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(72) Hageman, Robert, US
(72) Eisenberg, Stephen P., US
(72) Dripps, David, US
(72) Evans, Ronald, US
(72) Cudny, Henryk, US
(72) Thompson, Robert C., US
(73) AMGEN INC., US

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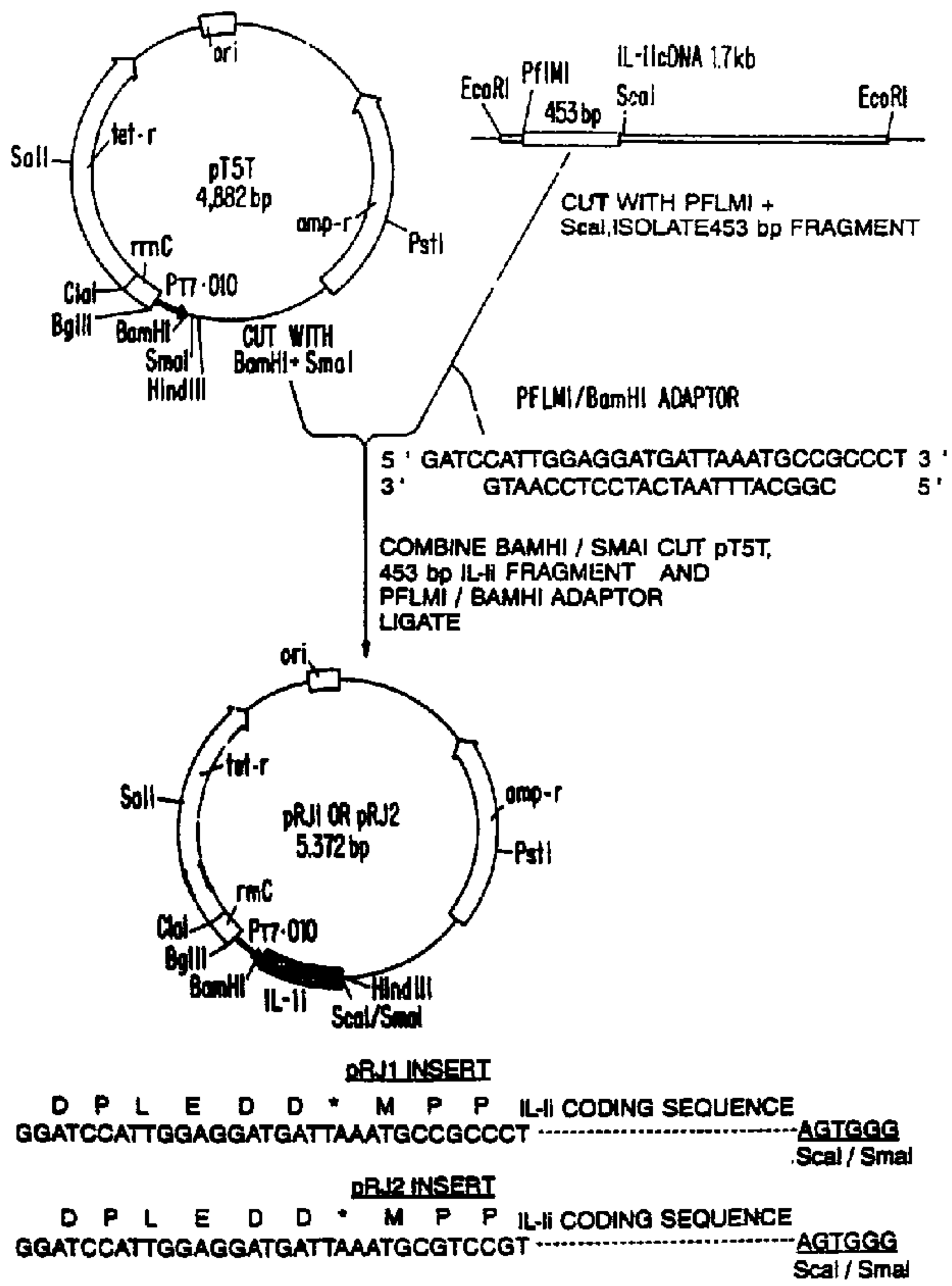
(54) **PRODUCTION D'UN INHIBITEUR RECOMBINANT DE L'INTERLEUKINE-1 HUMAINE**

(54) **PRODUCTION OF RECOMBINANT HUMAN INTERLEUKIN-1 INHIBITOR**



(57) Procédé de production de quantités commerciales d'inhibiteur d'interleukine-1 hautement purifiée (IL-1i) à partir d'un hôte recombiné. Un hôte de E. coli recombiné préféré utilisé dans ce procédé est également décrit.

(57) A method for the production of commercial quantities of highly purified interleukin-l inhibitor (IL-1i) from a recombinant host is disclosed. A preferred recombinant E. coli host for sue in this method is also disclosed.

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(71) Applicant: SYNERGEN, INC. [US/US]; 1885 33rd Street, Boulder, CO 80301 (US).

(72) Inventors: HAGEMAN, Robert ; 3784 Moffit Court, Boulder, CO 80302 (US). EISENBERG, Stephen, P. ; 2325 Panorama Ave., Boulder, CO 80302 (US). DRIPPS, David ; 3335 Moorhead Ave., Boulder, CO 80303 (US). EVANS, Ronald ; 404 W. Eisenhower, Louisville,CO 80027 (US). CUDNY, Henryk ; 4462 Hamilton Court, Boulder, CO 80302 (US). THOMPSON, Robert, C. ; 1820 Lehigh Street, Boulder, CO 80303 (US).

(74) Agents: PATTERSON, Herbert, W. et al.; Finnegan, Henderson, Farabow, Garrett & Dunner, 1300 I Street, N.W., Washington, DC 20005-3315 (US).

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(54) Title: PRODUCTION OF RECOMBINANT HUMAN INTERLEUKIN-1 INHIBITOR

(57) Abstract

A method for the production of commercial quantities of highly purified interleukin-1 inhibitor (IL-li) from a recombinant host is disclosed. A preferred recombinant *E. coli* host for sue in this method is also disclosed.

* (Referred to in PCT Gazette No. 06/1992, Section II)

PRODUCTION OF RECOMBINANT HUMAN INTERLEUKIN-1 INHIBITOR

BACKGROUND OF THE INVENTION

In the recombinant-DNA field, many proteins have been prepared in the laboratory in an amount suitable for research purposes. However, even though techniques to produce research quantities of these proteins have been optimized, these laboratory production and purification processes are often inadequate to produce commercial quantities of the desired protein which is of a quality sufficient to be used as a human pharmaceutical.

In order to produce commercial quantities of a given protein of an appropriate quality, unique fermentation, isolation, and purification techniques are often required. Moreover, the combination of the techniques and the order in which they are practiced often affect the amount of the protein recovered and the purity of the final product.

As described in Canadian patent application 600,825 filed May 26, 1989, and which claims priority from US application 266,531, a unique protein named human interleukin-1 inhibitor has been isolated and the DNA encoding it has been sequenced. This patent application also describes methods for producing recombinant human interleukin-1 inhibitor, hereinafter referred to as "IL-1i," in laboratory quantities in transformed organisms useful in laboratory methods. The term IL-1i refers to various IL-1i species including, non-exclusively, IL-1i X, IL-1iα and IL-1β. Likewise, the term "DNA encoding IL-1i" encompasses DNA encoding various species of IL-1i. Complementary DNA sequences as well as sequences which cross hybridize with the sequence are also contemplated. However, these methods did not result in production of commercial quantities of IL-1i of a quality suitable for administration to humans.

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The present inventors have found certain combinations of fermentations, isolation, and purification techniques which are capable of producing commercial quantities of highly purified IL-li. These methods are described in this application. As used herein, the term "commercial quantities" is intended to mean at least several to tens to hundreds of grams of highly purified product obtained from each 100 liters of fermentation broth. By "highly purified product" is meant a material of sufficient purity to be administered to humans. In a preferred embodiment, "highly purified product" has less than 5 E.U. per dose of endotoxin and less than 0.0025% contamination by E. coli protein.

SUMMARY OF THE INVENTION

It is an object of an aspect of the present invention to provide a method for the production of commercial quantities of recombinant human interleukin-1 inhibitor. This object is achieved by the methods described herein.

In order to achieve these objects, an improved strain for the production of IL-li is described herein. That strain, named SGE90, is capable of producing at least 50 grams of highly purified IL-li per 100 liters of fermentation broth when used in the methods described herein.

In accordance with an aspect of the invention, a method for the production of interleukin-1 inhibitor (IL-li) comprises:

(1) fermentation of Escherichia coli comprising a plasmid containing a DNA encoding IL-li;

(2) cell processing, including:

(a) cell recovery

(b) lysis, and

(c) clarification of the lysates;

(3) a first ion exchange step using a cationic resin;

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(4) a second ion exchange step using a anionic resin; and

(5) subsequent processing steps including concentration and diafiltration.

A third ion exchange step may be optionally added to achieve even greater product purity.

In a preferred embodiment, the fermentation step is carried out in microorganisms, particularly E. coli, while the first ionic exchange step is conducted with a column filled with the cation exchange resin S-Sepharose. Also in the preferred embodiment, the second ion exchange step is conducted with a column filled with an anion exchange resin, preferably Q-Sepharose®. If the optional third ion exchange step is added, a column filled with a cation exchange resin, preferably S—Sepharose®, is used.

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only, and are not restrictive of the invention as claimed. The accompanying drawings, which are incorporated in and constitute a part of this specification, illustrates various embodiments of the invention and, together with the description, serve to explain the principles of the invention.

In accordance with another aspect of the invention, a transformed E. coli host comprising at least one plasmid containing the plasmid pDD6 which is capable of producing commercial quantities of highly purified IL-li. In accordance with a further aspect of the invention, the plasmid is pDDS.

<u>BRIEF DESCRIPTION OF THE DRAWING</u>

Figure 1 depicts the construction of pRJ1 and pRJ2 as set forth in Example 1.

<u>DESCRIPTION OF THE PREFERRED EMBODIMENTS</u>

Reference will now be made in detail to the presently preferred embodiments of the invention, which,

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together with the following examples, serve to explain the principles of the invention.

As noted above, the present invention relates to a process for the production of commercial quantities of IL-li. As used herein, the term "commercial quantities" is intended to mean that at least several to tens to hundreds of grams of highly purified product from each 100 liters of fermentation broth are produced.

As noted previously, one of the preferred methods for production of commercial quantities of IL-li described herein includes the following steps:

(1) fermentation of *e. coli* comprising a plasmid containing a DNA encoding IL-li;

(2) cell processing, including:

(a) cell recovery,

(b) lysis, and

(c) clarification of the lysates;

(3) a first ion exchange step;

(4) a second ion exchange step;

(5) the final processing steps including concentration and diafiltration.

An optional third ion exchange step may also be conducted. Such an optional step would be performed immediately after the second ion exchange step.

The fermentation and cell processing steps for use in E. coli contemplated in this invention include those routinely known to one of ordinary skill in the art. Preferred embodiments of these steps are set forth in the examples which follow. However, any comparable procedures may be inserted in the place of those preferred procedures set forth below.

The process for the production of commercial quantities of IL-li utilizes a first ion exchange column. As noted previously, the preferred column (described in Example 2), is filled with cationic S-Sepharose® resin. Other interchangeable resins may also be used, including but not limited to resins such as SP-C25 Sephadex®, CM

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Sephadex®, CM Sepharose®, or CM cellulose®. A second ion exchange column is then used for further purification of the IL-li. As noted above, in the preferred embodiment Q-Sepharose® is used as an anion exchange resin in this column. In addition, other comparable resins including but not limited to resins such as DEAE-Sepharose®, Q-Sephadex® or DEAE-cellulose® may be employed.

In one embodiment of the present invention, a third ion exchange step is included immediately after the second ion exchange step. In this optional third step, a cation exchange column is used. This column preferably contains S-Sepharose resin, however other interchangeable resins may also be used. Such other resins include, but are not limited to, SP-25 Sephadex®, CM Sephadex®, CM Sepharose®, CM Cellulose® or CM Toyopearl®.

Following these steps, the final process steps are undertaken. These include a concentration step, if desired, and diafiltration of the IL-li. The parameters of these steps are routinely known to those of ordinary skill in the art, in light of the teachings found in the examples which follow.

Important to the operation of this process is a suitable set of quantitative analytical tools to evaluate yield and purity.

As described in greater detail in the procedures in Example 4, the assays which have been developed for these purposes include a reverse phase HPLC (RP-HPLC) assay, an ion exchange HPLC (IE-HPLC), an SDS-PAGE assay, a size exclusion assay, a trypsin peptide map, and an assay for biological activity. When tested in the first four of these assays, the highly-purified IL-li produced by the present methods is greater than 90% pure. Preferably, when tested in the IE-HPLC, the highly purified IL-li is at least 98% pure for both Mono Q and Mono S columns. Preferably, when tested in the SDS-PAGE assay, the highly purified IL-li is at least 99.5% pure, and is at least 98% pure when tested in size exclusion assay. The trypsin

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peptide map of the highly purified IL-li matches the pattern theoretically expected. The highly purified IL-li demonstrates inhibition of IL-1 in the bioassay.

The following examples are provided to illustrate certain preferred embodiment of the present invention. These examples are intended to be illustrative only and are not intended to limit the scope of the claims appended hereto.

EXAMPLE 1

1. Transfer of the IL-li cDNA from a lambda phage to a Bluescript® plasmid cloning vector.

The lambda phage GT10-IL-li-2a (ATCC #40488) was digested with EcoRI and the 1.7 kb fragment carrying the IL-li cDNA was purified by gel electrophoresis'. This fragment was ligated to EcoRI-digested Bluescript SKM13-(Stratagene), resulting in the plasmid BS-IL-li#2.

2. Development of an IL-li expression vector using the "T7' system

A. Description of pT5T.

The T7 expression vector used for IL-li production is called pT5T. It is essentially the same as pJU1003 [Squires, et al., J. Biol. Chem. (19B8) 31:16297–16302], except that there is a short stretch of DNA between the unique Bgl2 site 5' to the T7 promoter and the Clal site in the tetracycline resistance gene. The sequence of this DNA is:

ATCGATGATA AGCTGTCAAA CATGAGAATT GAGCTCCCCG GAGATCCTTA GCGAAAGCTA
Clal
AGGATTTTTT TTAGATCT
Bgl2

The vector was linearized with BamHl and Sinai restriction enzymes. The plasmid BS-IL-li#2 was digested with PflM1 and Scal and the 453 bp fragment carrying the sequence coding for amino acids 4 to 152 of the mature IL-li gene along with the termination codon and 3 bp of the 3' untranslated region was purified by polyacrylamide gel electrophoresis. Oligonucleotides with the sequences:

5' GATCCATTGGAGGATGATTAAATGCCGCCCT 3'
3' GTAACCTCCTACTAATTTACGGC 5'

were synthesized, phosphorylated at their 5' ends and annealed. These oligonucleotides contain sequences essential for the translational coupling of the T7 Φ10 gene to the IL-li gene. A mixture containing the annealed

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oligonucleotides, the linearized vector fragment and the 453 bp IL-1i gene fragment was treated with T4 DNA ligase and then used to transform the E. coli strain JM109 (See Figure 1).

B. Mutagenesis of IL-1i.

Once a plasmid was isolated and shown to have the correct sequence, it was designated pRJ1. pRJ1 carries sequences coding for a variant of the IL-1i protein. The amino-terminal sequence of this variant is Met-Pro-Pro-Ser-... rather than Arg-Pro-Ser-... which is the amino-terminal sequence of the natural human protein. The aim here was to express a protein that is as close as possible to the natural protein, and that was done by mutagenizing the DNA coding for the IL-1i protein such that it codes for Met-Arg-Pro-Ser-..., as follows. The gene for IL-1i in pRJ1 was removed by digesting the plasmid at the unique BamH1 and Pst1 sites. The 1375 bp fragment was cloned between the BamH1 and Pst1 sites of M13 mp 19 and designated M13-IL-1i1. Oligonucleotide site directed mutagenesis was performed on isolated single stand DNA of M13-IL-1i1 according to the procedure described in the BioRad Mutagene mutagenesis kit. The mutagenic oligonucleotide sequence is given below, along with the corresponding amino-terminal amino acid sequence of the mutated IL-1i:

5′ TGATTAAATGCGTCCGTCTGGGAG 3′

M R P S G R

This mutagenesis produced M13-IL-1i2 which differs from M13-IL-1i1 in that the IL-1i protein encoded on this plasmid has the desired amino-terminal sequence and that the codons for Arg and Pro are those used preferably by E. coli.

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C. Expression of IL-1i protein.

The mutagenized IL-1i gene was then transferred back into pT5T using the same procedure as described above. This second expression plasmid is designated pRJ2. pRJ2 was transformed into the *E. coli* strain BL21 (DE3) for expression. This strain [described in Studier and Moffat *J. Mol. Biol.* (1986) 189:113-130] contains the T7 RNA polymerase gene under control of the IPTG inducible lac promoter on a nonexcisable lysogenic lambda bacteriophage. High level expression of rIL-1i was achieved by growing the cells [BL21(DE3)pRJ2] in Luria broth with 15 µg/ml tetracycline up to a cell density corresponding to an A_{600} of 0.8. IPTG was added to a final concentration of 1.0 mM and the cells were allowed to grow for four hours. The cells were harvested by centrifugation and the rIL-1i was purified from the soluble cell lysate by standard protein chemistry techniques.

3. Development of an IL-1i expression vector using the "tac promoter" system.

A. Preparation of pDD1.

The plasmid pJU1003 (Squires, et al.) was cut with Hind3 and BamH1 and fused to a synthetic Human Pancreatic Secretory Trypsin Inhibitor (HPSTI) gene whose sequence is:

EcoR1

GAATTCGATA TCTCGTTGGA GATATTCATG ACGTATTTTG GATGATAACG
CTTAAGCTAT AGAGCAACCT CTATAAGTAC TGCATAAAAC CTACTATTGC

Pvu 1

AGGCGCAAAA AATGAAAAAG ACAGCTATCG CGATCGCAGT GGCACTGGCT
TCCGCGTTTT TTACTTTTTC TGTCGATAGC GCTAGCGTCA CCGTGACCGA

GGTTTCGCTA CCGTAGCGCA GGCTGACTCT CTGGGTCGTG AAGCTAAGTG
CCAAAGCGAT GGCATCGCGT CCGACTGAGA GACCCAGCAC TTCGATTCAC

CTACAACGAA CTGAACGGTT GCACTAAAAT CTACAACCCG GTATGTGGTA
GATGTTGCTT GACTTGCCAA CGTGATTTTA GATGTTGGGC CATACACCAT

CCGACGGTGA CACCTACCCG AACGAATGCG TGCTGTGCTT CGAAAACCGT
GGCTGCCACT GTGGATGGGC TTGCTTACGC ACGACACGAA GCTTTTGGCA

AAACGTCAGA CCTCCATCCT GATCCAGAAA TCTGGTCCGT GCTAAGTCGAC
TTTGCAGTCT GGAGGTAGGA CTAGGTCTTT AGACCAGGCA CGATTCAGCTG

Hind 3
CCTGCAGAAG CTT...
GGACGTCTTC GAA...

by cutting the HPSTI gene with PvuI and Hind3 and ligating the PvuI/Hind3 fragment to the BamHI-Hind3 cut plasmid using a double stranded oligonucleotide adaptor with the sequence:

5' GAT CCG ATC TTG GAG GAT GAT TAA ATG AAA AAG ACC GCT ATC
3' GC TAG AAC CTC CTA CTA ATT TAC TTT TTC TGG CGA TAG

GCC AT 3'
CGG 5'

This synthetic HPSTI gene codes for a protein consisting of the signal (or leader) peptide for the *E. coli ompA* protein fused to the mature HPSTI protein. Thus, the purpose of this manipulation was to incorporate sequences coding for the *ompA* signal peptide into pJU1003, for work described below. The resulting plasmid is pDD1. Plasmid pDD1 was digested with BstX1 and Hind3.

B. Construction of pDD3. Addition of *E. coli* translational signals to the IL-1i cDNA.

The plasmid pT5T (described above) was cut with BamH1 and Sma1. The plasmid BS-IL-1i#2 was cut with the PflM1 and Sca1, releasing a fragment 453 bp in length which codes for a portion of the IL-1i protein (see above). The

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BamH1/Sma1 cut pT5T, the 453 bp IL-1i fragment, and an oligonucleotide adaptor with the sequence:

```
                BstX1
5'    GA TCC ATC GCA GTG GCA CTG GCT GGT TTC GCT ACC GTA GCG
3'         G TAG CGT CAC CGT GAC CGA CCA AAG CGA TGG CAT CGC

CAG GCC CGT CCC T  3'
GTC CGG GCA G      5'
```

were fused to produce the plasmid pDD2. Plasmid pDD2 was cut with BstX1 and Hind3, releasing a 499 bp fragment which codes for all of the IL-1i protein and a portion of the ompA signal sequence. This 499 bp fragment was fused to BstX1/Hind3 cut pDD1, resulting in the plasmid pDD3.

C. <u>Construction of pT3XI-2. Modification of pKK223-3.</u>

The starting plasmid for this construction was plasmid pKK223-3 purchased from Pharmacia. Plasmid pKK223-3 carries a partial gene for tetracycline resistance. This non-functional gene was replaced by a complete tetracycline resistance gene carried on plasmid pBR322. Plasmid pKK223-3 was digested completely with Sph1 and partially with BamH1. A 4.4 kilobase pair fragment was gel purified and combined with a synthetic adaptor with the sequence:

```
5'  GATCTAGAATTGTCATGTTTGACAGCTTATCAT      3'
3'      ATCTTAACAGTACAAACTGTCGAATAGTAGC    5'
```

and a 539 base pair fragment of DNA from a Cla1 - Sph1 digest of the tetracycline resistance gene of pBR322 (PL Biochemicals, 27-4891-01). The resulting plasmid was designated pCJ1.

Next a Xhol linker purchased from New England Biolabs was inserted into plasmid pCJ1's PvuII site to form plasmid pCJX-1. This insertion disrupts the <u>rop</u> gene which controls plasmid copy number. An EcoR1 fragment containing the lac1 gene was purified from plasmid pMC9 [Calos, et al., Proc. Natl. Acad. Sci. USA (1983), 80:3015-3019] then inserted into the Xhol site with Xhol to EcoR1 adaptors having the sequence:

5′	TCGAGTCTAGA	3′
3′	CAGATCTTTAA	5′

The polylinker sequence between the EcoR1 and Pst1 sites in plasmid pKK223-3 was next replaced with a polylinker sequence shown here:

5′	AATTCCCGGG TACCAGATCT GAGCTCACTA GTCTGCA	3′
3′	GGGCCC ATGGTCTAGA CTCGAGTGAT CAG	5′

The plasmid vector so obtained is designated pCJXI-1.

Finally, the tetracycline resistance gene was replaced with a similar gene which had the recognition sites for restriction enzymes Hind3, BamH1, and Sal1 destroyed by bisulfite mutagenesis. The following procedure was used to mutate the tetracycline resistance gene of pBR322. Plasmid pBR322 was cut with Hind3, then mutagenized with sodium bisulfite [Shortle and Nathans, Proc. Natl. Acad. Sci. USA (1978) 5:2170-2174]. The mutagenized DNA was ligated to form circular DNA, then cut with Hind3 to linearize any plasmid that escaped mutagenesis. E. coli JM109 [Yanish-Perron et al., Gene (1985) 33:103-119] was transformed with the plasmid, then plated on selective media. Plasmids were isolated from tetracycline resistance colonies and checked for loss of the Hind3 site in the tetracycline resistance gene. The successfully mutated plasmid was designated pT1. A similar procedure was followed to mutagenize the BamH1 site in pT1, yielding plasmid pT2. Plasmid pT2 in turn was mutagenized to remove the Sal1 site, forming plasmid pT3. A Cla1-BsmH1 fragment of pT3 carrying the mutated tetracycline resistance gene was isolated and used to replace the

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homologous fragment of pCJXI-1 to form pT3XI-2. The mutated tetracycline resistance gene still encodes a functional protein.

D. Formation of pT3XI-2-Φ10TC3FGFsyn. Preparing the tac promoter vector for IL-1i.

Initially a "gene" for basic Fibroblast Growth Factor (FGF) was synthesized. This "gene" codes for the same sequence as that reported for FGF by Sommer et al., but uses the codons that are found preferably in highly expressed genes in *E. coli*. The structure of this is such that the coding portion is preceded by a translational coupler sequence (see Squires, et al., 1988) to ensure efficient initiation of translation.

The FGF synthetic gene was first inserted into M13mp18 between the EcoR1 and Hind3 sites and sequenced. The structure this gene is:

```
AATTCAGGA TCCGATCGTG GAGGATGATT AAATGGGTAC CATGGCTGCT GGCTCCATCA
    GTCCT AGGCTAGCAC CTCCTACTAA TTTACCCATG GTACCGACGA CCGAGGTAGT
EcoRI BamHI       RBS            FGFstart
      Translational Coupler 3

CTACCCTGCC GGCACTGCCG GAAGACGGTG GCTCCGGTGC TTTCCCGCCG GGCCACTTCA
GATGGGACGG CCGTGACGGC CTTCTGCCAC CGAGGCCACG AAAGGGCGGC CCGGTGAAGT

AAGACCCGAA ACGTCTGTAC TGTAAAAACG GTGGCTTCTT CCTGCGTATC CACCCGGATG
TTCTGGGCTT TGCAGACATG ACATTTTTGC CACCGAAGAA GGACGCATAG GTGGGCCTAC

GTCGTGTCGA CGGCGTACGT GAAAAAAGCG ACCCGCACA TCAAACTGCA GCTGCAGGCTG
CAGCACAGCT TGCCGCATGC ACTTTTTTCC TGGGCGTGT AGTTTGACGT CGACGTCCGAC

AAGAACGTG GTGTTGTATC TATCAAAGGC GTTTGCGCAA ACCGTTACCT GGCTATGAAAG
TTCTTGCAC CACAACATAG ATAGTTTCCG CAAACGCGTT TGGCAATGGA CCGATACTTTC

AAGACGGTC GTCTGCTGGC TAGCAAATGT GTAACTGACG AATGTTTCTT CTTCGAACGTC
TTCTGCCAG CAGACGACCG ATCGTTTACA CATTGACTGC TTACAAAGAA GAAGCTTGCAG
```

TGGAAAGCA ACAACTACAA CACCTACCGT TCTCGTAAAT ACACTTCTTG GTACGTTGCTC
ACCTTTCGT TGTTGATGTT GTGGATGGCA AGAGCATTTA TGTGAAGAAC CATGCAACGAG

TGAAACGTA CCGGCCAGTA CAAACTGGGT TCCAAAACTG GCCCGGGTCA GAAAGCAATCC
ACTTTGCAT GGCCGGTCAT GTTTGACCCA AGGTTTTGAC CGGGCCCAGT CTTTCGTTAGG

TGTTCCTGC CGATGAGCGC TAAATCTTAA ACTAGTA
ACAAGGACG GCTACTCGCG ATTTAGAATT TGATCATTCGA
FGFstop HinDIII

Relevant features of the gene are highlighted.

It was then isolated by digestion with BamH1 and Hind3 and inserted into BamH1/Hind3 cut pJU1003 (Squires, et al., 1988) yielding pJU1003-synFGF. This plasmid was cut with Xbal and Hind3 and the Xbal/Hind3 fragment carrying the FGF gene was isolated. This fragment was ligated into pT3Xl-2 cut with EcoR1 and Hind3, using an EcoR1-Xbal linker:

5′ pAAT TCC ACA ACG GTT TCC CT 3′
3′ GG TGT TGC CAA AGG GAG ATCp 5′

The new plasmid is designated pT3XI-2-Φ1OTC3FGFsyn.

E. Formation of pDD4. Inserting IL-1i into a tac promoter vector.

pT3XI-2-Φ1OTC3FGFsyn was cut with BamH1 and Hind3, which resulted in the linearization of the 7.4 kb expression vector and the release of the insert DNA. The DNA was then cut with Ncol and Smal, which further fragmented the insert DNA. pDD3 was digested with BamH1 and Hind3 and the 546 bp IL-1i fragment was gel purified and fused with the BamH1/Hind3-cut pT3XI-2-Φ1OTC3FGFsyn 7.4 kb vector DNA fragment, resulting in the plasmid pDD4.

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F. Formation of pDD5. Use of E. coli preferred codons.

The plasmid pDD4 carries DNA coding for the *ompA* signal sequence and the full length of the IL-1i protein as it was derived from the original cDNA. Plasmid pDD4 was cut with BamH1 and Spe1, thus releasing a small fragment (170 bp) carrying the sequences for the *ompA* signal peptide and the codons for the first 29 amino acid residues of the IL-1i protein, and the large (7.8 kb) vector fragment. The large BamH1/Spe1 vector fragment was fused to two small fragments of DNA assembled from four synthetic oligonucleotides. The sequences of these fragments are:

```
5'   GAT CCG ATC TTG GAG GAT GAT TAA ATG CGT CCG AGC GGC CGC
3'        GC TAG AAC CTC CTA CTA ATT TAC GCA GGC TCG CCG GCG

   SacI
AAG AGC TCC AAA AT          3'
TTC TCG AGG TTT TAC GTC CG  5'

5'   G CAG GCT TTC CGT ATC TGG GAC GTT AAC CAG AAA ACC TTC
TAC
3'           A AAG GCA TAG ACC CTG CAA TTG GTC TTT TGG AAG
ATG

CTG CGC AAC AAC CAA         3'
GAC GCG TTG TTG GTT GAT C   5'
```

These fragments carry sequences coding for the first 29 residues of the IL-1i protein using *E. coli* preferred codons [according to deBoer and Kastelein in From Gene to Protein: Steps Dictating the Maximal Level for Gene Expression (1986) Davis and Reznikoff, eds. pp. 225-283, Butterworths, NY] and a unique Sac1 site after the sixth codon of IL-1i. The resulting plasmid is called pDD5.

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G. Formation of pDD6. Changes to remove secondary structure in mRNA.

Plasmid pDD5 was digested with BamH1 and Sac1. The large (7.8 kb) vector fragment resulting from this digestion was ligated to a synthetic fragment of DNA:

```
5'   GAT CCG ATC TTG GAG GAT GAT TAA ATG CGA CCG TCC GGC CGT
3'        GC TAG AAC CTC CTA CTA ATT TAC GCT GGC AGG CCG GCA

AAG AGC T     3'
TTC           5'
```

that codes for the first 6 residues of the IL-1i protein, but utilizes codons that prevent the formation of any hairpin loops near the 5′ end of the mRNA, especially involving the "Shine-Dalgarno" sequence or the initiation codon for the IL-1i protein. This resulted in the formation of pDD6 which is the expression vector for production of IL-1i. Plasmid pDD6 was transformed into JM107 to yield the production strain SGE90.

EXAMPLE 2

1. Production of IL-1i from E. coli SGE90 Seed Growth.

Ampules of a culture of SGE90 are prepared to be used for seed as follows. A culture streak is grown on Luria agar supplemented with 15 mg/l tetracycline HCl at 37°C. A single colony is picked and grown in Luria broth supplemented with 15 mg/l tetracycline HCl at 37°C. Growth is monitored by absorbance at 660 nm (henceforth referred to as OD). When the culture reaches about 1 OD it is aseptically centrifuged and resuspended in 20% glycerol:Luria broth (1:1). It is then distributed into ampules (1.5 ml per ampule) and stored at -70°C. Working stocks are made from this cell bank by growing one ampule in Luria broth supplemented with 15 mg/l tetracycline HCl to about 1 OD, then preparing ampules as above.

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The fermentor used is prepared by thawing ampules in 40°C tap water and inoculating 1 ml from the ampule prep into each of two 2 liter flasks containing 0.5 liter of Seed Media (Formula 1). The flasks are incubated for about 8 hours on a shaker at 37°C at 350 rpm. The seed OD reaches about 3-4 by this time.

500 ml of the seed culture is used to inoculate 10 liters of Fermentation Media (Formula 2). This seed tank is then grown at 37°C for 5-6 hours with pH control at 7.0, until the OD reaches approximately 5. The seed tank is then used to inoculate the fermentor.

2. <u>Fermentation.</u>

The fermentation is carried out in 1600 liters of Fermentation Media (Formula 2). Temperature is controlled at 37°C. Dissolved oxygen is maintained at 30% (saturation with air at 3 psig). pH is controlled at 7.0 by the addition of HCl and NaOH as required.

Growth is monitored by OD. At approximately 10 OD synthesis of IL-1i is induced by the addition of Isopropyl-B-D-thiogalactoside (IPTG) to a final concentration of 150 uM. Fermentation is continued until the culture reaches an OD of about 40. Cell yield is about 150 kg solids per 1600 liters fermentation media.

3. <u>Cell recovery and washing.</u>

Cells are recovered using a desludging centrifuge (for example an Alfa Laval BTUX 510) and washed with 150 mM NaCl. Cells are resuspended to approximately 16% solids in 150 mM NaCl and then frozen and stored at -20°C.

4. <u>Cell rupture and debris removal.</u>

Fourteen kg of resuspended cells (about 2.2 kg ·ds) are thawed. EDTA is added to 5 mM and the cells ·th two passes through a high pressure homogenizer.

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The pH is adjusted to 5.5 using 1 M acetic acid. The lysate is diluted to 20±2 liters with water and clarified by centrifugation at 14,000 x G for 20 minutes.

5. First Ion Exchange.

(a) Column Specifications. The column used is an Amicon G300x250 filled with 7.5 liter of S-Sepharose resin (Pharmacia). All solutions are pumped through the column at 500 ml/min.

(b) Column Operation. The following buffer sequence is used for each cycle on the column. Buffer formulas are given in Example 4.

Solution	Formula Number	Volume
Equilibration	3	20 1
Clarified Cell lysate		15-25 1
Equilibration	3	20 1
Salt Gradient Elution*	3/4	40 1
NaOH Wash	5	10 1
Acetic Acid Wash	6	5 1
Storage	7	20 1

*Salt gradient is run from 150-400 mM NaCl.

Eluate is collected by following the absorbance at 280 nm and collecting the peak eluting during the salt gradient. Recovery is about 55 g of IL-1i in about 10 1 of the pooled fractions from 20 1 of clarified cell lysate.

6. Second Ion Exchange.

(a) Diafiltration. The pooled eluate is concentrated if desired using a YM10 membrane (Amicon) and then the salt is removed by diafiltration using 4 volumes of Second ion exchange Equilibration buffer (Formula 8). A precipitate which forms at this step is removed by filtration through 3 uM and 0.22 uM filters.

(b) Column Specifications. The column used is an Amicon G180x250, filled with 5 liters of Q-Sepharose (Pharmacia). All solutions are pumped through the columns at 350 ml/min.

(c) Column Operation. The following buffer sequence is used for each cycle on the column. Buffer formulas are given in Appendix A.

Solution	Formula Number	Volume
Equilibration	8	20 1
Diafiltrate		5-10 1
Equilibration	8	20 1
Salt Gradient Elution*	8/9	40 1
NaOH Wash	5	10 1
Acetic Acid Wash	6	5 1
Storage	7	20 1

*Salt gradient is run from 0 to 100 mM NaCl.

Eluate is collected by following the absorbance at 280 nm and collecting the peak eluting during the salt gradient. Recovery is about 45 g of IL-1i in about 10 1 of the pooled fractions from 7 1 of Diafiltrate 1.

7. Final Processing.

(a) Concentration and Diafiltration. The pooled eluate from the second ion exchange column is concentrated to approximately 6 1 using YM10 membrane (Amicon). The material is then diafiltered against 5 volumes of Diafiltration buffer (Formula 10). Final concentration then takes place to approximately 1-2 1, with a target concentration of 10-30 g/1. The precipitate which forms at this step is removed by filtration through 3 uM and 0.22 uM filters. The final concentrate is then filtered through a 0.22 uM filter into sterile, pyrogen free tubes and stored at -70°C. Recovery is about 80% from the pooled fractions from the second ion exchange column.

EXAMPLE 3

1. Removal of the N-terminal Methionine from E. coli produced IL-1i

IL-1i produced in E. coli has a sequence identical to that of IL-1i-x from human monocytes with the exception that the N-terminus has an additional methionine residue. This residue can be removed by incubating the inhibitor with the exoprotease Aminopeptidase 1 from S. cerevisiae.

10 mg of recombinant IL-1i (from the first S-Sepharose or the Q-Sepharose step of purification) is incubated with 1 mg of Yeast Aminopeptidase 1 purified as described by Change and Smith (J. Biol. Chem. 264, 6979, (1989)), in 50 mM ammonium carbonate pH 8.0 for 6 hours. The desmethionyl IL-1i is purified from the reaction mixture by further S-Sepharose chromatography.

If wished, this step of the production process for desmethionyl can be avoided by expressing the IL-1i in an E. coli which contains the cDNA for yeast Aminopeptidase 1 enzyme in a suitable expression vector. This E. coli should also be unable to express the gene for Aminopeptidase P (Yoshimoto et al. J. Biochem (Tokyo) 104 93 (1988)) since removal of the N-terminal methionine will otherwise lead to removal of the N-terminal arginine.

It will be apparent to those skilled in the art that various modifications and variations can be made in the processes of the present invention. Thus, it is intended that the present invention cover the modifications and variations of these processes provided they come within the scope of the appended claims and their equivalents.

EXAMPLE 4

A. Media and formula recipes

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Formula Number	Step	Name	Components	Conc.
1	Fermentation	Seed Medium	Yeast Extract	5 g/l
			Tryptone	10 g/l
			NaCl	10 g/l
			Antifoam*	0.2 ml/l
			Tetracycline	15 mg/l
			DI Water	Q.S.
		All ingredients except tetracycline are mixed and the pH adjusted to 7.5 with sodium hydroxide. Tetracycline is filter sterilized and added separately.		
2	Fermentation	Fermentation Media	NZ Amine HD	40 g/l
			KH_2PO_4	2 g/l
			$MgSO_4.7H_2O$	1 g/l
			$NaSO_4$	6 g/l
			Sodium Citrate	0.3 g/l
			Glycerol	50 g/l
			Antifoam* ca.	3 ml/l
			Trace minerals**	4 ml/l
			Thiamine HCl	10 ml/l
			Tetracycline HCl	15 mg/l
			DI Water	Q.S.
		All ingredients through antifoam are sterilized together. Trace minerals, thiamine and tetracycline are filter sterilized and added separately.		
		*Added as needed.		
*	Fermentation	Antifoam	Macol 19	750 ml/l
			GE60 antifoam	250 ml/l

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Formula Number	Step	Name	Components	Conc.
**	Fermentation	Trace Minerals	$FeCl_3.6H_2O$	27 g/l
			$ZnCl_2$	1.3 g/l
			$CoCl_2.6H_2O$	2 g/l
			$Na_2MoO_4.6H_2O$	2 g/l
			$CaCl_2.2H_2O$	2.5 g/l
			$CuCl_2.2H_2O$	1.27 g/l
			$MnCl_2.4H_2O$	3.3 g/l
			H_3BO_3	0.5 g/l
			HCl, conc.	160 ml/l
			DI Water	Q.S.
3	First Ion Exchange	Equilibration	Sodium Acetate	25 mM
			EDTA	1 mM
			NaCl	150 mM
			DI/UF Water	Q.S.
		Adjust pH to 5.5 with 5M Acetic Acid.		
4	First Ion Exchange	Elution/High Salt	Sodium Acetate	25 mM
			EDTA	1 mM
			NaCl	400 mM
			DI/UF Water	Q.S.
		Adjust pH to 5.5 with 5M Acetic Acid.		
5	First/Second Ion Exchange	NaOH Wash	NaOH	0.2 M
			NaCl	1.0 M
			DI/UF Water	Q.S.
6	First/Second Ion Exchange	Acetic Acid Wash	Acetic Acid	10 mM
			DI/UF Water	Q.S.
7	First/Second Ion Exchange	Storage	NaCl	1 M
			DI/UF Water	Q.S.

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Formula Number	Step	Name	Components	Conc.
8	Second Ion Exchange	Equilibration	Histidine	20 mM
			EDTA	1 mM
			DI/UF Water	Q.S.
		Adjust pH to 6.0 using 5M HCl.		
9	Second Ion Exchange	Elution/High Salt	Histidine	20 mM
			EDTA	1 mM
			NaCl	100 mM
			DI/UF Water	Q.S.
		Adjust pH to 6.0 using 5M HCl		
10	Diafiltration	Diafiltration	NaH_2PO_4	10 mM
			EDTA	0.1 mM
			DI/UF Water	Q.S.
		Adjust pH to 7.0 using 5M NaOH.		

B. Reverse-Phase HPLC of IL-1i - Non Reducing Conditions

REVERSE-PHASE HPLC OF IL-1i - NON REDUCING CONDITIONS

HPLC SYSTEM:

Beckman 114 Solvent Delivery Module
Beckman 165 Variable Wavelength Detector
Beckman System Gold Analog Interface Module 406
Beckman System Gold, Personal Chromatograph Software

COLUMN:

Brownlee RP-300 (C8)
(220 mm x 4.6mm, 7 micron)

DETECTOR SETTINGS:

Channel A, 215 nm
Channel B, 280 nm
Range: 0 - 0.05 AUFS

MOBILE PHASE:

A: 0.1% TFA in Water
B: 0.1% TFA in Acetonitrile

GRADIENT CONDITIONS:

Time (min)	Percent B	Duration
0	0	5
5	30	30 (Start Gradient)
35	50	40
75	100	5 (End Gradient)
85	0	5
95	0	End

FLOW RATE:

1.0 ml/min

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SAMPLE PREPARATION:

Dilute sample to 0.1 - 0.5 mg/ml with water.

INJECTION VOLUME:

100 ul

CHEMICALS:

Chemical	Supplier	Cat. No.
TFA	Sigma	T-6508
Acetonitrile, HPLC Grade	Baker	9017-03

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C. MONO Q HPLC OF IL-1i

HPLC SYSTEM:

Beckman System Gold
- Programmable Sovent Module 126
- Scanning Detector Module 167
- Remote Interface Module
- HP Series 1050 Autosampler
- System Gold, Personal Chromatograph Software

COLUMN:

Pharmacia Mono Q HR 5/5

DETECTOR SETTINGS:

280 nm

MOBILE PHASE:

A: 20 mM TRIS, pH 7.5

B: 20 mM TRIS, pH 7.5 + 250 mM NaCl

GRADIENT CONDITIONS:

0% to 100% B in 60 minutes

FLOW RATE:

0.5 ml/min.

SAMPLE PREPARATION:

None

INJECTION AMOUNT:

25 ug

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D. MONO S HPLC OF IL-1i

<u>HPLC SYSTEM:</u>

Beckman System Gold
- Programmable Solvent Module 126
- Scanning Detector Module 167
- Remote Interface Module
- HP Series 1050 Autosampler
- System Gold, Personal Chromatograph Software

<u>COLUMN:</u>

Pharmacia Mono S HR 5/5

<u>DETECTOR SETTINGS:</u>

280 nm

<u>MOBILE PHASE:</u>

A: 25 mM NaAc, pH 5.5 + 1 mM EDTA

B: 25 mM NaAc, pH 5.5 + 1 mM EDTA + 500 mM NaCl

<u>GRADIENT CONDITIONS:</u>

0% to 60% B in 36 minutes

<u>FLOW RATE:</u>

0.5 ml/min

<u>SAMPLE PREPARATION:</u>

None

<u>INJECTION AMOUNT:</u>

25 ug

E. SIZE EXCLUSION HPLC OF IL-1i

HPLC SYSTEM:

Beckman 114 Solvent Delivery Module
Beckman 165 Variable Wavelength Detector
Beckman System Gold Analog Interface Module 406
Beckman System Gold, Personal Chromatograph Software

COLUMN:

Bio-Sil TSK 250 (7.5 mm x 30 cm)

DETECTOR SETTING:

280 nm
Range: 0 - 0.2 AU

MOBILE PHASE:

25mM Na Acetate and 0.5M NaCl, pH 5.5

FLOW RATE:

0.5 mls/min

SAMPLE PREPARATION:

Dilute IL-1i solution with mobile phase to a final concentration of approximately 2 mg/ml

INJECTION VOLUME:

50 ul

A

F. REDUCING SDS PAGE OF IL-1i

GEL PREPARATION:

Follow procedure outlined by Lammli in J. Mol. Biol., 80, 575-599 (1973).

SEPARATING GEL:

Acrylamide	15%
TRIS pH 8.8	375 mM
SDS	0.1%

STACKING GEL:

Acrylamide pH 6.8	5%
SDS	0.1%

SAMPLE PREPARATION:

Sample is diluted 1:1 with Sample Buffer. The samples are then heated for 15 minutes at 65°C, spun and loaded onto the gel.

SAMPLE BUFFER:

TRIS pH 6.8	250mM
SDS	2.5%
2-Mercaptoethanol	5%
Glycerol	12.5%

ELECTROPHORESIS CONDITIONS:

50 V until samples have reached the separating gel. 100V until the bromophenol blue runs out of the gel.

STAINING:

Ethanol	45.4%
Acetic Acid	9.0%
Water	45.5%
Coomassie Brilliant Blue	2.5%

Stain overnight at room temperature with gentle shaking.

DESTAINING:

Methanol	30.0%
Acetic Acid	12.5%
Water	57.5%

Destain overnight or until background is clear at room temperature.

MOLECULAR WEIGHT STANDARDS:

Low Molecular Weight Range (BRL):

Protein	Reported MW
Insulin (A and B)	2,300 and 3,400
Bovine Trypsin Inhibitor	5,200
Lysozyme	14,300
β-Lactoglobulin	18,400
Alpha-Chymotrypsin	25,700
Ovalbumin	43,000

5 ug of the protein mixture is loaded onto the SDS PAGE gel.

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G. TRYPSIN PEPTIDE MAP OF RECOMBINANT HUMAN IL-1i

PROCEDURE:

1. Reagents
   - 1.1 Trypsin sequencing grade; Boehringer Mannheim GmbH.
   - 1.2 Urea ultra pure; BRL.
   - 1.3 Milli-Q water.
   - 1.4 Trifluoroacetic acid; Pierce.
   - 1.5 HPLC grade acetonitrile; J.T. Baker.
   - 1.6 Tris
   - 1.7 $CaCl_2$

2. Equipment
   - 2.1 HPLC system
     Beckman 114 Solvent Delivery Module
     Beckman 165 Variable Wavelength Detector
     Beckman System Gold Analog Interface Module 406
     Beckman System Gold, Personal Chromatograph Software
   - 2.2 Column
     BrowLee RP-300 (C8)
     (220mm x 4.6mm, 7 micron)
   - 2.3 Heating/cooling water bath

3. Solution
   - 3.1 Trypsin; Dissolve 0.1 mg in 0.1 ml of 0.1mM HCl; Store frozen at -20°C, stable for months without loss of activity.
   - 3.2 Urea: 8 M urea in Milli Q water, make fresh daily.
   - 3.3 2M Tris HCl pH 8.0 and 0.1M Tris HCl pH 8.0.
   - 3.4 3mM $CaCl_2$

4. Method

4.1 Denature of IL-1i in 6M urea and 0.1M Tris HCl pH 8.0 final concentration at about 3 mg/ml protein for 10 minutes at 37°C.

4.2 Dilute into a solution of 0.1M Tris HCl pH 8.0 containing 0.3mM $CaCl_2$ (1:2 vol/vol) to give a final concentration of 2M urea.

4.3 Add trypsin solution (solution number 3.1) to give 1% by weight of the protein. Mix well.

4.4 Incubate at 37°C for 1 hr and additional 1% by weight of trypsin is added.

4.5 Stop digest after an additional 3 hrs by freezing at -20°C or by acidification with 10% trifluoroacetic acid, final concentration 0.1%.

4.6 Inject onto the HPLC column.

5. Reverse-phase of peptide fragments produced by trypsin digestion.

5.1 HPLC system and column as in Section 2.

5.2 Detector settings:

Channel A: 215 nm
Channel B: 200 nm
Range: 0-0.5 AU

5.3 Mobile phase:

A: 0.1% TFA in water
B: 0.1% TFA in acetonitrile

5.4 Gradient conditions

Time (min)	Percent B	Duration
0	0	0
5	40	80
85	100	5
95	0	5
120	0	End

5.5 Flow rate

1.0 ml/min

A

5.6 Sample preparation

None

5.7 Injection volume

50 to 100 ul

H. IL-1i Bioassay.

The assay for IL-1 inhibitor is based on an IL-1 assay developed by S. Nakai, K. Mizuno, M. Kaneta and Y. Hirai. (Biochem. Biophys. Res. Comm. 154:1189-1196. 1988). The principle of this assay is that prolonged exposure to IL-1 is cytotoxic to the human melanoma cell line A375. The cytotoxicity is mediated via the IL-1 receptor. IL-1i antagonizes this cytotoxicity in a dose dependent manner by competing with IL-1 for binding to the IL-1 receptor. The level of toxicity can be quantitated by staining the live cells with crystal violet, extracting the stain from the cells by overnight incubation in 100% ethanol, and measuring the optical density of the extracted stain with a spectrophotometer. The rationale for the use of the A375 melanoma cell bioassay is that it is a simple and direct method for measuring both IL-1 and IL-1i activity. Most other assays that have been described in the literature depend on the ability of IL-1 to activate other products, such as prostaglandin E2 and lactic acid in fibroblasts, and interleukin-2 in T-cells. These secondary products are then measured in order to determine the level of IL-1 present. Although all of these IL-1 activities are receptor mediated, the existence of more than one stage makes these alternative assays cumbersome and subject to a greater probability of error.

CLAIMS

1. A method for the production of interleukin-1 inhibitor (IL-li) comprises:

(1) fermentation of Escherichia coli comprising a plasmid containing a DNA encoding IL-li;

(2) cell processing, including:
(a) cell recovery
(b) lysis, and
(c) clarification of the lysates;

(3) a first ion exchange step using a cationic resin;

(4) a second ion exchange step using a anionic resin; and

(5) subsequent processing steps including concentration and diafiltration.

2. The method of claim 1 wherein the DNA comprises a DNA that is selected from the group consisting of (1) a DNA that encodes IL-li X, IL-liα, or IL-liβ and (2) a DNA that cross-hybridizes to a DNA that is complementary to a DNA that encodes IL-li X, IL-liα, or IL-liβ, wherein said DNA of (1) or (2) encodes a protein having IL-1 inhibitor activity.

3. The method of claim 1 wherein the plasmid is pDD6.

4. The method of claim 1 wherein the cationic resin is selected from the group consisting of S-Sepharose®, SP-C25 Sephadex®, CM Sephadex®, CM Sepharose®, CM cellulose®, or CM Toyopearl®.

5. The method of claim 4 wherein the cationic resin is S-Sepharose®.

6. The method of claim 1 wherein the anionic resin is selected from the group consisting of Q–Sepharose®, DEAE-Sepharose®, Q-Sephadex® and DEAE® cellulose.

7. The method of claim 6 wherein the anionic resin is Q-Sepharose®.

8. The method of claim 1 which further comprises a third ion exchange step conducted immediately prior to the final processing steps.

9. The method of claim 8 wherein the third ion exchange step is conducted using a cationic resin.

10. The method of claim 9 wherein the cationic resin is selected from the group consisting of S-Sepharose®, SP-C25 Sephadex®, CM Sephadex®, CM Sepharose®, CM cellulose®, or CM Toyopearl®.

11. The method of claim 10 wherein the cationic resin is S-Sepharose®.

12. A transformed *E. coli* host comprising at least one plasmid containing the plasmid pDD6 which is capable of producing commercial quantities of highly purified IL-1i.

13. The plasmid pDD6.

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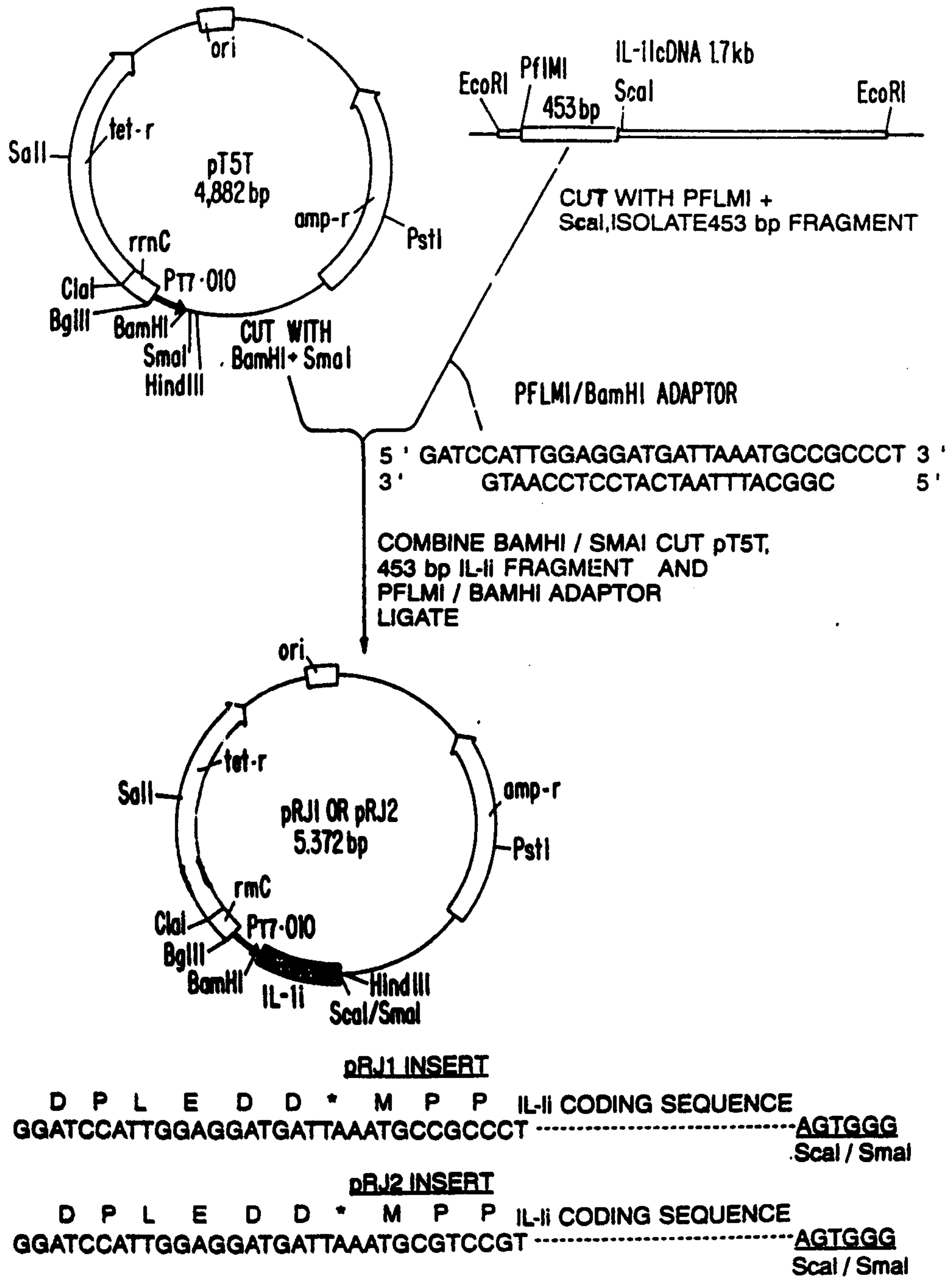
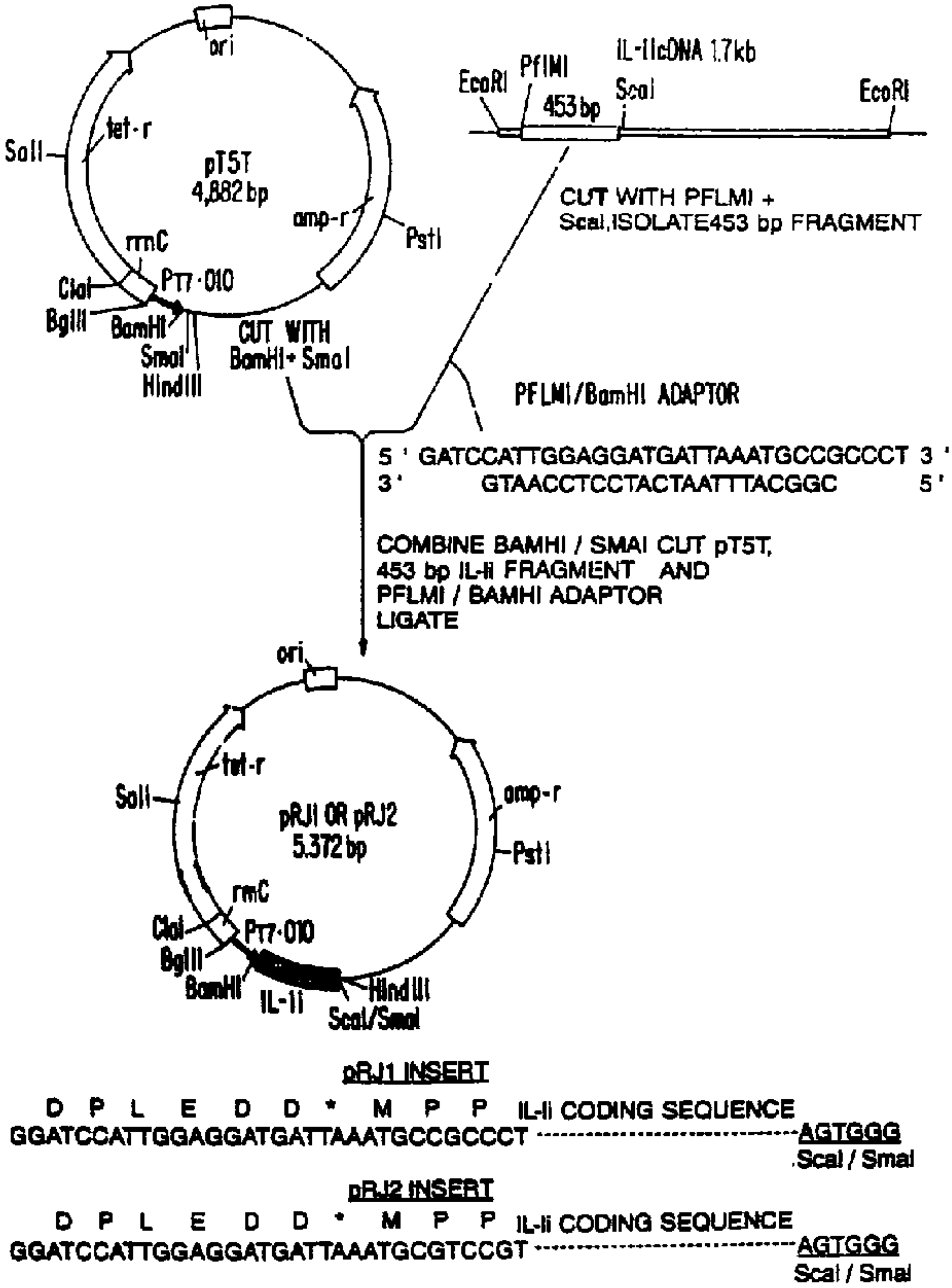
FIG. 1




ori
tet-r
SalI
pT5T
4,882 bp
amp-r
PstI
rrnC
ClaI
PT7·010
BglII
BamHI
SmaI
HindIII
CUT WITH
BamHI + SmaI
IL-1i cDNA 1.7kb
EcoRI
PflMI
453 bp
ScaI
EcoRI
CUT WITH PFLMI +
ScaI, ISOLATE453 bp FRAGMENT
PFLMI/BamHI ADAPTOR
5 ' GATCCATTGGAGGATGATTAAATGCCGCCCT 3 '
3 ' GTAACCTCCTACTAATTTACGGC 5 '
COMBINE BAMHI / SMAI CUT pT5T,
453 bp IL-1i FRAGMENT AND
PFLMI / BAMHI ADAPTOR
LIGATE
ori
tet-r
SalI
pRJ1 OR pRJ2
5,372 bp
amp-r
PstI
rrnC
ClaI
PT7·010
BglII
BamHI
IL-1i
HindIII
ScaI/SmaI
pRJ1 INSERT
D P L E D D * M P P IL-1i CODING SEQUENCE
GGATCCATTGGAGGATGATTAAATGCCGCCCT -------------------------- AGTGGG
ScaI / SmaI
pRJ2 INSERT
D P L E D D * M P P IL-1i CODING SEQUENCE
GGATCCATTGGAGGATGATTAAATGCGTCCGT -------------------------- AGTGGG
ScaI / SmaI