Figure 1

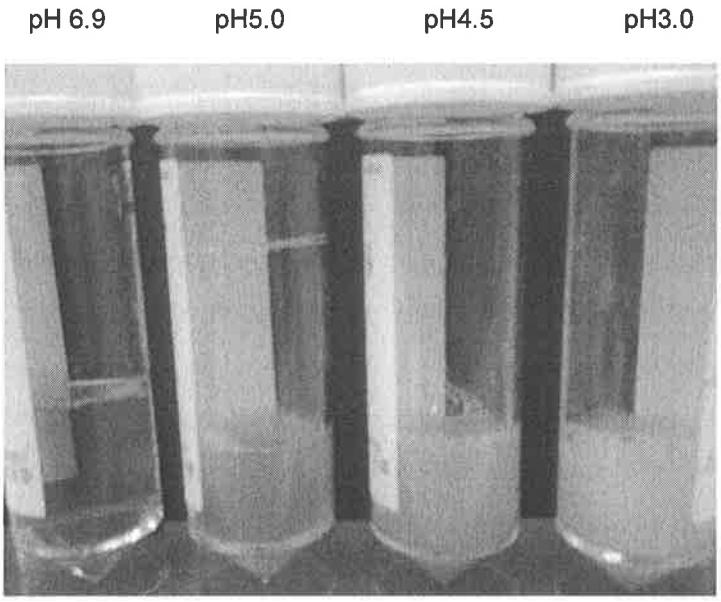


Figure 2

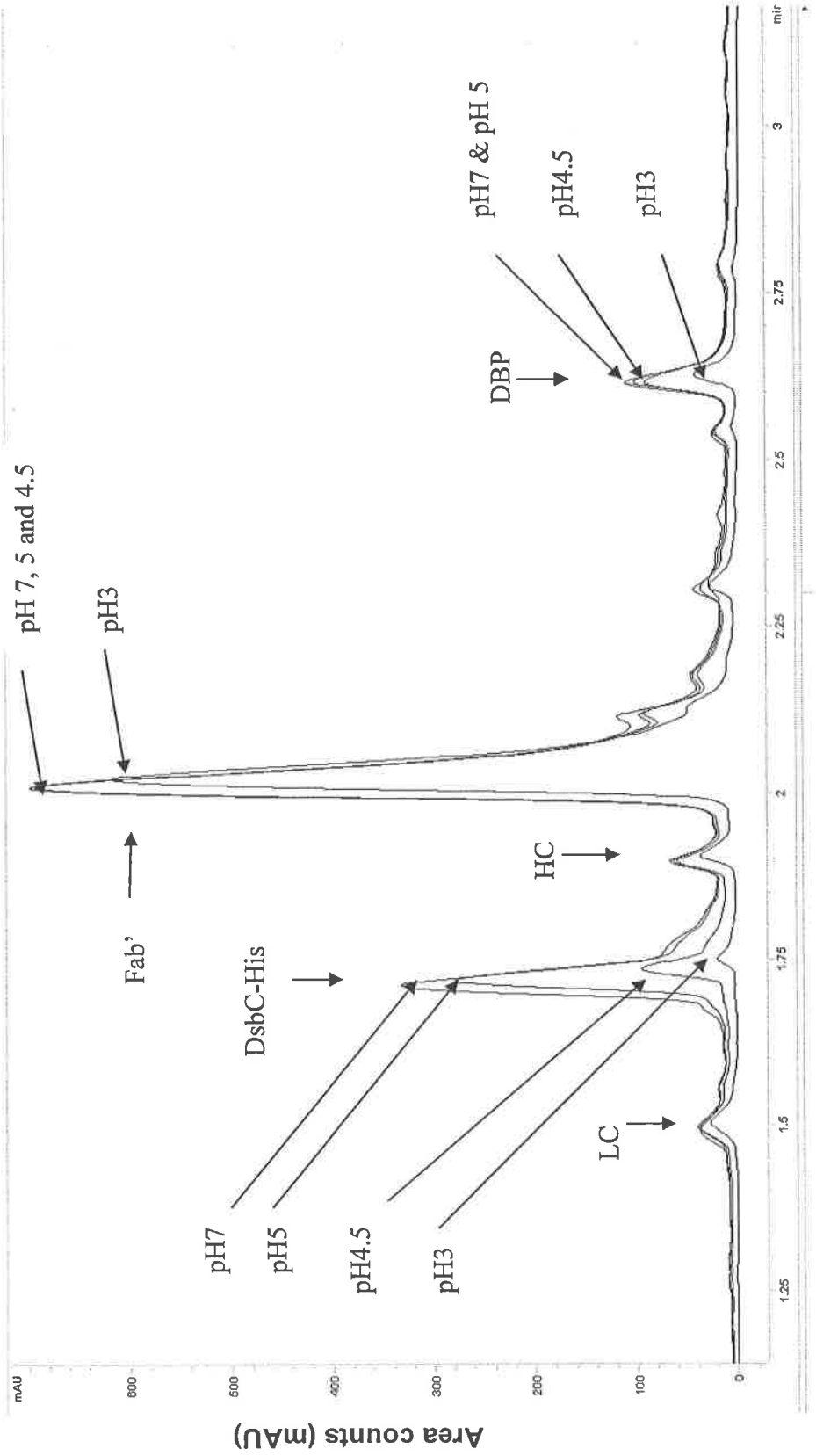

pH 7, 5 and 4.5
pH3
Fab'
DsbC-His
HC
LC
DBP
pH7 & pH 5
pH4.5
pH3
pH7
pH5
pH4.5
pH3
mAU
600
500
400
300
200
100
0
1.25
1.5
1.75
2
2.25
2.5
2.75
3
Area counts (mAU)
Time (mins)

Figure 3

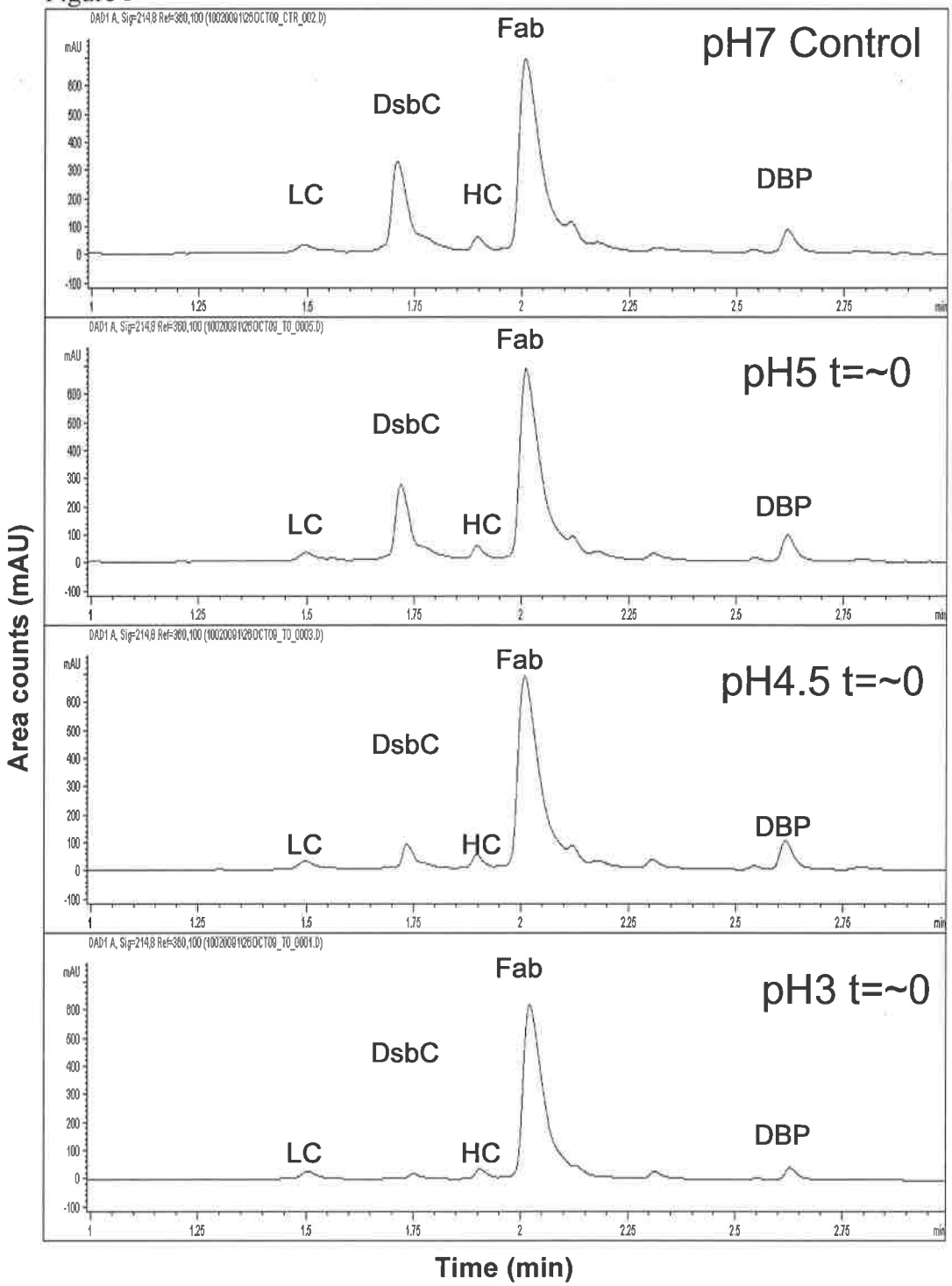

pH7 Control
pH5 t=~0
pH4.5 t=~0
pH3 t=~0
Fab
DsbC
LC
HC
DBP
Area counts (mAU)
Time (min)

Figure 4

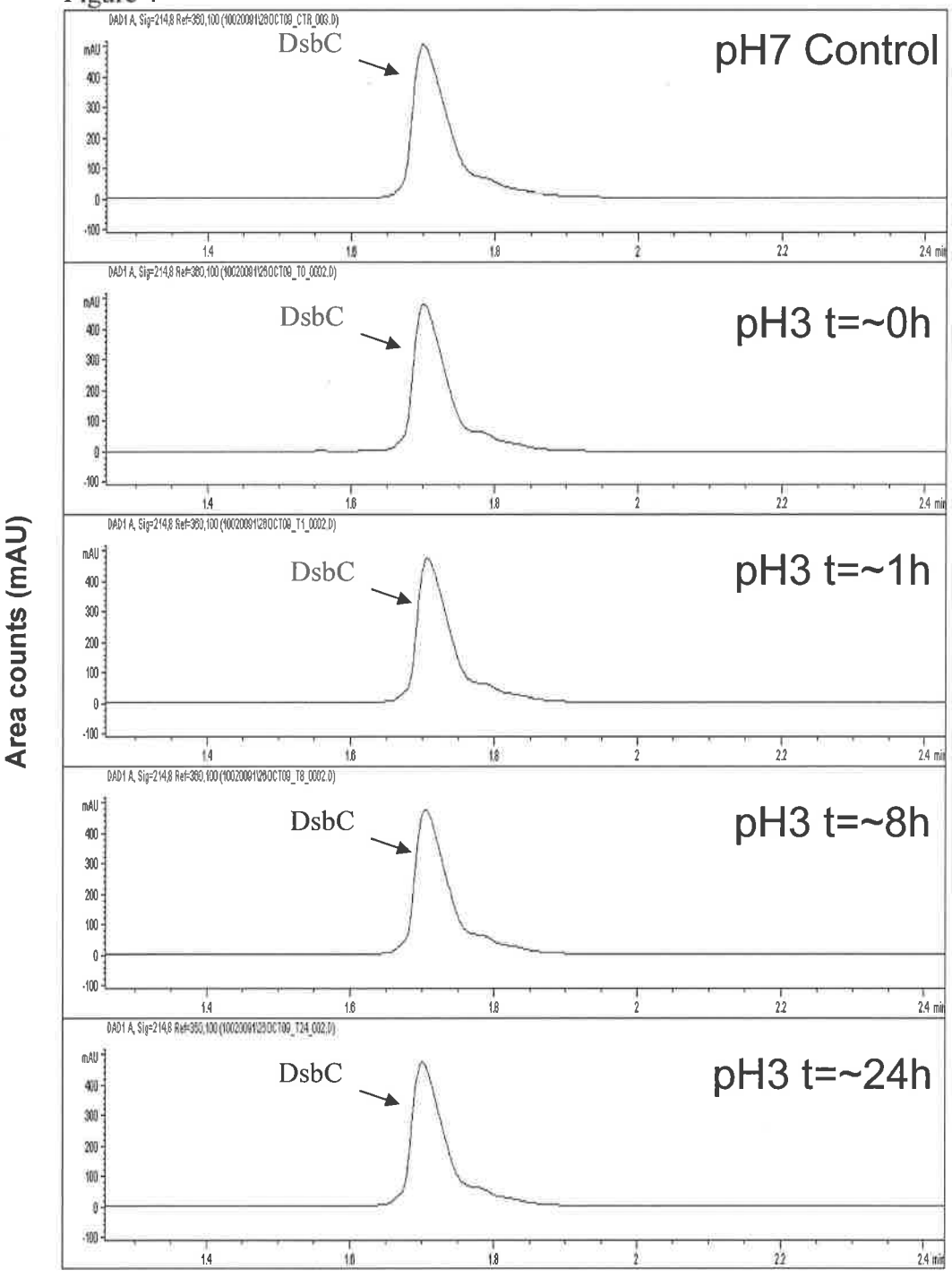

DsbC
pH7 Control
DsbC
pH3 t=~0h
DsbC
pH3 t=~1h
DsbC
pH3 t=~8h
DsbC
pH3 t=~24h
Area counts (mAU)
Time (min)

Figure 5

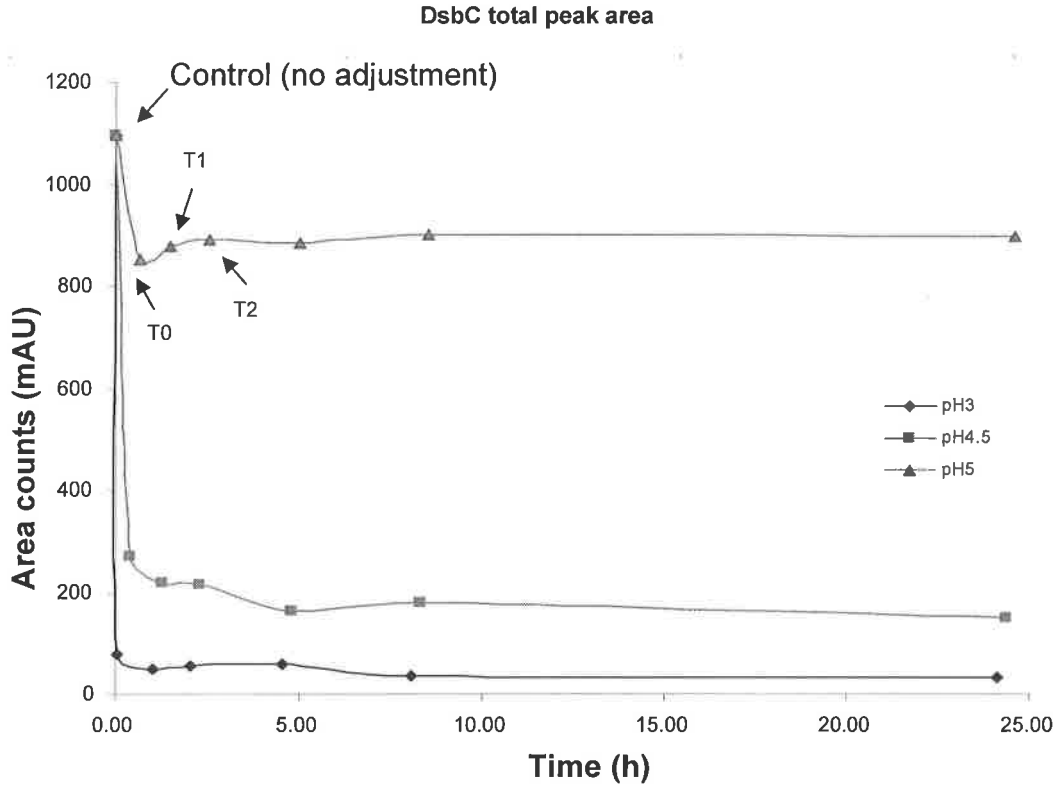

DsbC total peak area
Control (no adjustment)
T1
T0
T2
1200
1000
800
600
400
200
0
Area counts (mAU)
0.00
5.00
10.00
15.00
20.00
25.00
Time (h)
pH3
pH4.5
pH5

Figure 6

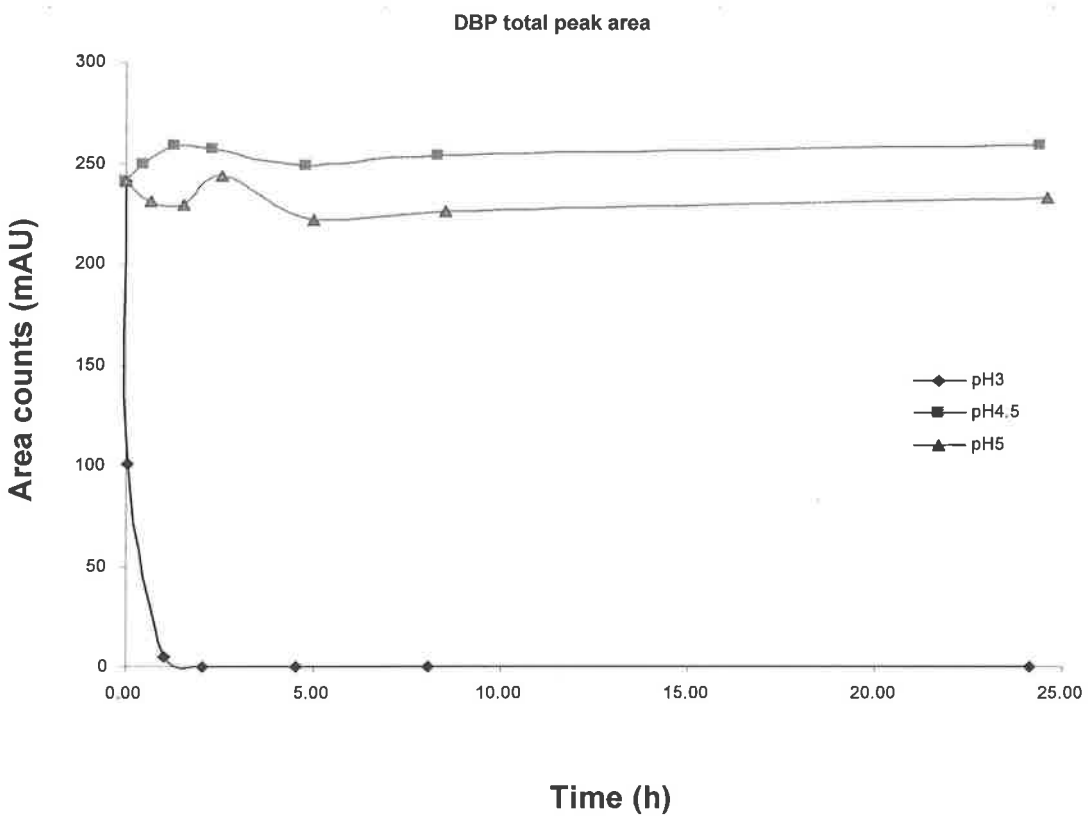
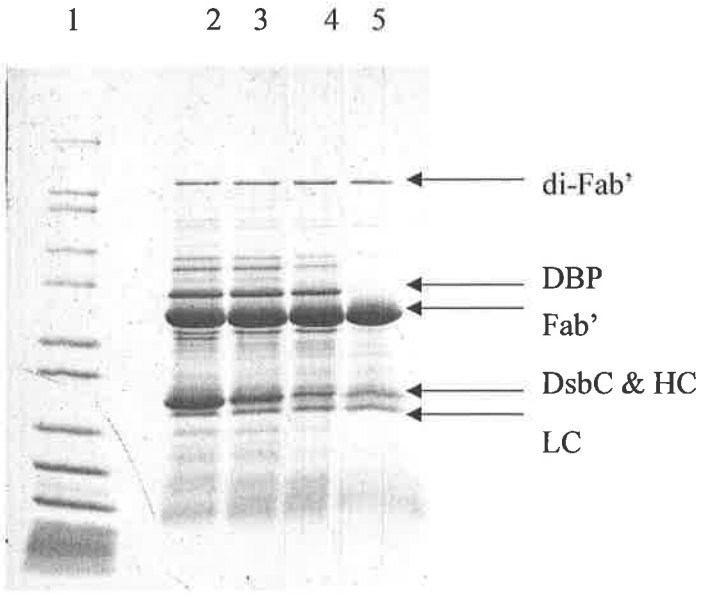

DBP total peak area
Area counts (mAU)
300
250
200
150
100
50
0
0.00
5.00
10.00
15.00
20.00
25.00
Time (h)
pH3
pH4.5
pH5

Figure 7



Lane	Sample
1	Molecular Weight Marker
2	Clarified Extract from MXE008 strain -control (pH6.9)
3	Clarified Extract from MXE008 strain pH adjustment to 5.0
4	Clarified Extract from MXE008 strain pH adjustment to 4.5
5	Clarified Extract from MXE008 strain pH adjustment to 3.0

Figure 8

SEQ ID NO: 1 shows the amino acid sequence of CDRH1 of CDP870.

Asp Tyr Gly Met Asn

SEQ ID NO: 2 shows the amino acid sequence of CDRH2 of CDP870
Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val Lys Gly

SEQ ID NO: 3 shows the amino acid sequence of CDRH3 of CDP870.

Gly Tyr Arg Ser Tyr Ala Met Asp Tyr

SEQ ID NO: 4 shows the amino acid sequence of CDRL1 of CDP870.

Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala

SEQ ID NO: 5 shows the amino acid sequence of CDRL2 of CDP870.

Ser Ala Ser Phe Leu Tyr Ser

SEQ ID NO: 6 shows the amino acid sequence of CDRL3 of CDP870.

Gln Gln Tyr Asn Ile Tyr Pro Leu Thr

SEQ ID NO: 7 shows the amino acid sequence of the light chain variable region CDP870 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

SEQ ID NO:8 shows the amino acid sequence of the heavy chain variable region CDP870.

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

SEQ ID NO: 9 shows the amino acid sequence of a grafted anti-TNFα Fab CDP870 light chain.

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

SEQ ID NO: 10 shows the amino acid sequence of a grafted anti-TNFα Fab CDP870 heavy chain.

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Ala Ala

SEQ ID NO: 11 is the nucleotide sequence of his-tagged DsbC.

```
atgaagaaag gttttatgtt gtttactttg ttagcggcgt tttcaggctt tgctcaggct
60
gatgacgcgg caattcaaca aacgttagcc aaaatgggca tcaaaagcag cgatattcag
120
cccgcgcctg tagctggcat gaagacagtt ctgactaaca gcggcgtgtt gtacatcacc
180
gatgatggta aacatatcat tcaggggcca atgtatgacg ttagtggcac ggctccggtc
240
aatgtcacca ataagatgct gttaaagcag ttgaatgcgc ttgaaaaaga gatgatcgtt
300
tataaagcgc cgcaggaaaa acacgtcatc accgtgttta ctgatattac ctgtggttac
360
tgccacaaac tgcatgagca aatggcagac tacaacgcgc tggggatcac cgtgcgttat
420
cttgctttcc cgcgccaggg gctggacagc gatgcagaga aagaaatgaa agctatctgg
480
tgtgcgaaag ataaaaacaa agcgtttgat gatgtgatgg caggtaaaag cgtcgcacca
540
gccagttgcg acgtggatat tgccgaccat tacgcacttg gcgtccagct tggcgttagc
600
ggtactccgg cagttgtgct gagcaatggc acacttgttc cgggttacca gccgccgaaa
660
gagatgaaag aatttctcga cgaacaccaa aaaatgacca gcggtaaaca ccatcaccat
720
```

SEQ ID NO: 12 is the amino acid sequence of his-tagged DsbC.

MKKGFMLFTL LAAFSGFAQA DDAAIQQTLA KMGIKSSDIQ PAPVAGMKTV LTNSGVLYIT
DDGKHIIQGP MYDVSGTAPV NVTNKMLLKQ LNALEKEMIV YKAPQEKHVI TVFTDITCGY
CHKLHEQMAD YNALGITVRY LAFPRQGLDS DAEKEMKAIW CAKDKNKAFD DVMAGKSVAP
ASCDVDIADH YALGVQLGVS GTPAVVLSNG TLVPGYQPPK EMKEFLDEHQ KMTSGKHHHH
HH

SEQ ID NO: 13 is the sequence of the wild-type spr gene including the signal sequence which is the first 26 amino acid residues

Met Val Lys Ser Gln Pro Ile Leu Arg Tyr Ile Leu Arg Gly Ile Pro Ala Ile Ala Val Ala Val Leu Leu Ser Ala Cys Ser Ala Asn Asn Thr Ala Lys Asn Met His Pro Glu Thr Arg Ala Val Gly Ser Glu Thr Ser Ser Leu Gln Ala Ser Gln Asp Glu Phe Glu Asn Leu Val Arg Asn Val Asp Val Lys Ser Arg Ile Met Asp Gln Tyr Ala Asp Trp Lys Gly Val Arg Tyr Arg Leu Gly Gly Ser Thr Lys Lys Gly Ile Asp Cys Ser Gly Phe Val Gln Arg Thr Phe Arg Glu Gln Phe Gly Leu Glu Leu Pro Arg Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys Ser Val Ser Arg Ser Asn Leu Arg Thr Gly Asp Leu Val Leu Phe Arg Ala Gly Ser Thr Gly Arg His Val Gly Ile Tyr Ile Gly Asn Asn Gln Phe Val His Ala Ser Thr Ser Ser Gly Val Ile Ile Ser Ser Met Asn Glu Pro Tyr Trp Lys Lys Arg Tyr Asn Glu Ala Arg Arg Val Leu Ser Arg Ser

SEQ ID NO: 14 is the sequence of the wild-type spr gene without the signal sequence.

Cys Ser Ala Asn Asn Thr Ala Lys Asn Met His Pro Glu Thr Arg Ala Val Gly Ser Glu Thr Ser Ser Leu Gln Ala Ser Gln Asp Glu Phe Glu Asn Leu Val Arg Asn Val Asp Val Lys Ser Arg Ile Met Asp Gln Tyr Ala Asp Trp Lys Gly Val Arg Tyr Arg Leu Gly Gly Ser Thr Lys Lys Gly Ile Asp Cys Ser Gly Phe Val Gln Arg Thr Phe Arg Glu Gln Phe Gly Leu Glu Leu Pro Arg Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys Ser Val Ser Arg Ser Asn Leu Arg Thr Gly Asp Leu Val Leu Phe Arg Ala Gly Ser Thr Gly Arg His Val Gly Ile Tyr Ile Gly Asn Asn Gln Phe Val His Ala Ser Thr Ser Ser Gly Val Ile Ile Ser Ser Met Asn Glu Pro Tyr Trp Lys Lys Arg Tyr Asn Glu Ala Arg Arg Val Leu Ser Arg Ser

SEQ ID NO: 15 is the DNA sequence of a mutated knockout Tsp gene including the 6 nucleotides ATGAAT upstream of the start codon.

atgaattcgt ttttaggctt accgcgttag ctggcctgct tgcaatagca ggccagacat 60
taattgtaga agatatcacg cgtgctgatc aaattccggt attaaaggaa gagacgcagc 120
atgcgacggt aagtgagcgc gtaacgtcgc gcttcacccg ttctcattat cgccagttcg 180
acctcgatca ggcattttcg gccaaaatct ttgaccgcta cctgaatctg ctcgattaca 240
gccacaacgt gctgctggca agcgatgttg aacagttcgc gaaaaagaaa accgagttag 300
gcgatgaact gcgttcaggc aaactcgacg ttttctacga tctctacaat ctggcgcaaa 360
agcgccgttt tgagcgttac cagtacgctt tgtcggtact ggaaaagccg atggatttca 420
ccggcaacga cacttataac cttgaccgca gcaaagcgcc ctggccgaaa aacgaggctg 480
agttgaacgc gctgtgggac agtaaagtca aattcgacga gttaagcctg aagctgacag 540
gaaaaacgga taaagaaatt cgtgaaaccc tgactcgccg ctacaaattt gccattcgtc 600
gtctggcgca aaccaacagc gaagatgttt tctcgctggc aatgacggcg tttgcgcgtg 660
aaatcgaccc gcataccaac tatctttccc cgcgtaatac cgaacagttc aacactgaaa 720
tgagtttgtc gctggaaggt attggcgcag tgctgcaaat ggatgatgac tacaccgtta 780
tcaattcgat ggtggcaggt ggtccggcag cgaagagtaa agctatcagc gttggtgaca 840
aaattgtcgg tgttggtcaa acaggcaagc cgatggttga cgtgattggc tggcgtcttg 900
atgatgtggt tgccttaatt aaagggccga agggcagtaa agttcgtctg gaaattttac 960
ctgctggtaa agggaccaag acccgtactg taacgttgac ccgtgaacgt attcgtctcg 1020
aagaccgcgc ggttaaaatg tcggtgaaga ccgtcggtaa agagaaagtc ggcgtgctgg 1080
atattccggg cttctatgtg ggtttgacag acgatgtcaa agtgcaactg cagaaactgg 1140
aaaaacagaa tgtcagcagc gtcatcatcg acctgcgtag caatggcggt ggggcgttaa 1200
ctgaagccgt atcgctctcc ggtctgttta ttcctgcggg tcccattgtt caggtccgcg 1260
ataacaacgg caaggttcgt gaagatagcg ataccgacgg acaggttttc tataaaggcc 1320
cgctggtggt gctggttgac cgcttcagtg cttcggcttc agaaatcttt gccgcggcaa 1380
tgcaggatta cggtcgtgcg ctggttgtgg gtgaaccgac gtttggtaaa ggcaccgttc 1440
agcaataccg ttcattgaac cgtatttacg atcagatgtt acgtcctgaa tggccagcgc 1500
tgggttctgt gcagtacacg atccagaaat tctatcgcgt taacggcggc agtacgcaac 1560
gtaaaggcgt aacgccagac atcatcatgc cgacgggtaa tgaagaaacg gaaacgggtg 1620
agaaattcga agataacgcg ctgccgtggg atagcattga tgccgcgact tatgtgaaat 1680
caggagattt aacggccttt gaaccggagc tgctgaagga acataatgcg cgtatcgcga 1740

aagatcctga gttccagaac atcatgaagg atatcgcgcg cttcaacgct atgaaggaca 1800

agcgcaatat cgtttctctg aattacgctg tgcgtgagaa agagaataat gaagatgatg 1860

cgacgcgtct ggcgcgtttg aacgaacgct ttaaacgcga aggtaaaccg gagttgaaga 1920

aactggatga tctaccgaaa gattaccagg agccggatcc ttatctggat gagacggtga 1980

atatcgcact cgatctggcg aagcttgaaa aagccagacc cgcggaacaa cccgctcccg 2040

tcaagtaa 2048

SEQ ID NO: 16 shows the oligonucleotide cassette encoding intergenic sequence 2 (IGS2) for *E. coli* Fab expression.

gagctcacca gtaacaaaaa gttttaatag aggggagtgt taaaatgaag aagactgcta 60

tagcaattg 69

Figure 9

