Figure 1

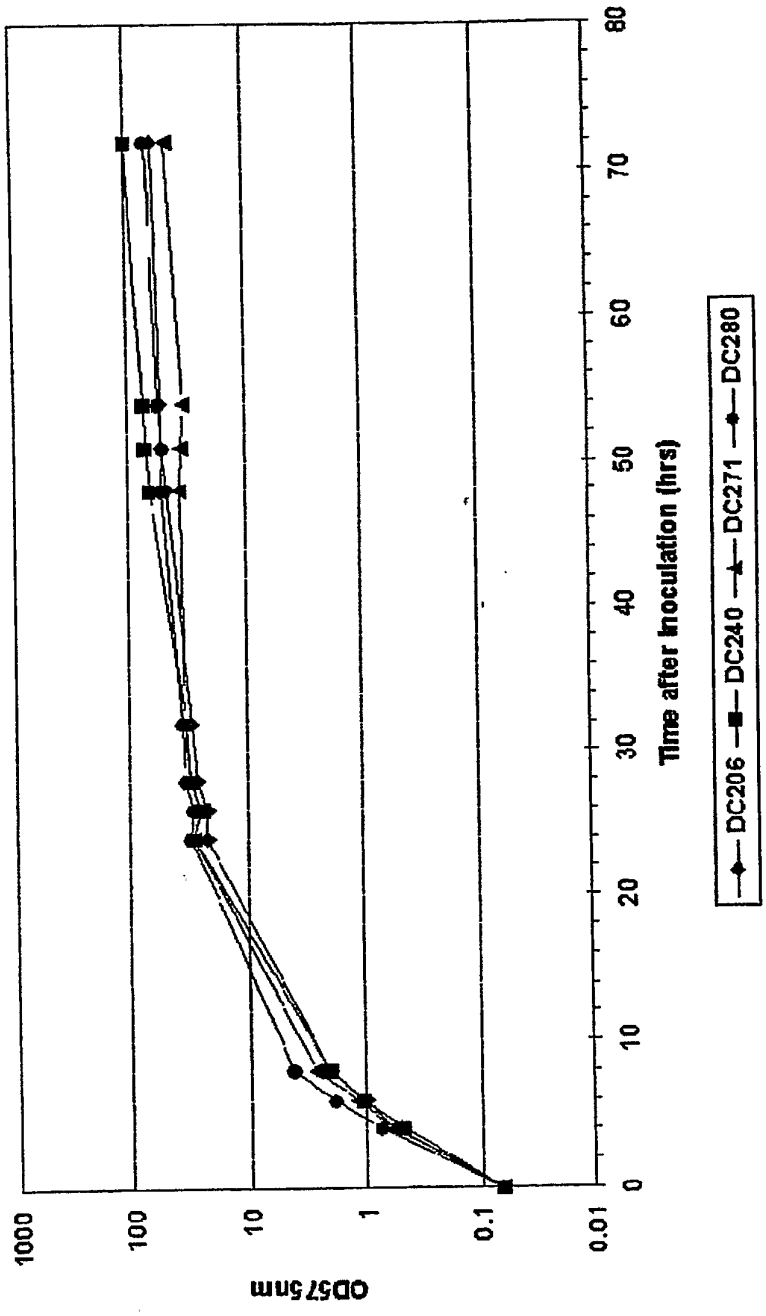

OD57 5nm
1000
100
10
1
0.1
0.01
0
10
20
30
40
50
60
70
80
Time after inoculation (hrs)
DC206
DC240
DC271
DC280

Figure 2

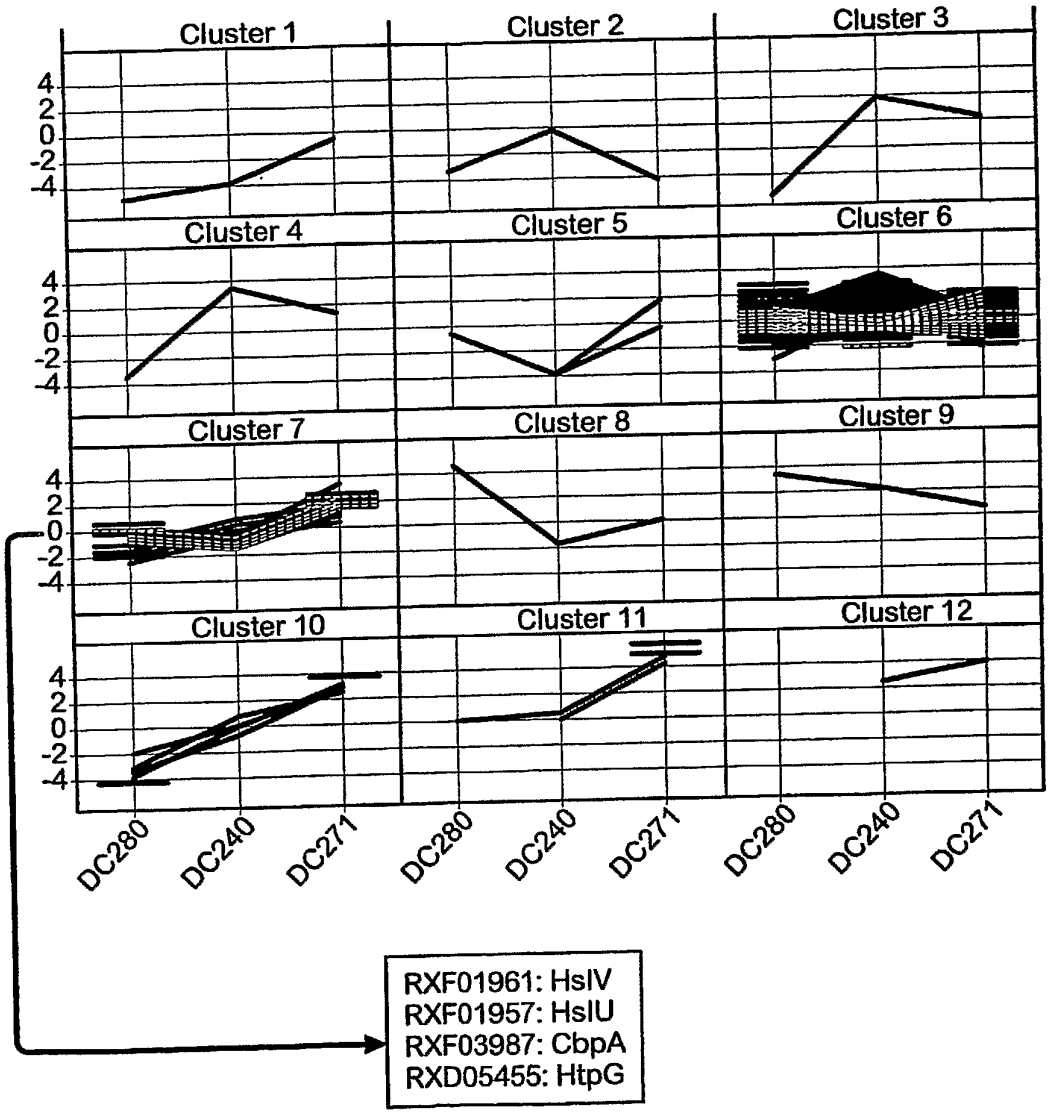

Cluster 1
Cluster 2
Cluster 3
Cluster 4
Cluster 5
Cluster 6
Cluster 7
Cluster 8
Cluster 9
Cluster 10
Cluster 11
Cluster 12
4
2
0
-2
-4
DC280
DC240
DC271
RXF01961: HslV
RXF01957: HslU
RXF03987: CbpA
RXD05455: HtpG

Figure 3

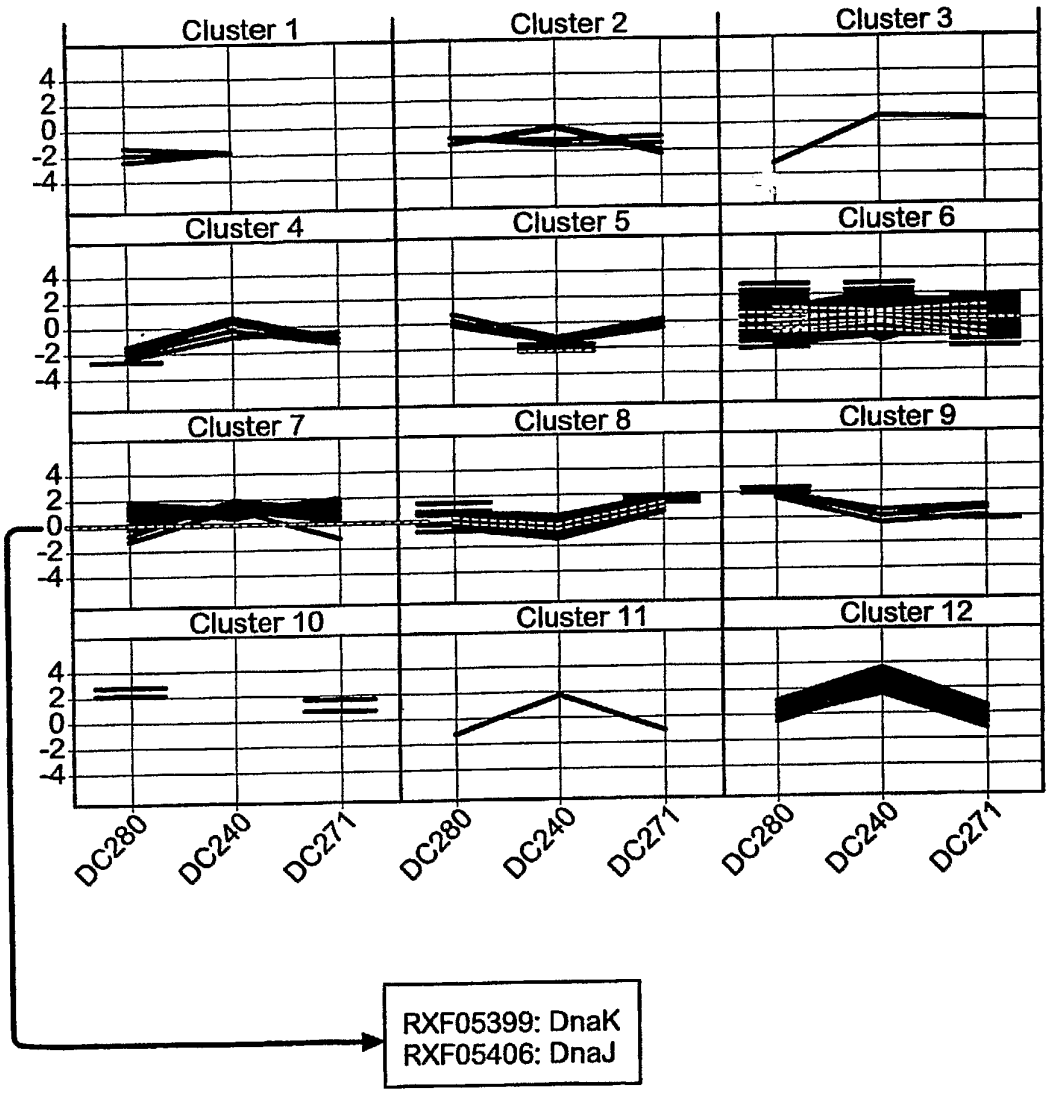
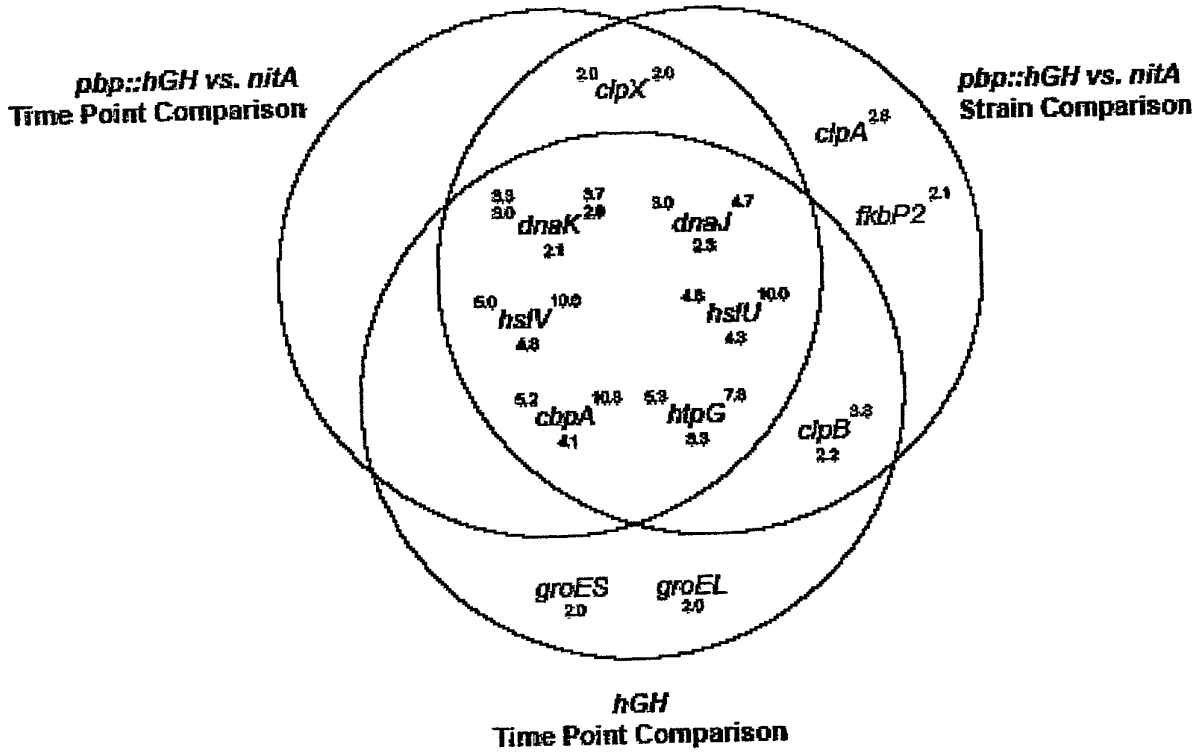

Cluster 1
Cluster 2
Cluster 3
Cluster 4
Cluster 5
Cluster 6
Cluster 7
Cluster 8
Cluster 9
Cluster 10
Cluster 11
Cluster 12
4
2
0
-2
-4
DC280
DC240
DC271
RXF05399: DnaK
RXF05406: DnaJ

Figure 4


pbp::hGH vs. nitA
Time Point Comparison
pbp::hGH vs. nitA
Strain Comparison
clpX
clpA
fkbP2
dnaK
dnaJ
hslV
hslU
clpA
htpG
clpB
groES
groEL
hGH
Time Point Comparison

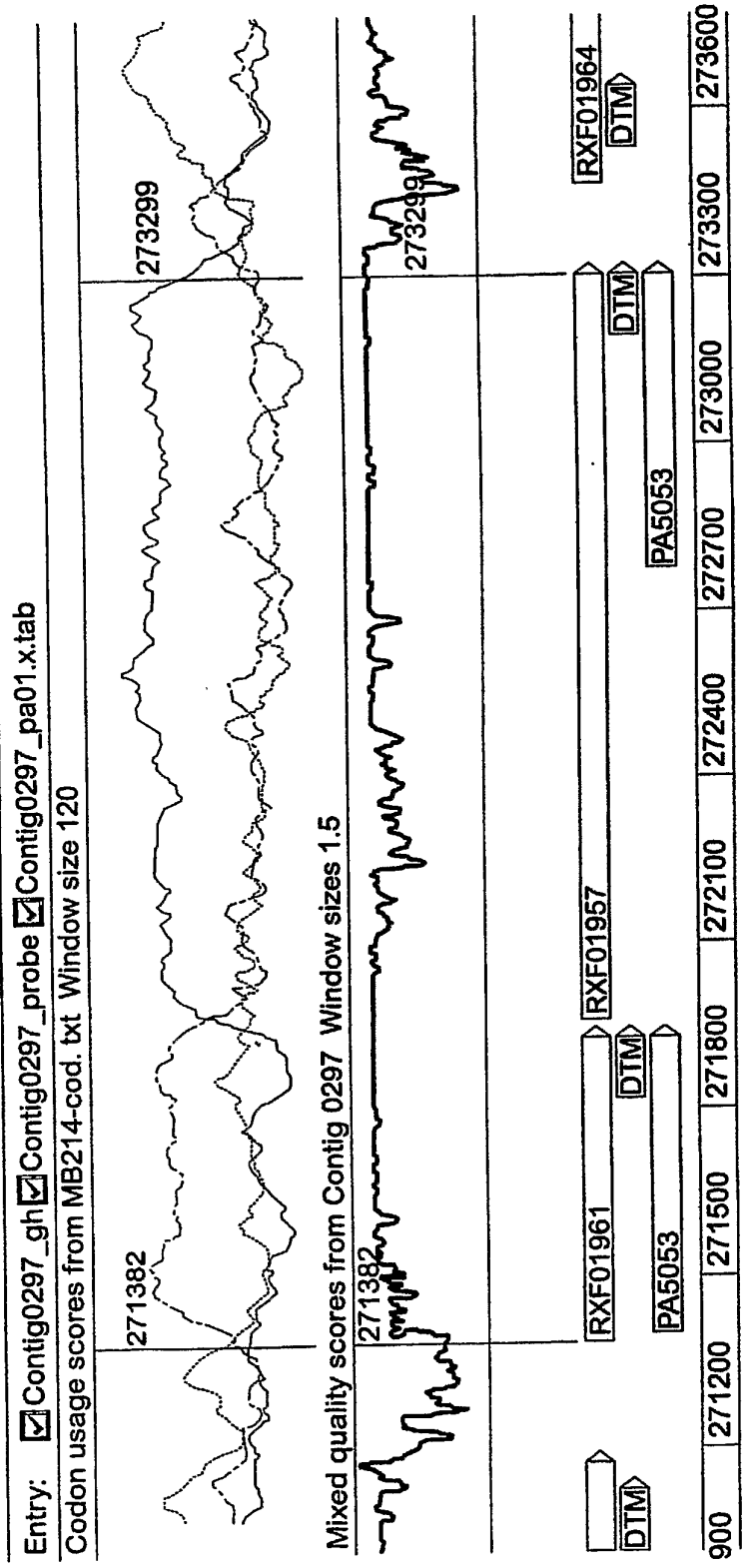

Entry: Contig0297_gh Contig0297_probe Contig0297_pa01.x.tab
Codon usage scores from MB214-cod. txt Window size 120
271382
273299
Mixed quality scores from Contig 0297 Window sizes 1.5
271382
273299
RXF01961
RXF01957
RXF01964
DTM
DTM
DTM
PA5053
PA5053
900
271200
271500
271800
272100
272400
272700
273000
273300
273600

Figure 5

Figure 6

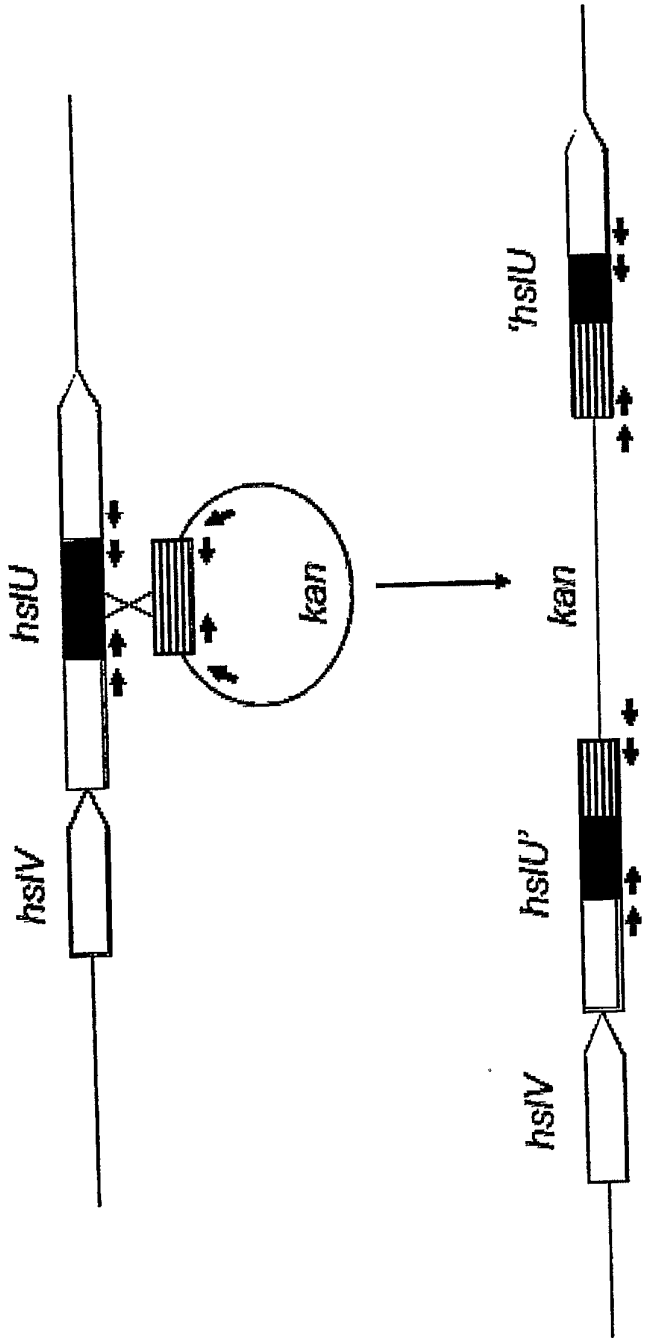


Figure 7

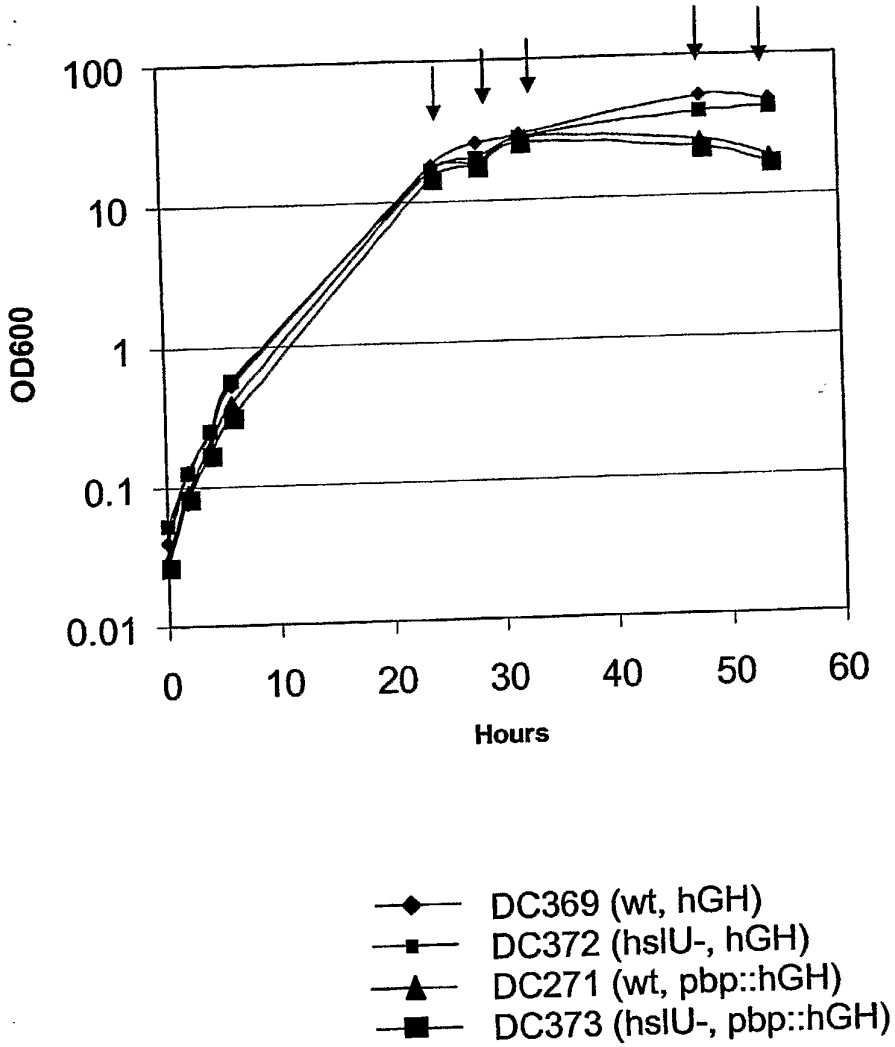

100
10
1
0.1
0.01
OD600
0
10
20
30
40
50
60
Hours
DC369 (wt, hGH)
DC372 (hslU-, hGH)
DC271 (wt, pbp::hGH)
DC373 (hslU-, pbp::hGH)

Figure 8

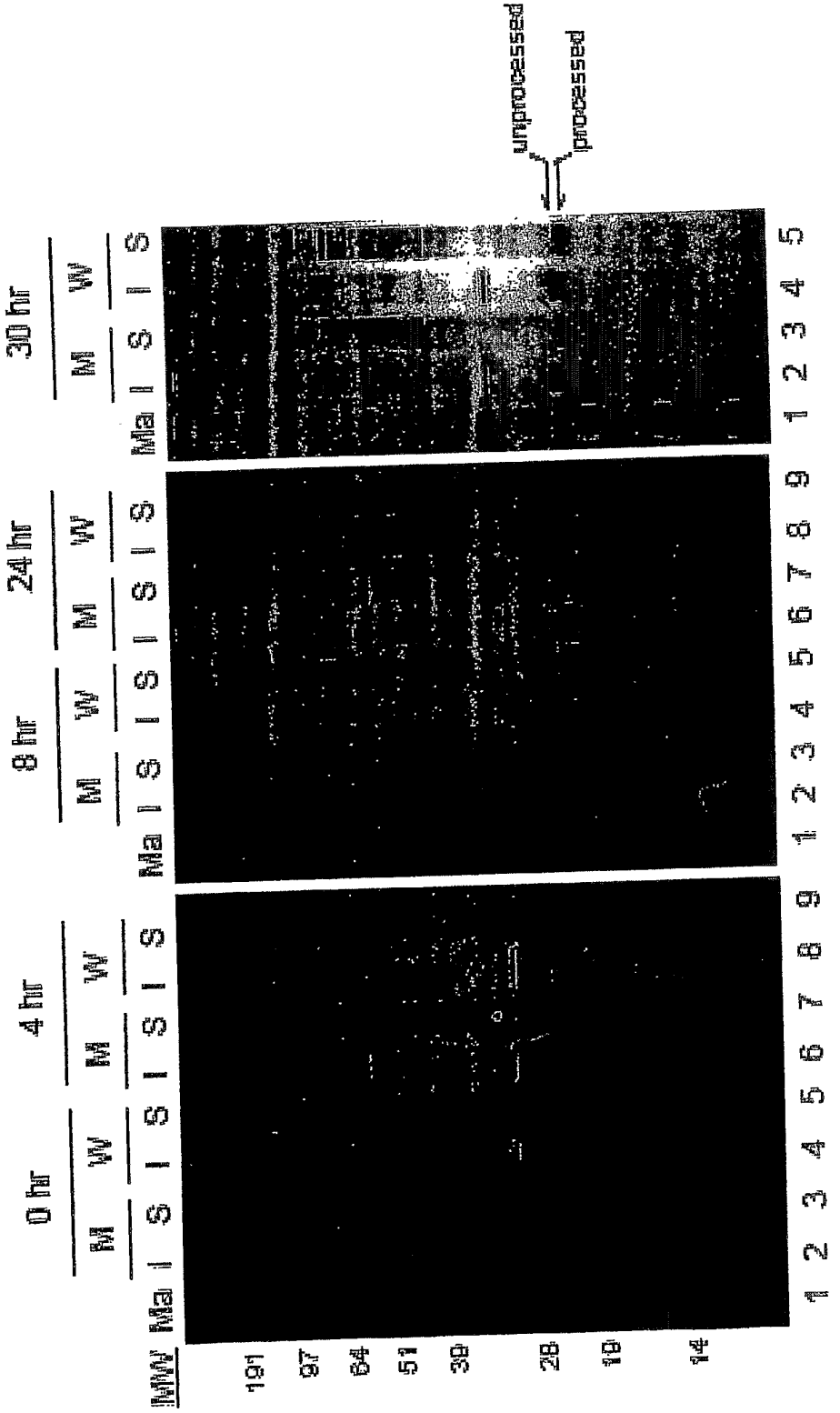

unprocessed
processed
0 hr
4 hr
8 hr
24 hr
30 hr
MW
Mal
M
W
S
I
1 2 3 4 5 6 7 8 9
191
97
64
51
39
28
18
14

Figure 9

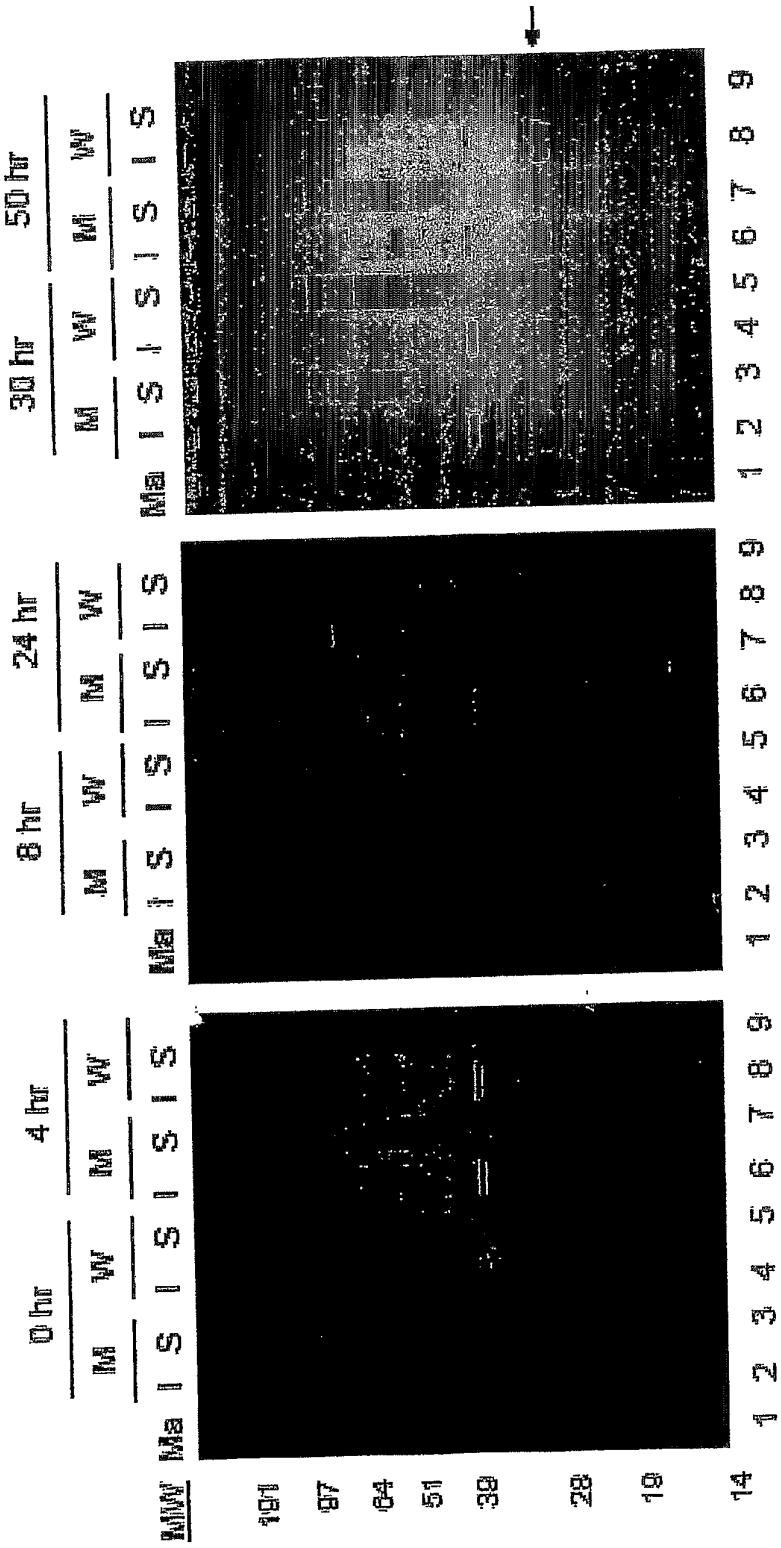

MWt
Ma
0 hr
4 hr
8 hr
24 hr
30 hr
50 hr
M
W
S
I
191
97
64
51
39
28
19
14
1 2 3 4 5 6 7 8 9

Figure 10

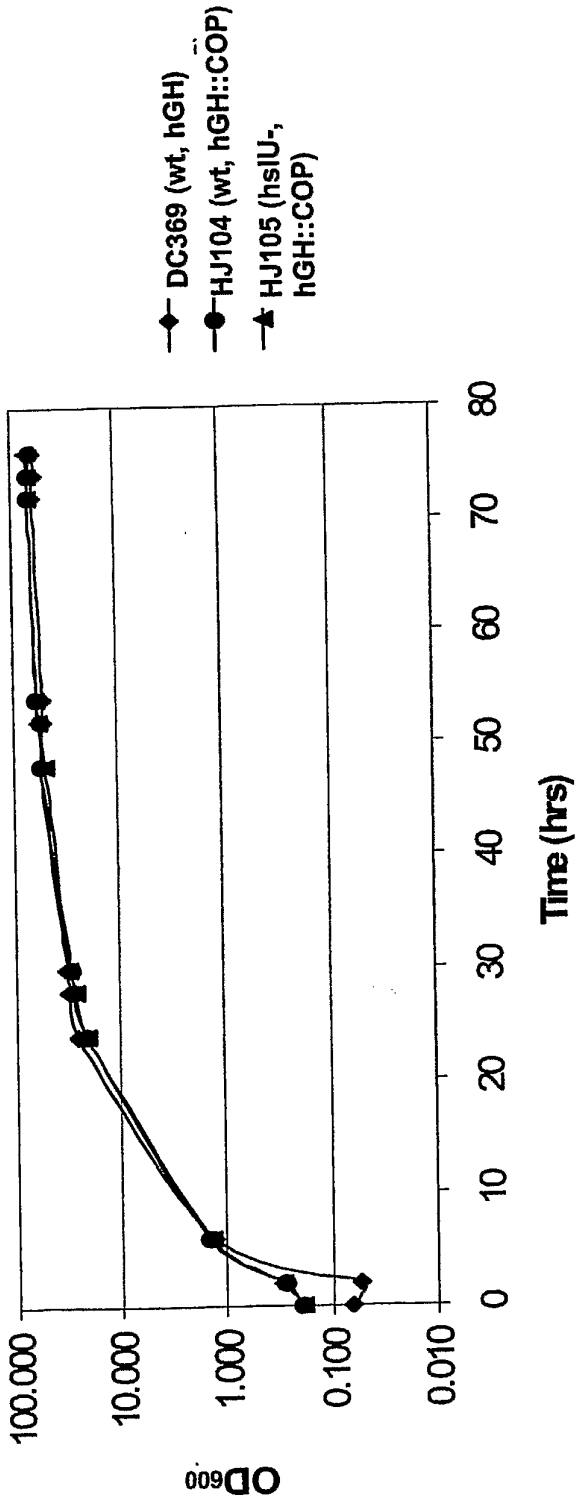
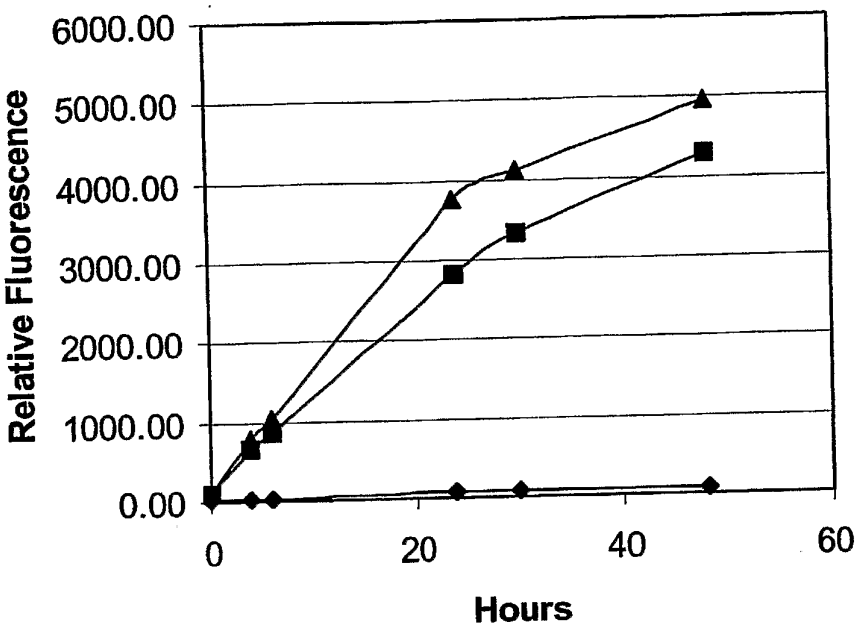

DC369 (wt, hGH)
HJ104 (wt, hGH::COP)
HJ105 (hslU-, hGH::COP)
100.000
10.000
1.000
0.100
0.010
OD600
0
10
20
30
40
50
60
70
80
Time (hrs)

Figure 11



Time	*hslu*%
0	5
4	17
6	22
24	33
30	24
48	16
52	15

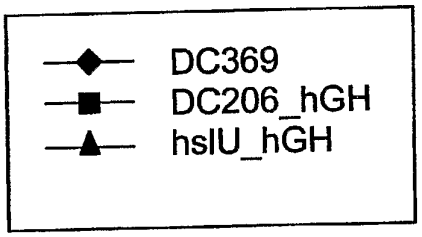


Figure 12

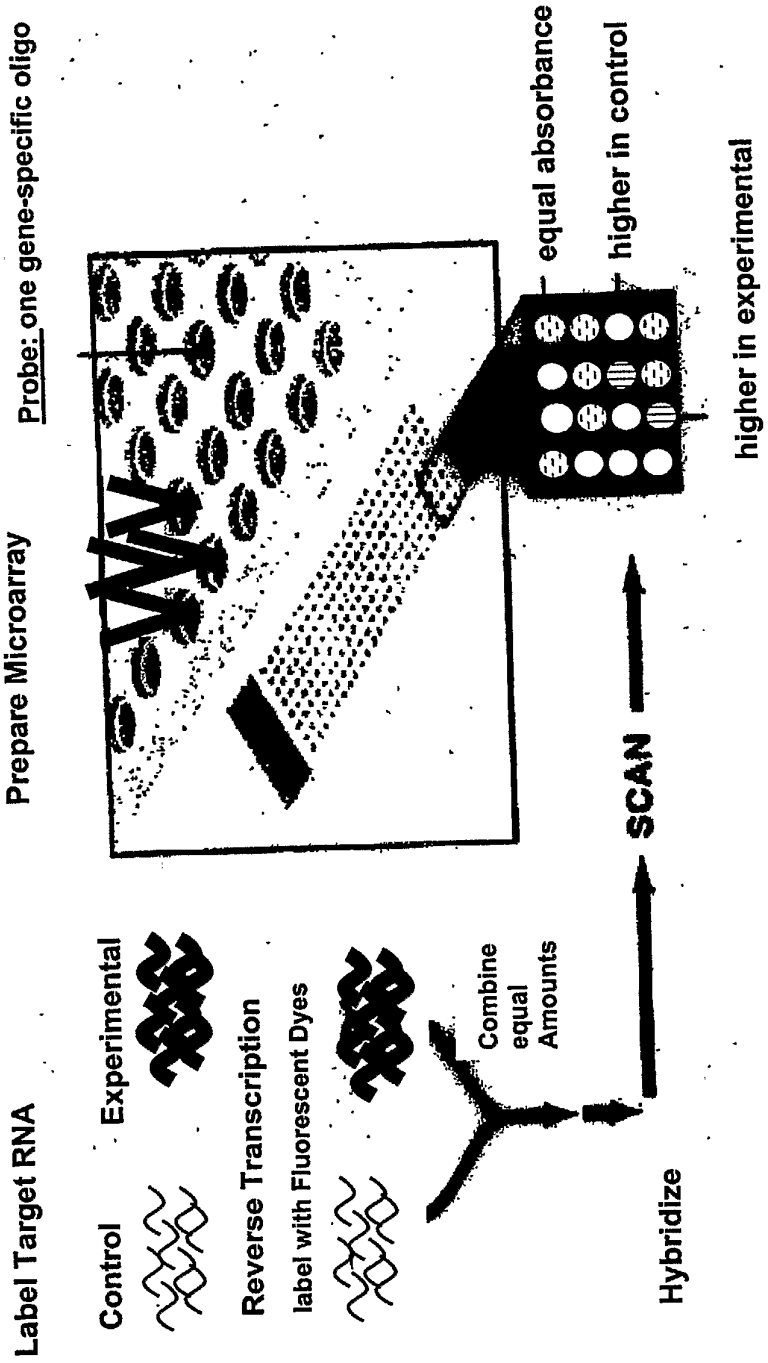

Label Target RNA
Control
Experimental
Reverse Transcription
label with Fluorescent Dyes
Combine equal Amounts
Hybridize
SCAN
Prepare Microarray
Probe: one gene-specific oligo
equal absorbance
higher in control
higher in experimental

Figure 13

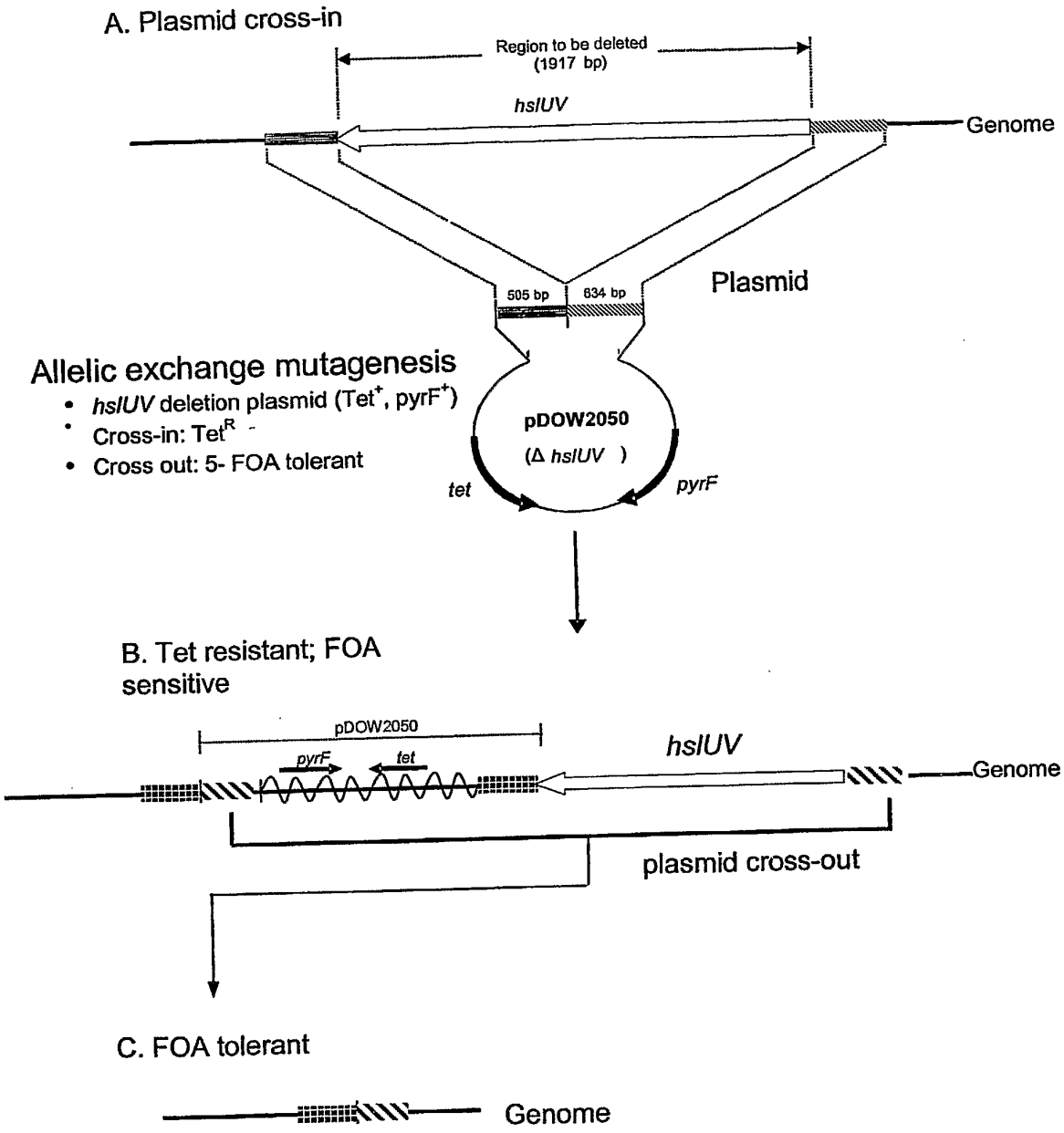

A. Plasmid cross-in
Region to be deleted
(1917 bp)
hslUV
Genome
505 bp
634 bp
Plasmid
Allelic exchange mutagenesis
• hslUV deletion plasmid (Tet+, pyrF+)
• Cross-in: TetR
• Cross out: 5- FOA tolerant
pDOW2050
(Δ hslUV)
tet
pyrF
B. Tet resistant; FOA sensitive
pDOW2050
pyrF
tet
hslUV
Genome
plasmid cross-out
C. FOA tolerant
Genome

Figure 14

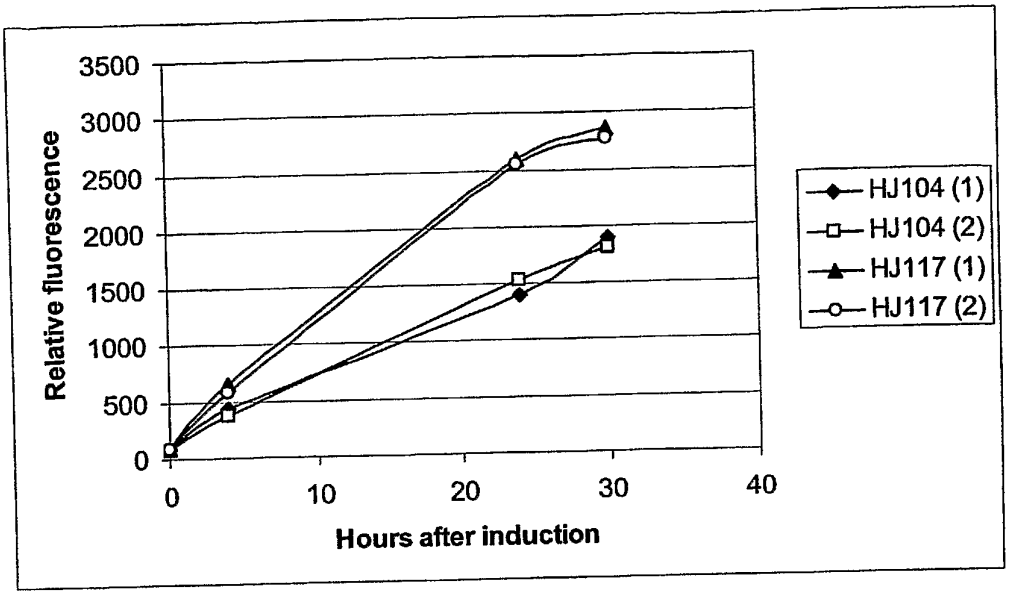
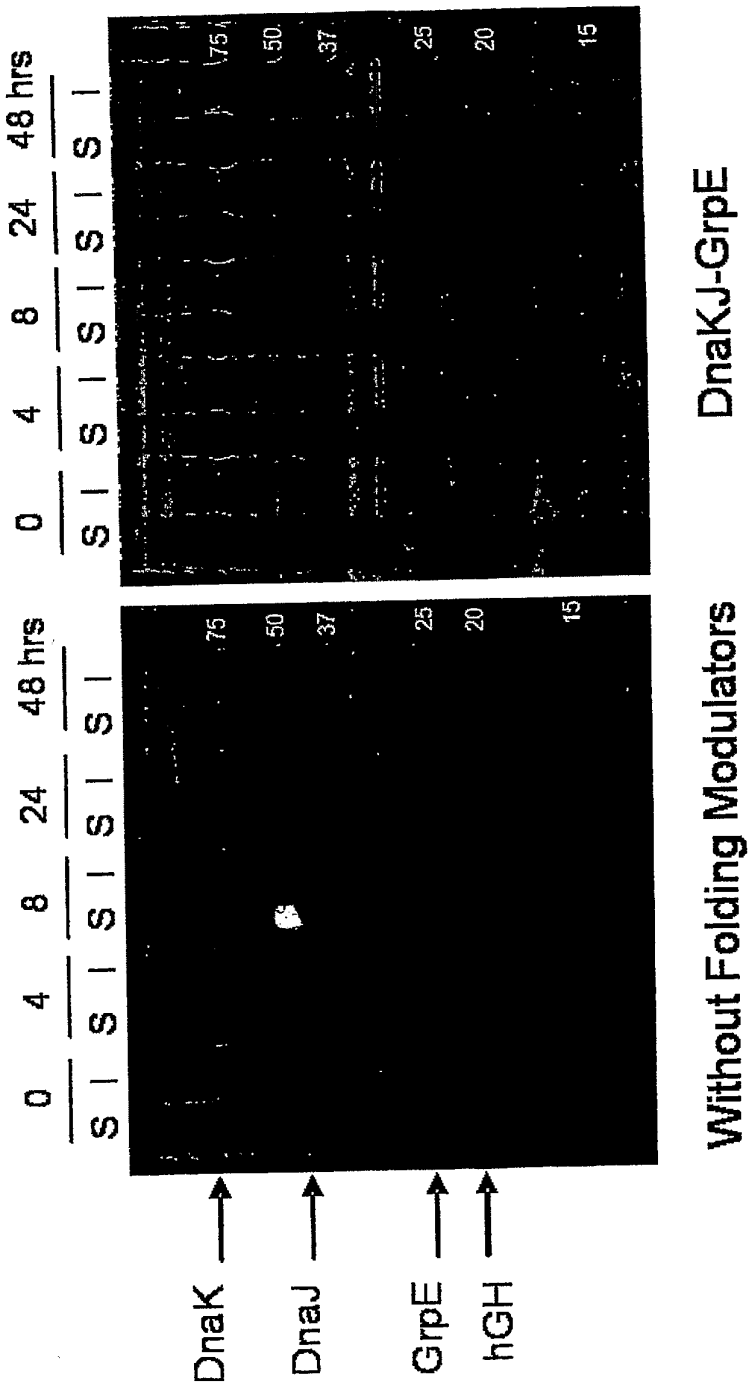

3500
3000
2500
2000
1500
1000
500
0
Relative fluorescence
0
10
20
30
40
Hours after induction
HJ104 (1)
HJ104 (2)
HJ117 (1)
HJ117 (2)

Figure 15


0 4 8 24 48 hrs
S I S I S I S I S I
75
50
37
25
20
15
DnaK
DnaJ
GrpE
hGH
Without Folding Modulators
DnaKJ-GrpE