



(86) Date de dépôt PCT/PCT Filing Date: 2002/12/05
(87) Date publication PCT/PCT Publication Date: 2003/06/12
(45) Date de délivrance/Issue Date: 2011/07/05
(85) Entrée phase nationale/National Entry: 2004/05/13
(86) N° demande PCT/PCT Application No.: GB 2002/005466
(87) N° publication PCT/PCT Publication No.: 2003/048208
(30) Priorité/Priority: 2001/12/05 (GB0129105.3)

(51) Cl.Int./Int.Cl. *C07K 16/00* (2006.01),
C07K 16/24 (2006.01), *C07K 16/28* (2006.01),
C12N 1/21 (2006.01), *C12N 15/70* (2006.01),
C12N 15/72 (2006.01)
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(54) Titre : REGULATION D'EXPRESSION AU MOYEN DE SEQUENCES INTERGENIQUES VARIABLES
(54) Title: EXPRESSION CONTROL USING VARIABLE INTERGENIC SEQUENCES

(57) **Abrégé/Abstract:**

The present invention relates to a method of production of antibodies wherein the heavy and light chains of a particular antibody molecule are encoded by the DNA present in a dicistronic message in which the two cistrons are linked by an optimised intergenic sequence.

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

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
12 June 2003 (12.06.2003)

PCT

(10) International Publication Number
WO 2003/048208 A3

(51) International Patent Classification⁷: **C07K 16/00**,
C12N 15/70, 1/21 // C07K 16/24

(21) International Application Number:
PCT/GB2002/005466

(22) International Filing Date: 5 December 2002 (05.12.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
0129105.3 5 December 2001 (05.12.2001) GB

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— with international search report

(88) Date of publication of the international search report:
31 December 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

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Expression control using variable intergenic sequences

Field of the invention

The present invention relates to a method of production of antibodies wherein the heavy
5 and light chains of a particular antibody molecule are encoded by the DNA present in a
dicistronic message in which the two cistrons are linked by an optimised intergenic
sequence.

Background to the invention

10 The ability of antibodies to recognise specific antigens has made them highly useful and
effective tools in medicine and biotechnology. Antibodies specific for antigens on selected
types of cell have been used to target these antibodies to the selected cell. The binding of
antibodies to receptors on cells has been found in some cases to affect the function of the
cell. Therapeutic and diagnostic agents have also been conjugated to antibodies to
15 specifically target these agents to selected cells. This technique has been used particularly
in the targeting of cancer cells. Antibodies have also been used to target antigens on
virally- or bacterially-infected cells, to target other molecules, such as TNF α , or for use in
assays. In biotechnology, antibodies have many uses such as probes, in purification and in
catalysis.

20

All whole antibody molecules consist of four polypeptide chains - two identical heavy
chains and two identical light chains. Each chain comprises both variable and constant
domains. Light chains comprise two domains: V_L and C_L, whilst heavy chains comprise at
least five domains: V_H, C_{H1}, hinge, C_{H2} and C_{H3} and an optional C_{H4}. The four chains are
25 always organised in the same general fashion: the two heavy chains are linked together by
at least one disulphide bond and each heavy chain is also linked to one of the light chains
by a disulphide bond such that both light chains are linked to a separate heavy chain.

Whole antibody molecules are roughly Y-shaped and consist essentially of two main
30 functional parts. The first functional part is responsible for the recognition of specific
antigens and is formed by the upper part of the arms of the Y. The antigen binding region
in each part comprises one V_H domain and one V_L domain. Each variable domain contains
three hypervariable regions which, together with the three hypervariable regions in the

other chain, form the antigen-binding site. These hypervariable regions are known as complementarity determining regions (CDR1, CDR2 and CDR3). The CDRs, which form loops, are supported on framework regions. Due to its variability between antibodies, the regions comprising V_H and V_L are known as the 'V' regions.

5

The second functional part is responsible for triggering the effector functions of other cells that will dispose of the antigen recognised by the antibody and is formed by the lower parts of the arms and the stem of the Y. This region is known as the constant 'C' region due to its relative constancy. It comprises the C_L domains and all the heavy chain C domains.

10

There are two types of light chain: κ and λ , and five types of heavy chain: α , δ , γ , ϵ and μ . The class of the antibody is determined by the type of heavy chain it has: IgA, IgD, IgE, IgG and IgM respectively.

15 Antibody fragments, which have had part of their constant region removed by enzymatic cleavage, are also used in medicine and biotechnology. These include Fab, Fab', $F(ab')_2$ and Fv fragments.

It is known to direct production of large amounts of monoclonal antibodies (having a particular antigen-specificity) by fusing an antibody-producing spleen cell with a myeloma cell, resulting in a hybridoma (Kohler, G. and Milstein, C. Continuous cultures of fused cells secreting antibody of predefined specificity. *Nature*, 256, 495-497 (1975)). However, such antibodies are unsuitable for use in human therapy as they are immunogenic in humans. Most monoclonal antibodies are produced by non-human cells.

25

Recombinant DNA techniques have been developed which enable the useful properties of more than one antibody to be combined to make one new antibody. The production of chimeric antibodies, in which the antigen-binding site comprising the complete V region of one antibody is linked to the constant region from a different antibody, is described in EP-A-0120694 (Celltech Limited), EP-A-0125023 (Genentech Inc. and City of Hope), EP-A-0171496 (Research Development Corporation, Japan), EP-A-0173494 (Stanford University) and WO-A-86/01533 (Celltech Limited).

30

WO-A-86/01533, for example, describes the preparation of a chimeric antibody in which murine V regions are joined to human constant regions. However, the large proportion of residues in chimeric non-human/human antibodies which are derived from the non-human donor result in the possibility of the antibody eliciting a potentially harmful immunological response, particularly if administered over a prolonged period (Begent et al., Br. J. Cancer, 62, 487 (1990)).

Antibody 'humanisation' is a technique which makes non-human/human chimeric antibodies appear more like human antibodies to the human immune system and has been developed in an attempt to overcome the unwanted immunological response mentioned above. EP-A-0239400 (Winter) describes how, instead of using a complete murine variable region, the CDRs of a murine monoclonal antibody are grafted onto the framework regions of the variable domains of a human antibody. Thus, it is only the CDRs forming the antigen-binding domain itself that are murine and the other residues are human.

Reichmann et al., ("Reshaping human antibodies for therapy", Nature, 332, 323-324, 1988) found it to be advantageous to convert other human residues in the variable domain to their non-human donor counterparts to improve antigen-binding activity. Such a residue was found at position 27 of the human heavy chain, which, when converted from the human serine to the corresponding rat residue (phenylalanine), resulted in improved antigen-binding ability. Another such residue was found at position 30. However, a construct which contained a human serine to rat tyrosine change at position 30 of the heavy chain in addition to the change at position 27 mentioned above, did not have a significantly altered binding activity over the humanised antibody with the serine to phenylalanine change at position 27 alone.

Heavy chain residues 27 and 30 are within the structural loop adjacent to CDR1. Queen et al., (WO 90/07861) conjectured that other residues which interact with the CDRs are also important in determining antigen-binding affinity. With this in mind, Queen et al., proposed four criteria for determining which residues should come from the donor and which from the acceptor when designing humanised antibodies. In a more definitive

analysis, Adair et al., (WO 91/09967) disclosed a hierarchy of residue numbers that will enable a humanised antibody to be designed.

A number of reviews discussing CDR-grafted antibodies have been published including
5 Vaughan et al., (Nature Biotechnology, 16, 535-539, 1998).

Antibody conjugates, in which the constant region has been fused to effector or reporter molecules which may act as therapeutic or diagnostic agents, have also been described (WO 95/01155, US 3927193, US 4331647, US 4348376, US 4361544, US 468457, US
10 4444744, US 4460459 and US 4460561 and reviews by Waldmann, T.A., Science, 252, 1657, (1991); Koppel, G.A., Bioconjug. Chem., 1, 13, (1990); Oeltmann, T.N. and Frankel, A.E., FASEB J., 5, 2334, (1991); and van den Bergh, H.E., Chemistry in Britain, May 1986, 430-439).

15 It was known to produce normal, chimeric or humanised antibodies by transfecting a suitable host cell with two expression vectors, one containing a DNA sequence encoding the heavy chain and one containing a DNA sequence encoding the light chain of the required antibody (WO-A-91/09967). Alternatively, it was known to transfect a suitable host cell with an expression vector that contains both the DNA sequence encoding the
20 heavy chain and the DNA sequence encoding the light chain of the required antibody. In the latter example, the DNA sequences encoding the heavy chain and the light chain are either under the control of their own individual promoters (WO-A-91/09967) or are present in a dicistronic message (Better, M., Paul Chang, C., Robinson, R.R. and Horwitz, A.H. *Escherichia coli*: Secretion of an Active Chimeric Antibody Fragment. Science, 240, 1041-
25 1043 (1988)).

A dicistronic message was used by Better et al., to produce a chimeric mouse L6 Fab antibody directed towards a ganglioside antigen expressed on the surface of many human carcinomas. A dicistronic message was chosen in this case in an attempt to ensure that
30 both the truncated heavy chains (Fd) and the κ light chains were translated in close physical proximity so that they would assemble correctly and be secreted. Dicistronic messages are only able to function in bacteria whereas the 'one gene, one promoter' concept functions in both mammals and bacteria. In a dicistronic message, a promoter is

associated only with the first cistron. The second cistron is transcribed by the polymerase 'reading through' to the second cistron such that both cistrons are represented by a single RNA molecule. The two coding DNA cistrons are separated by a stretch of DNA known as an 'intergenic sequence' or 'IGS'. This IGS region is also present in the RNA molecule
5 that is transcribed from the DNA.

Optimisation of the translational initiation rate has for some time been recognised as essential for high level expression of secreted heterologous proteins in *E. coli* (Simmons, L. and Yansura, D. Nature Biotech, 14, 629-634 (1996)). However, different Fab's have
10 different framework and CDR sequences which confer different properties to the molecule, including differences in the ease (or rate) of folding within the *E. coli* periplasm (Knappik, A. and Pluckthun, A. Prot Eng 8, 81-89 (1995)). For example, a Fab' which folds into its native conformation easily and rapidly within the *E. coli* periplasm is likely to be 'tolerated' at a high level and rapid translation can be accommodated to achieve high-level
15 accumulation. A Fab' which folds more poorly is likely to be tolerated less well by the host bacterium if rapidly translated, potentially saturating host folding / secretion machinery and having a deleterious effect on host cell physiology.

Thus, when producing antibodies using a host cell-expression vector system, a high level
20 of expression of a particular antibody may be tolerated, but for a different antibody, a high level of expression might prove toxic to the cell, perhaps because of different efficiencies of secretion or folding.

The level of expression of a particular antibody is determined by the amount of heavy and
25 light chains present. For maximal production, the ratio of heavy chains to light chains should be balanced, such as equal quantities of both. However, if either the heavy or the light chain is present in a lesser amount, this will limit the amount of antibody produced. Accumulation of excess heavy chain is likely to be particularly poorly tolerated.

30 In the case of an antibody encoded by a dicistronic message, the upstream cistron may contain either the DNA coding for the heavy chain or the light chain of an antibody with a particular antigen specificity. The downstream cistron would then encode the respective light chain or heavy chain partner. It would be advantageous if the level of expression of

the antibody chain corresponding to the coding DNA in the downstream cistron of a dicistronic message could be regulated to produce the desired level of expression for a particular antibody.

5 Summary of the invention

In one particular embodiment there is provided a dicistronic message for producing an antibody molecule with a particular antigen-binding specificity, in which the upstream cistron contains DNA coding for either the heavy chain or the light chain of the antibody and the downstream cistron contains DNA coding for the corresponding light
10 chain or heavy chain respectively, characterized in that the two cistrons are linked by an optimised intergenic sequence (IGS) wherein the IGS is IGS1 (SEQ ID NO:4), IGS2 (SEQ ID NO:7), IGS3 (SEQ ID NO:10) or IGS4 (SEQ ID NO:13), and wherein the antibody produced is not an anti-TNF α antibody or an anti-KDR antibody.

15 In a first aspect, the present invention provides a dicistronic message for producing an antibody molecule with a particular antigen-binding specificity, in which the upstream cistron contains DNA coding for either the heavy chain or the light chain of the antibody and the downstream cistron contains DNA coding for the corresponding light chain or heavy chain respectively, characterised in that the two cistrons are linked by an optimised
20 intergenic sequence (IGS) and wherein the antibody produced is not an anti-TNF α antibody (for example, see PCT/GB01/02477) or an anti-human kinase insert domain-containing receptor (anti-KDR) antibody (for example, see PCT/GB02/004619).

Preferably, the upstream cistron codes for the light chain of the antibody and the
25 downstream cistron codes for the corresponding heavy chain.

The IGS has been optimised to regulate the expression level of the antibody chain corresponding to the downstream cistron in the dicistronic message in order to achieve the desired expression level for the particular antibody.

30

In this specification, the length of the IGS is defined as the number of nucleotides between the stop codon of the upstream cistron and start codon of the downstream cistron (non-inclusive). The length of the IGS is involved in determining the rate of translation of the

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part of the RNA which corresponds to the downstream cistron. For example, a short intergenic sequence may result in very tight translational coupling between the heavy and the light chains, in that the translating ribosome may not fully dissociate from the mRNA after completing synthesis of the antibody chain encoded by the upstream cistron before
5 initiating synthesis of the antibody chain encoded by the downstream cistron (Adhin, M. and van Duin, J. J. Mol. Biol., 213, 811-818 (1990); Andre, A. et al., FEBS Letts., 468, 73-78 (2000)). Such a process, termed translational re-initiation, will only occur if the stop codon of the upstream gene is very close to the start codon of the downstream gene. Due to kinetic considerations, this will result in increased expression of the polypeptide

encoded by the downstream cistron since translation will not require a ribosome to bind to the mRNA molecule in its IGS.

If there is too much separation between the two genes, the ribosome will dissociate after
5 completion of synthesis of the upstream cistron, requiring a new ribosome to initiate translation of the downstream cistron. In general, this will reduce the efficiency of translational initiation.

The presence of a Shine Dalgarno (SD) ribosome binding site (complementary to 16S
10 rRNA) in the IGS allows a ribosome to bind to this IGS sequence and translate the downstream cistron. Where the distance between cistrons is sufficiently short to permit translational reinitiation to occur, there is some evidence to suggest that the presence of a SD site within the upstream cistron can increase the efficiency of translational initiation of the downstream cistron (Spanjaard, R.A. and van Duin, J. Nucl. Acids Res., 17, 5501-5507
15 (1989)).

There are several features of the SD site and the nucleotide sequence between the end of the SD site and the AUG initiation codon which have an influence on the strength of translational initiation (reviewed in Makrides, S. Microbiol. Revs., 60, 512-538 (1996)).
20 The distance between the SD site and the AUG start codon of the downstream cistron is one such feature, as is the 'strength' of the SD site itself. An SD site that is 100% complementary to the 16S rRNA sequence that binds to it will in general result in greater expression than if the SD site is only partly complementary to the 16S rRNA sequence.

25 The sequence of the region between the SD sequence and the start codon is another important determinant of the rate of translation of the downstream cistron. The distance and sequence affect the potential secondary structure of mRNA around the start codon (reviewed in Makrides, S. Microbiol. Revs., 60, 512-538 (1996)). The start codon should be in a 'loop' and not constrained within a 'stem', while the reverse applies to the SD
30 sequence. Thus by modifying the sequence and length of the IGS it is possible to modify the extent of translational coupling and/or the strength of translational initiation and therefore the level of translation of the downstream cistron and the subsequent rate of accumulation of the antibody chain it encodes.

The IGS of the dicistronic message of the present invention has been modified with respect to length, sequence and secondary structure such that optimal translational coupling of the two cistrons is achieved.

5

The optimal IGS sequence for use in the present invention can be empirically determined using the following method. The method comprises constructing a series of suitable expression vectors containing a series of IGS variants into which antibody molecules can be inserted for testing. Empirical testing of each IGS sequence for each antibody can be achieved by transforming the expression vector into a suitable host and analysing antibody expression and yield. The suite of IGS sequences described in the present application, which vary in length and sequence, can be used to construct such vectors from which the optimal IGS sequence for a particular antibody molecule can be selected. Said sequences include IGS sequences 1-4.

15

In a preferred embodiment, the IGS has been optimised such that maximum expression of the antibody chain encoded by the downstream cistron is achieved. This results in a maximal level of expression of the particular antibody as the amount of the antibody chain encoded by the downstream cistron is not limiting.

20

In a further embodiment, the IGS has been optimised such that the rate of translational initiation for translation of the downstream cistron is as high as possible.

In a further embodiment, the IGS has been optimised such that the rate of translational initiation for translation of the downstream cistron is not at the greatest possible achievable rate.

In a further embodiment, the IGS has been optimised such that the rate of translational initiation for translation of the downstream cistron is at a low rate.

30

The dicistronic message of the present invention codes for the heavy chain and the light chain of a particular antibody molecule. The antibody may be a whole antibody or in

particular a fragment thereof, such as a Fab or a Fab' fragment. The antibody may also be a chimeric or a humanised antibody.

The dicistronic message of the present invention may comprise synthetic DNA, cDNA or
5 genomic DNA, or any combination thereof.

The coding DNA sequence for a particular antibody can be obtained by methods well known to those skilled in the art. For example, DNA sequences coding for part or all of the antibody heavy and light chains may be synthesised as desired from the determined
10 DNA sequences or on the basis of the corresponding amino acid sequences.

Standard techniques of molecular biology may be used to prepare DNA sequences coding for the heavy and light chains of specific antibody molecules to be linked by the IGS in a dicistronic message of the present invention. Desired DNA sequences may be synthesised
15 completely or in part using oligonucleotide synthesis techniques. Site-directed mutagenesis and polymerase chain reaction (PCR) techniques may be used as appropriate.

The dicistronic message of the present invention may contain a DNA sequence encoding an effector or reporter protein that is fused to the DNA sequence encoding one of the
20 antibody chains.

The dicistronic message of the present invention may also contain a DNA sequence encoding a peptide linkage which is fused to the DNA sequence encoding one of the antibody chains such that it will allow the subsequent attachment of an effector or reporter
25 protein or molecule to the antibody expressed from the dicistronic message.

The dicistronic message of the present invention may also contain a secretory signal sequence that is fused upstream of the DNA sequence encoding one or both of the antibody chains in order to allow targeting of the antibody chains to the periplasm or to outside the
30 cell.

Preferably, the secretory signal sequence is an OmpA peptide sequence.

In a second aspect, the invention provides an expression vector containing a dicistronic message according to the first aspect of the present invention.

Preferably, the expression vector backbone is pTTO. The pTTO expression vector is
5 designed to give rise to soluble, periplasmic accumulation of recombinant proteins in *E. coli*. This vector has the following main features:

- (i) Tetracycline resistance marker - antibiotic not inactivated by the product of resistance gene, hence selection for plasmid-containing cells is maintained;
- 10 (ii) Low copy number - origin of replication derived from plasmid p15A, which is compatible with plasmids containing colE1 derived replicons;
- (iii) Strong, inducible tac promoter for transcription of cloned gene(s);
- (iv) LacIq gene - gives constitutive expression of the lac repressor protein, maintaining the tac promoter in the repressed state until induction with IPTG / allolactose;
- 15 (v) OmpA signal sequence - gives periplasmic secretion of cloned gene(s); and
- (vi) Translational coupling of OmpA signal sequence to a short lacZ peptide, giving efficient initiation of translation.

In a third aspect, the invention provides a cloning vector containing a dicistronic message
20 according to the first aspect of the present invention.

General methods by which the expression and cloning vectors may be constructed, transfection methods and culture methods are well known to those skilled in the art.

25 In a fourth aspect, the present invention also provides a process for the production of a particular antibody molecule comprising culturing a bacterial host cell that has been transformed with an expression vector of the present invention under conditions suitable for leading to expression of DNA encoding said antibody molecule, and isolating said antibody molecule, wherein the expression level of said antibody has been optimised.

30

Any suitable bacterial host cell may be used for expression of the heavy and light chains of the particular antibody molecule encoded by a dicistronic message according to the present

invention. However, preferably *E. coli* host cells are used. Other microbial systems may also be used.

5 The antibody molecule may be secreted from the cell or targeted to the periplasm by suitable signal sequences. Alternatively, the antibody molecules may accumulate within the cell's cytoplasm. Depending on the antibody being produced and the process used, it may be desirable to allow the antibody molecule to refold and form a functional conformation. Procedures for allowing the antibody molecule to refold are well known to those skilled in the art.

10

The antibody molecules produced by a dicistronic message according to the present invention may be used to make a therapeutic or diagnostic composition comprising a particular antibody in combination with a pharmaceutically acceptable excipient, diluent or carrier.

15

The antibody molecule may be the sole active ingredient in the therapeutic or diagnostic composition or may be accompanied by one or more other active ingredients including other antibody ingredients, for example, anti-T cell, anti-IFN γ or anti-LPS antibodies, or non-antibody ingredients such as xanthines.

20

The particular antibody molecule produced by the present invention may be administered in any appropriate form and amount according to the therapy in which it is employed.

25 Suitable forms for administration include forms suitable for parenteral administration, e.g. by injection or infusion, for example, by bolus injection or continuous infusion. Where the product is for injection or infusion, it may take the form of a suspension, solution or emulsion in an oily or aqueous vehicle and it may contain formulatory agents, such as suspending, preservative, stabilising and/or dispersing agents.

30 Alternatively, the antibody molecule may be in dry form, for reconstitution before use with an appropriate sterile liquid.

If the antibody molecule is suitable for oral administration, for example in the case of antibody fragments, the formulation may contain, in addition to the active ingredient, suitable additives used in the formulation of orally administered compositions.

- 5 The therapeutic and diagnostic compositions may be in unit dosage form, in which case each unit dose comprises an effective amount of the particular antibody molecule. The dose will also be selected according to the age and condition of the patient.

If the antibody molecule has a short half life (e.g. 2 to 10 hours) it may be necessary to
10 give one or more doses per day. Alternatively, if the antibody molecule has a long half life (e.g. 2 to 15 days) it may only be necessary to give a dosage once per day, once per week or even once every 1 or 2 months.

Detailed description of the invention

- 15 The present invention is further described by way of illustration only in the following examples which refer to the accompanying drawings in which:

Figure 1 shows vector pTTQ9;

- 20 Figure 2 shows the sequence of the OmpA polylinker region;

Figure 3 shows vector pACYC184;

Figure 4 shows vector pTTO-1;

25

Figure 5 shows the complete DNA sequence of vector pTTO-1;

Figure 6 shows vector pTTO-2;

- 30 Figure 7 shows vector pDNA_{AbEngG1};

Figure 8 shows vector pTTO(TNF α);

Figure 9 shows oligonucleotide cassettes encoding four different intergenic sequences for *E. coli* Fab' expression;

Figure 10 shows periplasmic Fab' accumulation of IGS variants pTTO(TNF α IGS-1),
5 pTTO(TNF α IGS-2), pTTO(TNF α IGS-3) and pTTO(TNF α IGS-4) as a result of shake-flask analysis;

Figure 11 shows a four way ligation used to generate four IGS variants of Fab' g163;

10 Figure 12 shows soluble Fab' accumulation of IGS variants pTTO(g163 IGS-1), pTTO(g163 IGS-2), pTTO(g163 IGS-3) and pTTO(g163 IGS-4) as a result of shake-flask analysis;

Figure 13 shows a restriction map of vector pTTOD(g163 IGS-3);

15

Figure 14 shows soluble Fab' accumulation of IGS variants pTTOD(g165 IGS-1), pTTOD(g165 IGS-2) and pTTOD(g165 IGS-3) as a result of shake-flask analysis;

Figure 15 shows soluble Fab' accumulation of IGS variants pTTOD(g165 IGS-1),
20 pTTOD(g165 IGS-2), pTTOD(g165 IGS-3) and pTTOD(g165 IGS-4) as a result of fermenter comparison analysis;

Figure 16 shows soluble Fab' accumulation of IGS variants pTTOD(gA33 IGS-2) and pTTOD(gA33 IGS-3) as a result of fermenter comparison analysis;

25

EXAMPLES

A dicistronic message encoding an anti-TNF α antibody

A dicistronic message of the present invention was used to achieve high level expression of
30 anti-TNF α Fab' fragments. The upstream cistron encoded the light chain of the antibody whilst the downstream cistron encoded the heavy chain of the antibody. A DNA sequence encoding the OmpA signal peptide was fused to the 5' end of the DNA coding for each of the light chain and the heavy chain to allow efficient secretion to the periplasm.

A series of oligonucleotide cassettes coding for a range of different IGSs were used in the dicistronic message in order to vary the level of expression of the heavy chain. The use of different cassettes altered the rate of translational initiation of the heavy chain, resulting in
5 a range of rates of accumulation of the translated heavy chain product.

A series of four IGSs were designed, permitting the experimental determination of the optimum sequence. The IGS variant that gave rise to the accumulation of the greatest amount of soluble Fab' was selected experimentally using shake flask expression as a
10 guide or fermenter expression as a definitive means. Surprisingly, different IGSs were selected for different Fab's, indicating that empirical selection will be required for each new Fab' fragment to be expressed.

Experimental

15

Materials and Methods

General microbiology and DNA manipulation techniques

E. coli strain INV α F' (Invitrogen, De Schelp, Netherlands) was used for transformation and
20 routine culture growth; *E. coli* strain W3110 (ATCC # 27325) was used for expression studies. DNA restriction and modification enzymes were obtained from Boehringer Mannheim (Lewes, East Sussex, UK) and New England Biolabs (Hitchin, Herts, UK). Plasmid preparations were performed using plasmid purification kits (QIAGEN, Crawley, West Sussex, UK). DNA fragment purification was performed using QIAGEN spin
25 columns. DNA fragments were purified from agarose using the GeneClean protocol (BIO 101). Oligonucleotides were supplied by Oswel Oligonucleotide Service and were synthesised at the 40nM scale. PCR was performed using Perkin Elmer 'Amplitaq'TM as recommended. DNA sequencing reactions were performed using the ABI Prism Dye-Deoxy chain termination kit and run on an ABI 373A automated sequencer (PE Applied
30 Biosystems, Warrington, Cheshire, UK). Data were analysed using the program AutoAssembler (PE Applied Biosystems).

Shake flask induction

E. coli W3110 cultures were grown in L-broth supplemented with tetracycline (7.5µg/ml). For inductions, fresh overnight cultures (grown at 30°C) were diluted to OD₆₀₀ = 0.1 into 200 ml L-broth in a 2L baffled flask and were grown at 30°C in an orbital incubator. At 5 OD₆₀₀ = 0.5, IPTG was added to 200 µM. Samples (normalised for OD) were taken at intervals.

Periplasmic Extraction

Culture samples were chilled on ice (5 minutes) then cells were harvested by 10 centrifugation. Following resuspension in extraction buffer (100mM Tris.HCl, 10mM EDTA; pH7.4) samples were incubated overnight at 30°C, then clarified by centrifugation.

Assembly Assay

Fab' concentrations were determined by ELISA. Plates were coated at 4°C overnight with 15 anti-human Fd 6045 (2µg/ml in coating buffer, physiological saline, 100µl per well) (see EP 491031). After washing, 100µl of sample was loaded per well; purified A5B7 gamma-1 Fab' (see EP 491031), initially at 2µg/ml, was used as a standard. Samples were serially diluted 2-fold across the plate in sample conjugate buffer (per litre: 6.05g tris aminomethane; 2.92g NaCl; 0.1ml Tween-20; 1ml casein (0.2%)); plates were incubated 20 for 1 hour at room temperature, with agitation. Plates were washed and dried, then 100µl of anti-human C-kappa (GD12)-peroxidase was added (diluted in sample conjugate buffer). Incubation was carried out at room temperature for 1 hour with agitation. Plates were washed and dried, then 100µl of substrate solution was added (10ml sodium acetate/citrate solution (0.1M, pH 6); 100µl H₂O₂ solution; 100µl tetramethyl benzidine 25 solution (10mg/ml in dimethylsulphoxide)). Absorbance at 630nm was read 4 - 6 minutes after substrate addition.

Fermentation

E. coli W3110 cultures were grown in shake flasks in L-broth supplemented with 30 tetracycline (7.5µg/ml) at 30°C to OD₆₀₀ = 1.0; 100ml of this culture was used to inoculate 1L of SM6 media (plus glycerol) (European Patent 651803) within a 1.5L fed-batch culture fermenter. pH was controlled at 7.0 with 50% NH₄OH and 5% H₂SO₄. The dissolved oxygen concentration was maintained at 30% by variable agitation. Tetracycline was not

included in the fermenter medium. The initial glycerol concentration was 3% w/v; glycerol was fed on one further occasion during fermentation, such that it would cease to be available once the culture reached $OD_{600} \sim 60$. Cultures were grown at 30°C to $OD_{600} = 55$, then 120ml of 50% lactose was added; lactose induction follows utilisation of available
5 glucose. A further 60ml batch of lactose was added 20 hours later. Fermentation was monitored for 25 to 30 hours post-induction and samples (normalised for OD) were taken at intervals.

Results

10

Construction of plasmids pTTO-1 and pTTO-2

Plasmid pTTQ9 was obtained from Amersham and is shown in Figure 1. An aliquot (2µg) was digested with restriction enzymes Sall and EcoRI, the digest was run on a 1% agarose gel and the large DNA fragment (4520 bp) was purified. Two oligonucleotides were
15 synthesized which, when annealed together, encode the OmpA polylinker region shown in Figure 2. This sequence has cohesive ends which are compatible with the Sall and EcoRI ends generated by restriction of pTTQ9. By cloning this oligonucleotide 'cassette' into the pTTQ9 vector, the Sall site is not regenerated, but the EcoRI site is maintained. The cassette encodes the first 13 amino acids of the signal sequence of the *E. coli* outer-
20 membrane protein Omp-A, preceded by the Shine Dalgarno ribosome binding site of the OmpA gene. In addition restriction sites for enzymes XbaI, MunI, StyI and SphI are present. The MunI and StyI sites are within the coding region of the OmpA signal sequence and are intended as the 5' cloning sites for insertion of genes. The two
25 oligonucleotides which make up this cassette were annealed together by mixing at a concentration of 5 pmoles/µl, heating in a waterbath to 95°C for 3 minutes, then slow cooling to room temperature. The annealed sequence was then ligated into the Sall / EcoRI cut pTTQ9. The resulting plasmid intermediate, termed pTQOmp, was verified by DNA sequencing.

30 Aliquots of this intermediate were then cleaved with SspI and EcoRI (2350 bp fragment purified) and with EcoRI and XmnI (350 bp fragment purified). The 2350 bp fragment encodes the transcriptional terminator region and the *lacI^q* gene and the 350 bp fragment encodes the *tac* promoter, OmpA signal sequence and multicloning site. Plasmid

pACYC184 (New England Biolabs – Figure 3) was digested with StyI, treated with Mung Bean Nuclease to generate blunt ends, then digested with PvuII (2348 bp fragment purified - this fragment encodes the tetracycline resistance marker and the p15A origin of replication). This fragment was treated with alkaline phosphatase to remove 5' terminal phosphates (to prevent self ligation) and was ligated to the other purified fragments. The resulting plasmid was termed pTTO-1 and is shown in the map in Figure 4. Figure 5 shows the complete DNA sequence of pTTO-1. Insertion of the human Ig light chain kappa constant domain, as a SphI-EcoRI fragment from plasmid pHCl32, created pTTO-2 (Figure 6).

10

Insertion of Fab' variable regions into pTTO-2

The variable region genes of Fab' TNF α were generated by PCR amplification from vectors for mammalian cell expression of whole antibody which contain sequence from SEQ ID8 of PCT/GB01/02477. DNA encoding the OmpA signal sequence and including the MunI restriction enzyme site for cloning in-frame into pTTO-2, was attached to the 5' end of each gene such that it replaced the native Ig leader.

20

The purified V_L gene (MunI/SphI) was then inserted into the MunI / SphI site of pTTO-2 to create the light chain intermediate pTTO(TNF α L).

The heavy chain V_H gene was cloned via the intermediate vector pDNAEng-G1 (figure 7), between the MunI-ApaI sites, creating pDNAEng(TNF α H). Cloning of the heavy chain gene from this plasmid as an EcoRI fragment into the EcoRI site of pTTO(TNF α L) created the *E. coli* expression plasmid pTTO(TNF α) (Figure 8).

25

Construction of IGS variants of pTTO(TNF α)

A series of four intergenic sequence (IGS) variants were designed (Figure 9), permitting the empirical determination of the optimum IGS for TNF α Fab'. IGS1 and IGS2 have very short intergenic sequences (-1 and +1 respectively) and might be expected to give closely coupled translation; the SD sequences (underlined) are subtly different. These two sequences will most likely confer a high level of translational initiation. IGS3 and IGS4 have a longer distance between stop and start codons (+13) and differ in their sequence composition. The SD sequence of IGS3 is stronger than that of IGS1, 2 or 4. All

30

sequences were studied for secondary structure (using m/fold program (Jaeger, J.A. et al. Methods Enzymology, 183: 281-306 (1990); part of GCG Wisconsin Package, Accelrys)) and 'optimised' as far as possible; however, with tight coupling of translation of the two chains the lack of ribosomal dissociation means that the mRNA may not be 'naked',
5 preventing secondary structure formation.

The IGS variants were constructed by ligation of two fragments into a vector prepared by SacI – NotI digestion of pTTO(TNF α). An insert fragment prepared by MunI-NotI digestion of pDNA_{AbEng}(TNF α) was purified and ligated along with each IGS cassette
10 (SacI-MunI) into the vector, creating the 4 expression plasmids pTTO(TNF α IGS-1), pTTO(TNF α IGS-2), pTTO(TNF α IGS-3) and pTTO(TNF α IGS-4).

Shake flask expression analysis of TNF α IGS variants

The four IGS variant vectors and the original expression vector pTTO(TNF α) were each
15 used to transform *E. coli* strain W3110. The transformed *E. coli* were then analysed for Fab' expression in shake flasks as described. The results of a typical experiment are shown in Figure 10.

The different intergenic sequences conferred different expression profiles. IGS1 and IGS2
20 accumulated periplasmic Fab' rapidly with a peak at 1 hour post induction, after which the level recovered fell. The peak was greater and the fall sharper for IGS1. These results were consistent with a high level of synthesis, as expected for close translational coupling for these constructs. IGS1 apparently conferred a higher level of heavy chain expression than did IGS2. In this instance, it appeared that this high level of expression was poorly
25 tolerated, since periplasmic expression levels fell after the 1 hour peak. This was seen on the growth profile of the IGS1 culture (not shown), which peaked at 1 hour post induction before falling, suggesting cell death and lysis.

IGS3 accumulated Fab' more slowly but peaked at 2 hours post induction with a higher
30 peak value (325 ng/ml/OD), before levels fell. The growth of this culture continued to 3 hours post induction and reached a higher peak biomass (not shown). This is consistent with a lower level of heavy chain synthesis.

IGS4 accumulated material at a slower rate still and failed to reach the high peak of productivity of the other three constructs.

All IGS variants significantly out-performed the original pTTO(TNF α) vector. The hypothesis that the different IGS sequences confer different rates of translational initiation is supported by these experimental results. For the TNF α Fab' it appears that a high rate of heavy chain translational initiation is poorly tolerated and is therefore not optimal. A slower rate, as conferred by IGS3, results in better growth characteristics and consequently a better yield accumulates over time.

10

Following comparison of productivity in the fermenter (not shown), the IGS3 construct was selected as the highest yielding.

A dicistronic message encoding a different Fab' antibody: creation of g163 Fab' IGS variants

The pTTO/IGS vector suite described above was then used for expression analysis of further Fab's. Initially, humanised Fab' g163 was used. A 4-way ligation was used to generate the 4 IGS variants of Fab' g163 (Figure 11). A heavy chain intermediate was generated by insertion of a MunI – ApaI fragment of the g163 V_H gene (obtained by PCR rescue from mammalian expression vector pGamma-4) into plasmid pDNAEngG1. This intermediate was cleaved with PvuII and NotI to generate a g163 V_H + C_{H1} fragment. The plasmid pTTO(TNF α) was cleaved with MunI and NotI and the large fragment was purified to give a vector fragment. A MunI – SphI V_L fragment was generated by PCR rescue from the mammalian expression vector pMR10.1(g163). Finally C κ -IGS fragments were generated by SphI – PvuII digestion of the 4 pTTO(TNF α) IGS variants described above. Four separate ligations then generated the constructs pTTO(g163 IGS-1), pTTO(g163 IGS-2), pTTO(g163 IGS-3) and pTTO(g163 IGS-4). The results of shake flask analysis of these constructs are shown in Figure 12.

The expression profile was quite similar to that seen with Fab' TNF α , in that IGS-1 and -2 resulted in very rapid Fab' accumulation, peaking at 1 hour post induction before reducing sharply. IGS-3 resulted in a slower initial rate of accumulation, peaking at a later time point (2-3 hours post induction) before reducing at a slower rate. The IGS-4 construct rose

slowly throughout the induction timecourse and again never reached the high yields of the other constructs. Because of the expression profiles, and the growth profiles showing that, for IGS-1 and -2, the biomass also peaked only 1 hour post induction (not shown), IGS-3 was chosen and expressed in the fermenter to high yields (not shown).

5

Construction of plasmid pTTOD

In order to simplify Fab' coding strategies, plasmid pTTOD was derived from plasmid pTTO-1 by removal of backbone restriction sites for PvuII (3 sites), EcoRV (2 sites) and ApaI (1 site). In making these changes, the protein coding sequences of the lacIq gene and
10 tetracycline resistance gene were not altered, although 'silent' changes were made at the DNA level. A PCR strategy was used, in which primers bearing 'silent' changes, which removed these restriction sites, were designed and used to amplify sections of the parent plasmid (pTTO-1). Flanking restriction sites (unaltered) were then used to replace sequences in the parent plasmid with these modified sequences. Plasmid pTTOD was
15 created by this multi-stage process. Transfer of existing g163 Fab' genes within vector pTTO into pTTOD was achieved using the unique PstI and EcoRI sites which flank the genes, creating pTTOD(g163) IGS variants 1-4. Figure 13 shows the restriction map of pTTOD(g163 IGS-3).

20 Expression of other Fab's as IGS variants

In addition to TNF α and g163, several more Fab's have been expressed as two or more IGS variants. These include Fab's termed g165 and gA33. Figure 14 shows pTTOD(g165) IGS-1 to -3 compared in the shake flask. In contrast to TNF α and g163, IGS-2 and IGS-1 out-perform IGS-3. Expression of this Fab' seems to be well tolerated by
25 the host cell even at a rapid rate, and the culture expressing IGS-2 continued to grow throughout the induction period (not shown). Figure 15 shows a fermenter comparison of IGS-1 to -4 with this Fab', and this essentially reproduces the observation made in the shake flask. IGS-2 was confirmed as the highest yielding variant. With Fab' gA33, pTTOD(gA33) IGS-2 and -3 were compared in the fermenter and both gave similar yields
30 (Figure 16). Hence, with different Fab's, different IGS sequences are required for optimum yield.

Shake flask versus fermenter analysis

In the shake flask, promoter de-repression is achieved with IPTG which gives very rapid induction of expression. The induction regime in the fermenter is different and more gentle, using lactose (which is converted by the bacterium to allolactose) to switch on the promoter. Despite these different induction kinetics, the shake flask has been shown to give an indication of how constructs will compare in the fermenter (see Figures 14 and 15).

The principle that different Fab's require a different IGS for optimum yield is clearly demonstrated. The novelty of the system described here is in the use of IGS cassettes to achieve optimal translational initiation rates of the second gene of a dicistronic message as a means of achieving high level Fab' expression. In the system described, the light chain expression remains unaltered and only the heavy chain translational initiation rate is optimised. There are two possible explanations for why this strategy succeeds:

- (i) The expression of the light chain is of little consequence to the overall level of Fab' accumulation, provided sufficient light chain is synthesised to prevent the heavy chain becoming in excess. Excess light chain is usually tolerated without problem, and it is the level of translation of the heavy chain that dictates the efficiency of soluble expression; or
 - (ii) The optimisation of heavy chain in effect is tuned for the fixed rate of light chain expression, so that the levels of the two chains are balanced. It is not the heavy chain folding/secretion rate per se that dictates the efficiency of soluble expression, but the balance of expression of the two heterologous chains.
- It should be understood that the above described examples are merely exemplary and do not limit the scope of the present invention as defined in the following claims.

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agaaaactgc tatagcaatt g 81

<210> 14

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> IGS cassette-4

<220>

<223> End of c-Kappa sequence

<400> 14

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

1 5 10

<210> 15

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> IGS cassette-4

<220>

<223> Start of OmpA sequence

<400> 15

Met Lys Lys Thr Ala Ile Ala Ile

1 5

<210> 16

<211> 84

<212> DNA

<213> Artificial Sequence

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<223> OmpA Oligonucleotide Adapter

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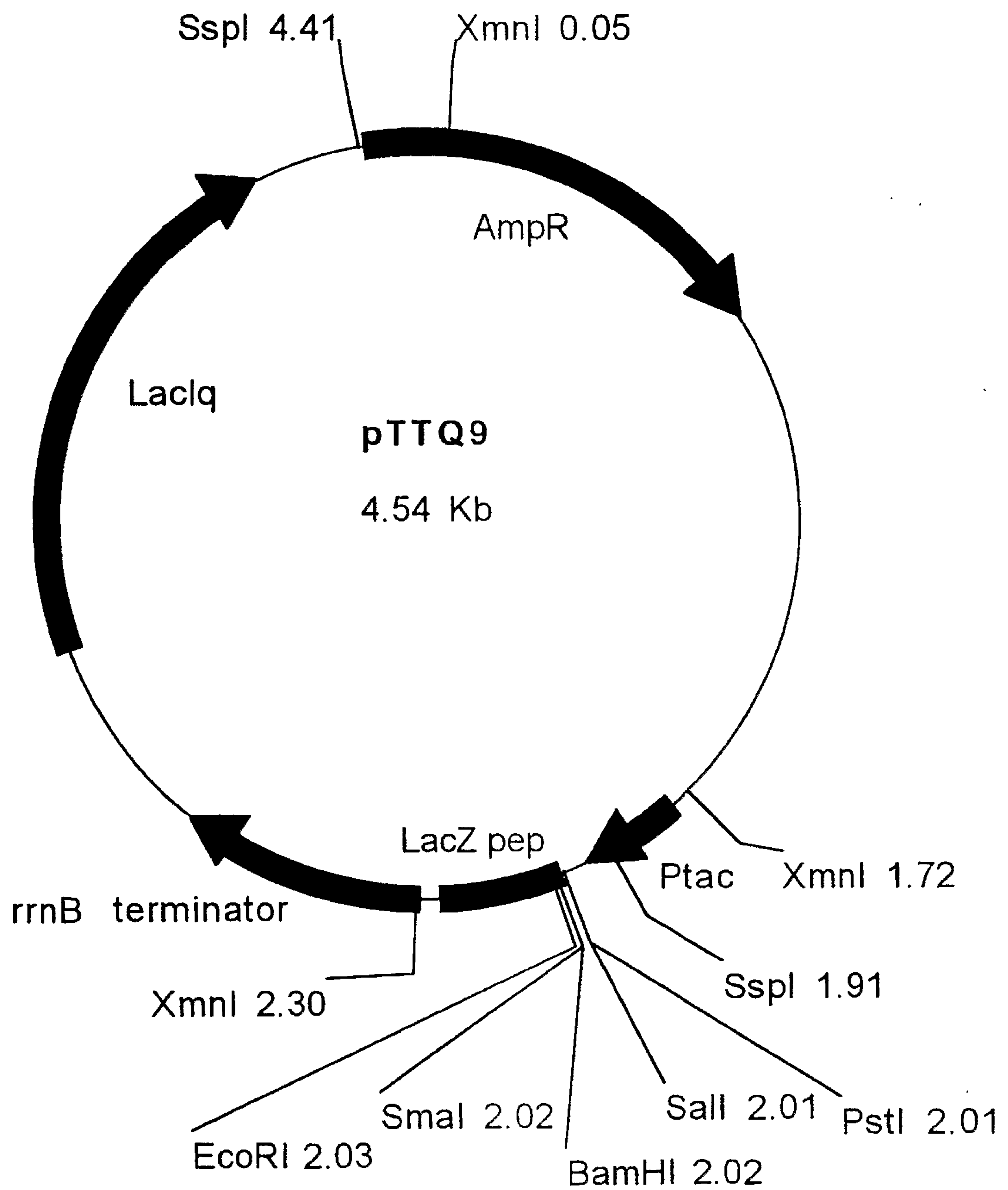
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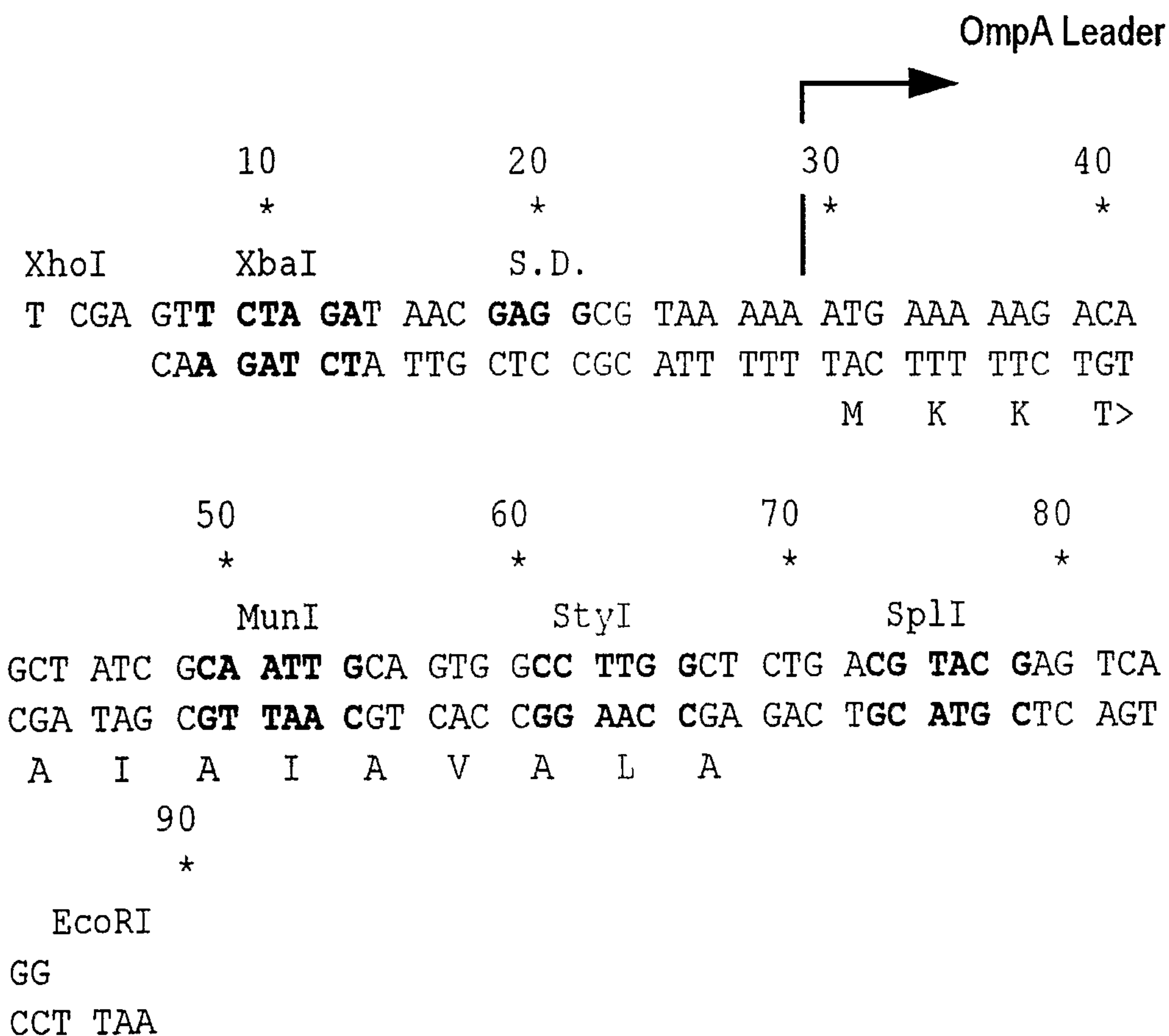
What is claimed:

1. A dicistronic message for producing an antibody molecule with a particular antigen-binding specificity, in which the upstream cistron contains DNA coding for either the heavy chain or the light chain of the antibody and the downstream cistron contains DNA coding for the corresponding light chain or heavy chain respectively, characterized in that the two cistrons are linked by an optimised intergenic sequence (IGS) wherein the IGS is IGS1 (SEQ ID NO:4), IGS2 (SEQ ID NO:7), IGS3 (SEQ ID NO:10) or IGS4 (SEQ ID NO:13), and wherein the antibody produced is not an anti-TNF α antibody or an anti-KDR antibody.
2. An expression vector containing the dicistronic message according to claim 1.
3. The expression vector according to claim 2 wherein the expression vector is pTTO-1 (SEQ ID NO:3).
4. A host cell that has been transformed with the expression vector according to claim 2 or claim 3.
5. The host cell according to claim 4, wherein the host cell is *E. coli*.
6. A process for the production of an antibody molecule comprising culturing the host cell of claim 4 or claim 5.

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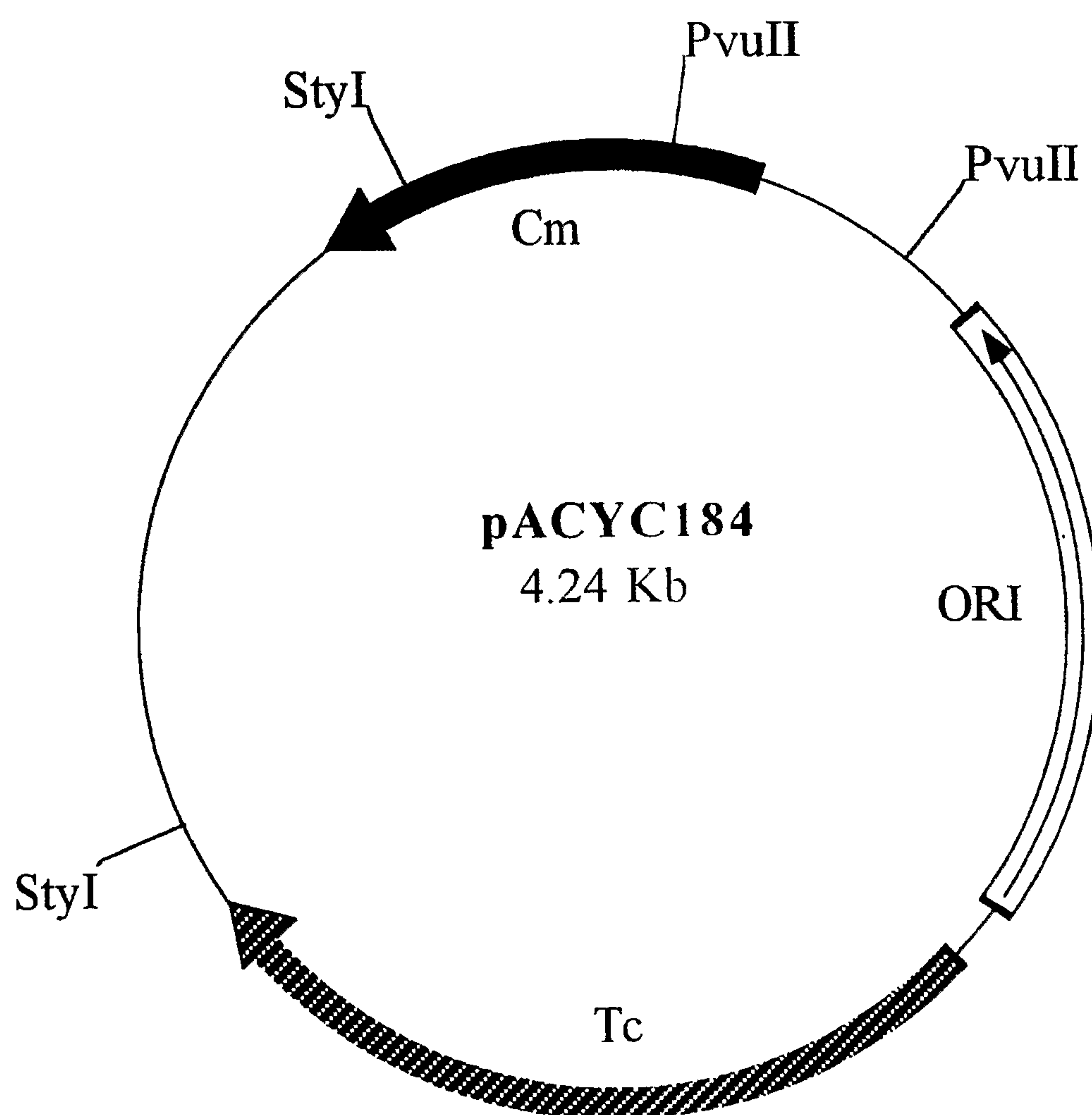
Fig. 1

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Fig. 2**Sequence of OmpA Oligonucleotide Adapter**

- Internal restriction sites are shown in bold
- The 5' XhoI cohesive end ligates into the vector Sall site, blocking it
- S.D. represents the OmpA Shine Dalgarno sequence

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Fig. 3

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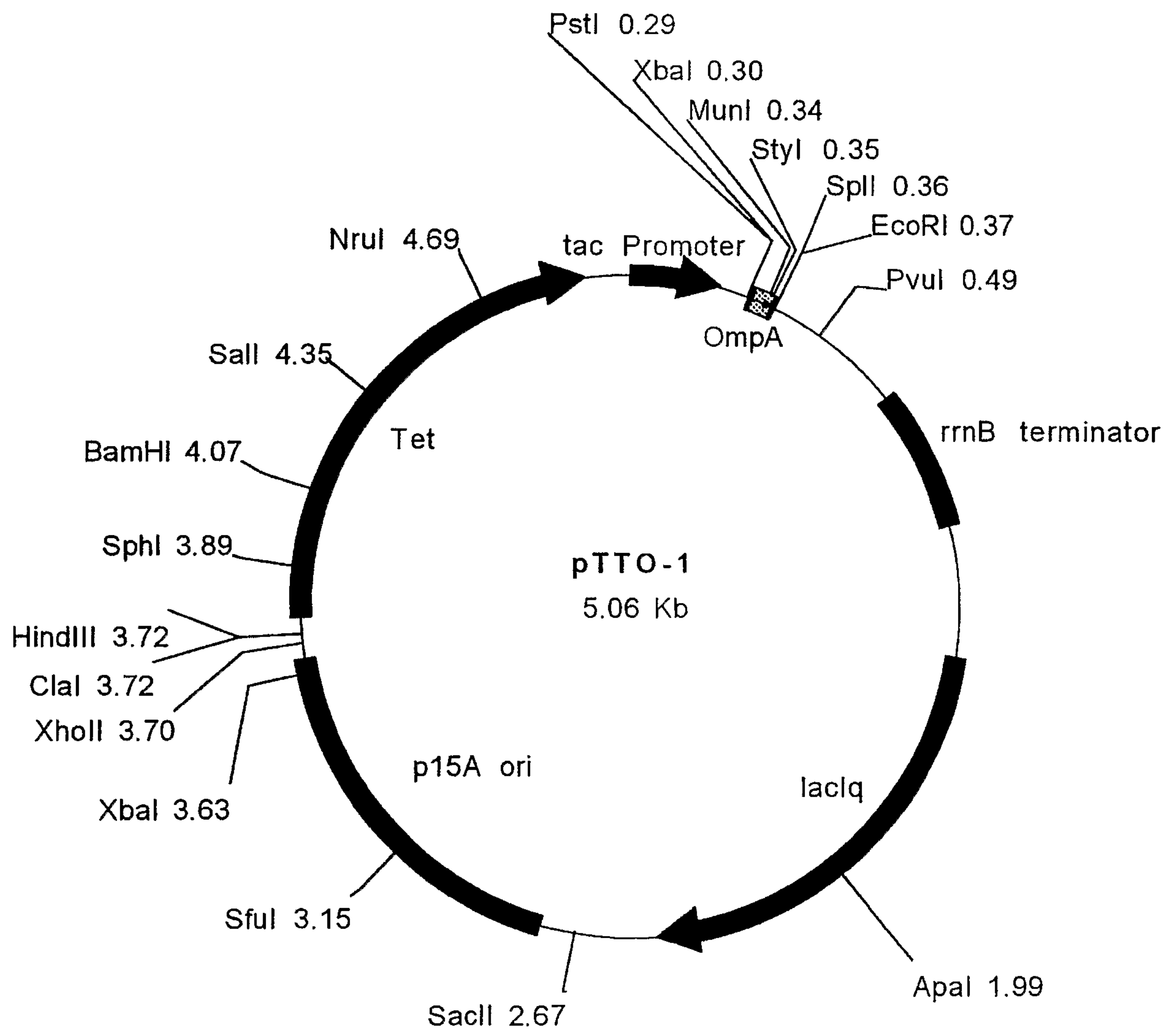
Fig. 4

Fig. 5**5/19****Nucleotide sequence of pTTO-1**

10	20	30	40	50	60	70
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TTAAGAGTAC	AAACTGTCGA	ATAGTAGCTG	ACGTGCCACG	TGGTTACGAA	GACCGCAGTC	CGTCGGTAGC
80	90	100	110	120	130	140
GAAGCTGTGG	TATGGCTGTG	CAGGTCGTAA	ATCACTGCAT	AATTCGTGTC	GCTCAAGGCG	CACTCCCGTT
CTTCGACACC	ATACCGACAC	GTCCAGCATT	TAGTGACGTA	TTAAGCACAG	CGAGTTCGCG	GTGAGGGCAA
150	160	170	180	190	200	210
CTGGATAATG	TTTTTTGCGC	CGACATCATA	ACGGTTCTGG	CAAATATTCT	GAAATGAGCT	GTTGACAATT
GACCTATTAC	AAAAAACGCG	GCTGTAGTAT	TGCCAAGACC	GTTTATAAGA	CTTTACTCGA	CAACTGTTAA
220	230	240	250	260	270	280
AATCATCGGC	TCGTATAATG	TGTGGAATTG	TGAGCGGATA	ACAATTTTAC	ACAGGAAACA	GCGATGAGCT
TTAGTAGCCG	AGCATATTAC	ACACCTTAAC	ACTCGCCTAT	TGTTAAAGTG	TGTCCTTTGT	CGCTACTCGA
290	300	310	320	330	340	350
TGGCTGCAGG	TCGAGTTCTA	GATAACGAGG	CGTAAAAAAT	GAAAAAGACA	GCTATCGCAA	TTGCAGTGGC
ACCGACGTCC	AGCTCAAGAT	CTATTGCTCC	GCATTTTTTA	CTTTTTCTGT	CGATAGCGTT	AACGTCACCG
360	370	380	390	400	410	420
CTTGGCTCTG	ACGTACGAGT	CAGGAATTCA	CTGGCCGTCG	TTTTACAACG	TCGTGACTGG	GAAAACCCTG
GAACCGAGAC	TGCATGCTCA	GTCTTAAGT	GACCGGCAGC	AAAATGTTGC	AGCACTGACC	CTTTTGGGAC
430	440	450	460	470	480	490
GCGTTACCCA	ACTTAATCGC	CTTGCAGCAC	ATCCCCCTTT	CGCCAGCTGG	CGTAATAGCG	AAGAGGCCCG
CGCAATGGGT	TGAATTAGCG	GAACGTCGTG	TAGGGGGAAA	GCGGTCGACC	GCATTATCGC	TTCTCCGGGC
500	510	520	530	540	550	560
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GTGGCTAGCG	GGAAGGGTTG	TCAACGCGTC	GGACTTACCG	CTTACCGCGG	ACTACGCCAT	AAAAGAGGAA
570	580	590	600	610	620	630
ACGCATCTGT	GCGGTATTTT	ACACCGCATA	AATTCCCTGT	TTTGGCGGAT	GAGAGAAGAT	TTTCAGCCTG
TGCGTAGACA	CGCCATAAAG	TGTGGCGTAT	TTAAGGGACA	AAACCGCCTA	CTCTCTTCTA	AAAGTCGGAC
640	650	660	670	680	690	700
ATACAGATTA	AATCAGAACG	CAGAAGCGGT	CTGATAAAAC	AGAATTTGCC	TGGCGGCAGT	AGCGCGGTGG
TATGTCTAAT	TTAGTCTTGC	GTCTTCGCCA	GACTATTTTG	TCTTAAACGG	ACCGCCGTCA	TCGCGCCACC
710	720	730	740	750	760	770
TCCCACCTGA	CCCCATGCCG	AACTCAGAAG	TGAAACGCCG	TAGCGCCGAT	GGTAGTGTGG	GGTCTCCCCA
AGGGTGGACT	GGGGTACGGC	TTGAGTCTTC	ACTTTGCGGC	ATCGCGGCTA	CCATCACACC	CCAGAGGGGT
780	790	800	810	820	830	840
TGCGAGAGTA	GGGAAGTGGC	AGGCATCAAA	TAAAACGAAA	GGCTCAGTCG	AAAGACTGGG	CCTTTCGTTT
ACGCTCTCAT	CCCTTGACGG	TCCGTAGTTT	ATTTTGCTTT	CCGAGTCAGC	TTTCTGACCC	GGAAAGCAAA
850	860	870	880	890	900	910
TATCTGTTGT	TTGTCGGTGA	ACGCTCTCCT	GAGTAGGACA	AATCCGCCGG	GAGCGGATTT	GAACGTTGCG
ATAGACAACA	AACAGCCACT	TGCGAGAGGA	CTCATCCTGT	TTAGGCGGCC	CTCGCCTAAA	CTTGCAACGC
920	930	940	950	960	970	980
AAGCAACGGC	CCGGAGGGTG	GCGGGCAGGA	CGCCCGCCAT	AAACTGCCAG	GCATCAAATT	AAGCAGAAGG
TTCGTTGCCG	GGCCTCCAC	CGCCCGTCCT	GCGGGCGGTA	TTTGACGGTC	CGTAGTTTAA	TTCGTCTTCC
990	1000	1010	1020	1030	1040	1050
CCATCCTGAC	GGATGGCCTT	TTTGCGTTTC	TACAAACTCT	TCCTGTGCTC	ATATCTACAA	GCCATCCCCC
GGTAGGACTG	CCTACCGGAA	AAACGCAAAG	ATGTTTGAGA	AGGACAGCAG	TATAGATGTT	CGGTAGGGGG
1060	1070	1080	1090	1100	1110	1120
CACAGATACG	GTAAACTAGC	CTCGTTTTTG	CATCAGGAAA	GCAGGGAATT	TATGGTGCAC	TCTCAGTACA
GTGTCTATGC	CATTTGATCG	GAGCAAAAAC	GTAGTCCTTT	CGTCCCTTAA	ATACCACGTG	AGAGTCATGT
1130	1140	1150	1160	1170	1180	1190
ATCTGCTCTG	ATGCCGCATA	GTAAAGCCAG	CCCCGACACC	CGCCAACACC	CGCTGACGCG	CCCTGACGGG
TAGACGAGAC	TACGGCGTAT	CAATTGCGTC	GGGGCTGTGG	GCGGTTGTGG	GCGACTGCGC	GGGACTGCCC
1200	1210	1220	1230	1240	1250	1260
CTTGTCTGCT	CCCGGCATCC	GCTTACAGAC	AAGCTGTGAC	CGTCTCCGGG	AGCTGCATGT	GTCAGAGGTT
GAACAGACGA	GGGCCGTAGG	CGAATGTCTG	TTCGACACTG	GCAGAGGCC	TCGACGTACA	CAGTCTCCAA
1270	1280	1290	1300	1310	1320	1330
TTCACCGTCA	TCACCGAAAC	GCGCGAGACG	AAAGGGCCTC	GTGATACGCC	TATTTTTATA	GGTTAATGTC
AAGTGGCAGT	AGTGGCTTTG	CGCGCTCTGC	TTTCCCGGAG	CACTATGCGG	ATAAAAATAT	CCAATTACAG
1340	1350	1360	1370	1380	1390	1400

Fig. 5(contd)**6/19**

ATGATAATAA	TGGTTTCTTA	GACGTGAGGT	TCTGTACCCG	ACACCATCGA	ATGGTGCAAA	ACCTTTCGCG
TACTATTATT	ACCAAAGAAT	CTGCACTCCA	AGACATGGGC	TGTGGTAGCT	TACCACGTTT	TGGAAAGCGC
1410	1420	1430	1440	1450	1460	1470
GTATGGCATG	ATAGCGCCCG	GAAGAGAGTC	AATTCAGGGT	GGTGAATGTG	AAACCAGTAA	CGTTATACGA
CATACCGTAC	TATCGCGGGC	CTTCTCTCAG	TTAAGTCCCA	CCACTTACAC	TTTGGTCATT	GCAATATGCT
1480	1490	1500	1510	1520	1530	1540
TGTCGCAGAG	TATGCCGGTG	TCTCTTATCA	GACCGTTTCC	CGCGTGGTGA	ACCAGGCCAG	CCACGTTTCT
ACAGCGTCTC	ATACGGCCAC	AGAGAATAGT	CTGGCAAAGG	GCGCACCAC	TGGTCCGGTC	GGTGCAAAGA
1550	1560	1570	1580	1590	1600	1610
GCGAAAACGC	GGGAAAAAGT	GGAAGCGGCG	ATGGCGGAGC	TGAATTACAT	TCCCAACCGC	GTGGCACAAC
CGCTTTTGCG	CCCTTTTTC	CCTTCGCCGC	TACCGCCTCG	ACTTAATGTA	AGGGTTGGCG	CACCGTGTTG
1620	1630	1640	1650	1660	1670	1680
AACTGGCGGG	CAAACAGTCG	TTGCTGATTG	GCGTTGCCAC	CTCCAGTCTG	GCCCTGCACG	CGCCGTCGCA
TTGACCGCCC	GTTTGTCAGC	AACGACTAAC	CGCAACGGTG	GAGGTCAGAC	CGGGACGTGC	GCGGCAGCGT
1690	1700	1710	1720	1730	1740	1750
AATTGTCGCG	GCGATTAAAT	CTCGCGCCGA	TCAACTGGGT	GCCAGCGTGG	TGGTGTCGAT	GGTAGAACGA
TTAACAGCGC	CGCTAATTTA	GAGCGCGGCT	AGTTGACCCA	CGGTCGCACC	ACCACAGCTA	CCATCTTGCT
1760	1770	1780	1790	1800	1810	1820
AGCGGCGTCG	AAGCCTGTAA	AGCGGCGGTG	CACAATCTTC	TCGCGCAACG	CGTCAGTGGG	CTGATCATT
TCGCCGCAGC	TTCGGACATT	TCGCCGCCAC	GTGTTAGAAG	AGCGCGTTGC	GCAGTCACCC	GACTAGTAAT
1830	1840	1850	1860	1870	1880	1890
ACTATCCGCT	GGATGACCAG	GATGCCATTG	CTGTGGAAGC	TGCCTGCACT	AATGTTCCGG	CGTTATTTCT
TGATAGGCGA	CCTACTGGTC	CTACGGTAAC	GACACCTTCG	ACGGACGTGA	TTACAAGGCC	GCAATAAAGA
1900	1910	1920	1930	1940	1950	1960
TGATGTCTCT	GACCAGACAC	CCATCAACAG	TATTATTTTC	TCCCATGAAG	ACGGTACGCG	ACTGGGCGTG
ACTACAGAGA	CTGGTCTGTG	GGTAGTTGTC	ATAATAAAG	AGGGTACTTC	TGCCATGCGC	TGACCCGCAC
1970	1980	1990	2000	2010	2020	2030
GAGCATCTGG	TCGCATTGGG	TCACCAGCAA	ATCGCGCTGT	TAGCGGGCCC	ATTAAGTTCT	GTCTCGGCGC
CTCGTAGACC	AGCGTAACCC	AGTGGTCGTT	TAGCGCGACA	ATCGCCCGGG	TAATTCAAGA	CAGAGCCGCG
2040	2050	2060	2070	2080	2090	2100
GTCTGCGTCT	GGCTGGCTGG	CATAAATATC	TCACTCGCAA	TCAAATTCAG	CCGATAGCGG	AACGGGAAGG
CAGACGCAGA	CCGACCGACC	GTATTTATAG	AGTGAGCGTT	AGTTTAAGTC	GGCTATCGCC	TTGCCCTTCC
2110	2120	2130	2140	2150	2160	2170
CGACTGGAGT	GCCATGTCCG	GTTTTCAACA	AACCATGCAA	ATGCTGAATG	AGGGCATCGT	TCCCACTGCG
GCTGACCTCA	CGGTACAGGC	CAAAAGTTGT	TTGGTACGTT	TACGACTTAC	TCCCGTAGCA	AGGGTGACGC
2180	2190	2200	2210	2220	2230	2240
ATGCTGGTTG	CCAACGATCA	GATGGCGCTG	GGCGCAATGC	GCGCCATTAC	CGAGTCCGGG	CTGCGCGTTG
TACGACCAAC	GGTTGCTAGT	CTACCGCGAC	CCGCGTTACG	CGCGGTAATG	GCTCAGGCCC	GACGCGCAAC
2250	2260	2270	2280	2290	2300	2310
GTGCGGATAT	CTCGGTAGTG	GGATACGACG	ATACCGAAGA	CAGCTCATGT	TATATCCCGC	CGTTAACCAC
CACGCCTATA	GAGCCATCAC	CCTATGCTGC	TATGGCTTCT	GTCGAGTACA	ATATAGGGCG	GCAATTGGTG
2320	2330	2340	2350	2360	2370	2380
CATCAAACAG	GATTTTCGCC	TGCTGGGGCA	AACCAGCGTG	GACCGCTTGC	TGCAACTCTC	TCAGGGCCAG
GTAGTTTGTC	CTAAAAGCGG	ACGACCCCGT	TTGGTCGCAC	CTGGCGAACG	ACGTTGAGAG	AGTCCCGGTC
2390	2400	2410	2420	2430	2440	2450
GCGGTGAAGG	GCAATCAGCT	GTTGCCCGTC	TCACTGGTGA	AAAGAAAAAC	CACCCTGGCG	CCCAATACGC
CGCCACTTCC	CGTTAGTCGA	CAACGGGCAG	AGTGACCACT	TTTCTTTTTG	GTGGGACCGC	GGGTTATGCG
2460	2470	2480	2490	2500	2510	2520
AAACCGCCTC	TCCCCGCGCG	TTGGCCGATT	CATTAATGCA	GCTGGCACGA	CAGGTTTCCC	GACTGGAAAG
TTTGCGGGAG	AGGGGCGCGC	AACCGGCTAA	GTAATTACGT	CGACCGTGCT	GTCCAAAGGG	CTGACCTTTC
2530	2540	2550	2560	2570	2580	2590
CGGGCAGTGA	GCGCAACGCA	ATTAATGTAA	GTTAGCTCAC	TCATTAGGCA	CCCCAGGCTT	TACACTTTAT
GCCCGTCACT	CGCGTTGCGT	TAATTACATT	CAATCGAGTG	AGTAATCCGT	GGGGTCCGAA	ATGTGAAATA
2600	2610	2620	2630	2640	2650	2660
GCTTCCGACC	TGCAAGAACC	TCACGTCAGG	TGGCACTTTT	CGGGGAAATG	TGCGCGGAAC	CCCTATTTGT
CGAAGGCTGG	ACGTTCTTGG	AGTGCAAGTCC	ACCGTGAAAA	GCCCCCTTAC	ACGCGCCTTG	GGGATAAACA
2670	2680	2690	2700	2710	2720	2730
TTATTTTTCT	AAATACATTC	AAATATGTAT	CCGCTCATGA	GACAATAACC	CTGATAAATG	CTTCAATAAT
AATAAAAAAG	TTTATGTAAG	TTTATACATA	GGCGAGTACT	CTGTTATTGG	GACTATTTAC	GAAGTTATTA
2740	2750	2760	2770	2780	2790	2800
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Fig. 5(contd)**7/19**

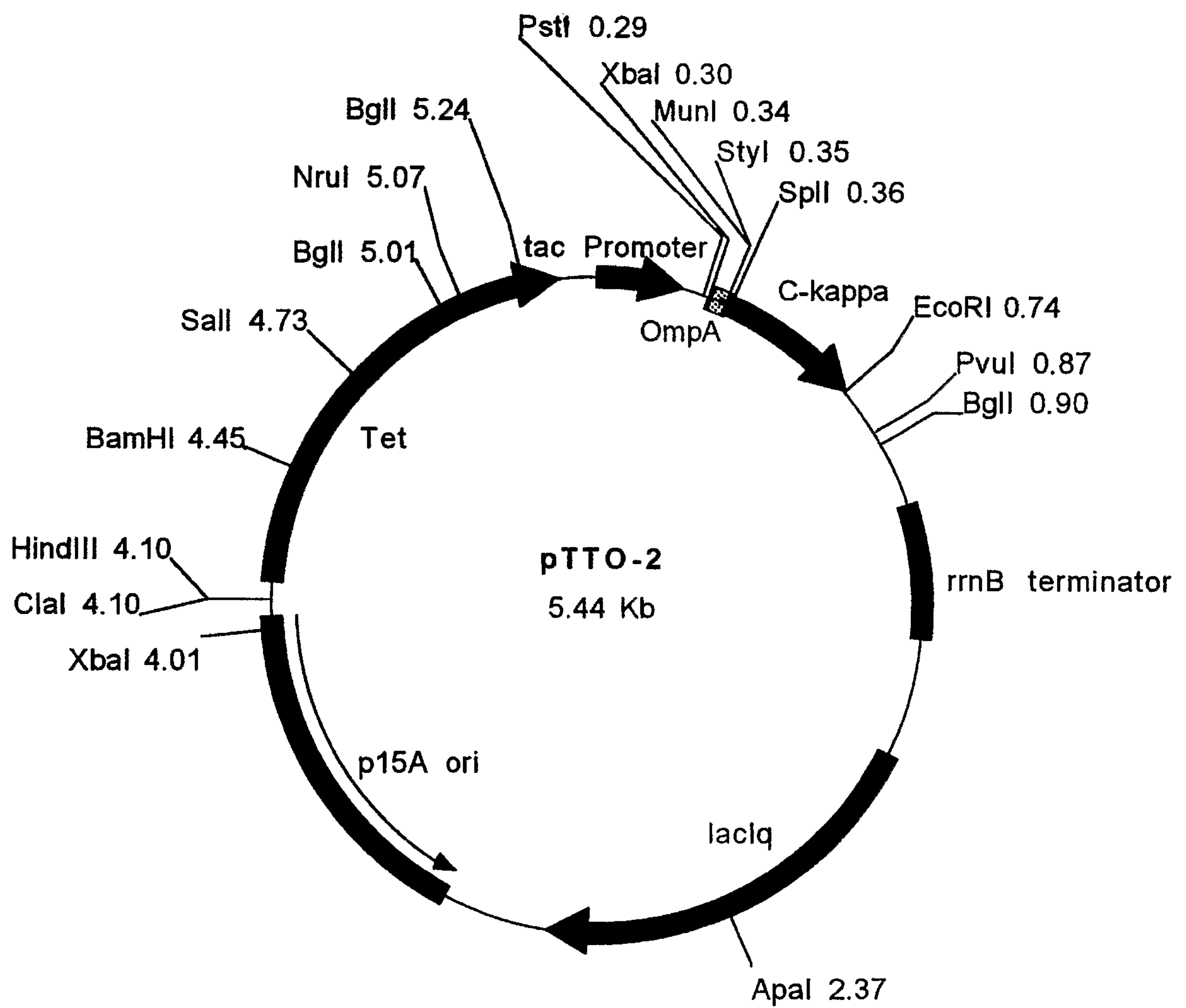
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CGGAGTGTAT	ACTGGCTTAC	TATGTTGGCA	CTGATGAGGG	TGTCAGTGAA	GTGCTTCATG	TGGCAGGAGA
GCCTCACATA	TGACCGAATG	ATACAACCGT	GACTACTCCC	ACAGTCACTT	CACGAAGTAC	ACCGTCCTCT
2880	2890	2900	2910	2920	2930	2940
AAAAAGGCTG	CACCGGTGCG	TCAGCAGAAT	ATGTGATACA	GGATATATTC	CGCTTCCTCG	CTCACTGACT
TTTTTCCGAC	GTGGCCACGC	AGTCGTCTTA	TACACTATGT	CCTATATAAG	GCGAAGGAGC	GAGTGACTGA
2950	2960	2970	2980	2990	3000	3010
CGCTACGCTC	GGTCGTTTCGA	CTGCGGCGAG	CGGAAATGGC	TTACGAACGG	GGCGGAGATT	TCCTGGAAGA
GCGATGCGAG	CCAGCAAGCT	GACGCCGCTC	GCCTTTACCG	AATGCTTGCC	CCGCCCTCTAA	AGGACCTTCT
3020	3030	3040	3050	3060	3070	3080
TGCCAGGAAG	ATACTTAACA	GGGAAGTGAG	AGGGCCGCGG	CAAAGCCGTT	TTTCCATAGG	CTCCGCCCCC
ACGGTCCTTC	TATGAATTGT	CCCTTCACTC	TCCC GGCGCC	GTTTCGGCAA	AAAGGTATCC	GAGGCGGGGG
3090	3100	3110	3120	3130	3140	3150
CTGACAAGCA	TCACGAAATC	TGACGCTCAA	ATCAGTGGTG	GCGAAACCCG	ACAGGACTAT	AAAGATACCA
GACTGTTTCGT	AGTGCTTTAG	ACTGCGAGTT	TAGTCACCAC	CGCTTTGGGC	TGTCCTGATA	TTTCTATGGT
3160	3170	3180	3190	3200	3210	3220
GGCGTTTCCC	CCTGGCGGCT	CCCTCGTGCG	CTCTCCTGTT	CCTGCCTTTC	GGTTTACCGG	TGTCATTCCG
CCGCAAAGGG	GGACCGCCGA	GGGAGCACGC	GAGAGGACAA	GGACGGAAAG	CCAAATGGCC	ACAGTAAGGC
3230	3240	3250	3260	3270	3280	3290
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GACAATACCG	GCGCAAACAG	AGTAAGGTGC	GGACTGTGAG	TCAAGGCCCA	TCCGTCAAGC	GAGGTTTCGAC
3300	3310	3320	3330	3340	3350	3360
GACTGTATGC	ACGAACCCCC	CGTTCAGTCC	GACCGCTGCG	CCTTATCCGG	TAAGTATCGT	CTTGAGTCCA
CTGACATACG	TGCTTGGGGG	GCAAGTCAGG	CTGGCGACGC	GGAATAGGCC	ATTGATAGCA	GAAGTCAGGT
3370	3380	3390	3400	3410	3420	3430
ACCCGGAAAG	ACATGCAAAA	GCACCACTGG	CAGCAGCCAC	TGGTAATTGA	TTTAGAGGAG	TTAGTCTTGA
TGGGCCTTTC	TGTACGTTTT	CGTGCTGACC	GTCGTCGGTG	ACCATTAACT	AAATCTCCTC	AATCAGAACT
3440	3450	3460	3470	3480	3490	3500
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TCAGTACGCG	GCCAATTCCG	ATTTGACTTT	CCTGTTCAAA	ACCACTGACG	CGAGGAGGTT	CGGTCAATGG
3510	3520	3530	3540	3550	3560	3570
TCGGTTCAAA	GAGTTGGTAG	CTCAGAGAAC	CTTCGAAAAA	CCGCCCTGCA	AGGCGGTTTT	TTCGTTTTCA
AGCCAAGTTT	CTCAACCATC	GAGTCTCTTG	GAAGCTTTTT	GGCGGGACGT	TCCGCCAAAA	AAGCAAAAGT
3580	3590	3600	3610	3620	3630	3640
GAGCAAGAGA	TTACGCGCAG	ACCAAAACGA	TCTCAAGAAG	ATCATCTTAT	TAATCAGATA	AAATATTTCT
CTCGTTCTCT	AATGCGCGTC	TGGTTTTGCT	AGAGTTCTTC	TAGTAGAATA	ATTAGTCTAT	TTTATAAAGA
3650	3660	3670	3680	3690	3700	3710
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TCTAAAGTCA	CGTTAAATAG	AGAAGTTTAC	ATCGTGGACT	TCAGTCGGGG	TATGCTATAT	TCAACATTAA
3720	3730	3740	3750	3760	3770	3780
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GAGTACAAAC	TGTCGAATAG	TAGCTATTTCG	AAATTACGCC	ATCAAATAGT	GTCAATTTAA	CGATTGCGTC
3790	3800	3810	3820	3830	3840	3850
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3860	3870	3880	3890	3900	3910	3920
GGCATAGGCT	TGGTTATGCC	GGTACTGCCG	GGCCTCTTGC	GGGATATCGT	CCATTCCGAC	AGCATCGCCA
CCGTATCCGA	ACCAATACGG	CCATGACGGC	CCGGAGAACG	CCCTATAGCA	GGTAAGGCTG	TCGTAGCGGT
3930	3940	3950	3960	3970	3980	3990
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CAGTGATACC	GCACGACGAT	CGCGATATAC	GCAACTACGT	TAAAGATACG	CGTGGGCAAG	AGCCTCGTGA
4000	4010	4020	4030	4040	4050	4060
GTCCGACCGC	TTTGGCCGCC	GCCAGTCCCT	GCTCGCTTCG	CTACTTGAGG	CCACTATCGA	CTACGCGATC
CAGGCTGGCG	AAACCGGCGG	CGGGTCAGGA	CGAGCGAAGC	GATGAACCTC	GGTGATAGCT	GATGCGCTAG
4070	4080	4090	4100	4110	4120	4130
ATGGCGACCA	CACCCGTCCT	GTGGATCCTC	TACGCCGGAC	GCATCGTGGC	CGGCATCACC	GGCGCCACAG
TACCGCTGGT	GTGGGCAGGA	CACCTAGGAG	ATGCGGCCTG	CGTAGCACCG	GCCGTAGTGG	CCGCGGTGTC
4140	4150	4160	4170	4180	4190	4200
GTGCGGTTGC	TGGCGCCTAT	ATCGCCGACA	TCACCGATGG	GGAAGATCGG	GCTCGCCACT	TCGGGCTCAT
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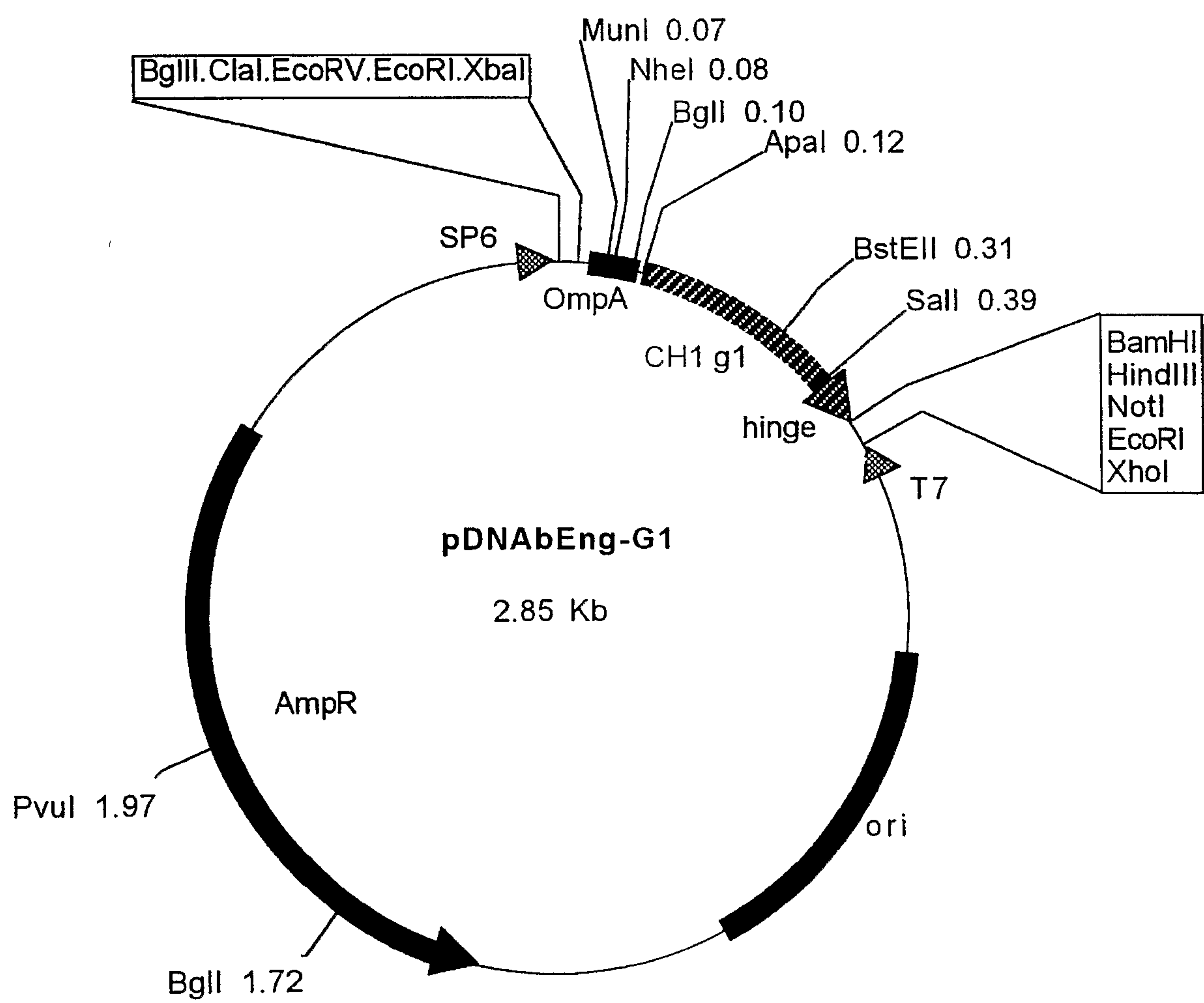
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CTCGCGAACA	AAGCCGCACC	CATACCACCG	TCCGGGGCAC	CGGCCCCCTG	ACAACCCGCG	GTAGAGGAAC
4280	4290	4300	4310	4320	4330	4340
CATGCACCAT	TCCTTGCGGC	GGCGGTGCTC	AACGGCCTCA	ACCTACTACT	GGGCTGCTTC	CTAATGCAGG
GTACGTGGTA	AGGAACGCCG	CCGCCACGAG	TTGCCGGAGT	TGGATGATGA	CCCGACGAAG	GATTACGTCC
4350	4360	4370	4380	4390	4400	4410
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4420	4430	4440	4450	4460	4470	4480
GCGGGGCATG	ACTATCGTCG	CCGCACCTAT	GACTGTCTTC	TTTATCATGC	AACTCGTAGG	ACAGGTGCCG
CGCCCCGTAC	TGATAGCAGC	GGCGTGAATA	CTGACAGAAG	AAATAGTACG	TTGAGCATCC	TGTCCACGGC
4490	4500	4510	4520	4530	4540	4550
GCAGCGCTCT	GGGTCATTTT	CGGCGAGGAC	CGCTTTCGCT	GGAGCGCGAC	GATGATCGGC	CTGTGCTTGG
CGTCGCGAGA	CCCAGTAAAA	GCCGCTCCTG	GCGAAAGCGA	CCTCGCGCTG	CTACTAGCCG	GACAGCGAAC
4560	4570	4580	4590	4600	4610	4620
CGGTATTTCG	AATCTTGAC	GCCCTCGCTC	AAGCCTTCGT	CACTGGTCCC	GCCACCAAAC	GTTTCGGCGA
GCCATAAGCC	TTAGAACGTG	CGGGAGCGAG	TTCGGAAGCA	GTGACCAGGG	CGGTGGTTTG	CAAAGCCGCT
4630	4640	4650	4660	4670	4680	4690
GAAGCAGGCC	ATTATCGCCG	GCATGGCGGC	CGACGCGCTG	GGCTACGTCT	TGCTGGCGTT	CGCGACGCGA
CTTCGTCCGG	TAATAGCGGC	CGTACCGCCG	GCTGCGCGAC	CCGATGCAGA	ACGACCGCAA	GCGCTGCGCT
4700	4710	4720	4730	4740	4750	4760
GGCTGGATGG	CCTTCCCCAT	TATGATTCTT	CTCGCTTCCG	GCGGCATCGG	GATGCCCGCG	TTGCAGGCCA
CCGACCTACC	GGAAGGGGTA	ATACTAAGAA	GAGCGAAGGC	CGCCGTAGCC	CTACGGGCGC	AACGTCCGGT
4770	4780	4790	4800	4810	4820	4830
TGCTGTCCAG	GCAGGTAGAT	GACGACCATC	AGGGACAGCT	TCAAGGATCG	CTCGCGGCTC	TTACCAGCCT
ACGACAGGTC	CGTCCATCTA	CTGCTGGTAG	TCCCTGTCGA	AGTTCCTAGC	GAGCGCCGAG	AATGGTCGGA
4840	4850	4860	4870	4880	4890	4900
AACTTCGATC	ATTGGACCGC	TGATCGTCAC	GGCGATTTAT	GCCGCCTCGG	CGAGCACATG	GAACGGGTTG
TTGAAGCTAG	TAACCTGGCG	ACTAGCAGTG	CCGCTAAATA	CGGCGGAGCC	GCTCGTGTAC	CTTGCCCCAAC
4910	4920	4930	4940	4950	4960	4970
GCATGGATTG	TAGGCGCCGC	CCTATACCTT	GTCTGCCTCC	CCGCGTTGCG	TCGCGGTGCA	TGGAGCCGGG
CGTACCTAAC	ATCCGCGGCG	GGATATGGAA	CAGACGGAGG	GGCGCAACGC	AGCGCCACGT	ACCTCGGCCC
4980	4990	5000	5010	5020	5030	5040
CCACCTCGAC	CTGAATGGAA	GCCGGCGGCA	CCTCGCTAAC	GGATTCACCA	CTCCAAGAAT	TGGAGCCAAT
GGTGGAGCTG	GACTTACCTT	CGGCCGCCGT	GGAGCGATTG	CCTAAGTGGT	GAGGTTCTTA	ACCTCGGTTA
5050	5060	5070				
CAATTCTTGC	GGAGAACTGT	GAATGCGCAA	ACCAACC			
GTTAAGAACG	CCTCTTGACA	CTTACGCGTT	TGGTTGG			

Fig. 5(contd)

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Fig. 6

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Fig. 7

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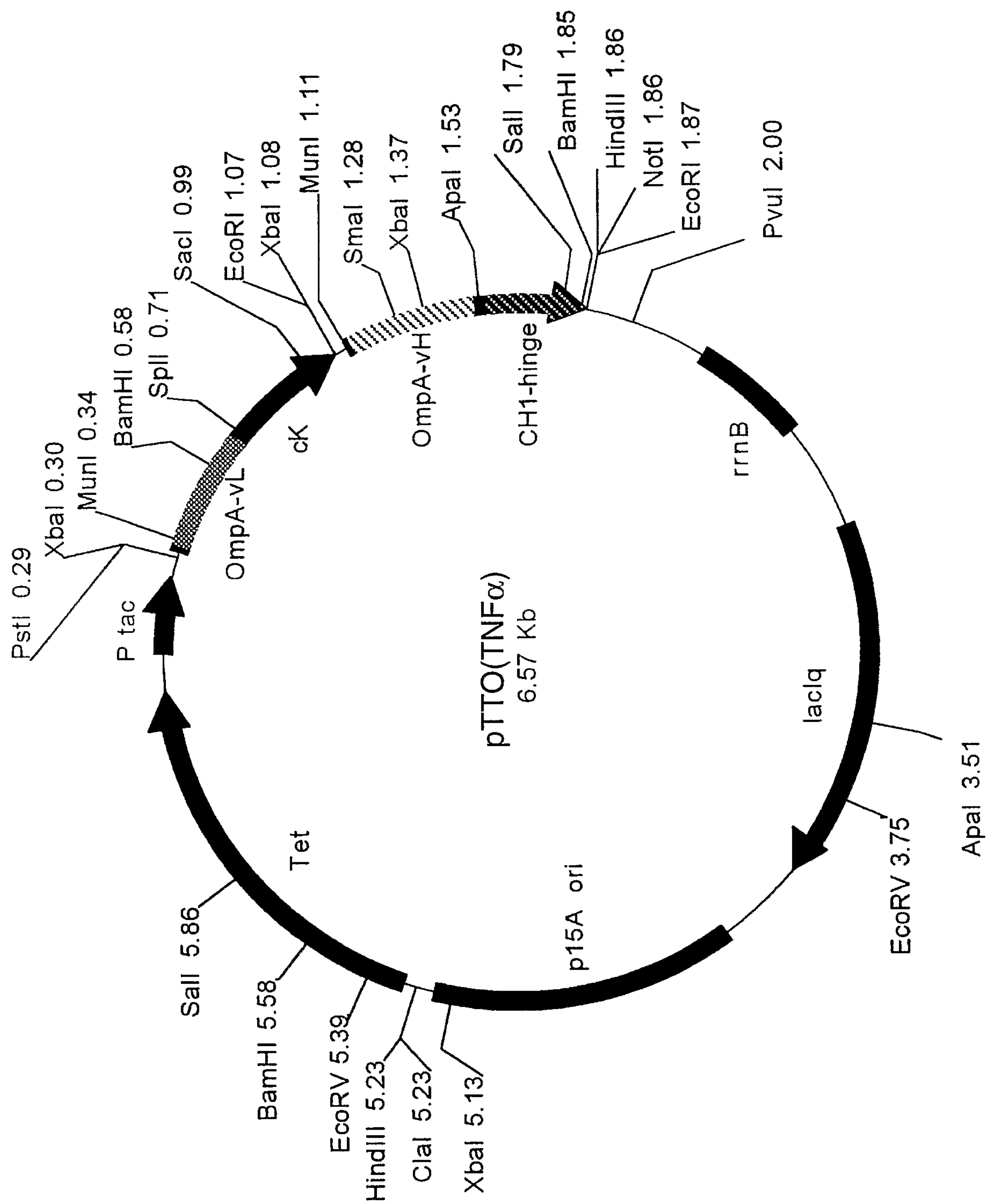


Fig. 8

Fig. 9

OLIGONUCLEOTIDE CASSETTES ENCODING DIFFERENT INTERGENIC SEQUENCES FOR E. Coli Fab' EXPRESSION

IGS CASSETTE-1;

Intergenic space = -1

SacI

MunI

G, AGC, TCA, CCA, GTA, ACA, AAA, AGT, TTT, AAT, AGA, GGA, GAG, TGT, TAATG, AAG, AAG, ACT, GCT, ATA, GCA, ATT, G

S S P V T K S F N R G E C * M K K T A I A I
End of c-Kappa sequence -> Start of OmpA sequence ->

IGS CASSETTE-2;

Intergenic space = +1

G, AGC, TCA, CCA, GTA, ACA, AAA, AGT, TTT, AAT, AGA, GGG, GAG, TGT, TAA AATG, AAG, AAG, ACT, GCT, ATA, GCA, ATT, G

S S P V T K S F N R G E C * M K K T A I A I

IGS CASSETTE-3;

Intergenic space = +13

G, AGC, TCA, CCA, GTA, ACA, AAA, AGC, TTT, AAT, AGA, GGA, GAG, TGT, TGA GGAGGAAAAAAATG, AAG, AAA, ACT, GCT, ATA, GCA, ATT, G

S S P V T K S F N R G E C * M K K T A I A I

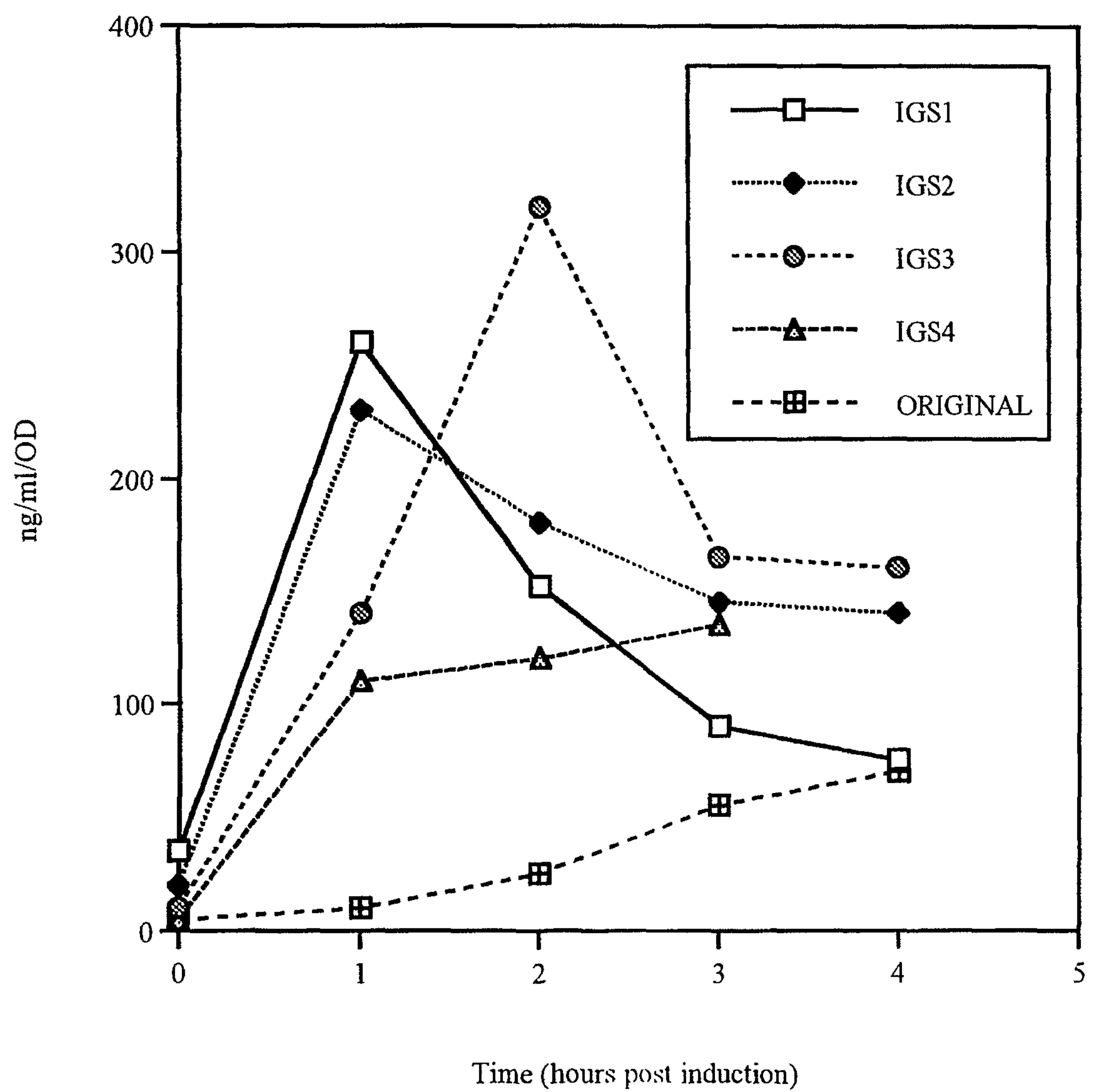
IGS CASSETTE-4;

Intergenic space = +13

G, AGC, TCA, CCA, GTA, ACA, AAA, AGT, TTT, AAT, AGA, GGA, GAG, TGT, TGA CGAGGATTATATAATG, AAG, AAA, ACT, GCT, ATA, GCA, ATT, G

S S P V T K S F N R G E C * M K K T A I A I

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Fig. 10**Periplasmic Fab' accumulation - IGS variants**

Construction of g163 Fab' IGS variants

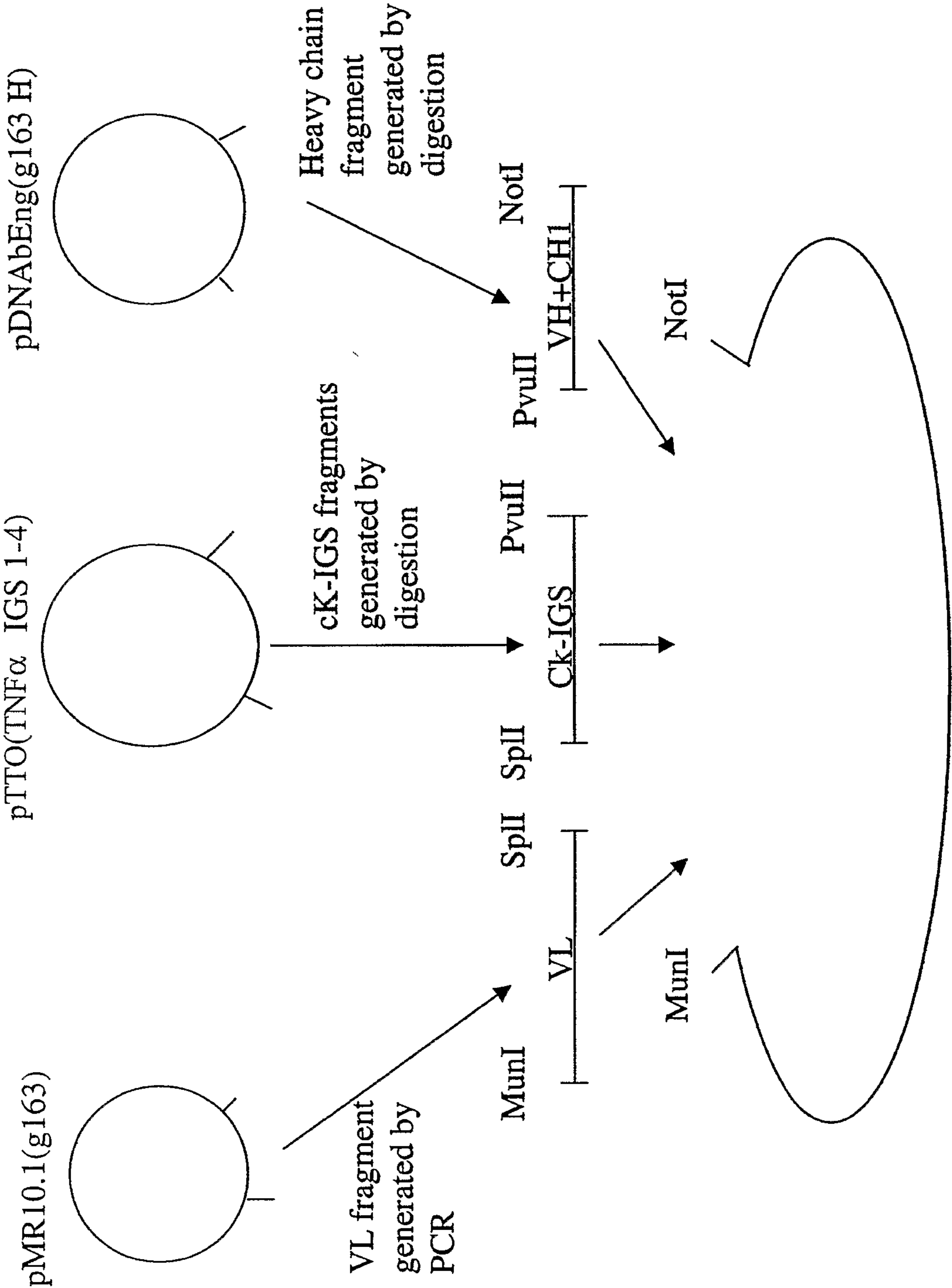
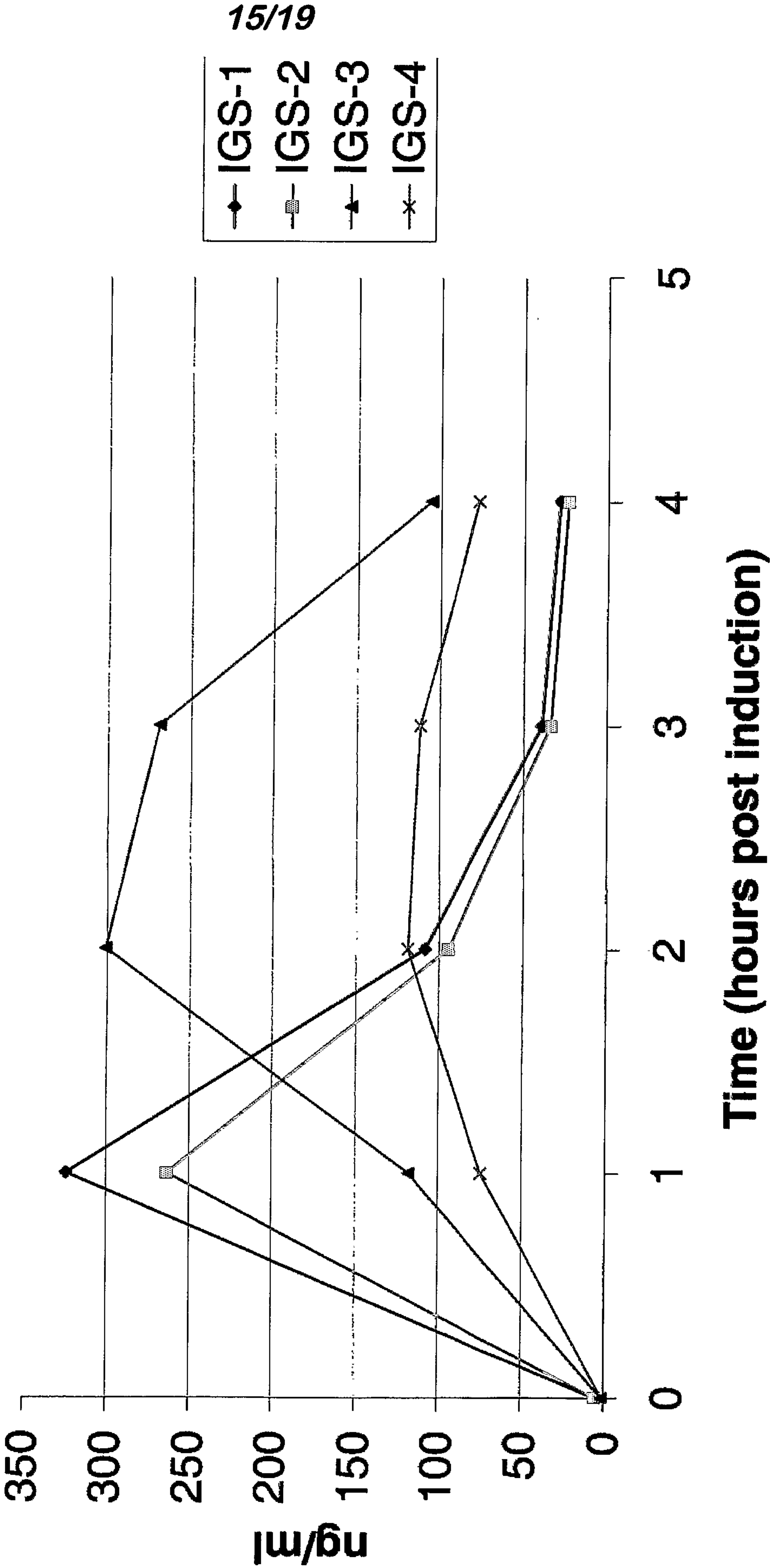


Fig. 11

Fig. 12
g163 Fab' expression (shake flask)



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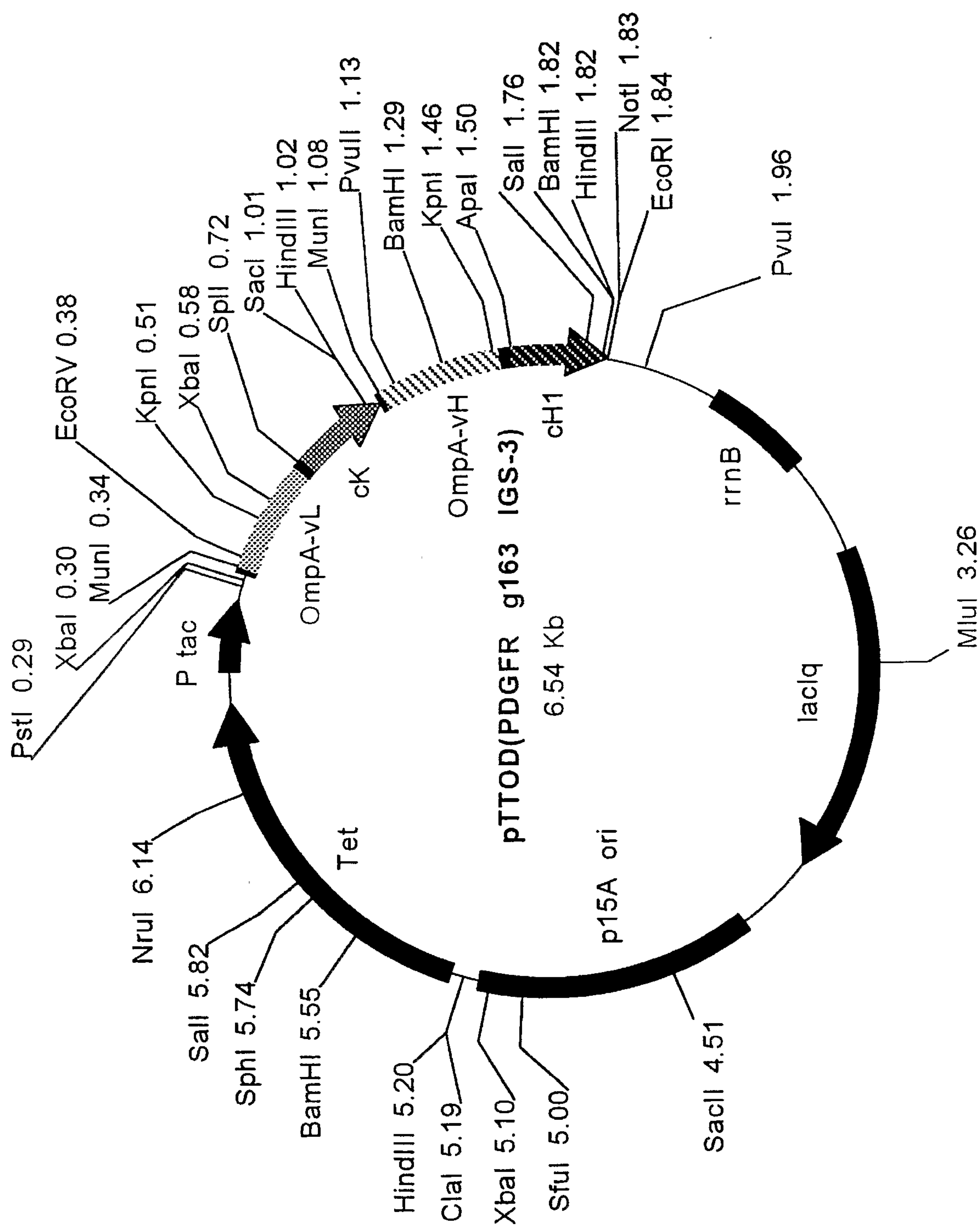


Fig. 13

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Fig. 14
Effect of IGS sequence on g165 Fab' titre in
shake flask culture

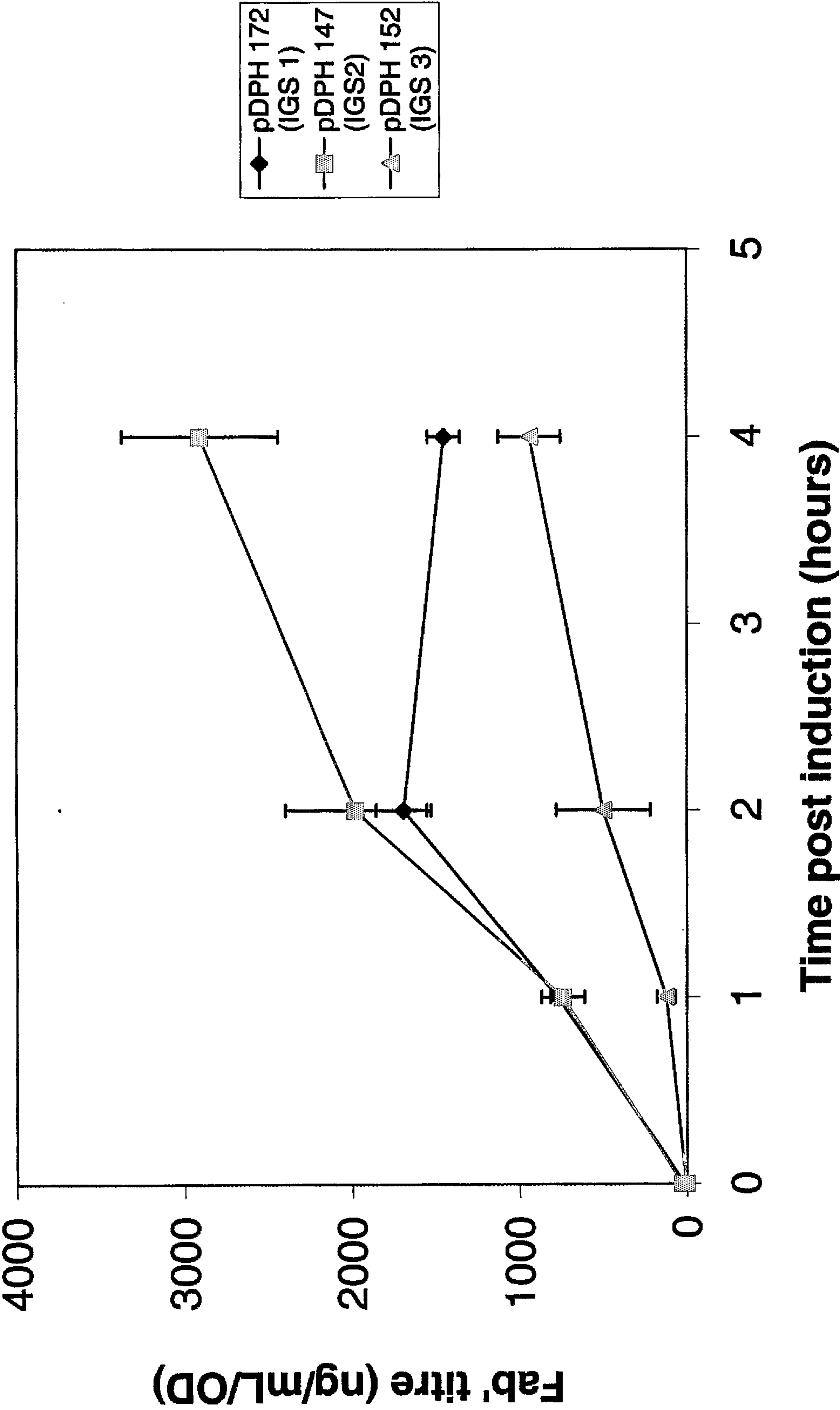


Fig. 15
pTTOD(g165) Fermenter Yields

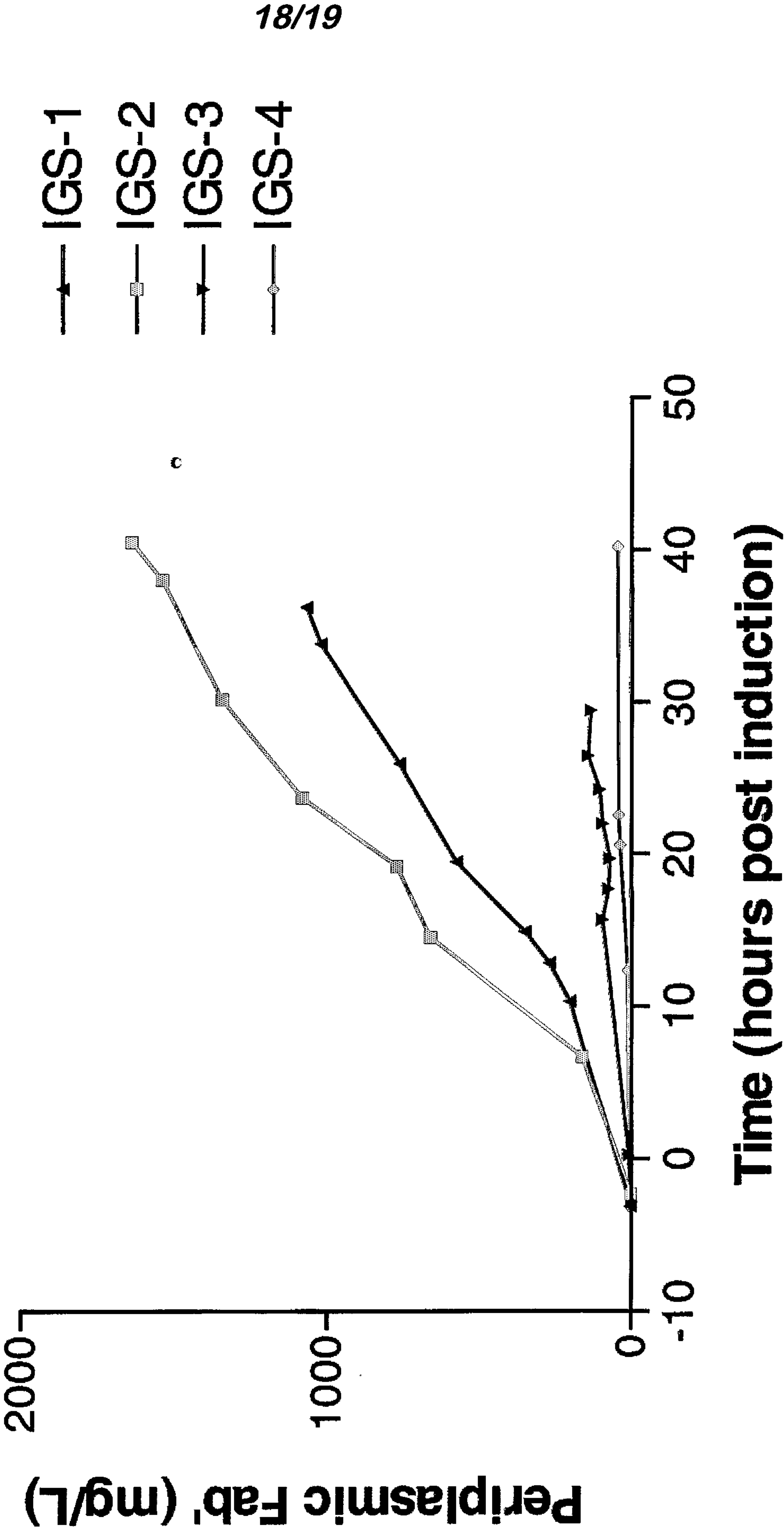


Fig. 16
Comparison of pTTO(gA33 IGS-2) and pTTO(gA33 IGS-3) Fab' expression in 1L fermentation

