1 (5'- AAC AGC TAT GAC CAT G -3') (SEQ ID NO: 11) and oligo2 (5'-TCT AGA GGA TCA TGC GGC GCA CGG TGG GCA TGT GTG AG-3') (SEQ ID NO: 12). The amplified 900bp fragment was purified, digested with SnaBI and XbaI and the 719bp SnaB1 to XbaI fragment generated was cloned into version of the the *Aspergillus* expression pGAMpR with the *amdS* gene as selectable marker. The final plasmid was named pCL2 (Fig.6). The *Aspergillus awamori glaA* (glucoamylase) promoter and *A. niger glaA* terminator are included to control expression of the open reading frame which includes the heavy chain encoding DNA. This plasmid was designed for the expression of a fusion protein consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 502 of mature glucoamylase, followed by amino acids YKR and then by the mature Fd' portion of the heavy chain. Free Fd' chain can be obtained after cleavage of this fusion protein immediately after the KR residues placed at the end of the glucoamylase linker region by Aspergillus KEX2 proteinase. The complete amino acid sequence of the fusion protein is given here. The YKR sequence between the end of the glucoamylase linker region and the start of the heavy chain sequence is underlined.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIV

VASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNPSGDLS
SGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTATDIVWPL
VRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCSWCDSQ
APEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCSPRALAN
HKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDALYQWDK
QGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHAASNGSM
SEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCAATSAIGT
YSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASKTSTYKREVQLVESGGGLV
QPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISA
DTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAA (SEQ ID NO: 13)

Example 8

Construction of an expression plasmid for an aglycosylated form of the trastuzumab heavy chain

There is known to be a single asparagine (at position 297) in the IgG heavy chain constant region which is the site of attachment for N-linked glycosylation. In order to prevent glycosylation of the antibody produced in *Aspergillus* the codon encoding this asparagine has been changed to a codon which encodes glutamine. The QuikChange Site-Directed Mutagenesis kit (Stratagene, La Jolla, CA) was used according to the manufacturers directions to make the appropriate change to the DNA sequence. A plasmid containing the assembled DNA encoding the heavy chain variable and constant regions was used as a template. The following two primers, one complementary to one DNA strand of the plasmid and the other complementary to the second strand of the plasmid, which overlap the asparagine codon to be mutated were used in the mutagenesis procedure: 5'-GAG CAG TAC CAG AGC ACG TAC CGT GTG GTC-3' (SEQ ID NO: 14) and 5'-GTA CGT GCT CTG GTA CTG CTC CTC CCG CGG CT-3' (SEQ ID NO: 15). The altered codon is underlined. DNA sequence analysis confirmed that the desired sequence change had been created and that no other undesired mutations had been introduced. The mutated version of full-length heavy chain was then cloned into the version of the *Aspergillus* expression vector pGAMpR with the *amdS* selectable marker.. The final plasmid was named pCL3 (Fig.7). The *Aspergillus awamori glaA* (glucoamylase) promoter and *A. niger glaA* terminator are included to control expression of the open reading frame which includes the heavy chain encoding DNA. This plasmid was designed for the expression of a fusion protein consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 502 of mature glucoamylase (Nunberg et al., 1984, Mol. Cell. Biol.

4:2306-2315), followed by amino acids YKR and then by the mature heavy chain containing the mutation to prevent glycosylation. Free heavy chain can be obtained after cleavage of this fusion protein immediately after the KR residues placed at the end of the glucoamylase linker region by Aspergillus KEX2 proteinase. The complete amino acid sequence of the fusion protein is given here. The YKR sequence between the end of the glucoamylase linker region and the start of the heavy chain sequence is underlined as is the glutamine residue which replaced the asparagine in the original heavy chain sequence.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIV
VASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNPSGDLS
SGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTATDIVWPL
VRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCSWCDSQ
APEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCSPRALAN
HKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDALYQWDK
QGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHAASNGSM
SEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCAATSAIGT
YSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASKTSTYKREVQLVESGGGLV
QPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISA
DTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC
LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 16)

Example 9
Trastuzumab light chain expression in *Aspergillus*

DNA of the integrative (i.e., it is designed to integrate into the host genomic DNA) expression plasmid pQ83 was prepared and transformed into *Aspergillus niger* var. *awamori* strain dgr246ΔGAP:pyr2-. This strain is derived from strain dgr246 P2 which has the *pepA* gene deleted, is *pyrG* minus and has undergone several rounds of mutagenesis and screening or selection for improved production of a heterologous gene product (Ward, M. et al., 1993, Appl. Microbiol. Biotech. 39:738-743 and references therein). To create strain dgr246ΔGAP:pyr2- the *glaA* (glucoamylase) gene was deleted in strain dgr246 P2 using exactly the same deletion plasmid (pΔGAM NB-Pyr) and procedure as reported by Fowler, T. et al (1990) Curr. Genet. 18:537-545. Briefly, the deletion was achieved by

transformation with a linear DNA fragment having *glaA* flanking sequences at either end and with part of the promoter and coding region of the *glaA* gene replaced by the *Aspergillus nidulans pyrG* gene as selectable marker. Transformants in which the linear fragment containing the *glaA* flanking sequences and the *pyrG* gene had integrated at the chromosomal *glaA* locus were identified by Southern blot analysis. This change had occurred in transformed strain dgr246ΔGAP. Spores from this transformant were plated onto medium containing fluoroorotic acid and spontaneous resistant mutants were obtained as described by van Hartingsveldt, W. et al. (1987) Mol. Gen. Genet. 206:71-75. One of these, dgr246ΔGAP:pyr2-, was shown to be a uridine auxotroph strain which could be complemented by transformation with plasmids bearing a wild-type *pyrG* gene.

The *Aspergillus* transformation protocol was a modification of the Campbell method (Cambell et at. (1989). Curr. Genet. 16:53-56). All solutions and media were either autoclaved or filter sterilized through a 0.2 micron filter. Spores of *A. niger* var. *awamori* were harvested from complex media agar (CMA) plates. CMA contained 20 g/l dextrose, 20 g/l DifcoBrand malt extract, 1 g/l Bacto Peptone, 20 g/l Bacto agar, 20 ml/l of 100 mg/ml arginine and 20 ml/l of 100 mg/ml uridine. An agar plug of approximately 1.5 cm square of spores was used to inoculate 100 mls of liquid CMA (recipe as for CMA except that the Bacto agar was omitted). The flask was incubated at 37°C on a shaker at 250-275 rpm, overnight. The mycelia were harvested through sterile Miracloth (Calbiochem, San Diego, CA, USA) and washed with 200 mls of Solution A (0.8M $MgSO_4$ in 10 mM sodium phosphate, pH 5.8). The washed mycelia were placed in a sterile solution of 300 mg of beta-D-glucanase (Interspex Products, San Mateo, CA) in 20 mls of solution A. This was incubated at 28°C at 200 rpm for 2 hour in a sterile 250 ml plastic bottle (Corning Inc, Corning, New York). After incubation, this protoplasting solution was filtered through sterile Miracloth into a sterile 50 ml conical tube (Sarstedt, USA). The resulting liquid containing protoplasts was divided equally amongst four 50 ml conical tubes. Forty ml of solution B (1.2 M sorbitol, 50 mM $CaCl_2$, 10 mM Tris, pH7.5) were added to each tube and centrifuged in a table top clinical centrifuge (Damon IEC HN SII centrifuge) at 3/4 speed for 10 minutes. The supernatant from each tube was discarded and 20 mls of fresh solution B was added to one tube, mixed, then poured into the next tube until all the pellets were resuspended. The tube was then centrifuged at 3/4 speed for 10 minutes. The supernatant was discarded, 20 mls of fresh solution B was added, the tube was centrifuged for 10 minutes at 3/4 speed. The wash occurred one last time before resuspending the washed protoplasts in solution B at a density of 0.5-1.0 X 10^7 protoplasts/l00ul. To each 100 ul of protoplasts in a sterile 15 ml conical tube (Sarstedt, USA), 10 ul of the transforming plasmid DNA was added. To this, 12.5 ul of solution C (50% PEG 4000, 50 mM $CaCl_2$, 10 mM Tris, pH 7.5) was added and

the tube was placed on ice for 20 minutes. One ml of solution C was added and the tube was removed from the ice to room temperature and shaken gently. Two ml of solution B was added immediately to dilute solution C. The transforming mix was added equally to 3 tubes of melted MMS overlay (6 g/l $NaNO_3$, 0.52 g/l KCl, 1.52 g/l KH_2PO_4, 218.5 g/l D-sorbitol, 1.0 ml/l trace elements-LW, 10 g/l SeaPlaque agarose (FMC Bioproducts, Rook1and, Maine, USA) 20 ml/l 50% glucose, 2.5 ml/l 20% $MgSO_4.7H_20$, pH to 6.5 with NaOH) that were stored in a 45°C water bath. Trace elements-LW consisted of 1 g/l $FeSO_4.7H_2O$, 8.8 g/l $ZnSO_4.7H_2O$, 0.4 g/l $CuSO_4.5H_2O$, 0.15 g/l $MnSO_4.4H_2O$, 0.1 g $Na_2B_4O_7.10H_2O$, 50 mg/l $(NH_4)_6Mo_7O_{24}.4H_2O$, 250 mls H2O, 200 ul/l concentrated HCl. The melted overlays with the transformation mix were immediately poured onto 3 MMS plates (same as MMS overlay recipe with the exception of 20 g/l of Bacto agar instead of 10 g/l of SeaPlaque agarose) that had been supplemented with 200 ul/plate of 100 mg/ml of arginine added directly on top of the agar plate. After the agar solidified, the plates were incubated at 37°C until transformants grew.

The sporulating transformants were picked off with a sterile toothpick onto a plate of minimal media + glucose (MM). MM consisted of 6 g/l $NaNO_3$, 0.52 g/l KC1, 1.52 g/l KH_2PO_4, 1 ml/l Trace elements-LW, 20 g/l Bacto agar, pH to 6.5 with NaOH, 25 ml/l of 40 % glucose, 2.5 ml/l of 20% $MgSO_4.7H_2O$ and 20 ml/l of 100 mg/ml arginine. Once the transformants grew on MM they were transferred to CMA plates.

A 1.5 cm square agar plug from a plate culture of each transformant was added to 50 mls, in a 250 ml shake flask, of an inoculum medium called CSL + fructose 100 g/1 com steep liquor (50 % solids, National), 1 g/1 $NaH_2P0_4.H_2O$, 0.5 g/l $MgSO_4$, 100 g/l maltose, 10 g/1 glucose, 50 g/1 fructose, 3 m1/l Mazu DF60-P (Mazur Chemicals, Gurnee, IL, USA), pH to 5.8 with NaOH. Flasks were incubated at 37°C, 200 rpm, for 2 days. Five ml of the 2 day old medium were inoculated into 50 ml of production medium called Promosoy special. This medium had the following components: 70 g/l sodium citrate, 15 g/l $(NH_4)_2$ $S0_4$, 1 g/l $NaH_2PO_4.H_2O$, 1 g/l $MgSO_4$, 1 ml Tween 80, pH to 6.2 with NaOH, 2 ml/l Mazu DF60-P, 45g/l Promosy 100 (Central Soya, Fort Wayne, IN), 120 g/l maltose. The production media flasks were incubated at 30°C, 200 rpm for 5 days and supernatant samples were harvested.

Samples of culture supernatant were mixed with an appropriate volume of 2X sample loading buffer and subjected to sodium dodecyl sulfate - polyacrylamide gel electrophoresis (SDS-PAGE) using precast gels according to the manufacturers instructions (The NuPAGE Bis-Tris Electrophoresis System from Invitrogen Corporation, Carlsbad, CA). The gels were either stained for protein with Coomassie Brilliant Blue stain or the protein was transferred to membrane filters by Western blotting (Towbin et al., 1979,

Proc. Natl. Acad. Sci. USA 76:4350-4354). Human kappa light chain was visualized on Western blots by sequential treatment with goat anti-human kappa light chain (bound and free) antibody and rabbit anti-goat IgG conjugated with horse radish peroxidase (HRP) followed by HRP color development by incubation with H_2O_2 and 4-chloro-l-napthol.

Transformants which produced trastuzumab light chain were identified by the appearance of extra protein bands compared to supernatant from the untransformed parental strain. The sizes and identities of these bands were as follows. A 25 kD band corresponding to the trastuzumab light chain which had been released from the glucoamylase-light chain fusion protein. A band with an apparent molecular weight of approximately 58 kD corresponding to the catalytic core and linker region of glucoamylase which had been released from the glucoamylase-light chain fusion protein. A band with an apparent molecular weight of approximately 85 kD corresponding to the glucoamylase-light chain fusion protein which had not been cleaved into separate glucoamylase and light chain proteins. The identities of the light chain bands were confirmed by Western analysis. The Western analysis employed an anti-human κ antibody to detect both the free light chain and the glucoamylase-light chain fusion protein. Quantification of the light chain in culture supernatants was performed by enzyme-linked immunosorption assays (ELISA). The best light chain expression strain was spore purified and was designated Q83-35-2. This strain produced approximately 1.5 g/l of trastuzumab light chain (κ chain) in shake flask culture according to ELISA. The ELISA was performed using goat anti-human κ (bound and free) antibody as a capture antibody coating the wells of microtiter plates. After adding appropriately diluted culture supernatant, incubation, and then washing the wells, the bound light chain from the supernatant was detected by addition of an goat anti human kappa (bound and free) antibody conjugated with horse radish peroxidase (HRP) followed by a color development reaction. A serial dilution of known concentration for human κ light chain was used to produce a standard for quantification purposes.

Example 10
Improved cleavage of the glucoamylase-light chain fusion protein

As indicated above, some of the trastuzumab light chain remained attached to glucoamylase when secreted by *Aspergillus niger* transformants containing pQ83. It was estimated that approximately 60-75% of the secreted light chain was attached to glucoamylase. This indicated that the KEX2 site between glucoamylase and the light chain was not efficiently cleaved by the KEX2 protease. In order to determine if the site of cleavage was as predicted (i.e., immediately after the KR residues of the KEX2 cleavage site) the N-terminus of the free light chain from transformant Q83-35-2 was determined. Proteins in culture supernatant samples were separated by SDS-PAGE and were blotted

onto a polyvinylidene difluoride (PVDF) membrane using a Novex transfer cell (Invitrogen Corporation, Carlsbad, CA) and transfer buffer consisting of 12 mM Tris base, 96mM glycine, 20% methanol, 0.01% SDS, pH8.3. The transfer was run at 20 V for 90 minutes. The membrane was rinsed three times for 30 minutes each in distilled water and stained with Coomassie Brilliant Blue R-250. The portion of the membrane with the 25 kD light chain band was excised and the N-terminal sequence was determined by Edman degradation. The data indicated that the population of light chain molecules had a mixture of N-termini, the dominant sequences were DIQM and KRDI and these were present in approximately equal amounts. This result demonstrates that some of the glucoamylase-light chain fusion proteins were cleaved at the expected position immediately after the KEX2 cleavage site but that approximately half of the cleaved fusion proteins had been cleaved at a position two residues towards the N-terminus.

In order to improve cleavage of the fusion protein we altered the position on the glucoamylase linker region to which the light chain was attached. Additionally, the amino acid sequence at the junction between glucoamylase and light chain was varied.

The expression plasmid used for these experiments was based on the same vector as pGAKHi+, a glucoamylase-hirulog expression vector which is described in detail in WO 9831821. The hirulog-encoding region of this plasmid, which is situated between unique *Nhe*I and *Bst*EII restriction endonuclease recognition sites, was replaced by light chain-encoding DNA. *Nhe*I cuts the plasmid within the coding region for the glucoamylase linker region and *Bst*EII cuts 5' of the glucoamylase terminator region. Using techniques known in the art the DNA sequence encoding the complete light chain was amplified by PCR using the following pair of primers. 5'-CCGCTAGCAAGCGTGATATCCAG-3' (SEQ ID NO:17) was the forward primer and 5'-CCGGTGACCGGATCAACACTCTCCC-3' (SEQ ID NO:18) was the reverse primer. These primers added *Nhe*I and *Bst*EII recognition sites at the 5' and 3' ends of the light chain DNA respectively. The light chain DNA was then inserted into the vector to create a plasmid identical to pGAKHi+ but with the light chain DNA replacing the hirulog-encoding region to create pQ87. This plasmid contained the *Aspergillus niger pyrG* gene as a selectable marker for transformation into *Aspergillus* or other fungi. The *Aspergillus niger* var *awamori glaA* (glucoamylase) promoter and *A. niger glaA* terminator were included to control expression of the open reading frame which includes the light chain encoding DNA. This plasmid was designed for the expression of the fusion protein shown below consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 498 (a serine) of mature glucoamylase (Nunberg, J.H. et al., 1984, Mol. Cell. Biol. 4:2306-2315), followed by amino acids KR (underlined below) and then by the mature light chain.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASKRDIQMTQSPSSL
SASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDF
TLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV
CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYA
CEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:19).

The amino acid sequence on either side of the KR residues (kexB cleavage site) was altered in a series of plasmids. To construct each new light chain expression plasmid, the following forward primers were used, each in combination with the same reverse primer as described for pQ87, to amplify the light chain DNA fragment in a PCR reaction. 5'-CCGCTAGCCAGAAGCGTGATATCCAGA-3' (SEQ ID NO:20) was the forward primer for pQ88; 5'-CCGCTAGCCTCAAGCGTGATATCCAG-3' (SEQ ID NO:21) was the forward primer for pQ90; 5'-CCGCTAGCATCTCCAAGCGTGATATCCAG-3' (SEQ ID NO:22) was the forward primer for pQ91; 5'-CCGCTAGCAACGTGATCTCCAAGCGTGATATCCAG-3' (SEQ ID NO:23) was the forward primer for pQ94; 5'-CCGCTAGCGTGATCTCCAAGCGTGATATCCAG-3' (SEQ ID NO:24) was the forward primer for pQ95; and 5'-CCGCTAGCATCTCCAAGCGTGGCGGTGGCGATATCCAGATGACCCAG-3' (SEQ ID NO:25) was the forward primer for pQ96; The PCR fragment was then digested with restriction enzymes *Nhe*I and *Bst*EII and inserted into the expression vector as for pQ87. In pQ88 and pQ90, an amino acid was inserted at the amino-terminal side of the KR residues which had been shown to be accepted at this position for cleavage of synthetic peptides by yeast KEX2 and *A. niger* KexB (Brenner, C. and Fuller, R.S., 1992, Proc. Natl. Acad. Sci. USA 89:922-926; Jalving, R. et al., 2000, Applied and Environmental Microbiology 66:363-368). In pQ91, pQ94 and pQ95, two, four or three residues respectively from the 6 amino acid propeptide of glucoamylase (which ends with KR and is cleaved by KEX2 protease) were placed on the amino-terminal side of the KR residues. Residues from the glucoamylase propeptide sequence have been placed in this position in glucoamylase

fusion proteins by others (Spencer, J.A. et al., 1998, European Journal of Biochemistry 258:107-112; Broekhuijsen, M.P. et al., 1993, Journal of Biotechnology 31:135-145). In pQ96, three glycine residues were placed on the carboxyl side of the KR residues as had been employed by (Spencer, J.A. et al., 1998, European Journal of Biochemistry 258:107-112). For each plasmid the amino acid sequence of the encoded glucoamylase-light chain fusion protein is shown below and the variable region around the KEX2 cleavage site (KR) is underlined.

Glucoamylase-light chain fusion protein encoded by pQ88:

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATAS<u>QKR</u>DIQMTQSPSS
LSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTD
FTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:26).

Glucoamylase-light chain fusion protein encoded by pQ90:

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATAS<u>LKR</u>DIQMTQSPSSL
SASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDF
TLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV
CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYA
CEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:27).

Glucoamylase-light chain fusion protein encoded by pQ91:

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASISKRDIQMTQSPSS
LSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTD
FTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:28).

Glucoamylase-light chain fusion protein encoded by pQ94:

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASNVISKRDIQMTQSP
SSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSG
TDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTA
SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK
VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:29).

Glucoamylase-light chain fusion protein encoded by pQ95:

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS

PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASVISKRDIQMTQSPS
SLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGT
DFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS
VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:30).

Glucoamylase-light chain fusion protein encoded by pQ96:

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASISKRGGGDIQMTQ
SPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSR
SGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK
HKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:31).

DNA of the expression plasmids pQ87, pQ88, pQ90, pQ91, pQ94, pQ95 and pQ96 were prepared and each was transformed individually into *Aspergillus niger* var. *awamori* strain dgr246ΔGAP:pyr2-. The transformants obtained were cultured in shake flasks in Promosoy special medium and the secreted proteins were visualized by SDS-PAGE and Coomassie Brilliant Blue staining. Cleavage of the glucoamylase-light chain fusion protein was assessed by examining the relative amounts of the 25 kD band corresponding to the trastuzumab light chain which had been released from the fusion protein, the 58 kD band corresponding to the catalytic core and linker region of glucoamylase which had been released from the fusion protein and the approximately 85 kD band corresponding to the glucoamylase-light chain fusion protein which had not been cleaved into separate glucoamylase and light chain proteins. In addition, the N-terminus of the released light chain was determined in some instances.

The extent of cleavage of the glucoamylase-light chain fusion protein was apparently unchanged, at approximately 25 to 40%, in *A. niger* transformants with the expression vectors pQ87, pQ88 or pQ90 compared to transformant Q83-35-2.

In contrast, approximately 90% of the glucoamylase-light chain fusion protein was cleaved in transformants with expression vectors pQ91, pQ94 and pQ95. The amino terminus of the free light chain in the supernatants of one transformant obtained with each of pQ91 and pQ94 was determined and a single dominant sequence of DIQMT was observed. This demonstrated that not only the extent of cleavage was improved in transformants with these expression vectors but also frequency at which the fusion protein was cleaved at the expected KEX2 site, i.e., the accuracy or fidelity of the cleavage had been improved.

100% of the glucoamylase-light chain fusion protein was apparently cleaved in transformants with expression vector pQ96. The amino terminus of the free light chain in the supernatant of one transformant obtained with pQ96 was determined and a single dominant sequence of GGGDI was observed.

Example 11
Trastuzumab heavy chain expression in *Aspergillus*

DNA of the integrative expression plasmid pCL1 was prepared and transformed into *Aspergillus niger* var. *awamori* strain dgr246ΔGAM. Transformants were cultured in liquid medium in shake flasks as above. In some experiments, the trastuzumab heavy chain was specifically precipitated from the supernatant by incubation with protein A–sepharose beads (Amersham Pharmacia) which has specific affinity for the heavy chain of IgG. The beads were pre-washed in SDS-PAGE running buffer and were further washed in this buffer after incubation with heavy chain and before being resuspended in SDS-PAGE sample buffer, heating at 70°C for 10 minutes prior and loading on a polyacrylamide gel. Samples of supernatant, or of material precipitated from supernatant with protein A-sepharose, were analyzed by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) under reducing conditions followed by Coomassie Brilliant Blue staining of the protein bands or blotting to nylon membranes for Western analysis. Trastuzumab heavy chain was visualized on Western blots by sequential treatment with goat anti-human IgG-Fc antibody and rabbit anti-goat IgG conjugated with horse radish peroxidase (HRP) followed by HRP color development by incubation with H_2O_2 and 4-chloro-l-napthol. Transformants which produced trastuzumab heavy chain were identified by the appearance of extra protein bands compared to supernatant from the untransformed parental strain. The sizes and identities of these bands were as follows. A pair of bands, one at 50 kD (which has the same mobility on SDS-PAGE as the secreted alpha-amylase of *Aspergillus niger*), and one

at approximately 53 KD, both corresponding to the trastuzumab heavy chain which had been released from the glucoamylase-heavy chain fusion protein (the appearance of free heavy chain of two different sizes is explained below). A band with an apparent molecular weight of 58 kD corresponding to the catalytic core and linker region of glucoamylase which had been released from the glucoamylase-heavy chain fusion protein. A band with an apparent molecular weight of 116 kD corresponding to the glucoamylase-heavy chain fusion protein which had not been cleaved into separate glucoamylase and heavy chain proteins. The best heavy-chain expressing transformant produced approximately 0.33 g per liter of culture supernatant of trastuzumab gamma heavy chain according to ELISA. The ELISA was performed using goat anti-human IgG-Fc antibody as a capture antibody coating the wells of microtiter plates. After adding appropriately diluted culture supernatant, incubation, and then washing the wells, the bound heavy chain from the supernatant was detected by addition of goat anti human IgG-Fc antibody conjugated with HRP followed by a color development reaction. A serial dilution of known concentration of human IgG was used to produce a standard for quantification purposes.

Example 12
Trastuzumab heavy and light chain expression in *Aspergillus*

Three different transformation strategies were used to construct *Aspergillus* transformants which produced both heavy and light chains of the trastuzumab antibody.

Strain construction by co-transformation. The expression plasmids pQ83 and pCL1 were mixed and transformed into *Aspergillus niger* var. *awamori* strain dgr246ΔGAM. Neither of these plasmids has a fungal origin of replication and would be expected to integrate into the *Aspergillus* chromosomal DNA at one or more sites. Transformants were cultured in shake flasks as described above and light and heavy chain production was evident from SDS-PAGE and Western analysis. A mix of the same light chain and heavy chain bands were observed as seen in the transformants which produced only light chain or only heavy chain. Up to approximately 0.3 g/l assembled IgG was measured by ELISA in shake flask cultures of the best transformant (1-LC/HC-3). The ELISA was performed using goat anti-human IgG-Fc antibody as a capture antibody coating the wells of microtiter plates. After adding appropriately diluted culture supernatant, incubation, and then washing the wells, the bound IgG1 from the supernatant was detected by addition of an goat anti human κ (bound and free) antibody conjugated with HRP followed by a color development reaction. By employing this combination of capture and detection antibodies in the ELISA, only assembled IgG1 would be measured whereas free light chain and heavy chain would not be measured. A serial dilution of known concentration of purified human IgG was used to produce a standard for quantification purposes. The capture and detection antibodies

were reversed in some experiments so that the capture antibody was anti human κ antibody and the detection antibody was anti-human IgG-Fc antibody conjugated with HRP. Results were comparable with either combination of antibodies.

Transformants were also obtained by co-transformation with the expression plasmids pQ83 and pCL5. These plasmids were mixed and transformed into *Aspergillus niger* var. *awamori* strain dgr246ΔGAM. Up to 0.9 g/l assembled IgG was measured by ELISA in shake flask cultures of the best transformant (2-LC/HC-38).

Strain construction using a replicating plasmid. The plasmids pQ83, pCL1 and pHELP1 were mixed and transformed into *Aspergillus niger* var. *awamori* strain dgr246ΔGAM. The plasmid pHELP1 (Gems, D. and Clutterbuck, A.J., 1993, Curr. Genet. 24:520-524) includes an *Aspergillus nidulans* sequence, AMA1, which confers autonomous replication in *aspergillus* strains. Based on previous results (Gems, D. and Clutterbuck, A.J., 1993, Curr. Genet. 24:520-524) it would be expected that the plasmids would recombine with one another and form a large replicating plasmid that contains elements of all three plasmids. Transformants were cultured in shake flasks and analyzed for expression of the trastuzumab heavy and light chains by SDS-PAGE and Western analysis. A mix of the same light chain and heavy chain bands were observed as seen in the transformants which produced only light chain or only heavy chain. Assembled IgG1 was assayed by ELISA. Up to 0.26 g/l assembled IgG was measured by ELISA in shake flask cultures.

Strain construction by two sequential transformations. The integrative plasmid pCL1 (heavy chain expression plasmid) was used to transform strain Q83-35-2, the best light chain producing strain identified above. Transformants were cultured in shake flasks and analyzed for expression of the trastuzumab heavy and light chains by SDS-PAGE and Western analysis. A mix of the same light chain and heavy chain bands were observed as seen in the transformants which produced only light chain or only heavy chain. Assembled IgG1 was assayed by ELISA. Up to 0.19 g/l assembled IgG was measured by ELISA in shake flask cultures.

In some experiments, the trastuzumab heavy chain and associated light chain was specifically precipitated from the supernatant by incubation with Protein A–Sepharose 4 Fast Flow beads (Amersham Pharmacia, Piscataway, NJ) as above. Purification of the heavy chain and associated light chain was also performed using affinity chromatography on a HiTrap Protein A HP chromatography column (Amersham Pharmacia, Piscataway, NJ) following the manufacturers protocol. Fig.8 shows the results of SDS-PAGE under reducing conditions and with Coomassie Brilliant Blue staining of samples which had been purified by protein A chromatography. The bands observed for transformant 1-LC/HC-3 were identified as the light chain (25 kDa), non-glycosylated and glycosylated forms of the heavy chain (50

and 53 kDa), glucoamylase-light chain fusion protein (85 kDa) and glucoamylase-heavy chain fusion (116 kDa). The fact that light chain was co-purified with heavy chain by Protein A affinity chromatography (which is specific for heavy chain) demonstrated that the antibody was assembled. The fact that both glucoamylase-heavy chain and glucoamylase-light chain fusion proteins co-purified by Protein A affinity chromatography demonstrated that the antibody assembled with glucoamylase attached.

Fig.9 shows the results of SDS-PAGE (NuPAGE Tris-Acetate Electrophoresis System from Invitrogen Corporation, Carlsbad, CA) under non- reducing conditions and with Coomassie Brilliant Blue staining of samples which had been purified by protein A chromatography. The major bands observed for transformant 1-LC/HC-3 were identified as assembled IgG1 (150 kDa), assembled IgG1 with one molecule of glucoamylase attached (~200 kDa) and assembled IgG1 with two molecules of glucoamylase attached (~250 kDa).

In order to understand why the two forms of the free heavy chain (i.e., that heavy chain which was released from the glucoamylase-heavy chain fusion protein) were produced differing in apparent molecular weight by approximately 3 kD, the following experiments were performed. The trastuzumab produced by Aspergillus was purified by protein A affinity chromatography. Samples of the purified trastuzumab were incubated for 1 hour in the presence or absence of 35 ug of endo-β-N-acetylglucosaminidase H (endo H) which is able to cleave high mannose type N-linked glycosylation from proteins leaving a single N-acetylglucosamine sugar attached to the asparagine of the protein. These samples were analyzed by SDS-PAGE under reducing conditions followed by Coomassie Brilliant Blue staining for proteins or staining which is specific for glycoproteins (GelCode Glycoprotein Staining Kit from Pierce, Rockford, IL used according to the manufactures instructions). The upper of the two bands of free heavy chain was greatly reduced in intensity by treatment with endo H. Only the upper free heavy chain band was stained with GelCode stain and this band was no longer visible with GelCode staining after endo H treatment. These observations indicate that the upper of the two free heavy chain bands represents heavy chain with N-linked high mannose glycan attached and that endo H treatment is able to remove this glycan.

It was possible to purify and separate the free IgG1 from the glucoamylase-IgG1 fusion proteins. The method used for purification was hydrophobic charge induction chromatography as described in co-pending application USSN 60/411,537 filed September 18, 2002, entitled "Protein Purification" (Attorney Docket Number GC775P). Firstly, fungal cells were removed from culture broth by filtration through Miracloth (Calbiochem, San Diego, CA). The filtered broth was concentrated approximately seven-fold by tangential ultrafiltration. Using a circulating pump, the broth was pressurized and flowed across a

membrane made of regenerated cellulose with a 30,000 molecular weight cutoff (Prep/Scale™ TFF, Millipore). To remove particulates, the concentrate was centrifuged at 25,000 times gravity for 15 minutes, and the supernatant was filtered through a series of membranes, with each membrane having a smaller pore size than the previous, ending with 0.2-micrometer pore size. IgG1 was purified from supernatant using hydrophobic charge induction chromatography (HCIC) This was performed with the aid of a high performance liquid chromatographic system (AKTA™explorer 10, Amersham Biosciences). HCIC provided an ability to separate antibody molecules from other supernatant proteins and from glucoamylase-fusion proteins. It was carried out using a column containing MEP HyperCel® (Ciphergen Biosystems) media. The column was equilibrated with 50 mM Tris, 200 mM NaCl, and pH 8.2 buffer. Supernatant, adjusted to pH 8.2, was applied to the column at a linear flow rate of 100 cm/h. After washing with five column volumes (5 CV) of equilibration buffer, bound molecules were eluted by incrementally decreasing the pH. Two CV of each of the following buffers were delivered to the column at 200 cm/h, in the order listed: 100 mM sodium acetate, pH 5.6; 100 mM sodium acetate, pH 4.75; 100 mM sodium acetate, pH 4.0; and 100 mM sodium citrate, pH 2.5. Free IgG1 eluted within the pH range 4.5-5.5 and was immediately neutralized with 1 M Tris and pH 8.2 buffer. The purity of the antibody exiting the column was assessed by SDS-PAGE.

Example 13
Aglycosylated Trastuzumab expression in *Aspergillus*

The plasmid pCL3 (the expression vector for the aglycosylated mutant form of the heavy chain) was used to transform strain Q83-35-2, the best light chain producing strain identified above. Transformants were cultured in shake flasks. Both light chain and heavy chain expression was evident from SDS-PAGE after precipitation of the heavy chain with protein A-sepharose beads or after purification by protein A affinity chromatography. A mix of the same light chain and heavy chain bands were observed on SDS-PAGE under reducing conditions as seen in transformant 1-LC/HC-3 except that only a single band of free heavy chain at 50 kD was observed (strain 1-HCΔ-4 in Fig.8). A similar pattern of bands were observed on SDS-PAGE under non-reducing conditions as seen in transformant 1-LC/HC-3 (strain 1-HCΔ-4 in Fig.9). Fully assembled IgG1 was measured by ELISA. 0.1 g/l of aglycosylated trastuzumab was produced in shake flask cultures by the best transformant.

Example 14
Trastuzumab Fab' fragment expression in *Aspergillus*

The plasmid pCL2 (the expression vector for the Fd' fragment of the trastuzumab heavy chain) was used to transform strain Q83-35-2, the best light chain producing strain identified above. Transformants were cultured in shake flasks. Assembled Fab' was measured by ELISA. Two transformants were studied in more detail; 1-Fab-1 and 1-Fab-12. 1.2 g/l Fab' was produced in shake flask cultures by the best transformant (strain 1-Fab-12). Expression of the Fab' fragment of the trastuzumab was evident from SDS-PAGE after precipitation of the heavy chain with protein A-sepharose beads or after purification by protein A affinity chromatography. SDS-PAGE under reducing conditions showed a band at approximately 25 kDa representing both the light chain and Fd' chains as well as a band at approximately 85 kDa representing both the glucoamylase-light chain and glucoamylase-Fd' chain fusion proteins (strain 1-Fab-1 in Fig.8). The major bands observed on SDS-PAGE under non-reducing conditions were one at approximately 50 kDa representing the assembled Fab' and one at approximately 100 kDa representing Fab' with a single glucoamylase molecule attached (strain 1-Fab-1 in Fig.9). A fainter band at approximately 150 kDa may represent Fab' with glucoamylase molecules attached to both the light chain and the Fd' chain. It is of interest to determine if Fab' produced by *A. niger* can covalently dimerize through the free cysteines near the carboxyl terminus of the Fd' chain to form $F(ab')_2$. The size of $F(ab')_2$ would be approximately 100 kDa and would therefore run at the same position as Fab' with a single glucoamylase molecule attached on non-reducing SDS-PAGE. Similarly, the size of $F(ab')_2$ with one glucoamylase attached would be approximately 150 kDa and would therefore run at the same position as Fab' with two glucoamylase molecules attached. However, the higher molecular weight band at approximately 200 kDa observed for strain 1-Fab-1 in Fig. 9 is best explained as representing $F(ab')_2$ with two glucoamylase molecules attached.

To confirm that $F(ab')_2$ was secreted by transformant 1-Fab-12 the secreted antibody fragments were purified to separate the Fab' and $F(ab')_2$ from the glucoamylase-Fab' and glucoamylase-$F(ab')_2$ fusion proteins. The method used for purification was hydrophobic charge induction chromatography as described in co-pending application USSN 60/411,537 filed September 18, 2002, entitled "Protein Purification" (Attorney Docket Number GC775P) followed by size exclusion chromatography. Firstly, fungal cells were removed from culture broth by filtration through Miracloth (Calbiochem, San Diego, CA). The filtered broth was concentrated approximately seven-fold by tangential ultrafiltration. Using a circulating pump, the broth was pressurized and flowed across a membrane made of regenerated cellulose with a 30,000 molecular weight cutoff (Prep/Scale™ TFF, Millipore). To remove particulates, the concentrate was centrifuged at 25,000 times gravity for 15 minutes, and the supernatant was filtered through a series of membranes, with each

membrane having a smaller pore size than the previous, ending with 0.2-micrometer pore size. Fab' (monomer and dimer) antibody fragments were purified from supernatant using a combination of hydrophobic charge induction chromatography (HCIC) and size exclusion chromatography (SEC). Each of these methods was performed with the aid of a high performance liquid chromatographic system (AKTA™explorer 10, Amersham Biosciences). HCIC provided an ability to separate antibody molecules from other supernatant proteins and from glucoamylase-fusion proteins. SEC served to separate Fab from $F(ab')_2$. HCIC was carried out using a column containing MEP HyperCel® (Ciphergen Biosystems) media. The column was equilibrated with 50 mM Tris, 200 mM NaCl, and pH 8.2 buffer. Supernatant, adjusted to pH 8.2, was applied to the column at a linear flow rate of 100 cm/h. After washing with five column volumes (5 CV) of equilibration buffer, bound molecules were eluted by incrementally decreasing the pH. Two CV of each of the following buffers were delivered to the column at 200 cm/h, in the order listed: 100 mM sodium acetate, pH 5.6; 100 mM sodium acetate, pH 4.75; 100 mM sodium acetate, pH 4.0; and 100 mM sodium citrate, pH 2.5. Fab' and $F(ab')_2$ eluted within the pH range 4.5-5.5 and were immediately neutralized with 1 M Tris and pH 8.2 buffer. A HiLoad™ 26/60 column with Superdex 200™ Prep Grade media (Amersham Biosciences) was used for SEC. The flow rate was kept at 17 cm/h. After equilibrating the column with 20 mM sodium acetate, 136 mM NaCl, and pH 5.5 buffer, a 6.5-mL sample was driven through the column with 1 CV of equilibration buffer. The purity of the antibody exiting the column was assessed by SDS-PAGE.

On SDS-PAGE under reducing conditions the Fd' and light chains of the HCI-purified Fab' and $F(ab')_2$ both run as bands of 25 kDa (Fig.10). Under these conditions it is clear that no glucoamylase-light chain or glucoamylase-Fd' fusion proteins are present in the purified samples because these would run as a band of approximately 50 kDa. On SDS-PAGE under non-reducing conditions it is clear that $F(ab')_2$ is present in the purified samples (Fraction A5 in Fig.10) because this runs as a band of approximately 100 kDa compared to the 50 kDa of Fab'(Fraction B7 in Fig.10).

Example 15
Assays to demonstrate that Trastuzumab made in *Aspergillus* is functional (it binds to and inhibits proliferation of her2 expressing breast cancer cells)

The effect of the trastuzumab produced by *Aspergillus* transformant 1-LC/HC-3 was compared to that of commercial trastuzumab (Herceptin, Genentech, South San Francisco, CA) on the proliferation of a human breast adenocarcinoma cell line, SK-BR-3 (ATCC number: HTB-30), which expresses high levels of HER2. In order to assay proliferation of the cells in 96 well microtiter plates the "CellTiter 96 Aqueous One Solution Cell

Proliferation Assay" (Promega Corporation, Madison, WI) was used according to the manufacturers instructions. SK-BR-3 cells were plated at 1800 cells per well and allowed to adhere for 6 hours prior to antibody addition then assayed 72 hours later. Protein A purified IgG1 from transformant 1-LC/HC-3 was tested for anti-proliferative effects on SK-BR-3 cells relative to Herceptin and untreated cells. As a control cell line A-431 cells (ATCC number: CRL-1555) were used. A-431 is human epidermoid carcinoma that expresses high levels of the EGF receptor and low levels of HER2. Herceptin should have little or no anti-proliferative effect on this cell line. Data is presented as the percent proliferation (mean of triplicate wells) relative to untreated cells (see Fig.11). These results are in excellent agreement with the reported anti-proliferative effects of trastuzumab on the SK-BR-3 cell line (Carter, P. et al., 1992, Proc. Natl. Acad. Sci. USA 89:4285-4289) and demonstrate that the antibody purified from culture supernatant of transformant 1-LC/HC-3 is assembled and functional in its ability to bind to the specific antigen, HER2.

Example 16
Production of Hu1D10 antibody in *Aspergillus*

Expression vectors were constructed in the same manner as described in Example 10 to allow the production of the light and heavy chains of Hu1D10 antibody (of the IgG1κ subclass; Kostelny, S.a. et al., 2001, Int. J. Cancer 93:556-565) in *Aspergillus niger*. The cDNA encoding Hu1D10 was modified by site directed mutagenesis to remove internal *Bst*EII sites. PCR primers were designed to amplify and add *Nhe*I sites at the 5' end, add *Bst*EII sites at the 3' end and to add specific codons at the 5' ends.

Two forms of the cDNA encoding the Hu1D10 light chain were generated which varied at the 5' end sequence. The cDNA sequence encoding the Q101 form of Hu1D10 light chain was as follows. The nucleotides represented in lower case are those added by the PCR primers.

GctagcatctccaagcgcGACATCCAGATGACTCAGTCTCCATCTTCTCTATCTGCATC
TGTGGGAGACAGGGTCACAATCACATGTCGAGCAAGTGAAAATATTTACAGTTATTTA
GCATGGTACCAGCAGAAACCTGGAAAAGCTCCTAAGCTCCTGGTCTCTAATGCTAAAA
CCTTAGCAGAAGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGCAAACAGTTTA
CTCTGACAATCAGCAGCCTGCAGCCTGAAGATTTTGCTACTTATTACTGTCAACATCAT
TATGGTAATTCGTACCCGTTCGGACAGGGGACCAAACTGGAAATAAAACGAACTGTGG
CTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGC
CTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG
GTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGC

AAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAG
AAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA
AAGAGCTTCAACAGGGGAGAGTGTTAGggtgacc (SEQ ID NO:32).

The cDNA sequence encoding the Q100 form of Hu1D10 light chain was as follows. The nucleotides represented in lower case are those added by the PCR primers.

GctagcatctccaagcgcggtggcggaGACATCCAGATGACTCAGTCTCCATCTTCTCTAT
CTGCATCTGTGGGAGACAGGGTCACAATCACATGTCGAGCAAGTGAAAATATTTACAG
TTATTTAGCATGGTACCAGCAGAAACCTGGAAAAGCTCCTAAGCTCCTGGTCTCTAAT
GCTAAAACCTTAGCAGAAGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGCAAA
CAGTTTACTCTGACAATCAGCAGCCTGCAGCCTGAAGATTTTGCTACTTATTACTGTCA
ACATCATTATGGTAATTCGTACCCGTTCGGACAGGGGACCAAACTGGAAATAAAACGA
ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG
GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA
GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA
GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGA
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC
CGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGggtgacc (SEQ ID NO:33).

The above amplified light chain cDNAs could then be inserted into the *Aspergillus* expression vector to create pQ101 or pQ100. The *Aspergillus niger* var *awamori glaA* (glucoamylase) promoter and *A. niger glaA* terminator were present in the plasmid to control expression of the open reading frame which included the light chain encoding cDNA.

Plasmid pQ101 was designed for the expression of a fusion protein with the amino acid sequence shown below and consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 498 (a serine) of mature glucoamylase (Nunberg, J.H. et al., 1984, Mol. Cell. Biol. 4:2306-2315), followed by amino acids ISKR (underlined below) and then by the mature Hu1D10 light chain. This plasmid did not include a selectable marker for *Aspergillus* transformation.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA

LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASISKRDIQMTQSPSS
LSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLVSNAKTLAEGVPSRFSGSGSGKQ
FTLTISSLQPEDFATYYCQHHYGNSYPFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:34).

Plasmid pQ100 was designed for the expression of a fusion protein with the amino acid sequence shown below and consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 498 (a serine) of mature glucoamylase (Nunberg, J.H. et al., 1984, Mol. Cell. Biol. 4:2306-2315), followed by amino acids ISKRGGG (underlined below) and then by the mature Hu1D10 light chain. This plasmid also contained the *A. niger pyrG* gene as a selectable marker for *Aspergillus* transformation.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASISKRGGGDIQMTQ
SPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLVSNAKTLAEGVPSRFSGSG
SGKQFTLTISSLQPEDFATYYCQHHYGNSYPFGQGTKLEIKRTVAAPSVFIFPPSDEQLKS
GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:35).

Two forms of the cDNA encoding the Hu1D10 heavy chain were generated which varied at the 5' end sequence. The cDNA sequence encoding the CL17 form of Hu1D10 light chain was as follows. The nucleotides represented in lower case are those added by the PCR primers.

gctagcatctccaagcgcCAGGTGCAGCTGCAGGAGTCAGGACCAGGCCTAGTGAAG
CCCTCAGAGACTCTGTCCCTAACCTGCACAGTCTCTGGTTTCTCATTAACTAACTATG
GTGTACACTGGGTTCGCCAGTCTCCAGGAAAGGGTCTGGAATGGATCGGAGTGAAAT

GGAGTGGTGGGTCGACAGAATATAATGCAGCTTTCATATCCAGACTGACCATCAGCAA
GGACACCTCCAAGAACCAAGTTTCCCTTAAACTGAACAGTCTGACCGCTGCTGACACA
GCCGTGTACTACTGTGCCAGAAATGATAGATATGCTATGGACTACTGGGGTCAAGGAA
CTCTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC
TACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT
GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACAGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA
GCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCAC
ACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA
CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA
GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC
CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA
AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAggtgacc (SEQ ID NO:36).

The cDNA sequence encoding the CL16 form of Hu1D10 heavy chain was as follows. The nucleotides represented in lower case are those added by the PCR primers.

gctagcatctccaagcgcggtggcggaCAGGTGCAGCTGCAGGAGTCAGGACCAGGCCTA
GTGAAGCCCTCAGAGACTCTGTCCCTAACCTGCACAGTCTCTGGTTTCTCATTAACTA
ACTATGGTGTACACTGGGTTCGCCAGTCTCCAGGAAAGGGTCTGGAATGGATCGGAG
TGAAATGGAGTGGTGGGTCGACAGAATATAATGCAGCTTTCATATCCAGACTGACCAT
CAGCAAGGACACCTCCAAGAACCAAGTTTCCCTTAAACTGAACAGTCTGACCGCTGCT
GACACAGCCGTGTACTACTGTGCCAGAAATGATAGATATGCTATGGACTACTGGGGTC
AAGGAACTCTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCC
TGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC
GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
GTGGTGACAGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT

CACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAA
CTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCC
TCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACAT
GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAG
CACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA
GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT
CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGA
CCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAggtgac
c (SEQ ID NO:37).

The above amplified heavy chain cDNAs could then be inserted into the *Aspergillus* expression vector to create pCL17 or pQCL16. The *Aspergillus niger* var *awamori glaA* (glucoamylase) promoter and *A. niger glaA* terminator were present in the plasmid to control expression of the open reading frame which included the heavy chain encoding DNA.

Plasmid pCL17 was designed for the expression of a fusion protein with the amino acid sequence shown below and consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 498 (a serine) of mature glucoamylase (Nunberg, J.H. et al., 1984, Mol. Cell. Biol. 4:2306-2315), followed by amino acids ISKR (underlined below) and then by the mature Hu1D10 heavy chain. This plasmid also contained the *A. niger pyrG* gene as a selectable marker for *Aspergillus* transformation.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATAS<u>ISKR</u>QVQLQESGP
GLVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTI

SKDTSKNQVSLKLNSLTAADTAVYYCARNDRYAMDYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD
TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK (SEQ ID NO:38).

Plasmid pCL16 was designed for the expression of a fusion protein with the amino acid sequence shown below and consisting of the glucoamylase signal sequence, prosequence, catalytic domain and linker region up to amino acid number 498 (a serine) of mature glucoamylase (Nunberg, J.H. et al., 1984, Mol. Cell. Biol. 4:2306-2315), followed by amino acids ISKRGGG (underlined below) and then by the mature Hu1D10 heavy chain. This plasmid did not include a selectable marker for *Aspergillus* transformation.

MSFRSLLALSGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWVSGA
DSGIVVASPSTDNPDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGISNP
SGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSTAT
DIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCS
WCDSQAPEILCYLQSFWTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCS
PRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWFLCTLAAAEQLYDA
LYQWDKQGSLEVTDVSLDFFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGFVSIVETHA
ASNGSMSEQYDKSDGEQLSARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCA
ATSAIGTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATAS<u>ISKRGGG</u>QVQLQE
SGPGLVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFIS
RLTISKDTSKNQVSLKLNSLTAADTAVYYCARNDRYAMDYWGQGTLVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK (SEQ ID NO:39).

Plasmids pQ101 and pCL17 were co-transformed into *Aspergillus niger* var *awamori* strain dgr246ΔGAP:pyr2- by the methods described in Examples 9 and 12. The best Hu1D10 producing transformant (3-Hu1D10-20e) was identified and found to produce approximately 0.2 g/l of IgG1κ.

Plasmids pQ100 and pCL16 were co-transformed into *Aspergillus niger* var *awamori* strain dgr246ΔGAP:pyr2- by the methods described in Examples 9 and 12. The best Hu1D10 producing transformant (2-Hu1D10-16b) was identified and found to produce approximately 0.2 g/l of IgG1κ.

Antibody was purified from culture supernatant of these transformants by the methods described in Example 12. The purified antibody preparation obtained from strain 3-Hu1D10 was designated An-Hu1D10 and that from strain 2-Hu1D10-16b was designated An-3G-Hu1D10.

Example 17
Antibody affinity and avidity

The human Burkitt's lymphoma-derived cell line Raji (ATCC, Manassas, VA), which expresses the HLA-DR β chain allotype recognized by Hu1D10 (Kostelny et al., 2001, Int J Cancer, 93:556), was maintained in RPMI-1640 (Gibco BRL, Grand Island, NY) containing 10% fetal bovine serum (FBS; HyClone, Logan, UT) in a 7.5% CO_2 incubator. The affinity of Hu1D10 binding to HLA-DR β chains was determined by measuring the amount of antibody that bound to Raji cells. Raji cells (5×10^5 cells/test) were incubated with varying amounts (serial 2-fold dilutions starting at 1 µg/test) of control Hu1D10 (derived from the NS0 mouse myeloma cell line), An-Hu1D10 or An-3G-Hu1D10 for 30 min on ice in 100 µl of FACS Staining Buffer (FSB; PBS containing 1% bovine serum albumin and 0.2% sodium azide). After incubation, cells were washed three times in FSB and incubated with fluorescein isothiocyanate (FITC)-conjugated AffiniPure goat anti human IgG antibodies (Jackson ImmunoResearch, West Grove, PA) for additional 30 min on ice. The cells were washed three times with FSB and analyzed by flow cytometry using a FACScan (Becton Dickinson, San Jose, CA). Antibody concentration (ng/test) was plotted versus mean channel fluorescence (Fig. 12). A competition binding experiment was also performed in which a mixture of FITC-labeled NS0-Hu1D10 (0.25 µg/test) and competitor antibody (serial 2-fold dilutions of control NS0-derived Hu1D10, An-Hu1D10 or An-3G-Hu1D10 starting at 6.25 µg/test) in FSB was added to Raji cells (5×10^5 cells/test) in a final volume of 100 µl per test in duplicate. All samples were incubated on ice for 30 min. The cells were washed three times with FSB and analyzed by flow cytometry. Competitor concentration (ng/test) was plotted versus mean channel fluorescence (Fig. 13). No significant difference was observed in the binding to Raji cells among the NS0-derived and *Aspergillus*-derived Hu1D10 antibodies (Figs 12 and 13), indicating that the production of Hu1D10 in *Aspergillus niger* had no measurable effect on the structure of its antigen binding site.

In addition, the avidity of Hu1D10 was measured by monitoring the degree of apoptosis in a population of Raji cells (as determined by staining with FITC-Annexin V and

propidium iodide; Vermes, I. et al., 1995, J. Immunol. Methods 184:38-51). To measure the ability control NS0-derived Hu1D10, An-Hu1D10 or An-3G-Hu1D10 antibodies to induce apoptosis, Raji cells resuspended at 5 x 10^5 cells/ml in RPMI-1640 containing 10% FBS were incubated with 2 µg antibody at 37°C for 5 hr or 24 hr. Cells were then washed three times in 1X binding buffer provided in the Apoptosis Detection Kit (Pharmingen, San Diego, CA) and stained with FITC-conjugated annexin V and propidium iodide according to the manufacturer's protocol. Cell death was determined by 2-color flow cytometry. Percent apoptosis was defined as the sum of the percentage of annexin V staining cells and the percentage of annexin V and propidium iodide staining cells. Relative cell fluorescence was analyzed on FACScan (Fig. 14).

No significant difference in ability to induce apoptosis was observed between NS0-Hu1D10, An-Hu1D10 or An-3G-Hu1D10 in these experiments.

Example 18
Antibody-dependent cellular cytotoxicity (ADCC)

The ability of NS0-Hu1D10, An-Hu1D10 or An-3G-Hu1D10 to kill Raji cells by ADCC was measured (Kostelny et al, 2001). ADCC was analyzed with the LDH Detection Kit (Roche Molecular Biochemicals, Indianapolis, IN) using human PBMC as effector cells (E) and Raji cells as target cells (T). Human peripheral blood mononuclear cells (PBMC) were isolated from healthy donors using Ficoll-Paque PLUS lymphocyte isolation solution (Amersham Biosciences, Uppsala, Sweden). Target and effector cells were washed in RPMI-1640 (Gibco BRL) supplemented with 1% BSA and added to 96-well U-bottom plates (Becton Dickinson) at an E:T ratio of 40:1. Hu1D10 antibodies were added to the wells at desired concentrations. After a 4 hr incubation at 37°C, all plates were centrifuged and cell-free supernatants were incubated with LDH reaction mixture in separate 96-well flat-bottom plates for 30 min at 25°C. The absorbance of reaction samples was measured at 490 nm. Antibody-independent cellular cytotoxicity (AICC) was measured by adding effector and target cells in the absence of antibodies. Spontaneous release (SR) was measured by adding only target or effector cells. Maximal release (MR) was measured by adding 2% Triton-X100 to target cells. Percent lysis was determined by the following equation: {(LDH release of sample - SR of effector cells - SR of target cells)/(MR of target cells - SR of target cells)} x 100. Each condition was examined in duplicate.

Human PBMC from two different donors were used in the analysis. With donor 1 (Fig. 15, left panel), the maximal cytotoxicity level reached nearly 40% with either of the three Hu1D10 antibodies. In this particular experiment, the *Aspergillus*-derived An-Hu1D10 induced cytotoxicity slightly better than the other two Hu1D10 antibodies. Between the NS0-derived Hu1D10 and the *Aspergillus*-derived An-3G-Hu1D10 antibodies, however,

there was no significant difference in induction of cytotoxicity. With donor 2 (Fig. 15, right panel), the maximal cytotoxicity levels were between 15 to 20% with the three Hu1D10 antibodies. In this experiment, the An-Hu1D10 antibody was not as active in inducing cytotoxicity as the other two Hu1D10 antibodies, although the difference among the three antibodies was minimal. These results clearly indicate that the *Aspergillus*-derived Hu1D10 antibodies exhibit ADCC activities.

Example 19
Pharmacokinetics

An in vivo rat study was performed in order to compare the pharmacokinetics of trastuzumab purified from *A. niger* strain 2-LC/HC-38b with that of trastuzumab (Herceptin) purchased from Genentech Inc., South San Francisco.

Two groups of Sprague Dawley rats (weight range of approximately 250 –300 g) received a 2 mg/kg IV bolus dose of *A. niger*- derived trastuzumab (N=3) or of the commercial trastuzumab (N=4). Animals were dosed according to individual body weight using trastuzumab preparations that had been diluted to a final concentration of 0.9 mg/mL. Blood for serum (0.5 mL/sample) was collected at 0, 1, 4, 8, 24, 48, 72 and 96 hours and 7, 12, and 14 days post-dose. Serum was prepared by centrifugation of the blood sample within 30 minutes of collection. The serum was decanted and the serum samples were stored on ice until transfer for storage at –80°C. Human IgG1 levels in these serum samples were measured by ELISA as described above. The serum concentration versus time profiles of the fungal-derived and commercial trastuzumabs are shown in Figure 16. A noncompartmental analysis of the data was performed (Table 1). The parameters from this analysis as well as the serum concentration versus time profiles of trastuzumab from 2 LC/HC-38b and the commercial source were similar. Given the long survival time in the serum of both commercial trastuzumab and the antibody from 2 LC/HC-38b an accurate estimate of half-life could not be determined in this 14 day study. However, the parameters commonly used to evaluate bioequivalence, namely C_{max} (the mean peak concentration of antibody in the serum) and AUC_{last} (area under the concentration-time curve), were comparable for the 2 LC/HC 38b and mammalian cell-derived trastuzumabs. These results indicated that the fungal expression of trastuzumab did not affect the pharmacokinetic disposition of the antibody *in vivo*.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity and understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

Table 1 Pharmacokinetics of CHO-derived and *Aspergillus*-derived trastuzumab

Meaned parameters from individual animals			
		CHO Ab	Fungal Ab
Parameter	Units	n=4	n=3
Cmax	ug/mL	49.5(6.2)	48.3(3)
No_points_Lambda_z		8.25(1.5)	4.67(1.5)
AUClast	day*ug/mL	153(4.4)	143(11)
HL_Lambda_z	day	11.1(3.3)	15(2)
AUCINF_obs	day*ug/mL	297(45)	285(5.4)
AUC_%Extrap_obs	%	47.7(6.9)	49.8(3)
Vz_obs	mL/kg	106(16)	152(23)

CLAIMS

1. A monoclonal antibody comprising two heavy chains and two light chains wherein each of the chains comprising the monoclonal antibody has been expressed in a filamentous fungal host cell as a fusion protein, wherein the fusion protein comprises a secreted polypeptide or portion thereof normally secreted from a filamentous fungus and an immunoglobulin chain.

2. The monoclonal antibody of claim 1 wherein the secreted polypeptide, or functional part thereof, is selected from the group consisting of an *Aspergillus* glucoamylase, *Aspergillus* alpha-amylase, *Aspergillus* aspartyl protease, *Trichoderma* cellobiohydrolase and *Trichoderma* endoglucanase.

3. The monoclonal antibody of claim 1 wherein the fusion protein comprises an antibody chain and a glucoamylase.

4. The monoclonal antibody of claim 1 wherein the filamentous fungus host is an *Aspergillus*, *Neurospora*, *Fusarium*, *Trichoderma*, *Cephalosporium Penicillium* or *Chrysosporium*.

5. The monoclonal antibody of claim 1 wherein the filamentous fungus is an *Aspergillus*.

6. The monoclonal antibody of claim wherein the filamentous fungus is an *Aspergillus niger*.

7. The monoclonal antibody of claim 1 which is conjugated to a label.

8. The monoclonal antibody of claim 7 wherein the label is a cytotoxic agent, an antibiotic, or a detectable marker.

9. The monoclonal antibody of claim 8 wherein the detectable marker is a radioisotope or an enzyme.

10. A monoclonal antibody comprising two heavy chains and two light chains wherein at least one of the heavy chains and at least one of the light chains comprising the monoclonal antibody has been expressed in a filamentous fungal host cell as a fusion protein, wherein the fusion protein comprises a secreted polypeptide or portion thereof normally secreted from a filamentous fungus and an immunoglobulin chain.

11. The monoclonal antibody of claim 10 wherein the secreted polypeptide, or functional part thereof, is selected from the group consisting of an *Aspergillus* glucoamylase, *Aspergillus* alpha-amylase, *Aspergillus* aspartyl protease, *Trichoderma* cellobiohydrolase and *Trichoderma* endoglucanase.

12. The monoclonal antibody of claim 10 wherein the fusion protein comprises an immunoglobulin chain and a glucoamylase.

13. A monoclonal antibody fragment selected from the group consisting of $F(ab')_2$, Fab' and Fab, said fragment comprising at least one heavy chain and at least one light chain wherein each of the chains comprising the monoclonal antibody fragment has been expressed in a filamentous fungal host cell as a fusion protein, wherein the fusion protein comprises a secreted polypeptide or portion thereof normally secreted from a filamentous fungus and an immunoglobulin chain.

14. The monoclonal antibody of claim 13 wherein the secreted polypeptide, or functional part thereof, is selected from the group consisting of an *Aspergillus* glucoamylase, *Aspergillus* alpha-amylase, *Aspergillus* aspartyl protease, *Trichoderma* cellobiohydrolase and *Trichoderma* endoglucanase.

15. The monoclonal antibody fragment of claim 13 wherein the fusion protein comprises an immunoglobulin chain and a glucoamylase.

16. The monoclonal antibody of claim 13 which is conjugated to a label.

17. The monoclonal antibody of claim 16 wherein the label is a cytotoxic agent, an antibiotic, or a detectable marker.

18. The monoclonal antibody of claim 17 wherein the detectable marker is a radioisotope or an enzyme.

19. A monoclonal antibody according to claim 1 that is non-glycosylated.

20. The monoclonal antibody of claim 19, wherein the antibody has been treated with an enzyme.

21. The monoclonal antibody according to claim 20, wherein the enzyme is selected from the group consisting of endoglycosidase H, endoglycosidase F1, endoglycosidase F2, endoglycosidase A, PNGase F, PNGase A, and PNGase At.

22. The monoclonal antibody of claim 19, wherein the antibody is aglycosylated.

23. The monoclonal antibody of claim 22, wherein aglycosylation is due to an amino acid substitution.

24. The monoclonal antibody of claim 23, wherein aglycosylation is due to the amino acid substitution N297Q.

25. The monoclonal antibody of claim 1 having a fungal glycosylation pattern.

26. The monoclonal antibody of claim 25, having a high mannose glycosylation pattern.

27. A fusion nucleic acid encoding a fusion polypeptide comprising, from a 5' end of said fusion nucleic acid, first, second, third and fourth nucleic acids, wherein said first nucleic acid encodes a signal polypeptide functional as a secretory sequence in a first filamentous fungus, said second nucleic acid encodes a secreted polypeptide or functional portion thereof normally secreted from said first or a second filamentous fungus, said third nucleic acid encodes a cleavable linker and said fourth nucleic acid encodes an immunoglobulin light chain or fragment thereof.

28. The fusion nucleic acid according to claim 27 wherein the fourth nucleic acid encodes an immunoglobin light chain.

29. The fusion nucleic acid according to claim 27 wherein the fourth nucleic acid encodes a fragment of an immunoglobin light chain.

30. A composition comprising the nucleic acid of claim 27.

31. A composition according to claim 30 further comprising a fusion nucleic acid encoding a fusion polypeptide comprising, from a 5' end of said fusion nucleic acid, first, second, third and fourth nucleic acids, wherein said first nucleic acid encodes a signal polypeptide functional as a secretory sequence in a first filamentous fungus, said second nucleic acid encodes a secreted polypeptide or functional portion thereof normally secreted from said first or a second filamentous fungus, said third nucleic acid encodes a cleavable linker and said fourth nucleic acid encodes an immunoglobulin heavy chain or fragment thereof.

32. An expression vector comprising the nucleic acid of any one of claims 27 - 29.

33. The expression vector according to claim 32 further comprising a fusion nucleic acid encoding a fusion polypeptide comprising, from a 5' end of said fusion nucleic acid, first, second, third and fourth nucleic acids, wherein said first nucleic acid encodes a signal polypeptide functional as a secretory sequence in a first filamentous fungus, said second nucleic acid encodes a secreted polypeptide or functional portion thereof normally secreted from said first or a second filamentous fungus, said third nucleic acid encodes a cleavable linker and said fourth nucleic acid encodes an immunoglobulin heavy chain or fragment thereof.

34. A process for producing an immunoglobulin molecule or an immunologically functional immunoglobulin fragment comprising at least the variable domains of the immunoglobulin heavy and light chains, in a host filamentous fungus, comprising the steps of:

a. transforming said host with a first expression vector containing the

fusion DNA sequence of Claim 27;

b. transforming said host with a second expression vector containing the a fusion nucleic acid encoding a fusion polypeptide comprising, from a 5' end of said fusion nucleic acid, first, second, third and fourth nucleic acids, wherein said first nucleic acid encodes a signal polypeptide functional as a secretory sequence in a first filamentous fungus, said second nucleic acid encodes a secreted polypeptide or functional portion thereof normally secreted from said first or a second filamentous fungus, said third nucleic acid encodes a cleavable linker and said fourth nucleic acid encodes an immunoglobulin heavy chain or fragment thereof;

c. growing said host under conditions which permit expression of said fusion DNA sequences to cause the expression of the desired polypeptides encoded by said fusion DNA sequences; and

d. isolating said immunoglobulin or molecule or immunologically functional immunoglobulin fragment therefrom.

35. The process of Claim 34, wherein the immunoglobulin or fragment thereof is secreted.

36. A process for producing an immunoglobulin molecule or an immunologically functional immunoglobulin fragment comprising at least the variable domains of the immunoglobulin heavy and light chains, in a host filamentous fungus, comprising the steps of:

a. transforming said host with a composition according to Claim 31;

b. growing said host under conditions which permit expression of said fusion DNA sequences to cause the expression of the desired polypeptides encoded by said fusion DNA sequences; and

c. isolating said immunoglobulin or molecule or immunologically functional immunoglobulin fragment therefrom.

37. The process of Claim 36, wherein the immunoglobulin or fragment thereof is secreted.

38. A filamentous fungal host cell capable of secreting a monoclonal antibody wherein the monoclonal antibody is expressed by the process of claim 34 or Claim 36.

39. A filamentous fungal host cell that has been transformed with a first and second fusion nucleic acid wherein

a. the first fusion nucleic acid encodes at least the variable domain of either the immunoglobulin heavy or light chain one chain; and

b. the second fusion nucleic acid encodes the other chain.

40. A filamentous fungal host cell that has been transformed with a composition according to claim 31.

41. A therapeutic composition comprising a monoclonal antibody or fragment thereof, wherein the antibody is produced by the method of claim 34 or Claim 36.

42. A therapeutic composition comprising a monoclonal antibody or fragment thereof according to claim 1.

43. A therapeutic composition comprising a monoclonal antibody conjugated to a label according to claim 7.

44. A diagnostic or assay kit comprising an antibody or fragment thereof, wherein the antibody is produced by the method of claim 34 or claim 36.

45. The kit of Claim 44 wherein the monoclonal antibody is conjugated to a label.

46. The kit of Claim 45 wherein the label is a cytotoxic agent, an antibiotic, or a detectable marker.

47. The kit of Claim 46 wherein the detectable marker is a radioisotope or an enzyme.

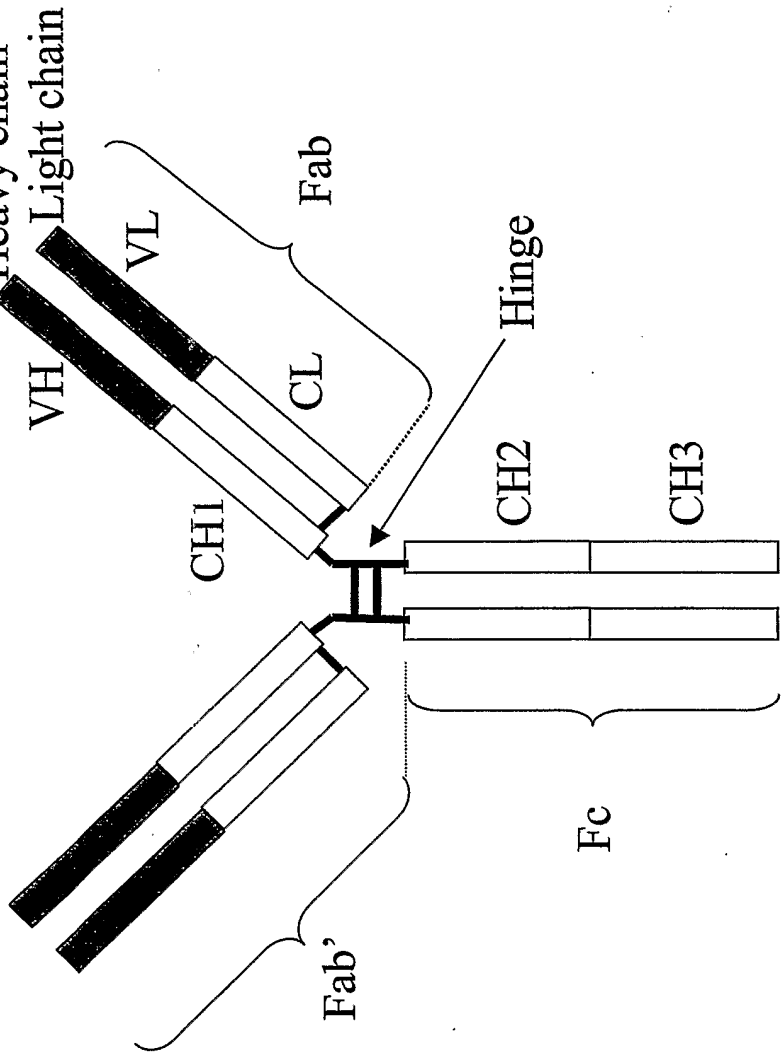
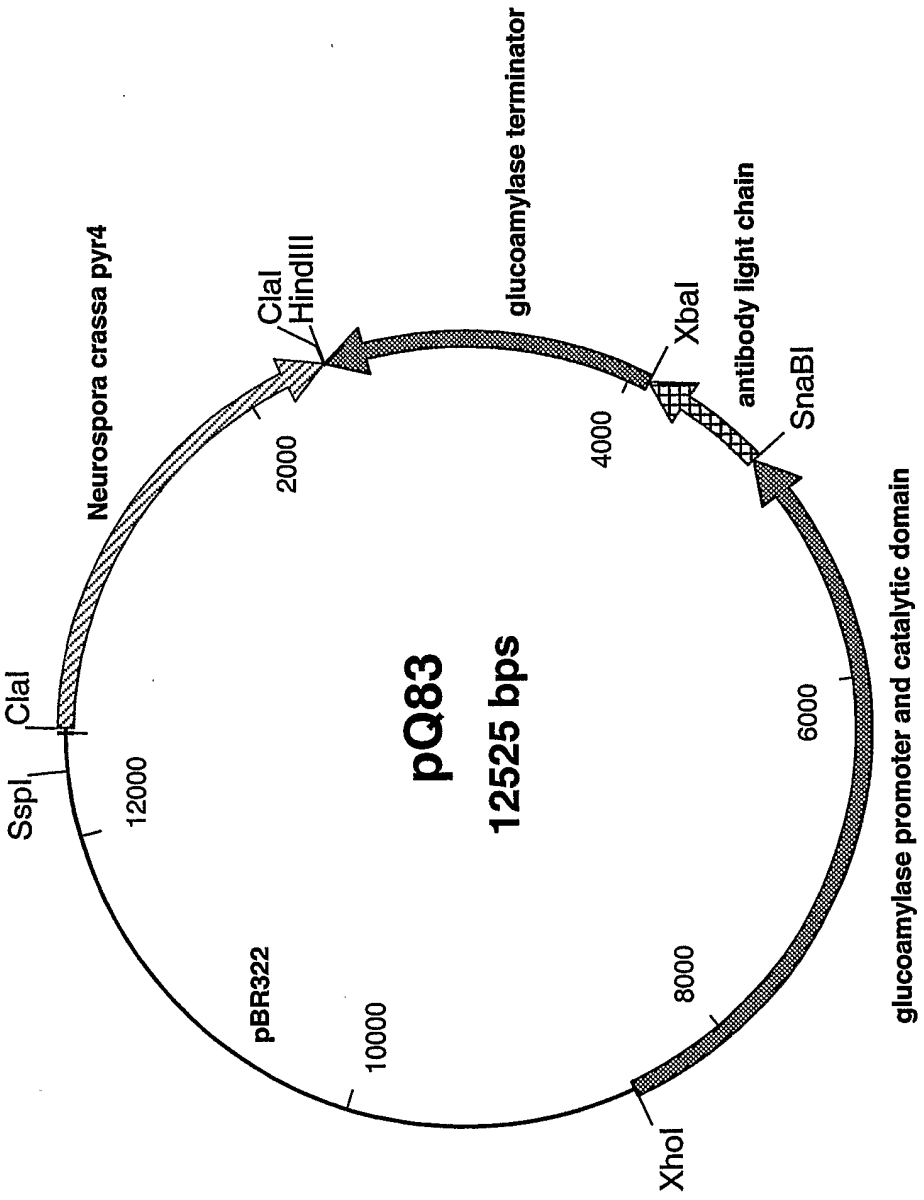


Fig. 1

Fig. 2 *Aspergillus niger* glucoamylase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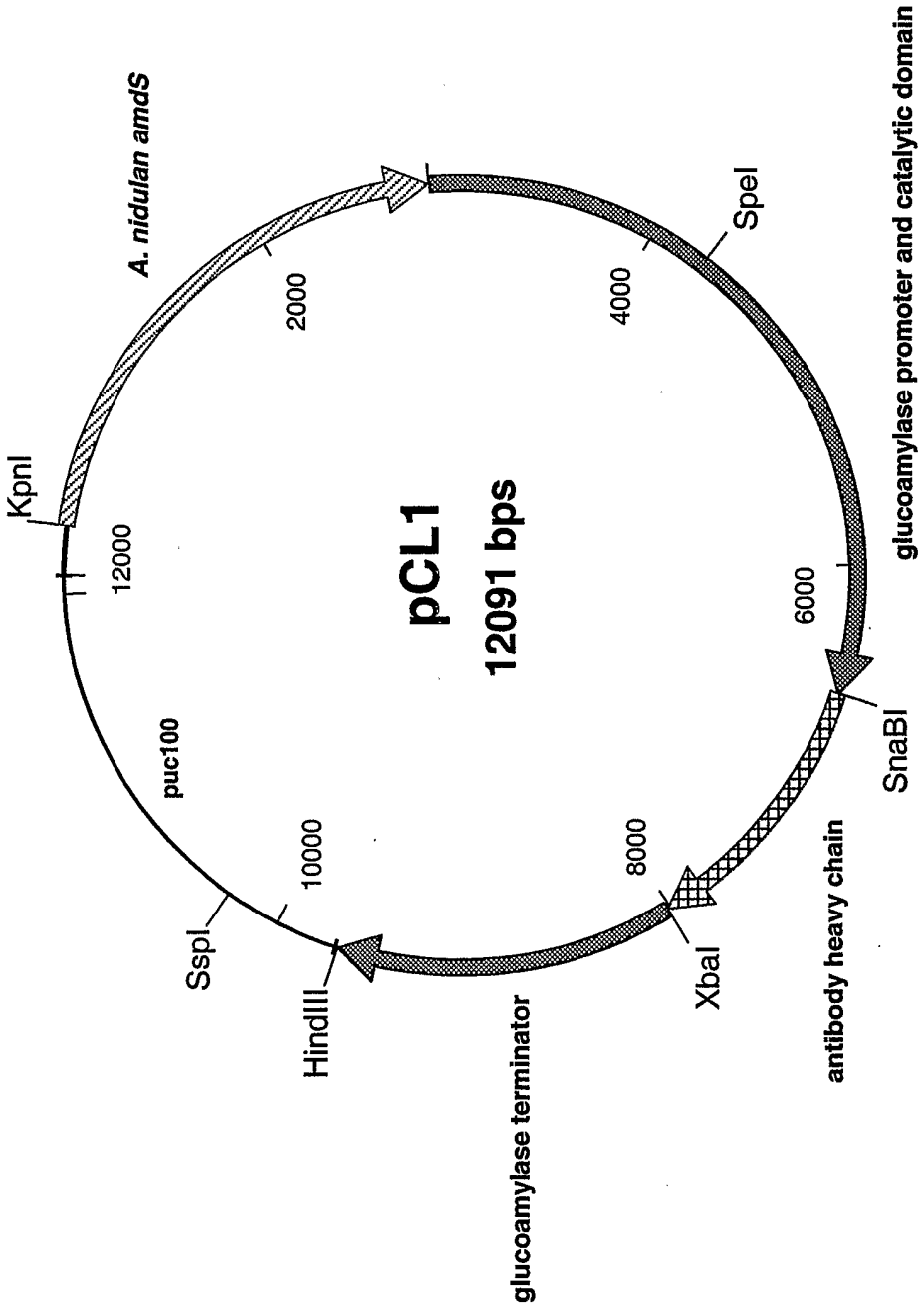
12525 bps
ClaI
HindIII
XbaI
SnaBI
XhoI
SspI
ClaI
2000
4000
6000
8000
10000
12000
Neurospora crassa pyr4
glucoamylase terminator
antibody light chain
glucoamylase promoter and catalytic domain
pBR322

Fig. 3

Fig. 4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12091 bps
A. nidulan amdS
glucoamylase promoter and catalytic domain
antibody heavy chain
glucoamylase terminator
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SpeI
SnaBI
XbaI
HindIII
SspI
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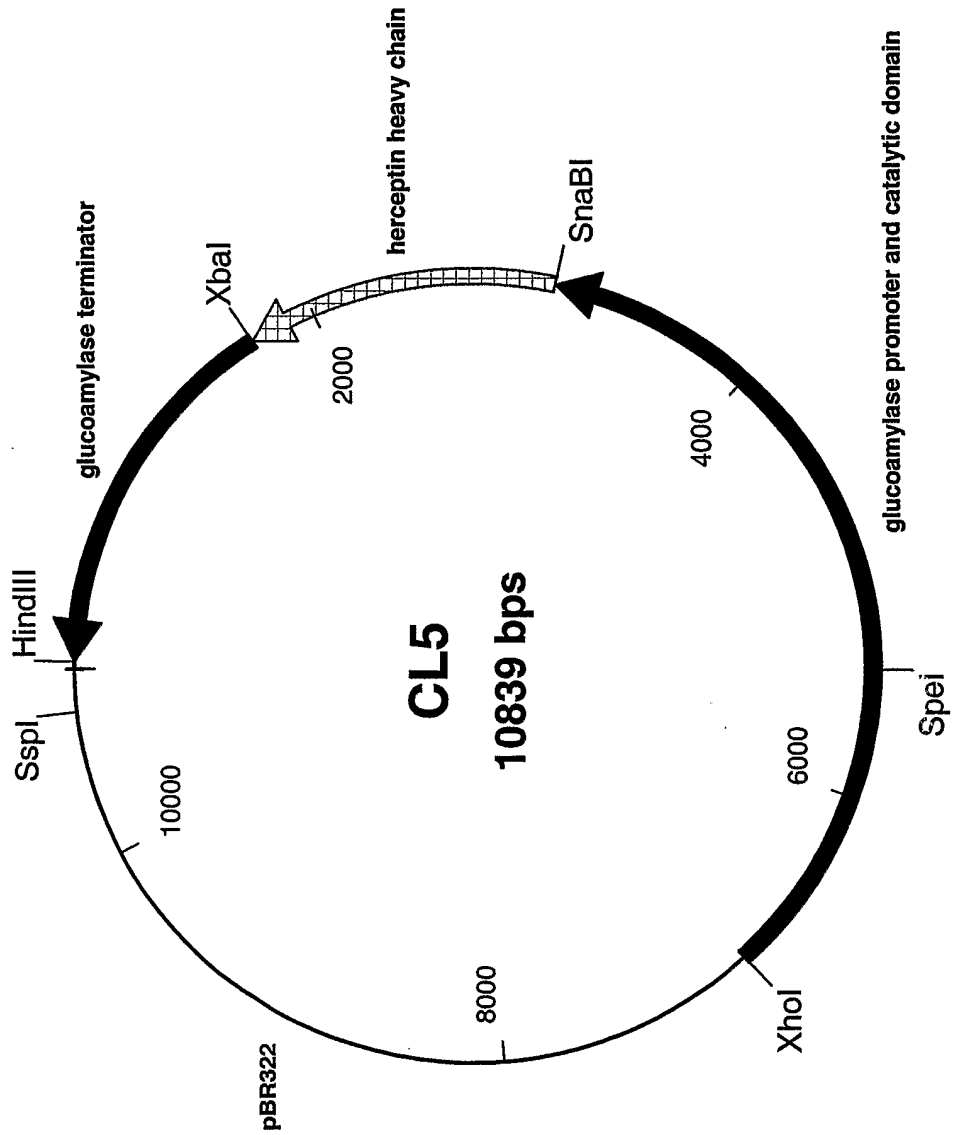
4000
6000
8000
10000
12000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SnaBI
SpeI
XhoI
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8000
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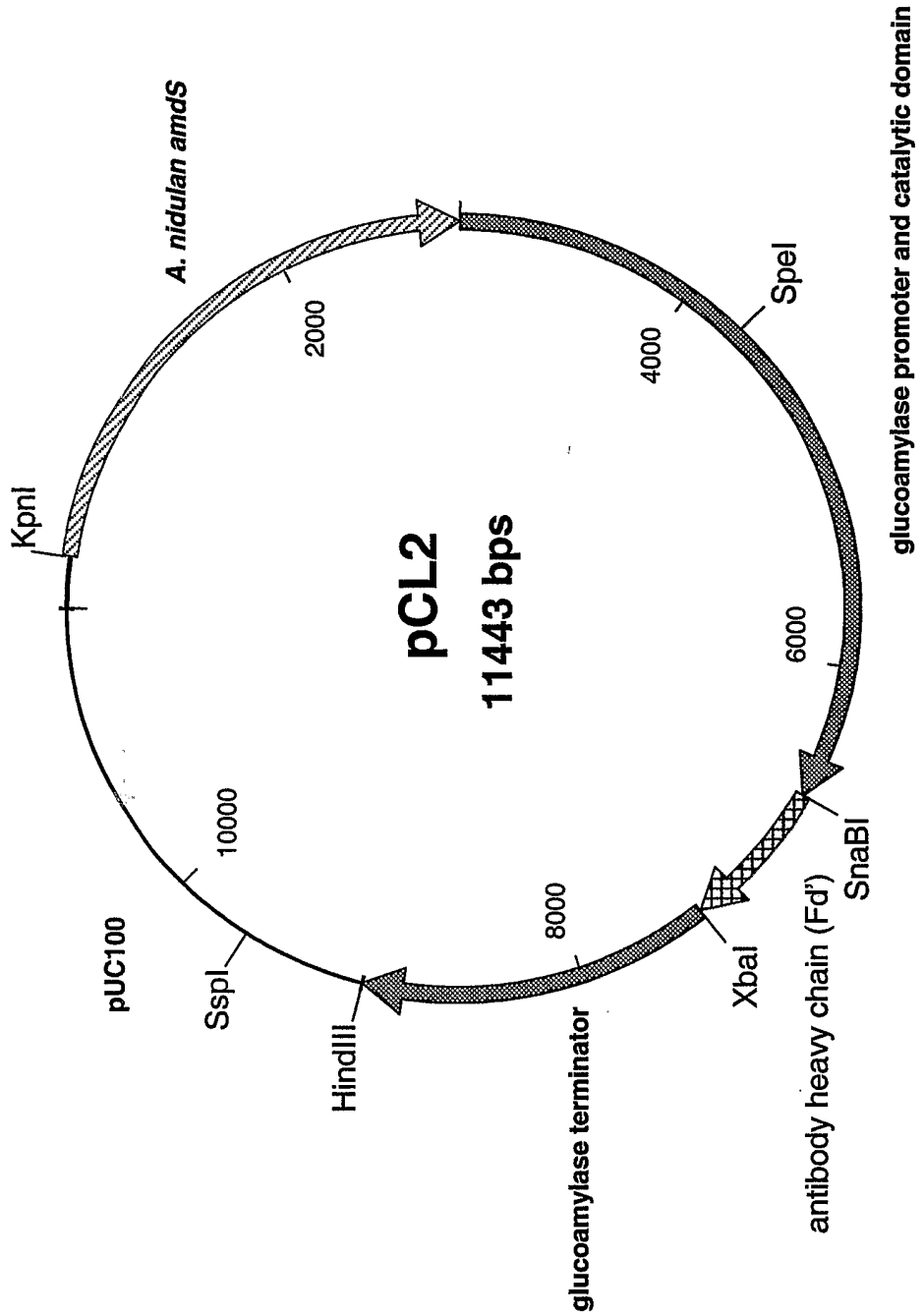
herceptin heavy chain
glucoamylase promoter and catalytic domain
pBR322

Fig. 5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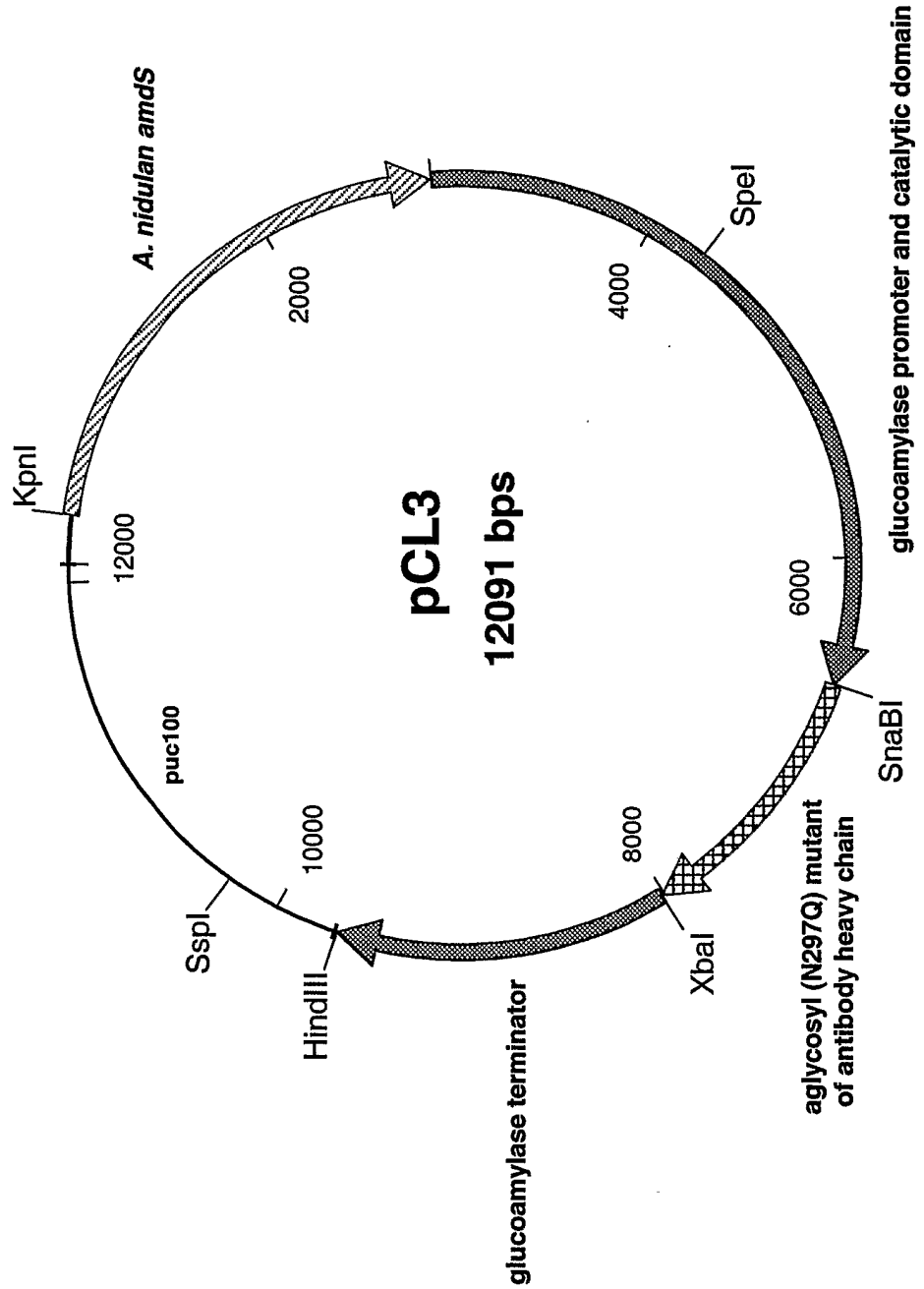
XbaI
SnaBI
SpeI
2000
4000
6000
8000
10000

Fig. 6

Fig. 7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A. nidulan amdS
KpnI
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4000
SpeI
glucoamylase promoter and catalytic domain
6000
SnaBI
aglycosyl (N297Q) mutant
of antibody heavy chain
8000
XbaI
glucoamylase terminator
HindIII
10000
SspI
puc100
12000

Fig. 8

Strain 1-Fab-1
Strain 1-HCA-4
Strain 1-LC/HC-3
Mol. Wt. Markers
116.3 kDa
97.4 kDa
66.3 kDa
55.4 kDa
36.5 kDa
31 kDa
21.5 kDa
14.4 kDa
Glucoamylase-heavy chain
Glucoamylase-light chain
Glucoamylase-light chain and Glucoamylase-Fd' chain
Glycosylated heavy chain
Non-glycosylated heavy chain
Light chain
Light chain and Fd' chain

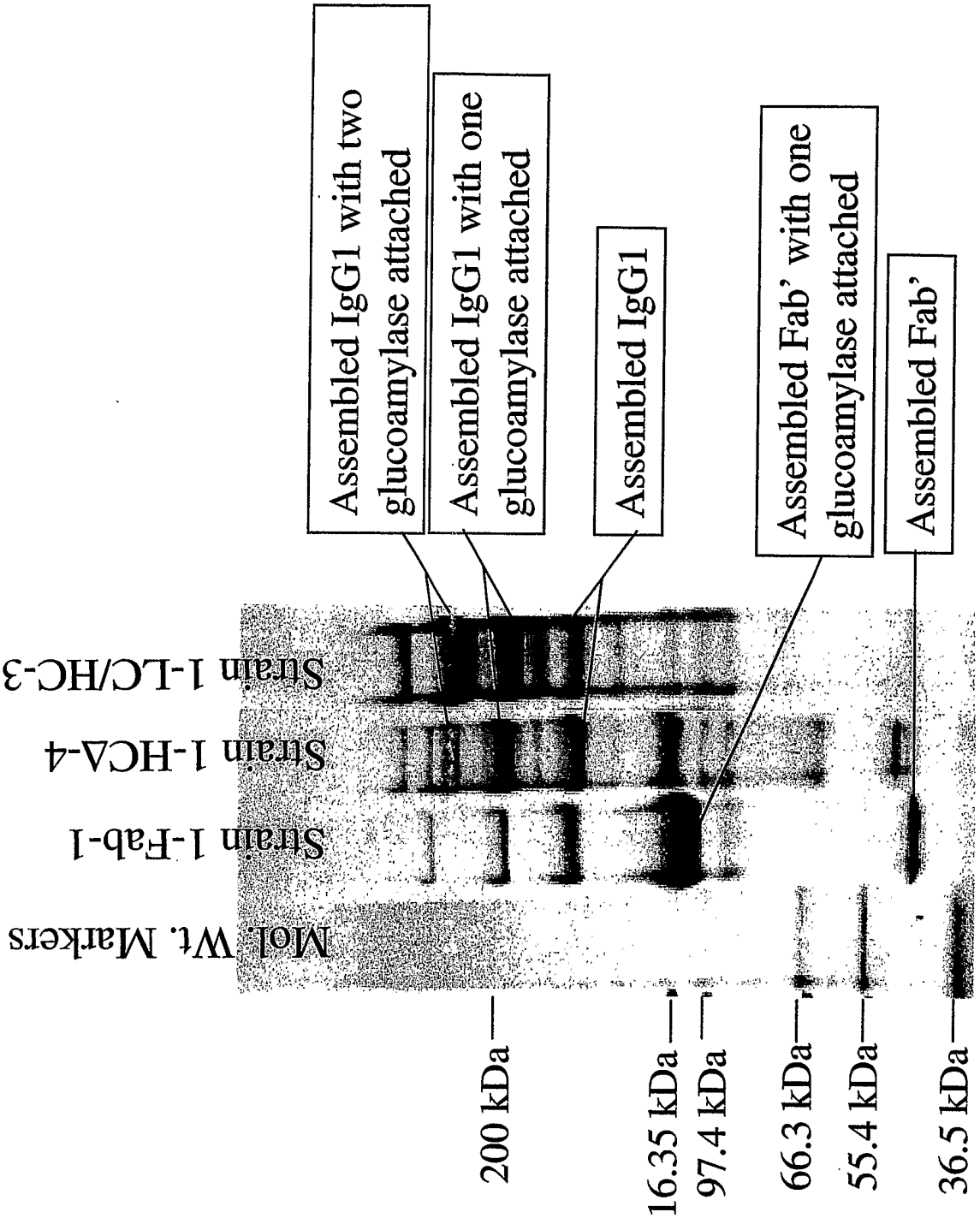
Assembled IgG1 with two glucoamylase attached
Assembled IgG1 with one glucoamylase attached
Assembled IgG1
Assembled Fab' with one glucoamylase attached
Assembled Fab'
Mol. Wt. Markers
Strain 1-Fab-1
Strain 1-HCΔ-4
Strain 1-LC/HC-3
200 kDa
116.35 kDa
97.4 kDa
66.3 kDa
55.4 kDa
36.5 kDa

Fig. 9

Fig. 10

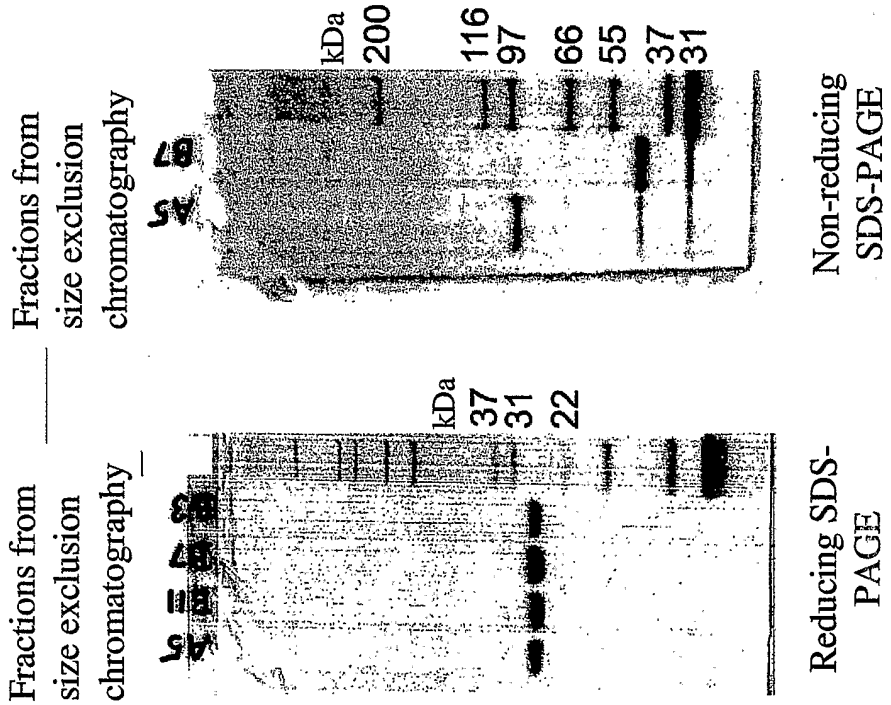
Fractions from size exclusion chromatography
kDa
37
31
22
Reducing SDS-PAGE
Fractions from size exclusion chromatography
kDa
200
116
97
66
55
37
31
Non-reducing SDS-PAGE

Fig. 11 Relative Proliferation of SK-BR-3 and A-431 cells treated with herceptin or antibody purified from *Aspergillus* transformant 1-LC/HC-3

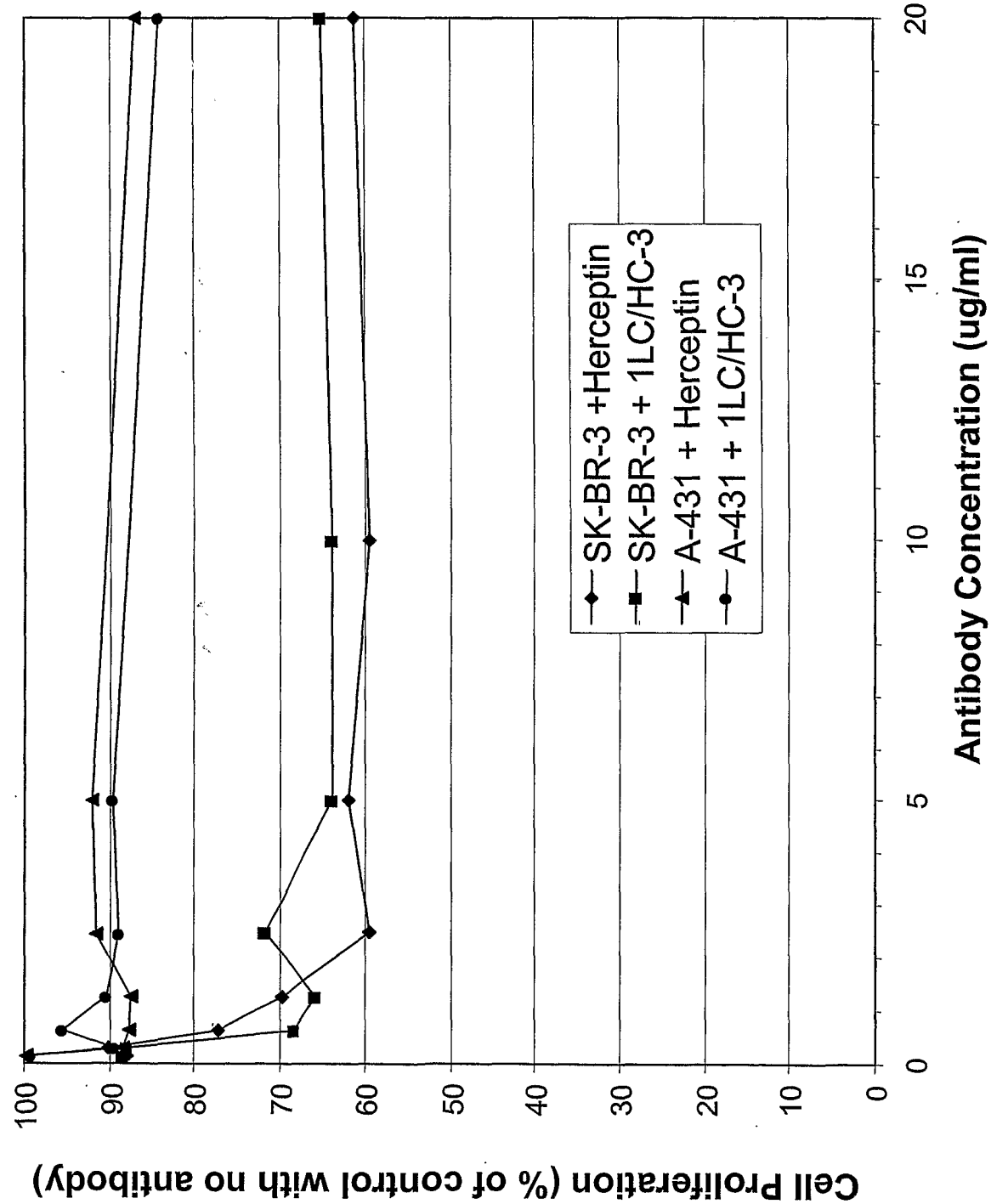

Fig.12 Binding of NS0 Hu1D10, An-3G-Hu1D10 and An-Hu1D10 to Raji Cells

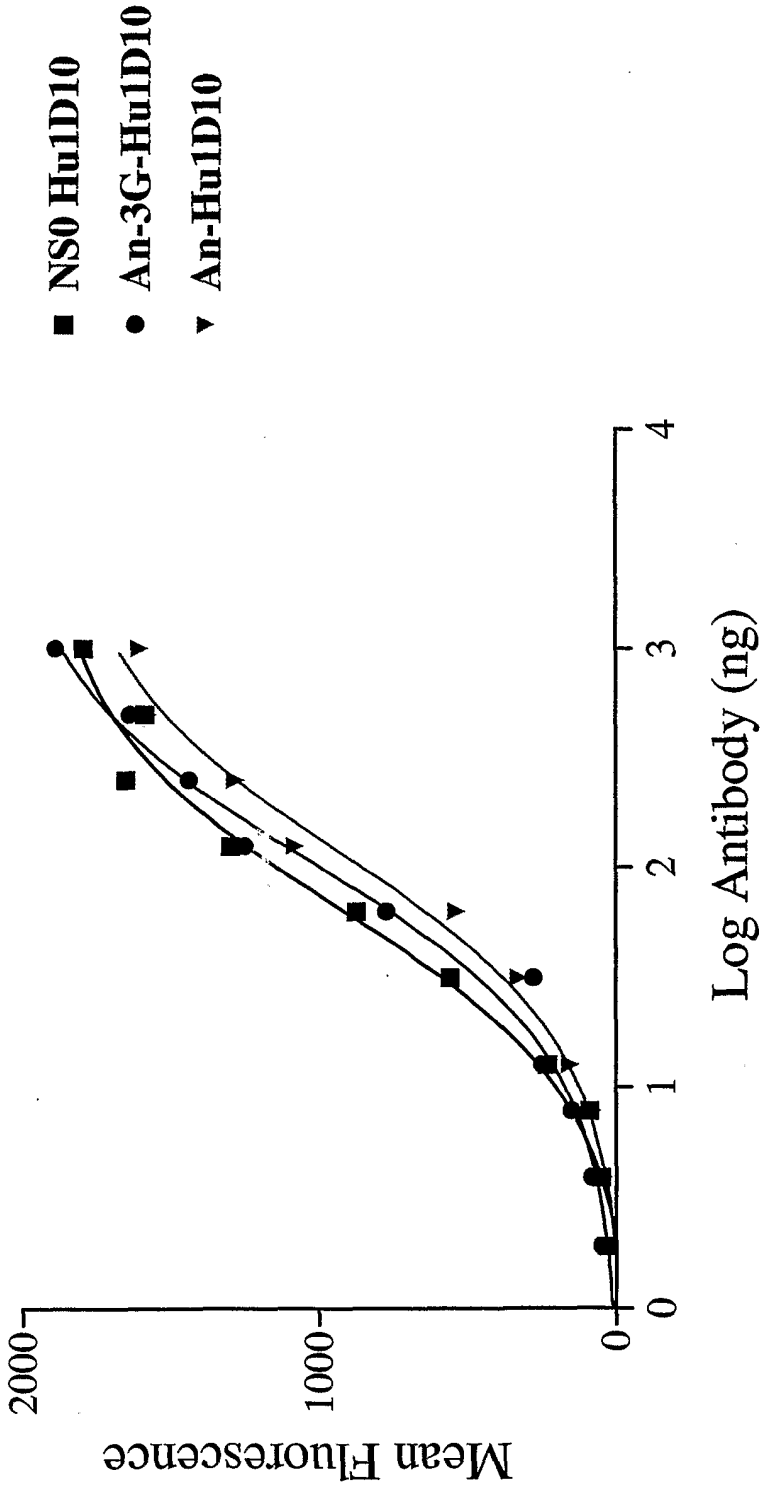

Fig.13 Competition Binding Assay by FACS (250ng FITC-Hu1D10)

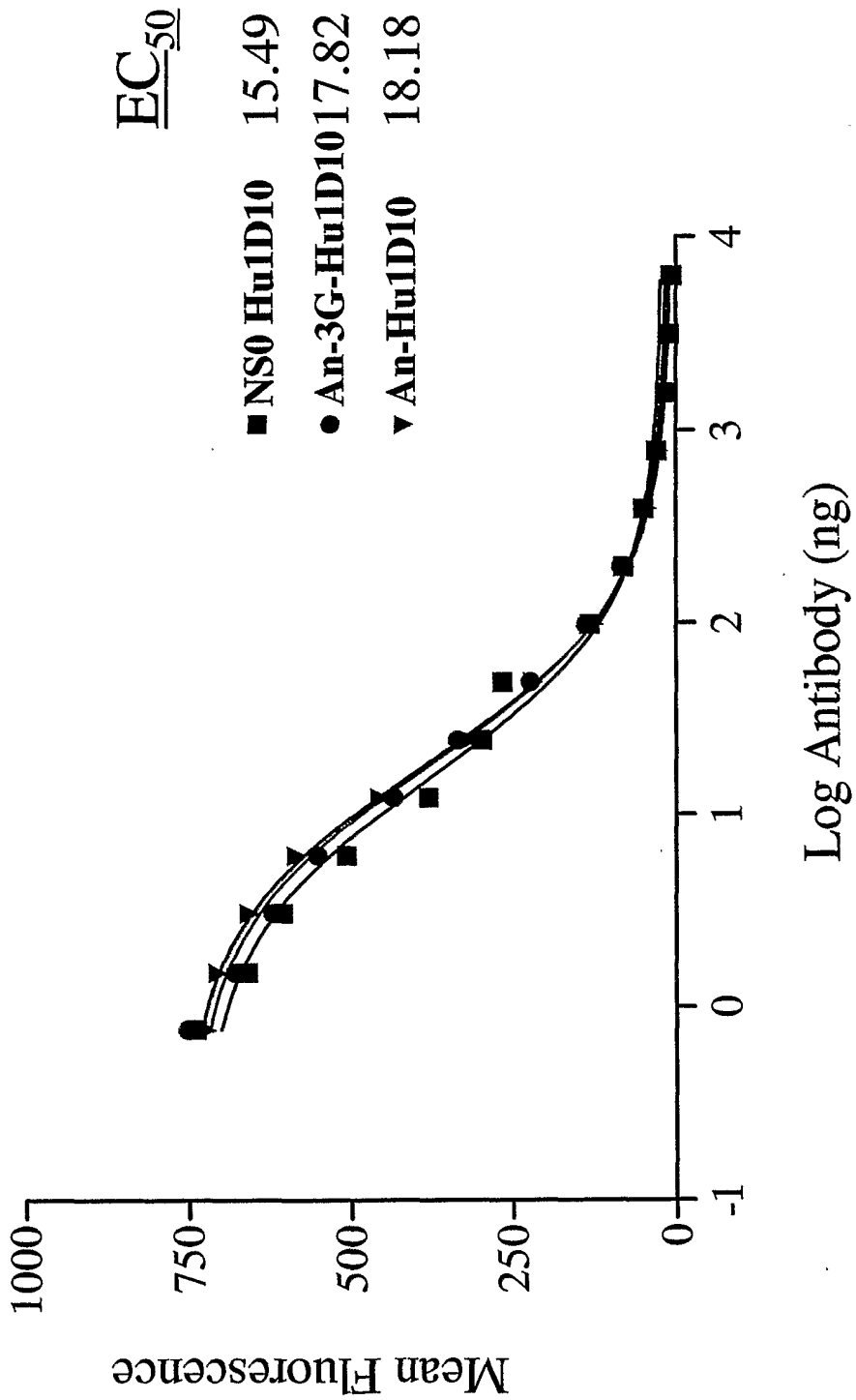

Fig. 14 Apoptosis of Raji cells Induced by NS0 Hu1D10, An-3G-Hu1D10 and An-Hu1D10

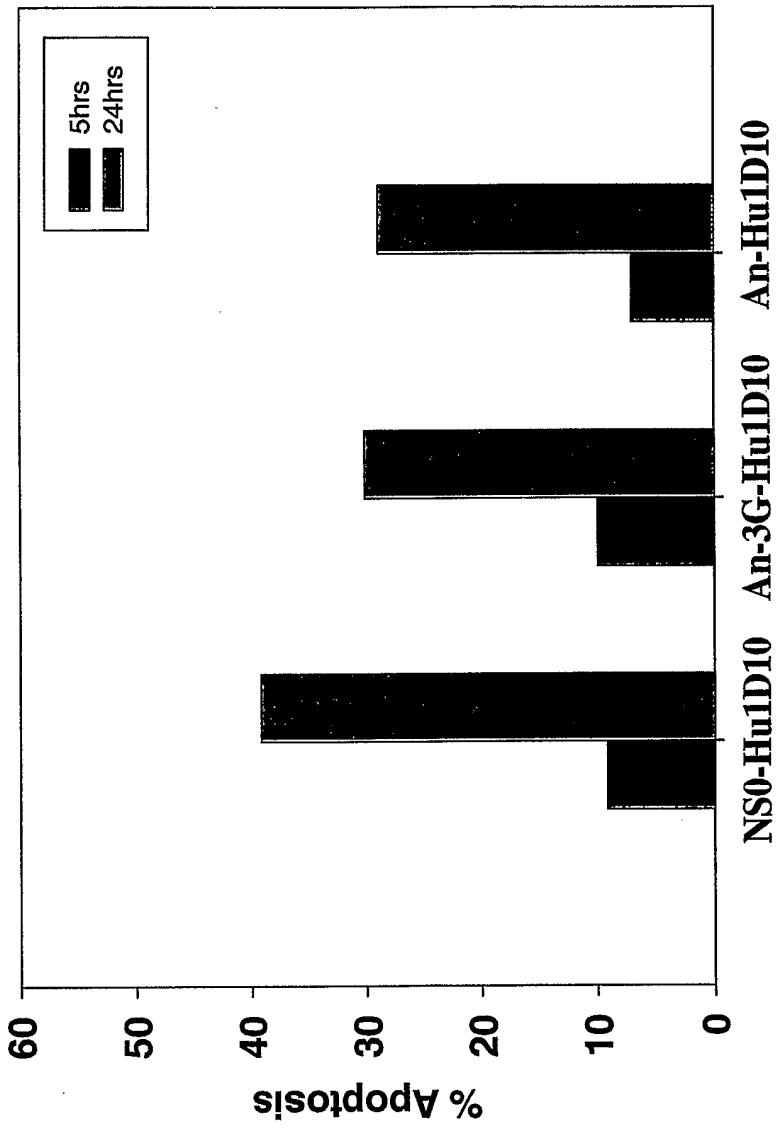

Fig.15 Antibody-Dependent Cellular Cytotoxicity Assay

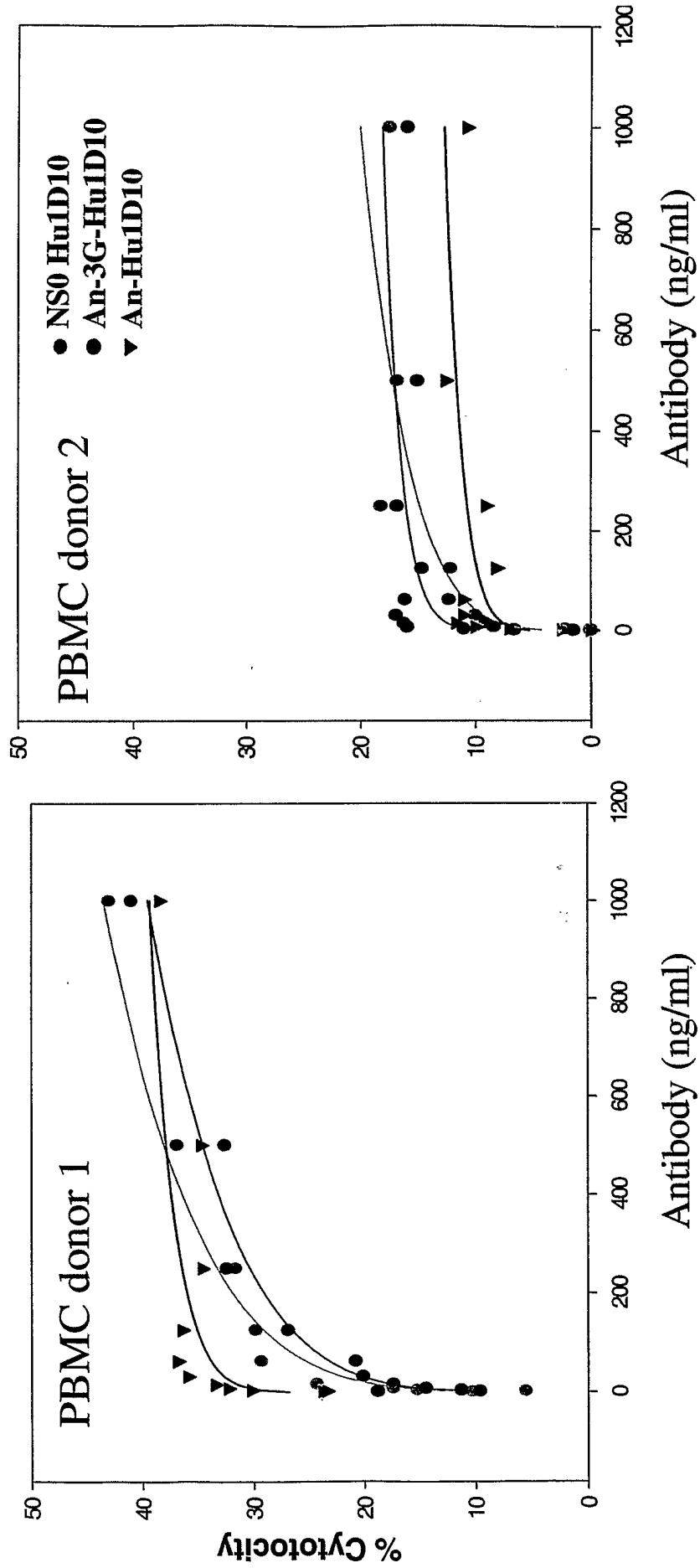

Fig 16. Pharmacokinetics of CHO-derived and *Aspergillus*-derived trastuzumab