FIGURE 1

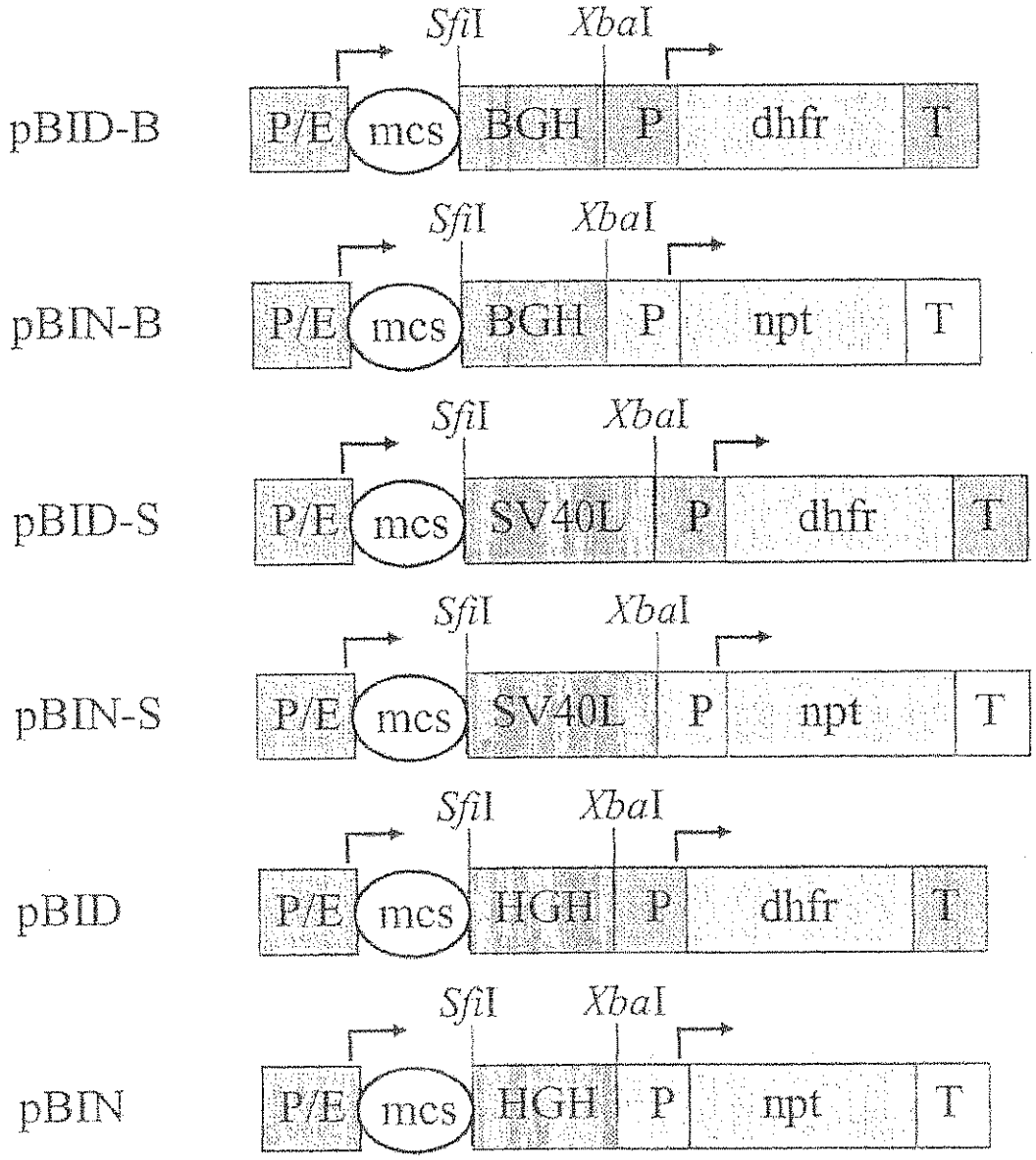

SfiI
XbaI
pBID-B
P/E
mcs
BGH
P
dhfr
T
SfiI
XbaI
pBIN-B
P/E
mcs
BGH
P
npt
T
SfiI
XbaI
pBID-S
P/E
mcs
SV40L
P
dhfr
T
SfiI
XbaI
pBIN-S
P/E
mcs
SV40L
P
npt
T
SfiI
XbaI
pBID
P/E
mcs
HGH
P
dhfr
T
SfiI
XbaI
pBIN
P/E
mcs
HGH
P
npt
T

FIGURE 2

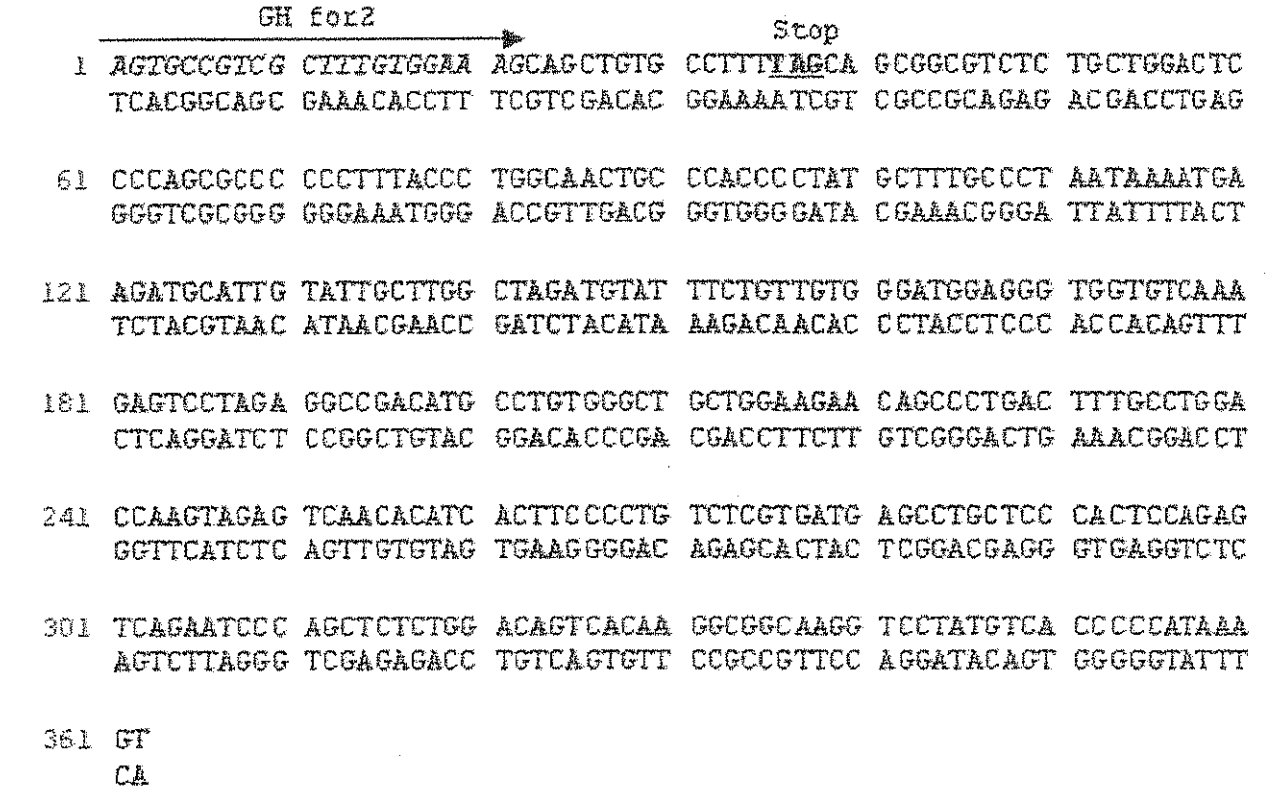
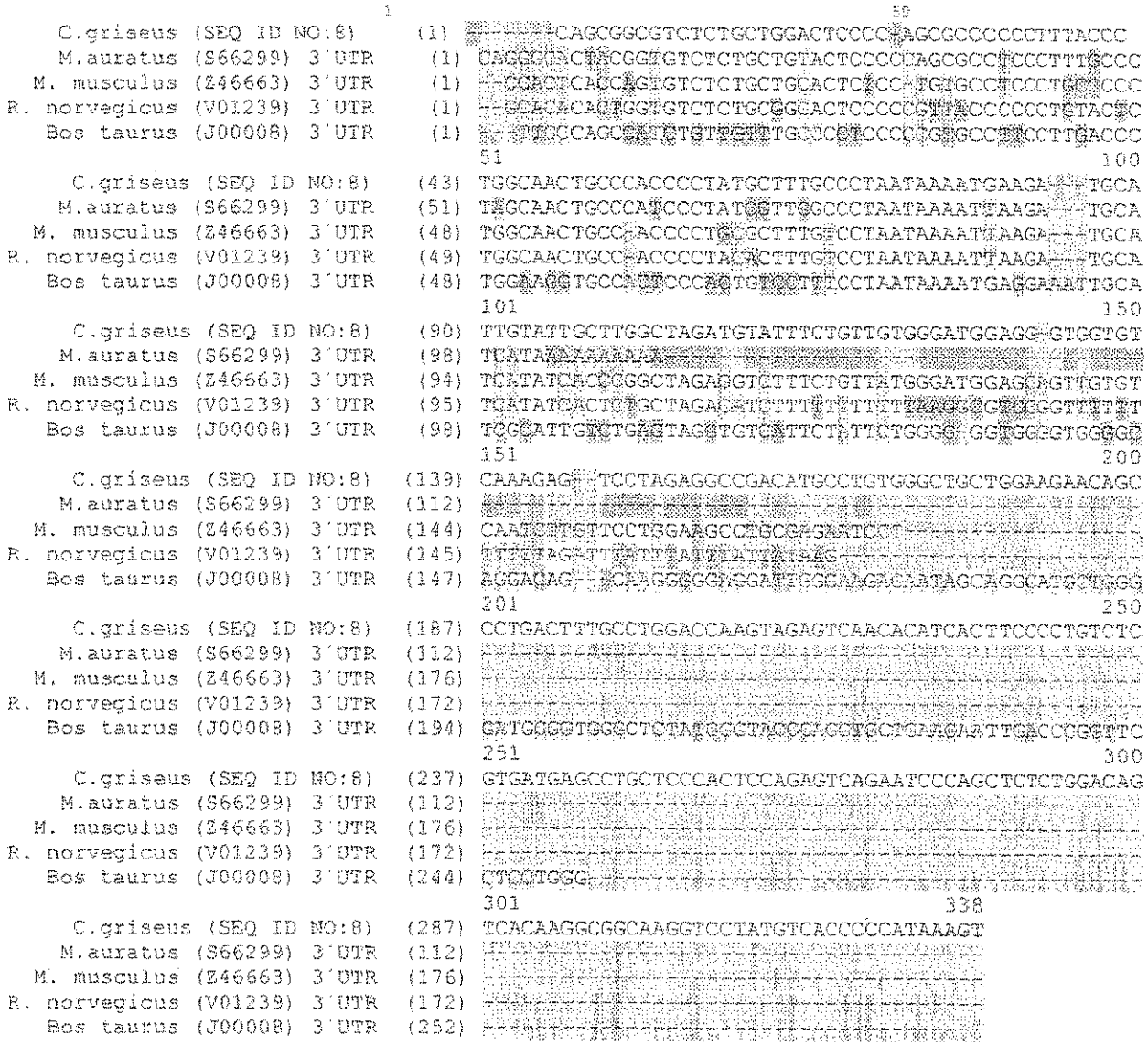

GH for2
Stop
1 AGTGCCGTCG CTTTGTGGAA AGCAGCTGTG CCTTTTTAGCA GCGGCGTCTC TGCTGGACTC
TCACGGCAGC GAAACACCTT TCGTCGACAC GGAAAATCGT CGCCGCAGAG ACGACCTGAG
61 CCCAGCGCCC CCCTTTACCC TGGCAACTGC CCACCCCTAT GCTTTGCCCT AATAAAATGA
GGGTCGCGGG GGGAAATGGG ACCGTTGACG GGTGGGGATA CGAAACGGGA TTATTTTACT
121 AGATGCATTG TATTGCTTGG CTAGATGTAT TTCTGTTGTG GGATGGAGGG TGGTGTCAAA
TCTACGTAAC ATAACGAACC GATCTACATA AAGACAACAC CCTACCTCCC ACCACAGTTT
181 GAGTCCTAGA GGCCGACATG CCTGTGGGCT GCTGGAAGAA CAGCCCTGAC TTTGCCTGGA
CTCAGGATCT CCGGCTGTAC GGACACCCGA CGACCTTCTT GTCGGGACTG AAACGGACCT
241 CCAAGTAGAG TCAACACATC ACTTCCCCTG TCTCGTGATG AGCCTGCTCC CACTCCAGAG
GGTTCATCTC AGTTGTGTAG TGAAGGGGAC AGAGCACTAC TCGGACGAGG GTGAGGTCTC
301 TCAGAATCCC AGCTCTCTGG ACAGTCACAA GGCGGCAAGG TCCTATGTCA CCCCCATAAA
AGTCTTAGGG TCGAGAGACC TGTCAGTGTT CCGCCGTTCC AGGATACAGT GGGGGTATTT
361 GT
CA

FIGURE 3


C.griseus (SEQ ID NO:8)
M.auratus (S66299) 3'UTR
M. musculus (Z46663) 3'UTR
R. norvegicus (V01239) 3'UTR
Bos taurus (J00008) 3'UTR

# FIGURE 4

```
                                  1                                                  Stop        60
HGH 362 nt (SEQ ID NO:7)      (1) AGTGCCGTCGCTTTGTGGAAAGCAGCTGTGCCTTTTAGCAGCGGCGTCTC
HGH 324 nt (SEQ ID NO:8)      (1) ------------------------------------------CAGCGGCGTCTC
HGH 189 nt (SEQ ID NO:9)      (1) ------------------------------------------CAGCGGCGTCTC
HGH 113 nt (SEQ ID NO:10)     (1) ------------------------------------------CAGCGGCGTCTC
                                  51                                                 100
HGH 362 nt (SEQ ID NO:7)     (51) TGCTGGACTCCCCAGCGCCCCCCTTTACCCTGGCAACTGCCCACCCCTAT
HGH 324 nt (SEQ ID NO:8)     (13) TGCTGGACTCCCCAGCGCCCCCCTTTACCCTGGCAACTGCCCACCCCTAT
HGH 189 nt (SEQ ID NO:9)     (13) TGCTGGACTCCCCAGCGCCCCCCTTTACCCTGGCAACTGCCCACCCCTAT
HGH 113 nt (SEQ ID NO:10)    (13) TGCTGGACTCCCCAGCGCCCCCCTTTACCCTGGCAACTGCCCACCCCTAT
                                 101                                                 150
HGH 362 nt (SEQ ID NO:7)    (101) GCTTTGCCCTAATAAAATGAAGATGCATTGTATTGCTTGGCTAGATGTAT
HGH 324 nt (SEQ ID NO:8)     (63) GCTTTGCCCTAATAAAATGAAGATGCATTGTATTGCTTGGCTAGATGTAT
HGH 189 nt (SEQ ID NO:9)     (63) GCTTTGCCCTAATAAAATGAAGATGCATTGTATTGCTTGGCTAGATGTAT
HGH 113 nt (SEQ ID NO:10)    (63) GCTTTGCCCTAATAAAATGAAGATGCATTGTATTGCTTGGCTAGATGTAT
                                 151                                                 200
HGH 362 nt (SEQ ID NO:7)    (151) TTCTGTTGTGGGATGGAGGGTGGTGTCAAAGAGTCCTAGAGGCCGACATG
HGH 324 nt (SEQ ID NO:8)    (113) TTCTGTTGTGGGATGGAGGGTGGTGTCAAAGAGTCCTAGAGGCCGACATG
HGH 189 nt (SEQ ID NO:9)    (113) TTCTGTTGTGGGATGGAGGGTGGTGTCAAAGAGTCCTAGAGGCCGACATG
HGH 113 nt (SEQ ID NO:10)   (113) T-----------------------------------------------------
                                 201                                                 250
HGH 362 nt (SEQ ID NO:7)    (201) CCTGTGGGCTGCTGGAAGAACAGCCCTGACTTTGCCTGGACCAAGTAGAG
HGH 324 nt (SEQ ID NO:8)    (163) CCTGTGGGCTGCTGGAAGAACAGCCCTGACTTTGCCTGGACCAAGTAGAG
HGH 189 nt (SEQ ID NO:9)    (163) CCTGTGGGCTGCTGGAAGAACAGCCCT------------------------
HGH 113 nt (SEQ ID NO:10)   (114) -----------------------------------------------------
                                 251                                                 300
HGH 362 nt (SEQ ID NO:7)    (251) TCAACACATCACTTCCCCTGTCTCGTGATGAGCCTGCTCCCACTCCAGAG
HGH 324 nt (SEQ ID NO:8)    (213) TCAACACATCACTTCCCCTGTCTCGTGATGAGCCTGCTCCCACTCCAGAG
HGH 189 nt (SEQ ID NO:9)    (190) -----------------------------------------------------
HGH 113 nt (SEQ ID NO:10)   (114) -----------------------------------------------------
                                 301                                                 350
HGH 362 nt (SEQ ID NO:7)    (301) TCAGAATCCCAGCTCTCTGGACAGTCACAAGGCGGCAAGGTCCTATGTCA
HGH 324 nt (SEQ ID NO:8)    (263) TCAGAATCCCAGCTCTCTGGACAGTCACAAGGCGGCAAGGTCCTATGTCA
HGH 189 nt (SEQ ID NO:9)    (190) -----------------------------------------------------
HGH 113 nt (SEQ ID NO:10)   (114) -----------------------------------------------------
                                 351       362
HGH 362 nt (SEQ ID NO:7)    (351) CCCCCATAAAGT
HGH 324 nt (SEQ ID NO:8)    (313) CCCCCATAAAGT
HGH 189 nt (SEQ ID NO:9)    (190) ------------
HGH 113 nt (SEQ ID NO:10)   (114) ------------
```

FIGURE 5

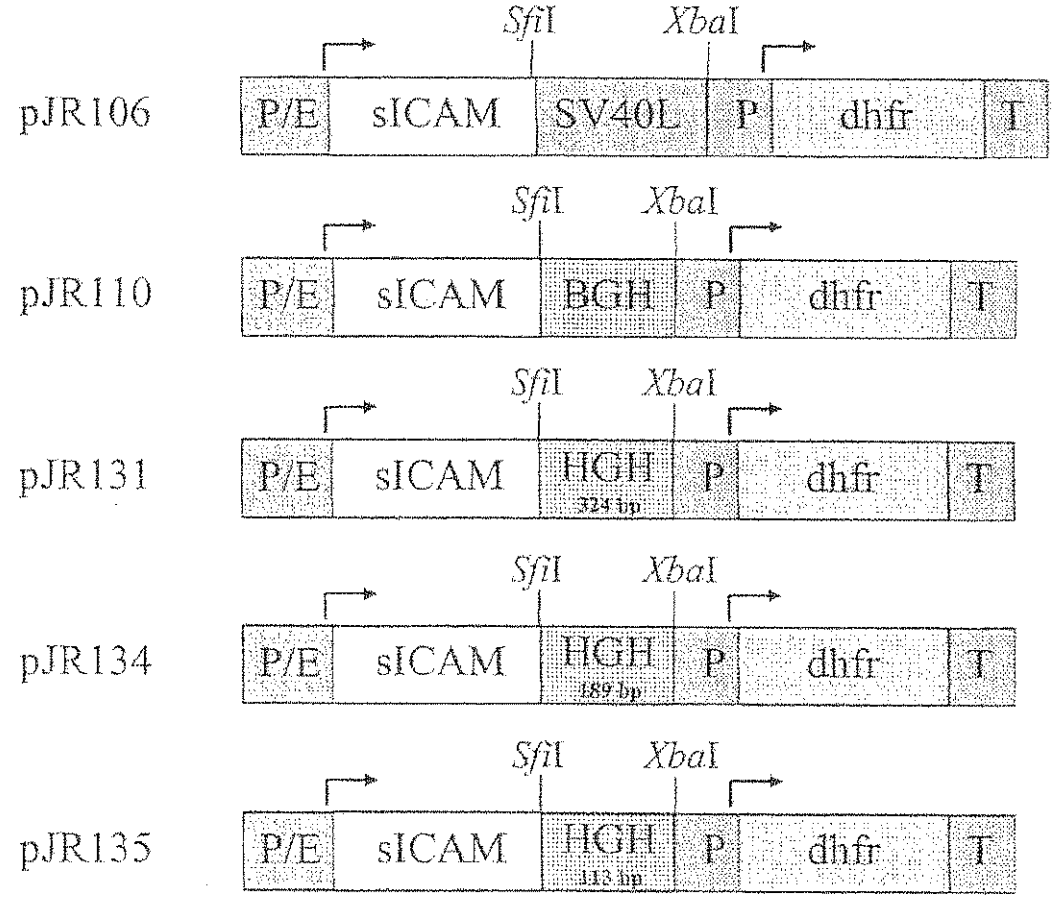

SfiI
XbaI
pJR106
P/E
sICAM
SV40L
P
dhfr
T
SfiI
XbaI
pJR110
P/E
sICAM
BGH
P
dhfr
T
SfiI
XbaI
pJR131
P/E
sICAM
HGH
324 bp
P
dhfr
T
SfiI
XbaI
pJR134
P/E
sICAM
HGH
189 bp
P
dhfr
T
SfiI
XbaI
pJR135
P/E
sICAM
HGH
113 bp
P
dhfr
T

FIGURE 6

| Vector | Termination Sequence | Transient Transfection #1 (n=2) | Transient Transfection #2 (n=2) |
|---|---|---|---|
| pJR106 | SV40 late (SEQ ID NO: 11) | 193 ng/mL sICAM | 207 ng/mL sICAM |
| pJR110 | BGH (SEQ ID NO: 12) | 222 ng/mL sICAM | 234 ng/mL sICAM |
| pJR131 | HGH (SEQ ID NO: 8) | 269 ng/mL sICAM | 257 ng/mL sICAM |

FIGURE 7

| Vector combination | Termination Sequence | Transient Transfection (n=6) |
|---|---|---|
| pBID-B/IgG4 + pBIN-B/kappa | BGH (SEQ ID NO: 12) | 40 ± 6 ng/mL IgG4 |
| pBID/IgG4 + pBIN/kappa | HGH (SEQ ID NO: 8) | 54 ± 8 ng/mL IgG4 |

FIGURE 8

| Vector | HGH Sequence (3'UTR) | Transient Transfection #1 (n=2) | Transient Transfection #2 (n=2) |
|---|---|---|---|
| pJR131 | bp 1 – 324 (SEQ ID NO: 8) | 111 ng/mL sICAM | 108 ng/mL sICAM |
| pJR134 | bp 1- 189 (SEQ ID NO: 9) | 98 ng/mL sICAM | 83 ng/mL sICAM |
| pJR135 | bp 1- 113 (SEQ ID NO: 10) | 25 ng/mL sICAM | 25 ng/mL sICAM |

FIGURE 9

| Product | Cell Clone/ Cell Pool | Specific Productivity (pg/cell/day) | Titer in Fed Batch Process |
|---|---|---|---|
| IgG1 (1) | cell clone | 23 | 6.3 g/L (40 L bioreactor) |
| IgG1 (2) | cell pool (800 nM MTX) | 32 | 2.5 g/L (shake flask) |
| IgG2 | cell clone | 10 | 2.1 g/L (2 L bioreactor) |
| IgG4 | cell pool (800 nM MTX) | 44 | 2.1 g/L (shake flask) |
| Fc fusion protein (IgG1) | cell pool (800 nM MTX) | 45 | 3.9 g/L (shake flask) |
| Fc fusion protein (IgG2) | cell pool (800 nM MTX) | 34 | 3.4 g/L (shake flask) |