FIGURE 1

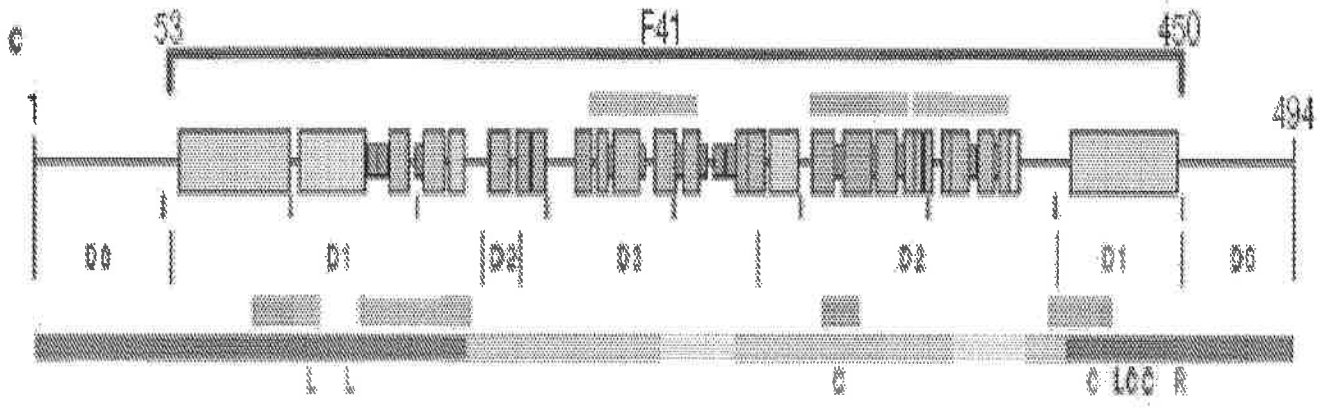


FIGURE 2

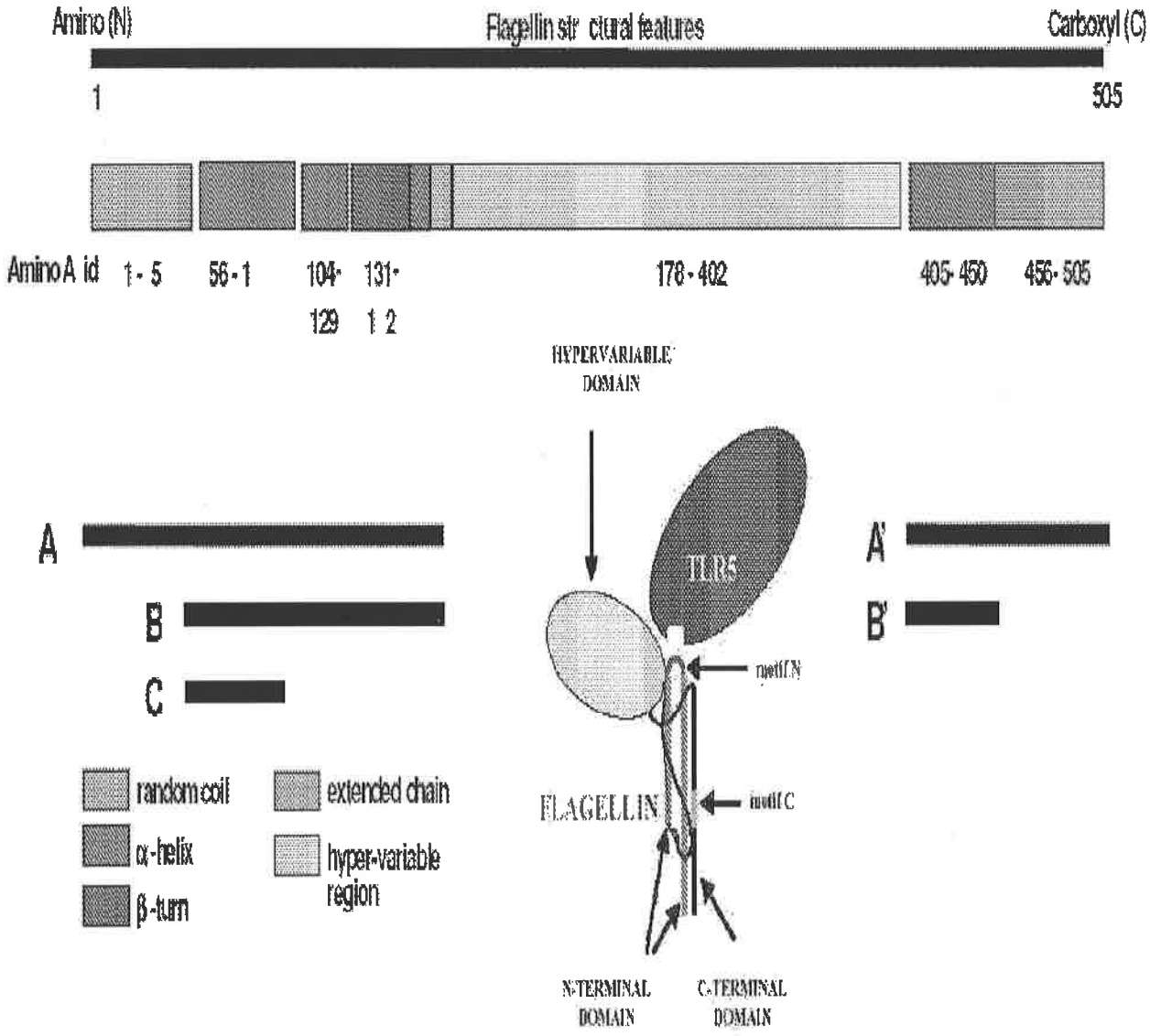

Amino (N)
Flagellin structural features
Carboxyl (C)
1
505
Amino Acid
1-5
56-1
104-129
131-12
178-402
405-450
456-505
HYPERVARIABLE DOMAIN
A
B
C
A'
B'
HR5
motif N
motif C
FLAGELLIN
random coil
α-helix
β-turn
extended chain
hyper-variable region
N-TERMINAL DOMAIN
C-TERMINAL DOMAIN

FIGURE 3

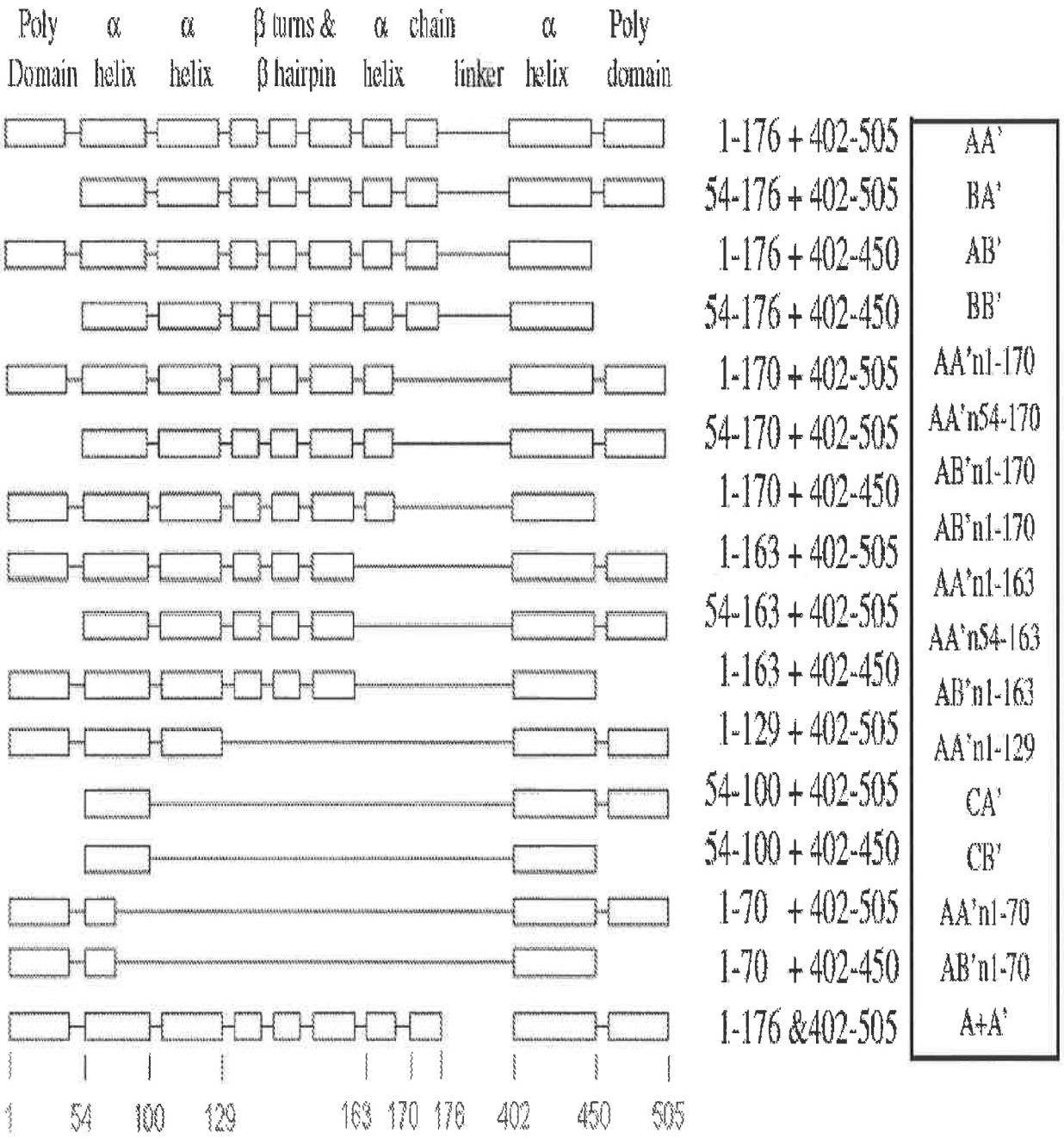

Poly Domain
α helix
α helix
β turns & β hairpin
α helix
chain linker
α helix
Poly domain
1-176 + 402-505
AA'
54-176 + 402-505
BA'
1-176 + 402-450
AB'
54-176 + 402-450
BB'
1-170 + 402-505
AA'n1-170
54-170 + 402-505
AA'n54-170
1-170 + 402-450
AB'n1-170
1-163 + 402-505
AB'n1-170
54-163 + 402-505
AA'n1-163
1-163 + 402-450
AA'n54-163
1-129 + 402-505
AB'n1-163
54-100 + 402-505
AA'n1-129
54-100 + 402-450
CA'
1-70 + 402-505
CB'
1-70 + 402-450
AA'n1-70
1-176 &402-505
AB'n1-70
A+A'
1
54
100
129
163
170
176
402
450
505

FIGURE 4

AA'

Nucleotide sequence (990 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTTGATGGGTTCAATGTTAATTCCCCGGGAATTTCCGGTGGTGGTGGTGGAATT
CTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCT
AACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTG
GGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAAT
CTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATG
TCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTT
CCGCAAAACGTCCTCTCTTTACTGCGTTAG

Protein sequence (329 AA):

MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPMAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GLDGFNVNSPGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFD
SAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AB'

Nucleotide sequence (825 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTTGATGGGTTCAATGTTAATTCCCCGGGAATTTCCGGTGGTGGTGGTGGAATT
CTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCT
AACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTG
GGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (274 AA):

MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPMAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GLDGFNVNSPGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFD
SAITNL

FIGURE 4, CONTINUED

BA'

Nucleotide sequence (831 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATTGATGTCAAAAGCCTTGGCCTTGATGGGTTCAATGTTAAT**TCCCCGGGAATT**
TCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCC
GCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTG
GACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAAC
CTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTAT
GCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTT
CTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGTTAG

Protein sequence (276 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPF*TSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKIDVKSLGLDGFNVN**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVD
AVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVP
QNVLSLLR

BB'

Nucleotide sequence (666 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATTGATGTCAAAAGCCTTGGCCTTGATGGGTTCAATGTTAAT**TCCCCGGGAATT**
TCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCC
GCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTG
GACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAAC
CTTTAG

Protein sequence (221 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPF*TSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKIDVKSLGLDGFNVN**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVD
AVRSSLGAIQNRFDSAITNL

CA'

Nucleotide sequence (603 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT

FIGURE 4, CONTINUED

GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
TCCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAAT
GAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCA
TTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCA
GCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGCCGTATCGAA
GATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTGCAGCAGGCT
GGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGT
TAG

Protein sequence (200 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQAT**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAI
QNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

CB'

Nucleotide sequence (438 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
TCCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAAT
GAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCA
TTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCA
GCCATTACCAACCTTTAG

Protein sequence (145 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQAT**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAI
QNRFDSAITNL

A

Nucleotide sequence (639 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGC*ACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGTCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTGTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTTGATGGGTTCAATGTTAAT**TCCCCGGGA**TGA

Protein sequence (212 AA), last three amino acids are derived from primer and pRSETb polylinker:

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPMA*QVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GLDGFNVN**SPG**

FIGURE 4, CONTINUED

B

Nucleotide sequence (480 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGT
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTGTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATTGATGTGAAAAGCCTTGGCCTTGATGGGTTCAATGTTAATTCCCCGGGATGA

Protein sequence (159 AA), last three amino acids are derived from primer and pRSETb polylinker:

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKIDVKSLGLDGFNVN**SPG**

C

Nucleotide sequence (252 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGT
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
TCCCCGGGATGA

Protein sequence (83 AA), last three amino acids are derived from primer and pRSETb polylinker:

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQAT**SPG**

GST-A'

Nucleotide sequence (1038 bp), GST highlighted:

ATGTCCCCTATACTAGGTTATTGGAAAATTAGGGCCTTGTGCAACCCACTCGACTTCTT
TTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAA
TGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGAT
GGTGATGTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAC
ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG
GATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTT
GATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAA
ACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAA
AACGTATTGAAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA
TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGAT
CTGGTTCCGCGTGGA**TCCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATG**
GGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCT
TCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAA
AACCGTTTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCG
CGTAGCCGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAG
ATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTC
CTCTCTTTACTGCGTTAG

Protein sequence (345 AA):

FIGURE 4, CONTINUED

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFE
DRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAW
PLQGWQATFGGGDHPPKSDLVPRG**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSK
VDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQ
VPQNVLSLLR

GST-B'

Nucleotide sequence (873 bp), GST highlighted:

ATGTCCCCTATACTAGTTATTGGAAATTRAGGCCTTGTGCAACCCACTCGACTTCTT
TTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAA
TGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGAT
GGTGATGTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAC
ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG
GATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTT
GATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAA
ACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAA
AAACGTATTGAAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA
TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGAT
CTGGTTCCGCGTGGA**TCCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATG**
GGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCT
TCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAA
AACCGTTTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (290 AA):

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFE
DRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAW
PLQGWQATFGGGDHPPKSDLVPRG**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSK
VDAVRSSLGAIQNRFDSAITNL

AA'n1-170

Nucleotide sequence (972 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTT**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGC
CGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTG
CAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAAGCAGGTTCCGCAAAACGTCCTCTCT

FIGURE 4, CONTINUED

TTACTGCGTTAG

Protein sequence (323 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPMAQ*VINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GL**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL
GNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AA'n1-163

Nucleotide sequence (951 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATT**ATCCCGGGAATT**
TCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCC
GCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTG
GACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAAC
CTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTAT
GCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTT
CTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGTTAG

Protein sequence (316 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPMAQ*VINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKI**IPGIS**
GGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNL
NSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AA'n54-170

Nucleotide sequence (813 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATTGATGTGAAAAGCCTTGGCCTT**ATCCCGGGAATTTCCGGTGGTGGTGGTGGA**
ATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACC
GCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCT
CTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACC
AATCTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAAT
ATGTCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAG
GTTCCGCAAAACGTCCTCTCTTTACTGCGTTAG

FIGURE 4, CONTINUED

Protein sequence (270 AA):

*MRGSHHHHHH*GMASMTGGQQMGRDLYDDDDKDPFTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKIDVKSLGL**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSL
GAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSL
LR

AA'n54-163

Nucleotide sequence (792 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGTTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATT**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGC
CGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTG
CAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCT
TTACTGCGTTAG

Protein sequence (263 AA):

*MRGSHHHHHH*GMASMTGGQQMGRDLYDDDDKDPFTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKI**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRF
DSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AB'n1-170 (or AA'n1-170e402-450)

Nucleotide sequence (807 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCT**TATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (268 AA):

*MRGSHHHHHH*GMASMTGGQQMGRDLYDDDDKDP*M*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN

FIGURE 4, CONTINUED

GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GLIPGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

AB'n1-163 (or AA'n1-163c402-450)

Nucleotide sequence (786 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATT**ATCCCGGGAATT**
TCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCC
GCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTG
GACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAAC
CTTTAG

Protein sequence (261 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKI**IPGIS**
GGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

AA'n1-129

Nucleotide sequence (849 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAG**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACATTA
ATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGAT
TCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTT
GATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGCCGT
ATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTGCAG
CAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCTTTA
CTGCGTTAG

Protein sequence (282 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQ**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDS
ALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLA
QANQVPQNVLSLLR

FIGURE 4, CONTINUED

AA'n54-129

Nucleotide sequence (690 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAG**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATT**
CTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCT
AACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTG
GGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAAT
CTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATG
TCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTT
CCGCAAAACGTCCTCTCTTTACTGCGTTAG

Protein sequence (229 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQ**IPGISGGGGGILDSMG**TLINEDAAA
AKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMS
KAQILQQAGTSVLAQANQVPQNVLSLLR

AB'n1-129

Nucleotide sequence (684 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGG*CACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAG**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACATTA
ATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGAT
TCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTT
GATTCAGCCATTACCAACCTTTAG

Protein sequence (227 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQ**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDS
ALSKVDAVRSSLGAIQNRFDSAITNL

AB'n54-129

Nucleotide sequence (525 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT

FIGURE 4, CONTINUED

AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAG**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATT**
CTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCT
AACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTG
GGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (174 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPF*TSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQ**IPGISGGGGGILDSMG**TLINEDAAA
AKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

AA'n1-100

Nucleotide sequence (762 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGG*CACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT**ATCCCGGGAATTTCCGGTGGT**
GGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAG
AAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTT
CGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTGGCAAT
ACGGTAACCAATCTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTATGCAACGGAA
GTTTCTAATATGTCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAG
GCTAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGTTAG

Protein sequence (253 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQAT**I**
PGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNT
VTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AB'n1-100

Nucleotide sequence (597 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGG*CACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT**ATCCCGGGAATTTCCGGTGGT**
GGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAG
AAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTT
CGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (198 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQAT**I**
PGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

FIGURE 4, CONTINUED

AA'n1-70

Nucleotide sequence (672 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGAC**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGC
CGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTG
CAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCT
TTACTGCGTTAG

Protein sequence (223 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNAND**IPGISGGGGGILDSMG**TLINEDAAAAKKSTA
NPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQ
QAGTSVLAQANQVPQNVLSLLR

AB'n1-70

Nucleotide sequence (507 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGAC**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (168 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNAND**IPGISGGGGGILDSMG**TLINEDAAAAKKSTA
NPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

FIGURE 5A

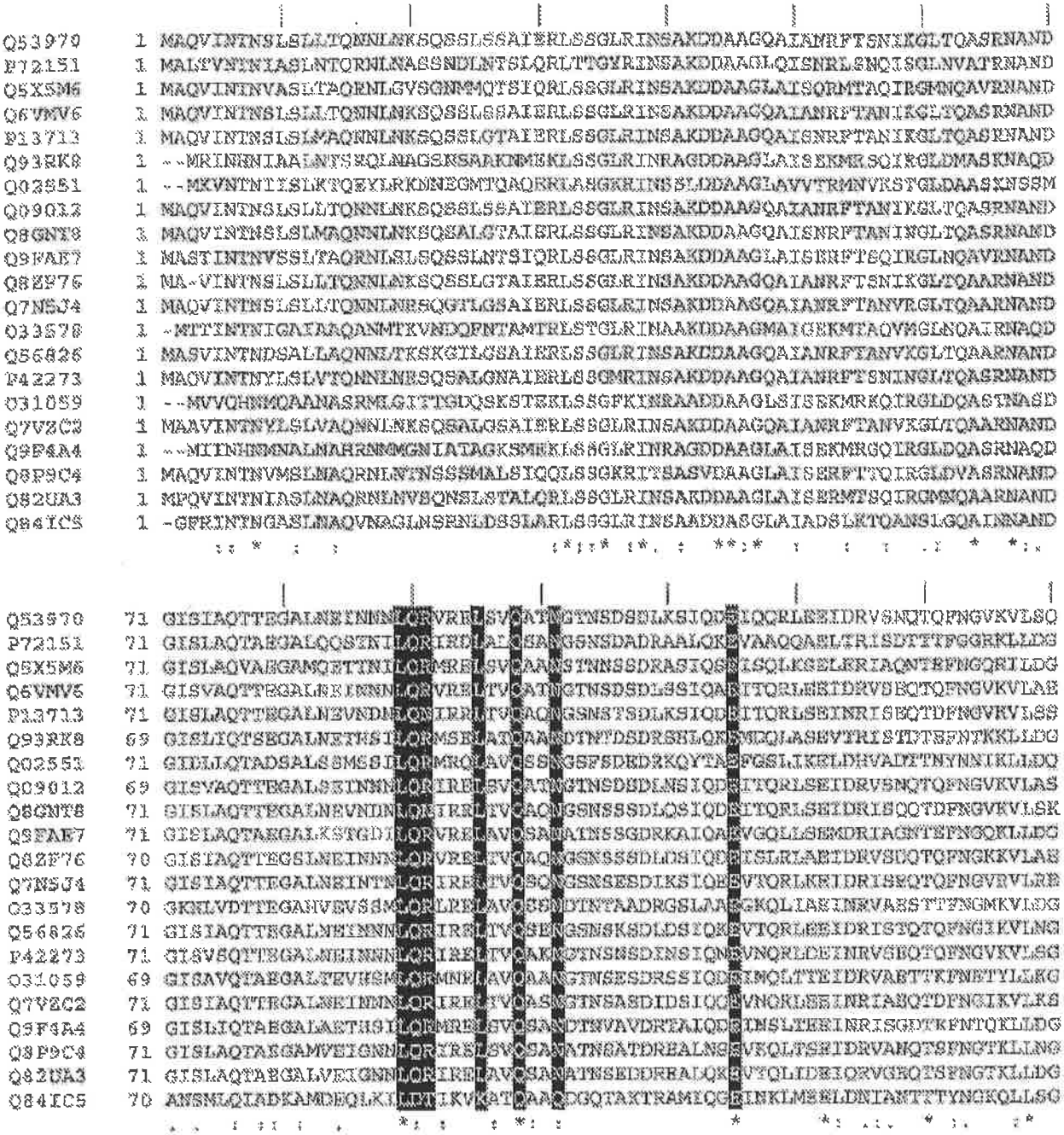

Q53979
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Q7NSJ4
Q33578
Q56826
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O31059
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Q9F4A4
Q8P9C4
Q82UA3
Q84IC5

FIGURE 5A, CONTINUED

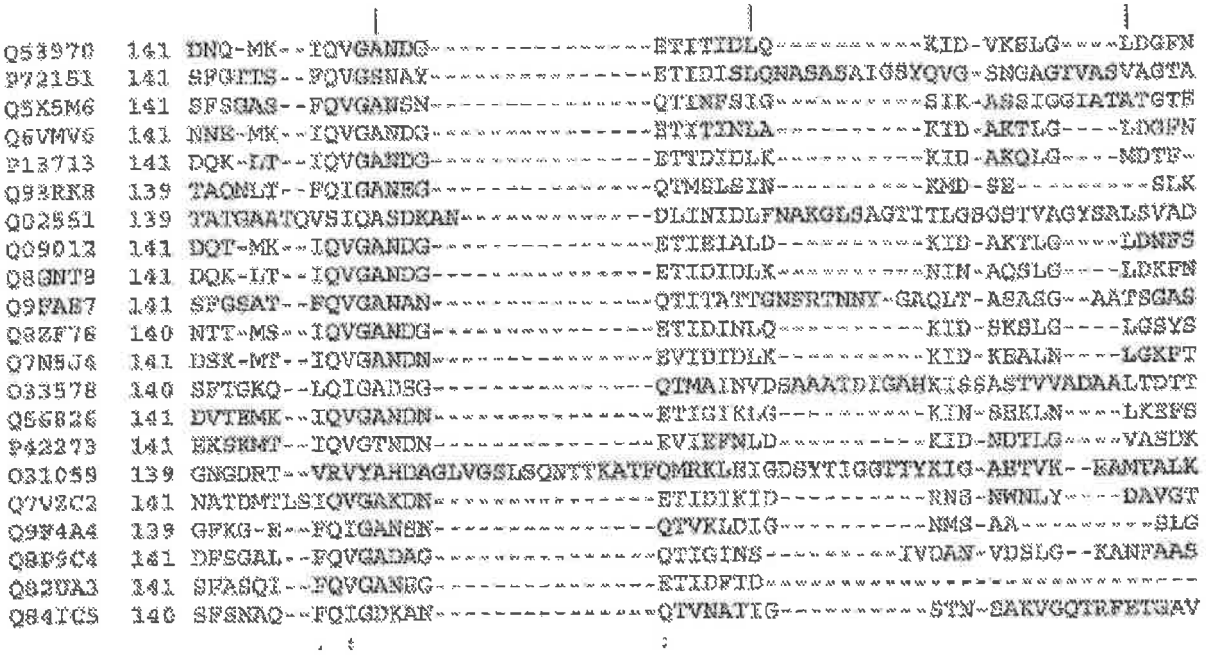


FIGURE 5B

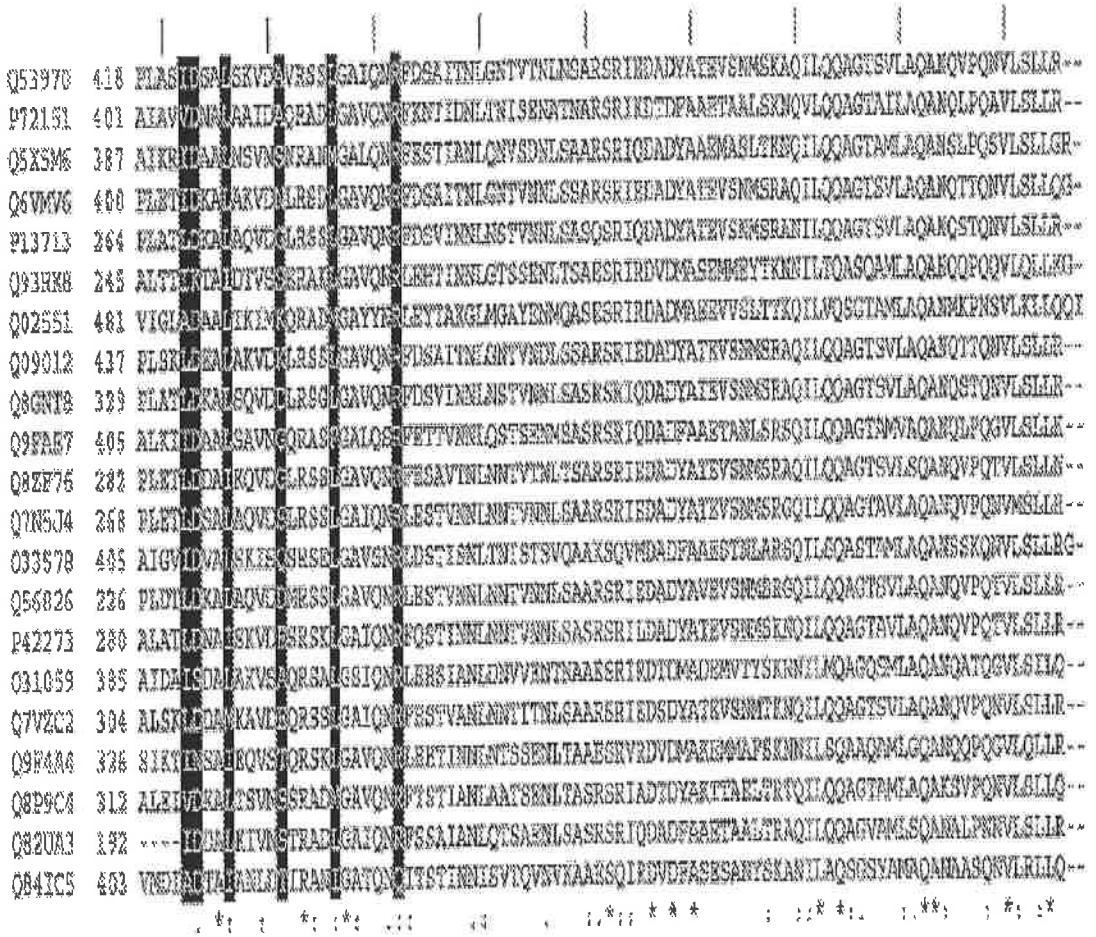


FIGURE 6

Homo Sapiens TLR5

```
   1 mgdhldlllg vvlmagpvfg ipscsfdgri afyrfcnltq vpqvlntter lllsfnyirt
  61 vtassfpfle qlqllelgsq ytpltidkea frnlpnlril dlgsskiyfl hpdafqglfh
 121 lfelrlyfcg lsdavlkdgy frnlkaltrl dlsknqirsl ylhpsfgkln slksidfssn
 181 qiflvcehel eplqgktlsf fslaanslys rvsvdwgkcm npfrnmvlei ldvsgngwtv
 241 ditgnfsnai sksqafslil ahhimgagfg fhnikdpdqn tfaglarssv rhldlshgfv
 301 fslnsrvfet lkdlkvlnla ynkinkiade afygldnlqv lnlsynllge lyssnfyglp
 361 kvayidlqkn hiaiiqdqtf kfleklqtld lrdnalttih fipsipdifl sgnklvtlpk
 421 inltanlihl senrlenldi lyfllrvphl qililnqnrf sscsgdqtps enpsleqlfl
 481 genmlqlawe telcwdvfeg lshlqvlyln hnylnslppg vfshltalrg lslnsnrltv
 541 lshndlpanl eildisrnql lapnpdvfvs lsvldithnk ficecelstf inwlnhtnvt
 601 iagppadiyc vypdsfsgvs lfslstegcd eeevlkslkf slfivctvtl tlflmtiltv
 661 tkfrgfcfic yktaqrlvfk dhpqgtepdm ykydaylcfs skdftwvqna llkhldtqys
 721 dqnrfnlcfe erdfvpgenr ianiqdaiwn srkivclvsr hflrdgwcle afsyaqgrcl
 781 sdlnsalimv vvgslsqyql mkhqsirgfv qkqqylrwpe dfqdvgwflh klsqqilkke
 841 kekkkdnnip lqtvatis
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FIGURE 7

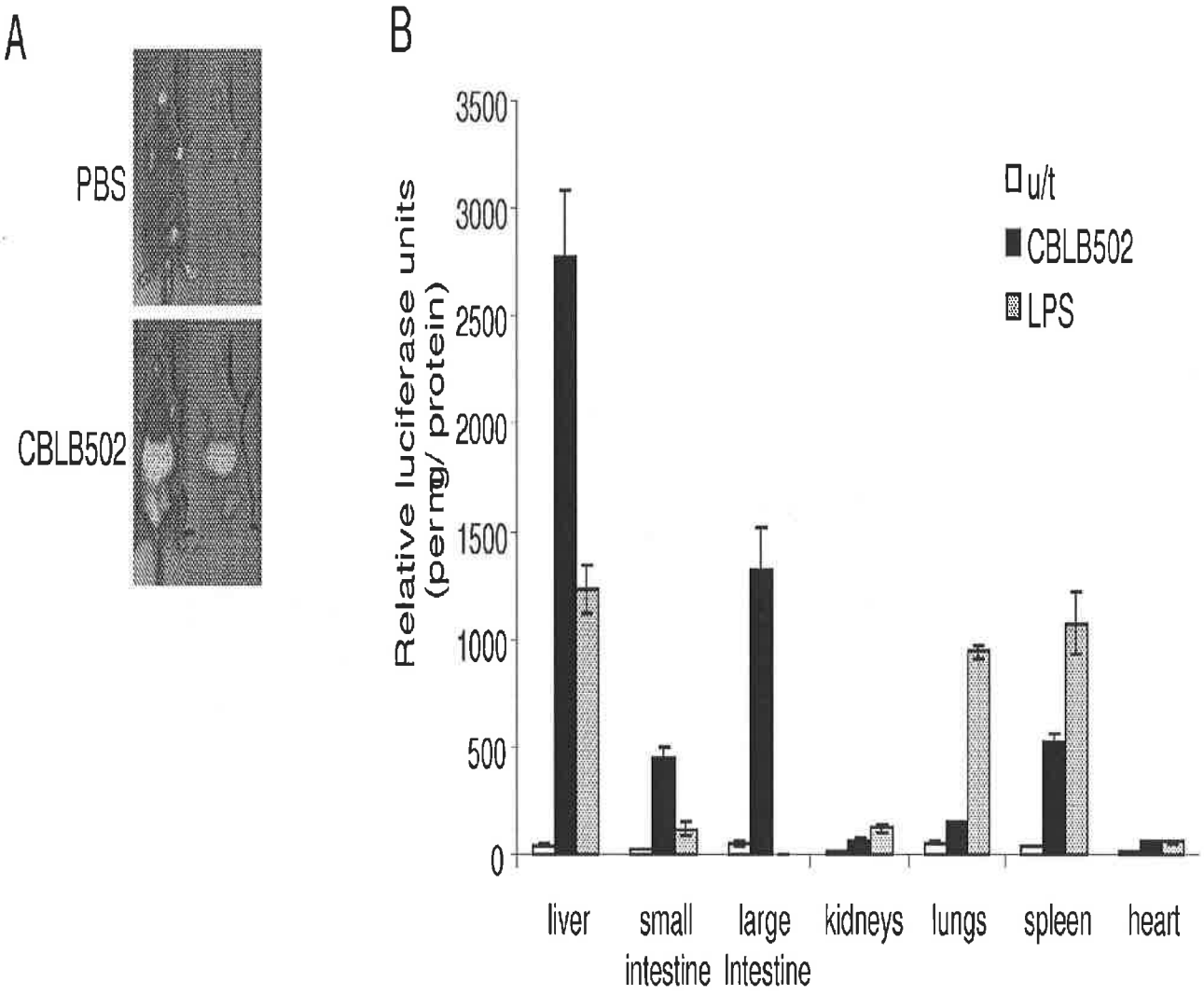

A
PBS
CBLB502
B
Relative luciferase units (per mg/ protein)
3500
3000
2500
2000
1500
1000
500
0
u/t
CBLB502
LPS
liver
small intestine
large Intestine
kidneys
lungs
spleen
heart

FIGURE 7, CONTINUED

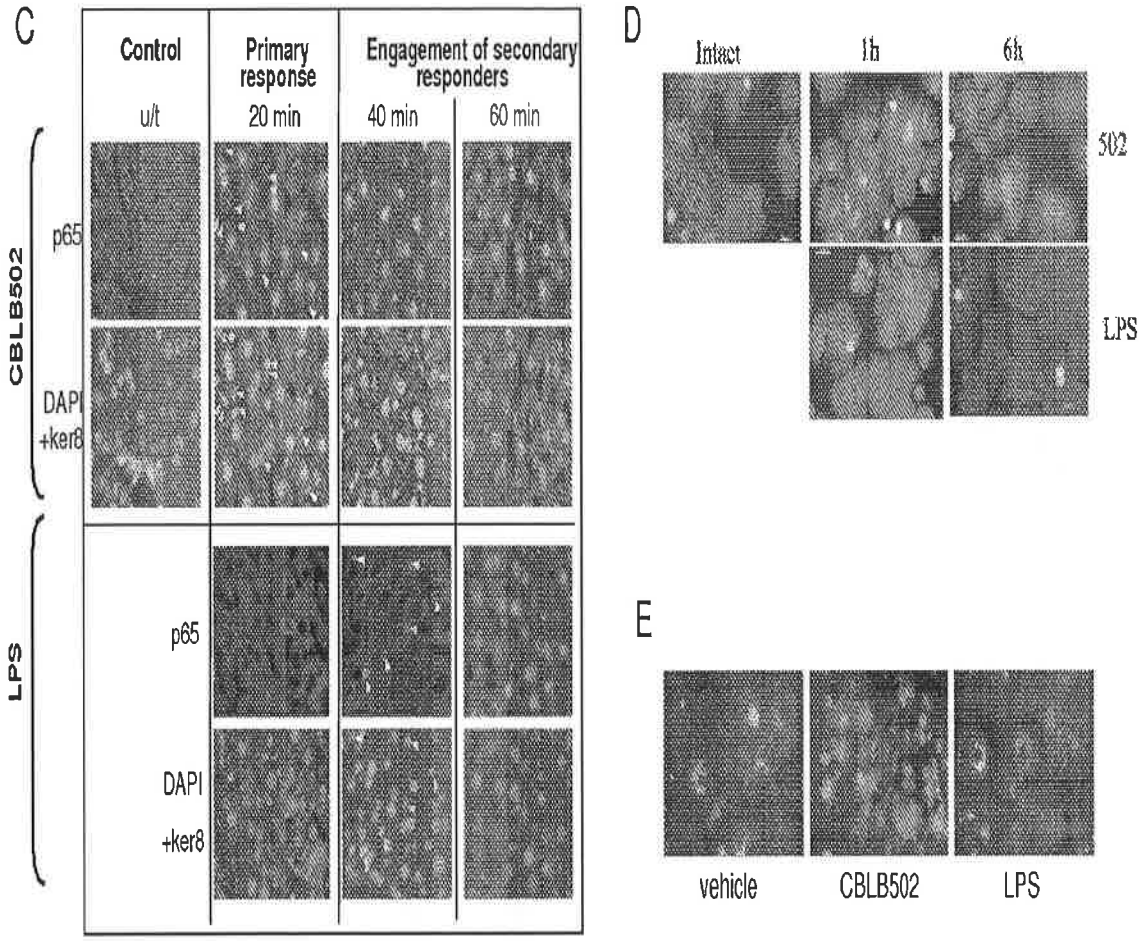


FIGURE 8

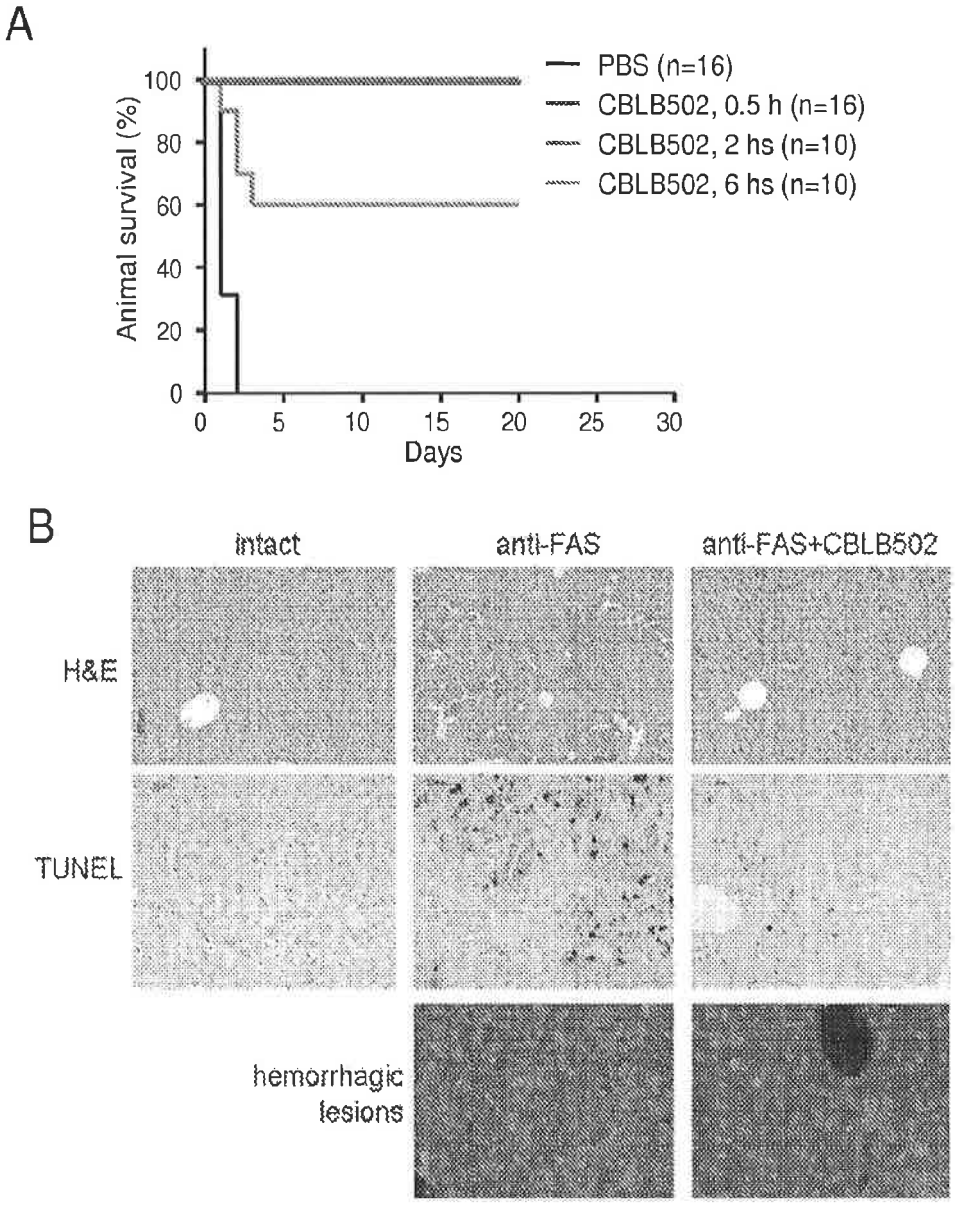
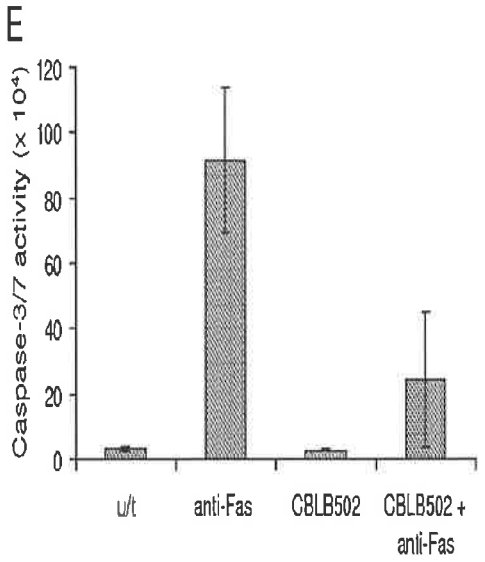
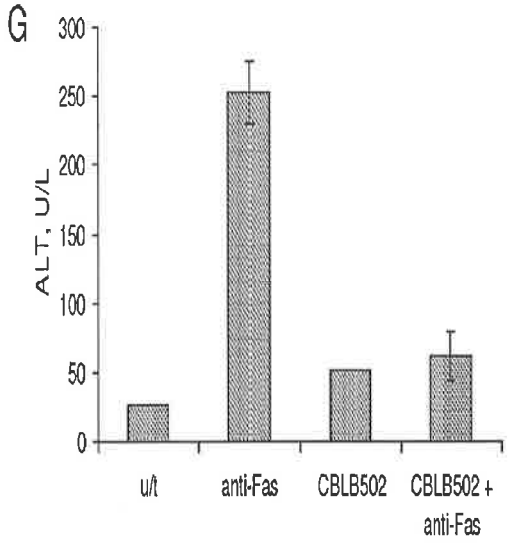

A
Animal survival (%)
100
80
60
40
20
0
0
5
10
15
20
25
30
Days
PBS (n=16)
CBLB502, 0.5 h (n=16)
CBLB502, 2 hs (n=10)
CBLB502, 6 hs (n=10)
B
intact
anti-FAS
anti-FAS+CBLB502
H&E
TUNEL
hemorrhagic lesions

FIGURE 8, CONTINUED





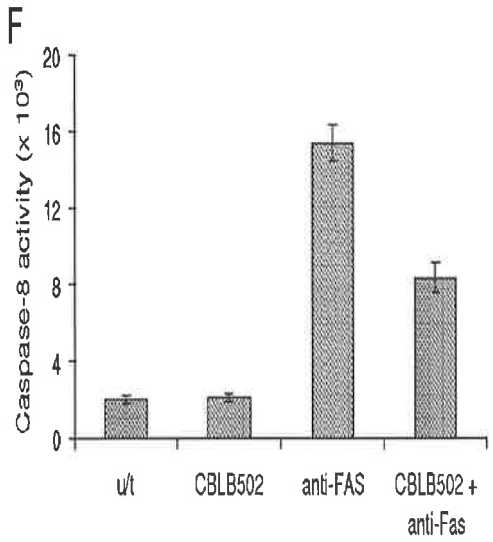


FIGURE 9

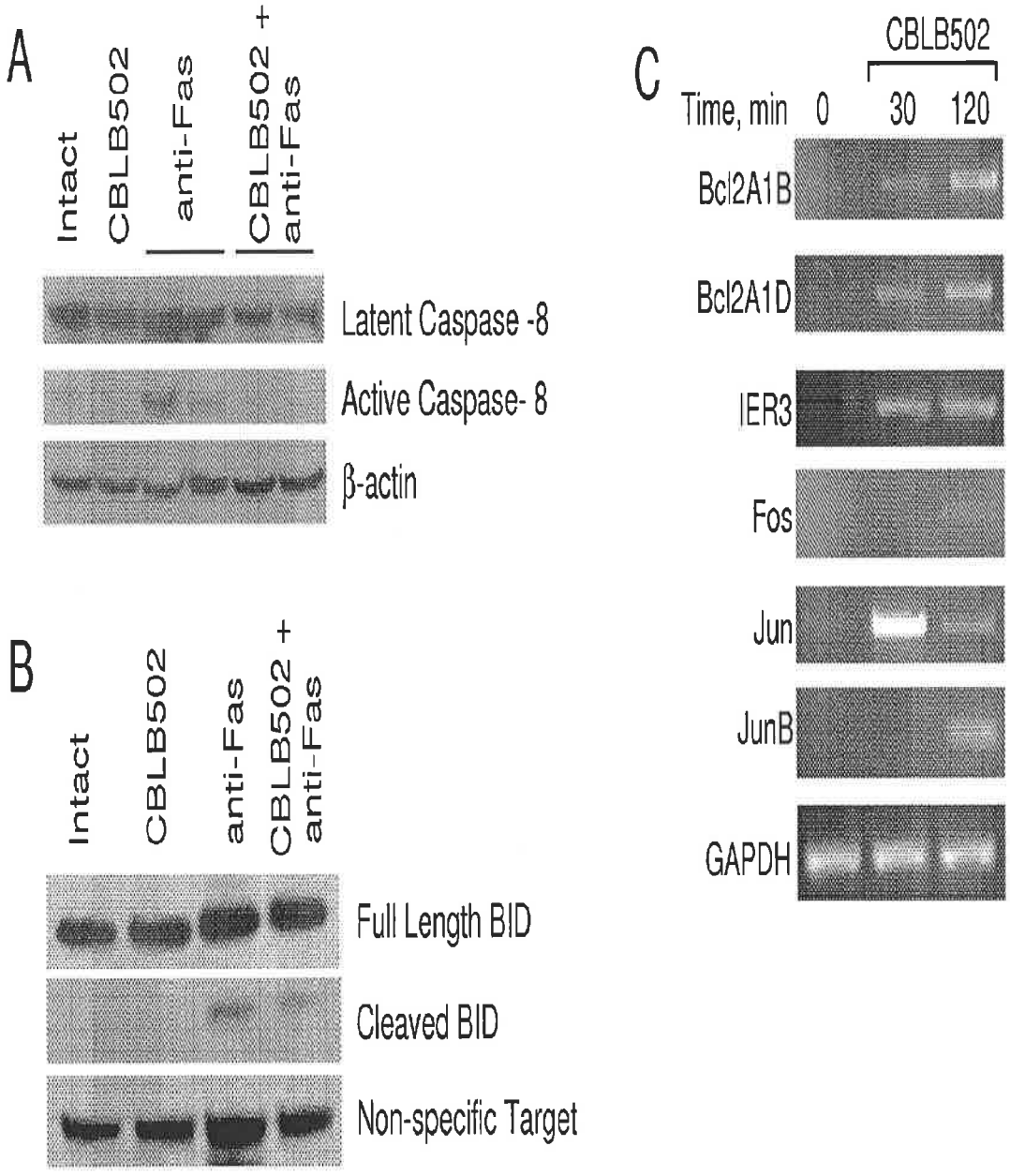

A
Intact
CBLB502
anti-Fas
CBLB502 + anti-Fas
Latent Caspase -8
Active Caspase- 8
β-actin
B
Intact
CBLB502
anti-Fas
CBLB502 + anti-Fas
Full Length BID
Cleaved BID
Non-specific Target
C
CBLB502
Time, min 0 30 120
Bcl2A1B
Bcl2A1D
IER3
Fos
Jun
JunB
GAPDH

FIGURE 9, CONTINUED

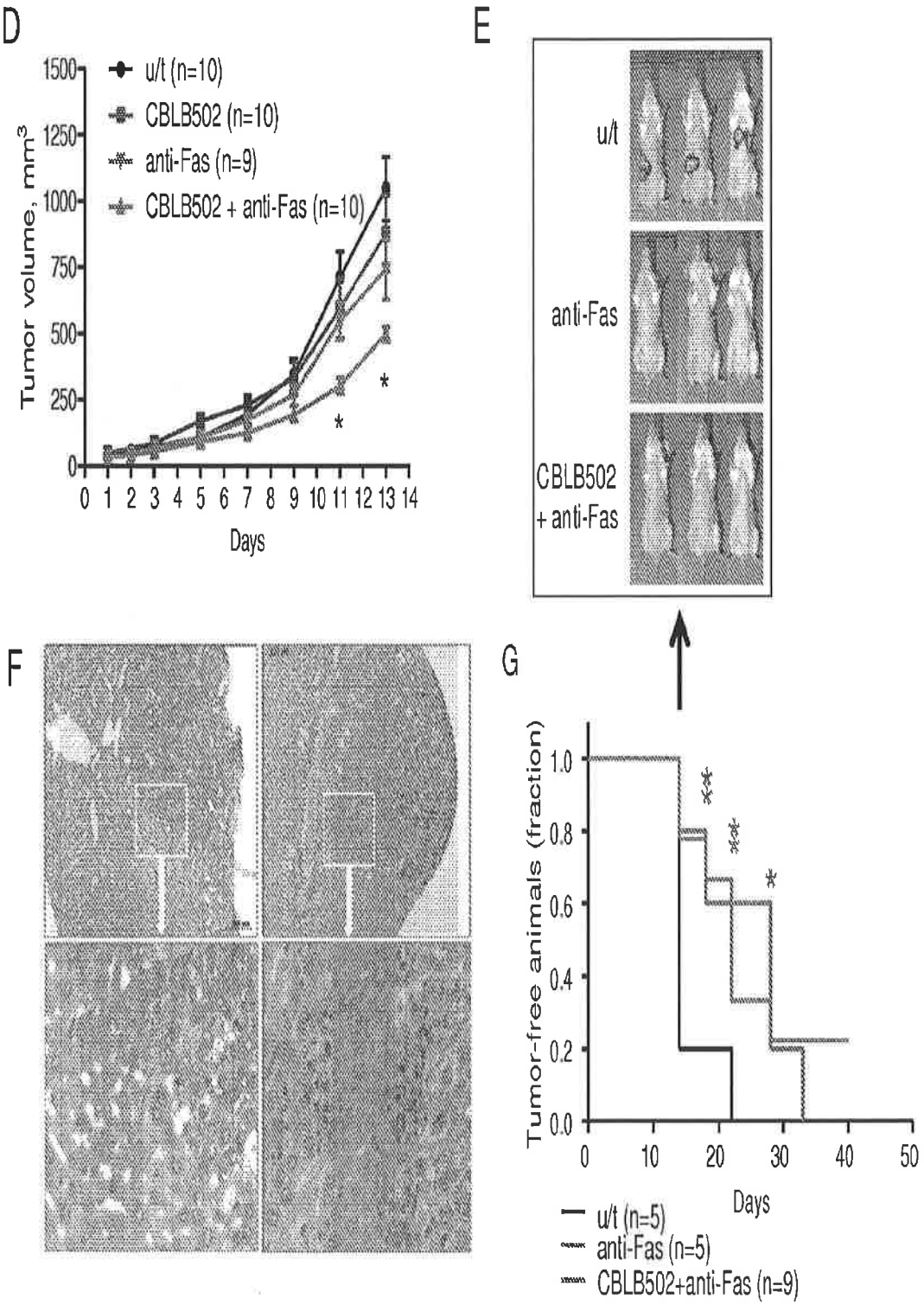


FIGURE 10

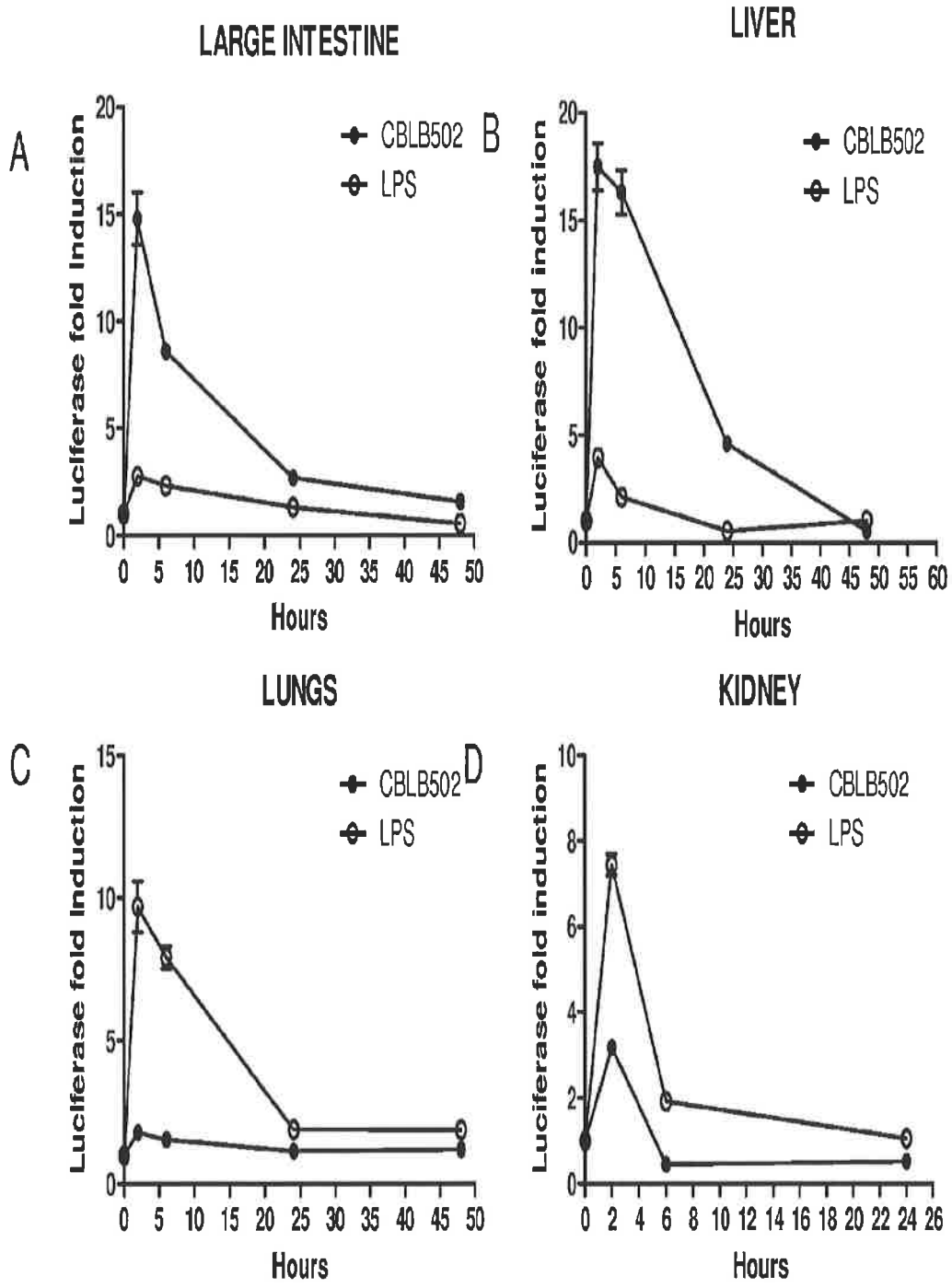

A
LARGE INTESTINE
Luciferase fold Induction
CBLB502
LPS
Hours
B
LIVER
Luciferase fold induction
CBLB502
LPS
Hours
C
LUNGS
Luciferase fold Induction
CBLB502
LPS
Hours
D
KIDNEY
Luciferase fold induction
CBLB502
LPS
Hours

FIGURE 11

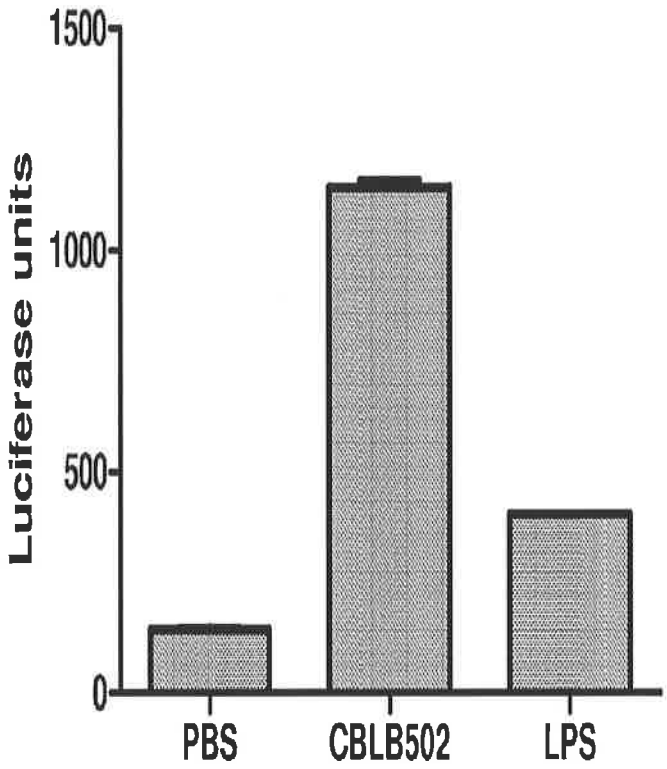


FIGURE 12

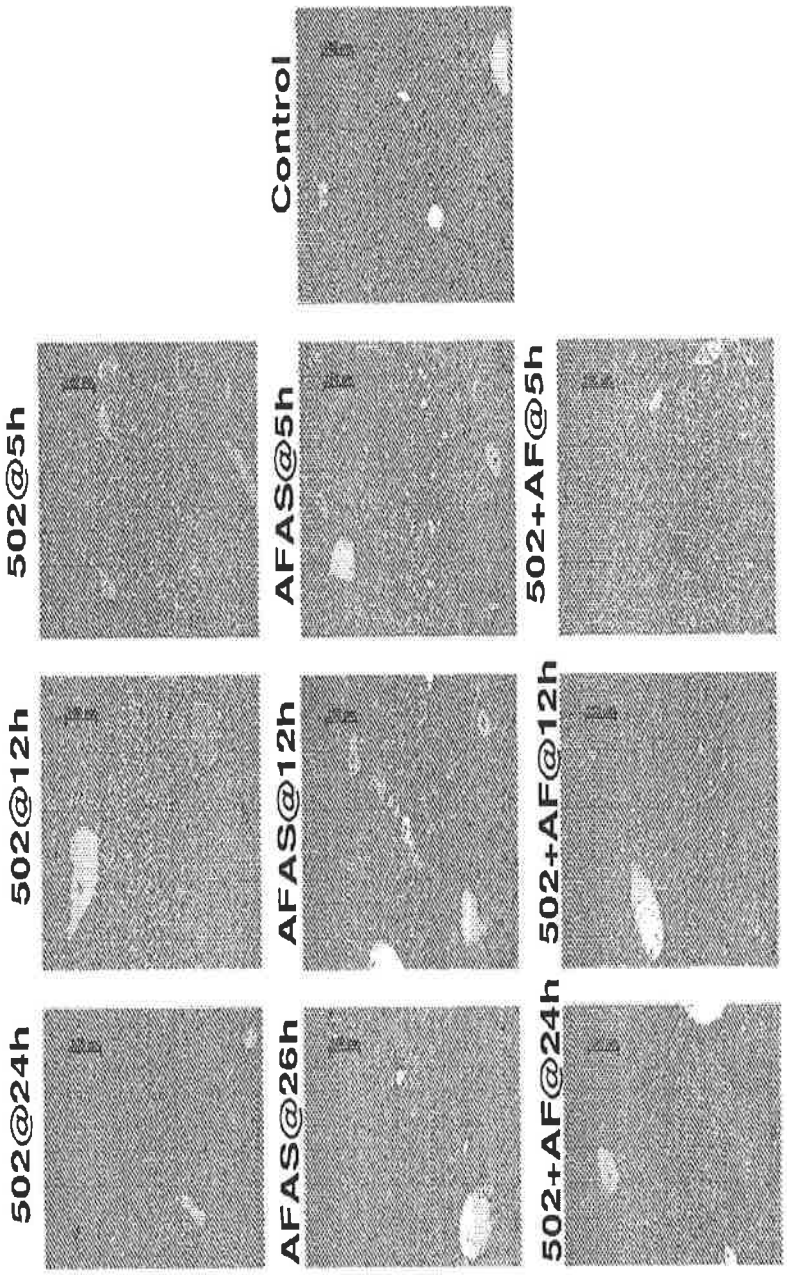

Control
502@5h
AFAS@5h
502+AF@5h
502@12h
AFAS@12h
502+AF@12h
502@24h
AFAS@26h
502+AF@24h

FIGURE 13

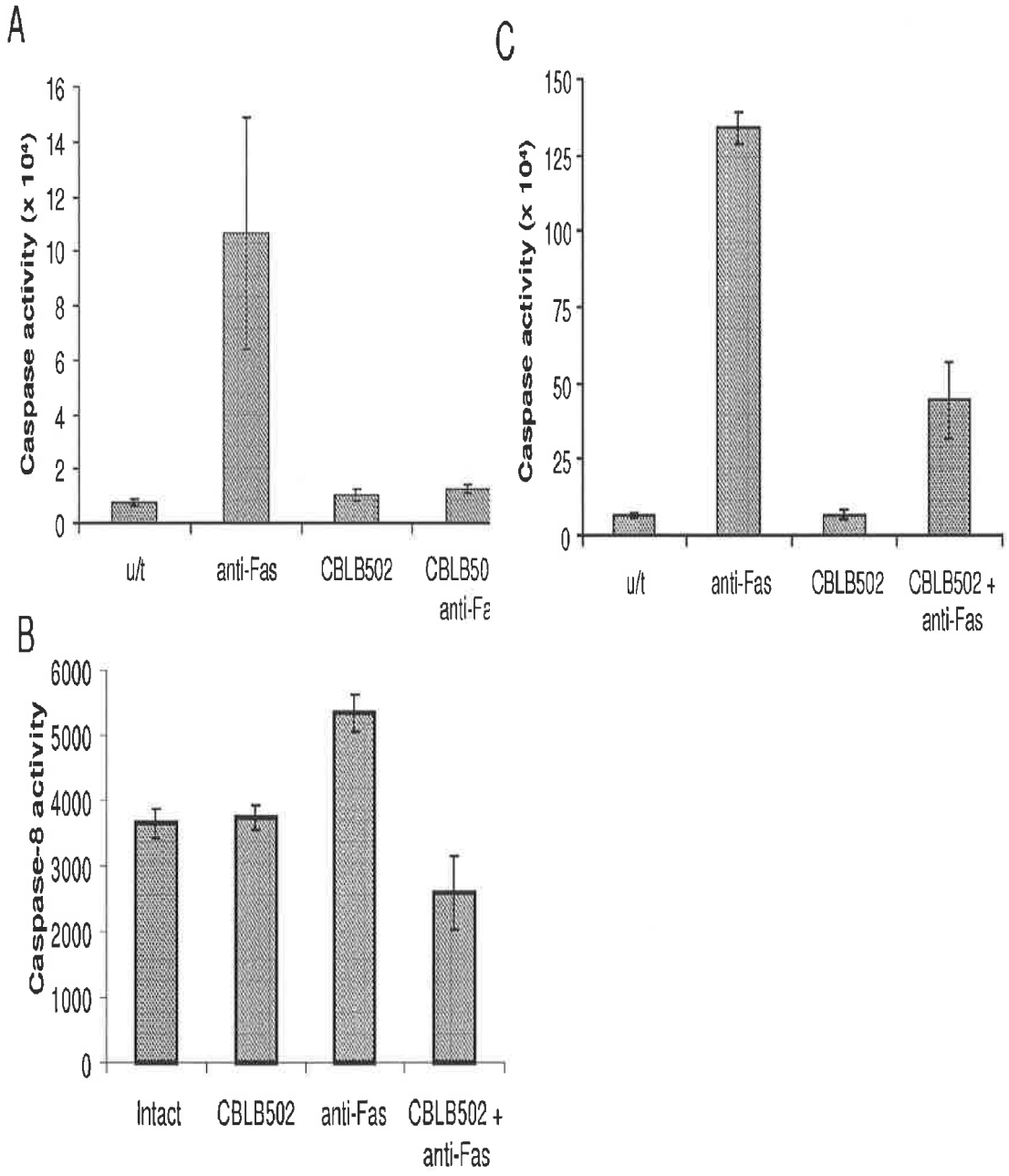

A
Caspase activity (x 10⁴)
16
14
12
10
8
6
4
2
0
u/t
anti-Fas
CBLB502
CBLB50
anti-Fa
C
Caspase activity (x 10⁴)
150
125
100
75
50
25
0
u/t
anti-Fas
CBLB502
CBLB502 +
anti-Fas
B
Caspase-8 activity
6000
5000
4000
3000
2000
1000
0
Intact
CBLB502
anti-Fas
CBLB502 +
anti-Fas

FIGURE 14

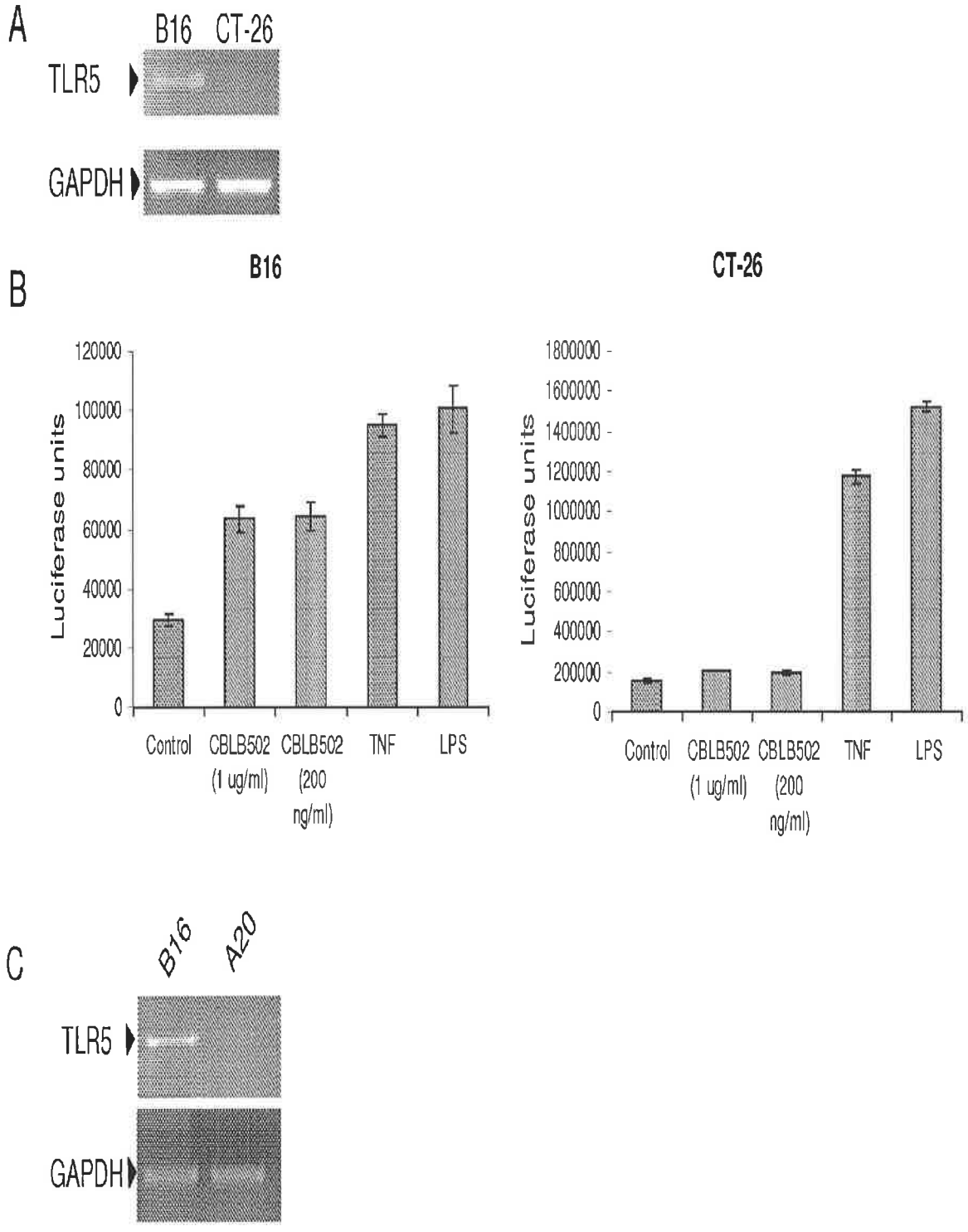

A
B16
CT-26
TLR5
GAPDH
B
B16
CT-26
Luciferase units
120000
100000
80000
60000
40000
20000
0
1800000
1600000
1400000
1200000
1000000
800000
600000
400000
200000
Control
CBLB502 (1 ug/ml)
CBLB502 (200 ng/ml)
TNF
LPS
C
B16
A20
TLR5
GAPDH

FIGURE 15

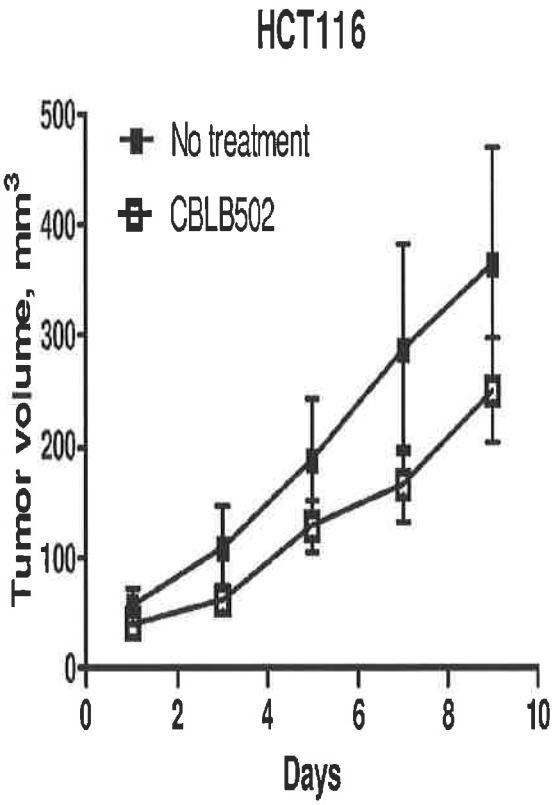

HCT116
No treatment
CBLB502
Tumor volume, mm3
500
400
300
200
100
0
0
2
4
6
8
10
Days

FIGURE 16

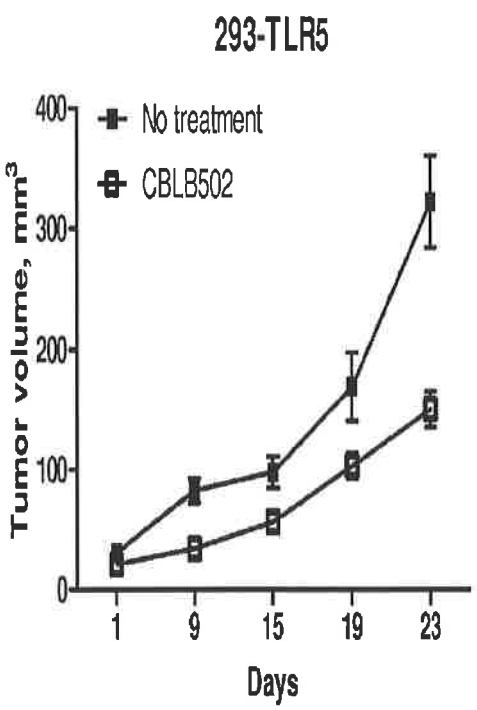

293-TLR5
No treatment
CBLB502
Tumor volume, mm3
400
300
200
100
0
1
9
15
19
23
Days

FIGURE 17

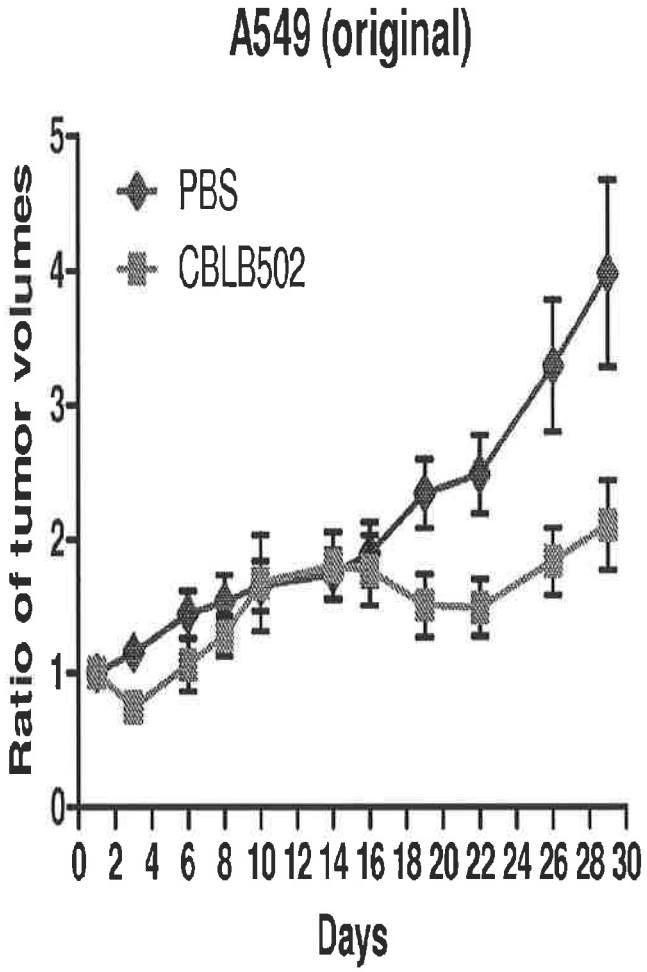

A549 (original)
PBS
CBLB502
Ratio of tumor volumes
0
1
2
3
4
5
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
Days

FIGURE 18

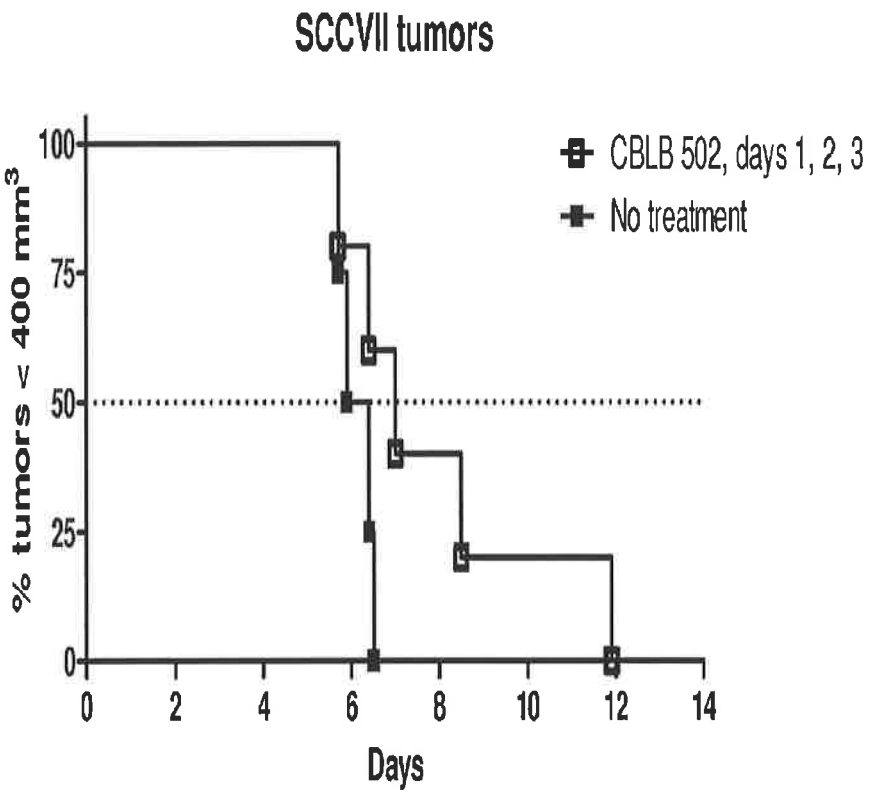
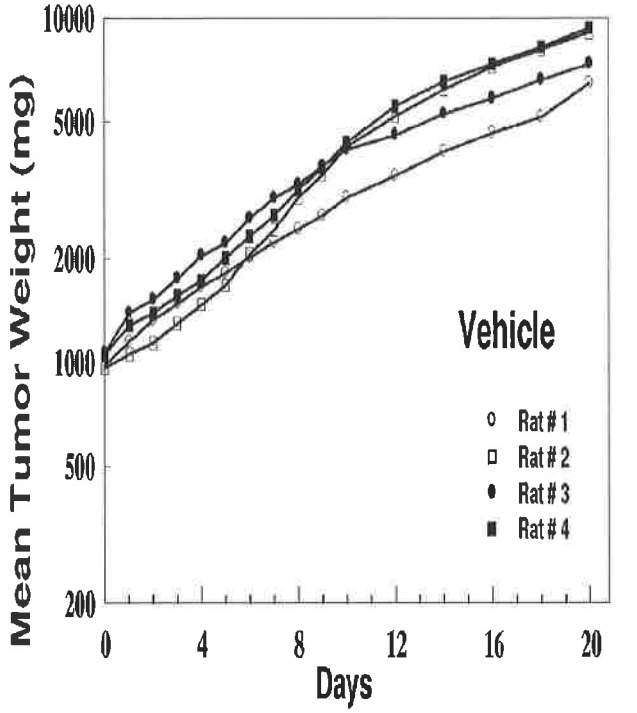

SCCVII tumors
CBLB 502, days 1, 2, 3
No treatment
% tumors < 400 mm3
100
75
50
25
0
0
2
4
6
8
10
12
14
Days

FIGURE 19


Mean Tumor Weight (mg)
10000
5000
2000
1000
500
200
0
4
8
12
16
20
Days
Vehicle
Rat # 1
Rat # 2
Rat # 3
Rat # 4

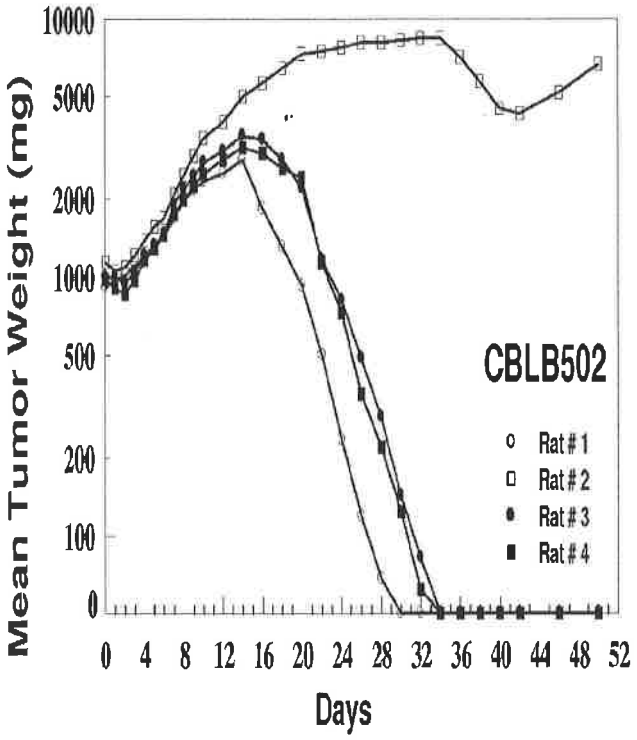

Mean Tumor Weight (mg)
10000
5000
2000
1000
500
200
100
0
0 4 8 12 16 20 24 28 32 36 40 44 48 52
Days
CBLB502
Rat # 1
Rat # 2
Rat # 3
Rat # 4

FIGURE 20

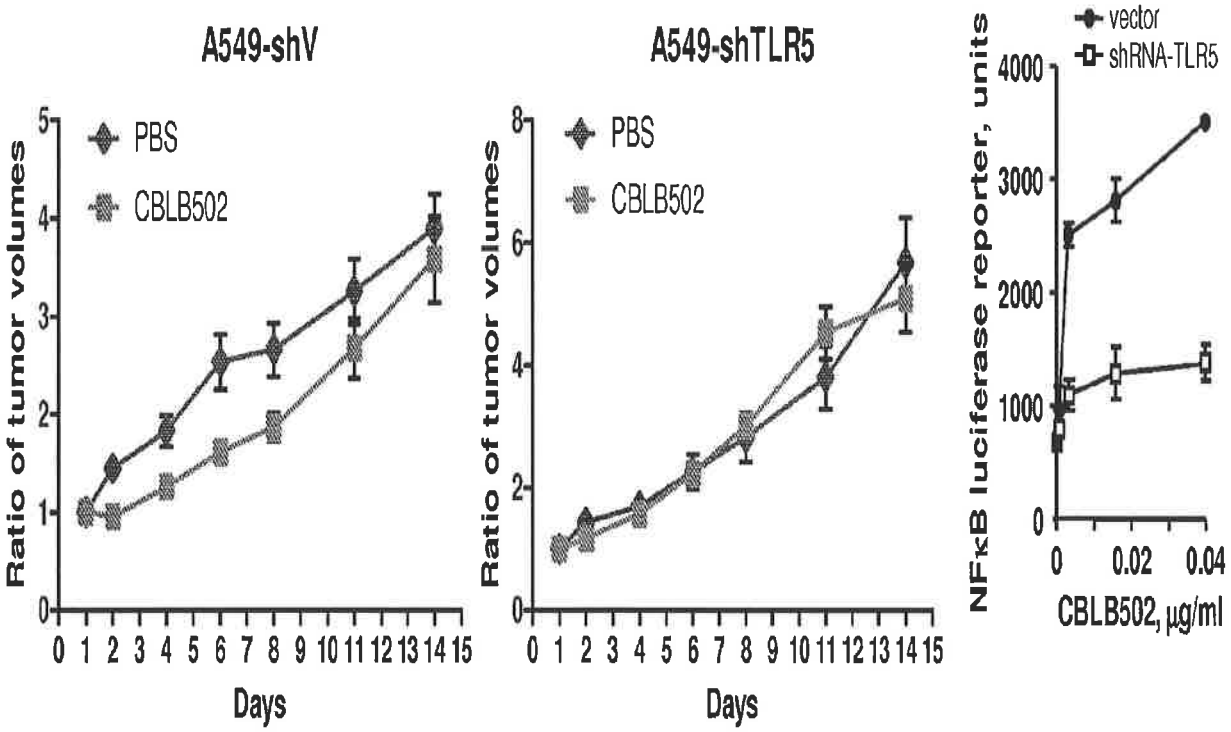

A549-shV
PBS
CBLB502
Ratio of tumor volumes
Days
A549-shTLR5
PBS
CBLB502
Ratio of tumor volumes
Days
vector
shRNA-TLR5
NFκB luciferase reporter, units
CBLB502, µg/ml

FIGURE 21

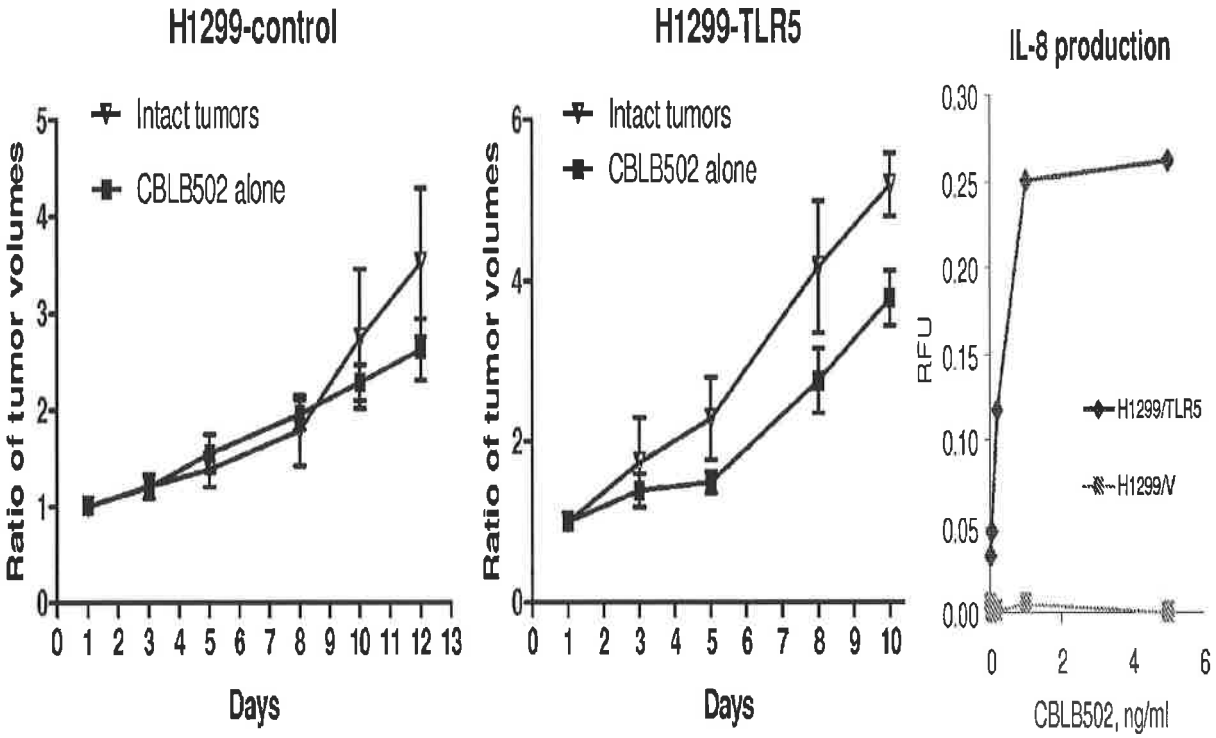

H1299-control
Intact tumors
CBLB502 alone
Ratio of tumor volumes
Days
H1299-TLR5
Intact tumors
CBLB502 alone
Ratio of tumor volumes
Days
IL-8 production
RFU
H1299/TLR5
H1299/V
CBLB502, ng/ml

FIGURE 22

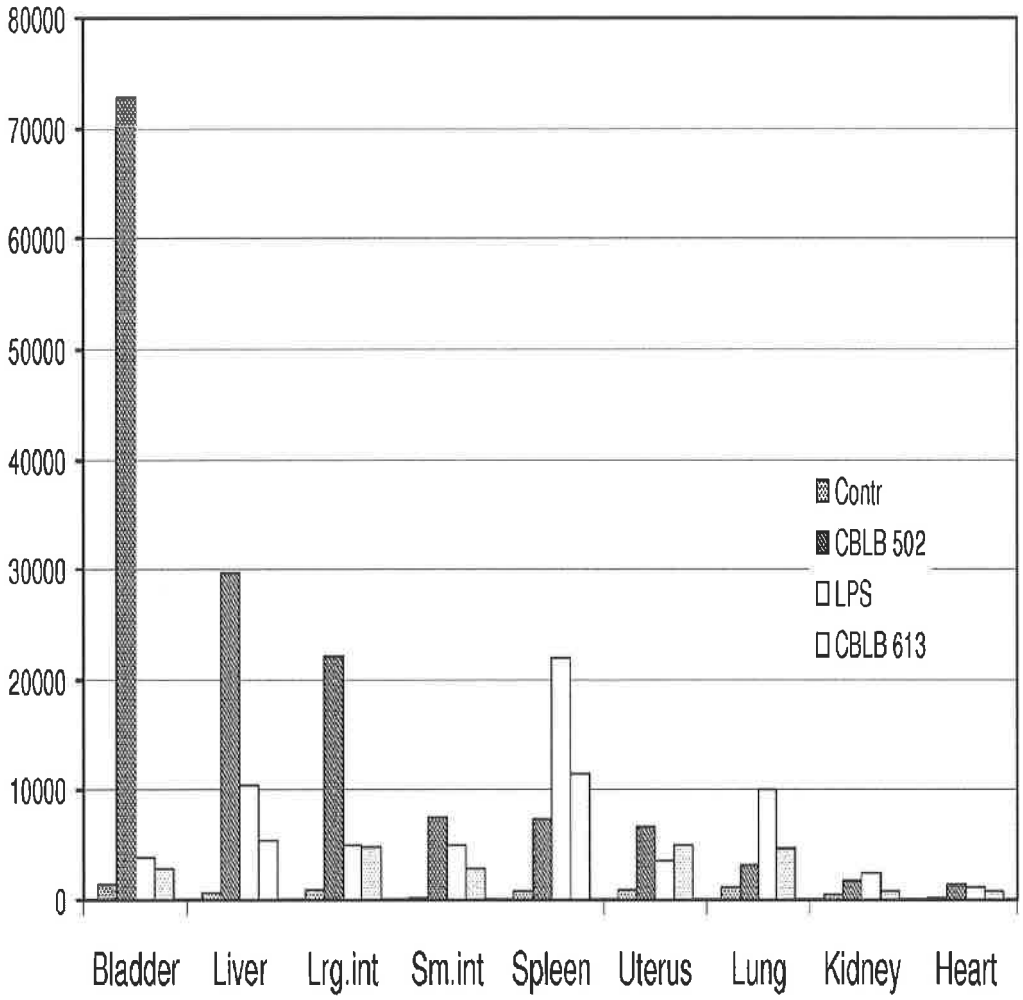

80000
70000
60000
50000
40000
30000
20000
10000
0
Contr
CBLB 502
LPS
CBLB 613
Bladder
Liver
Lrg.int
Sm.int
Spleen
Uterus
Lung
Kidney
Heart

FIGURE 23

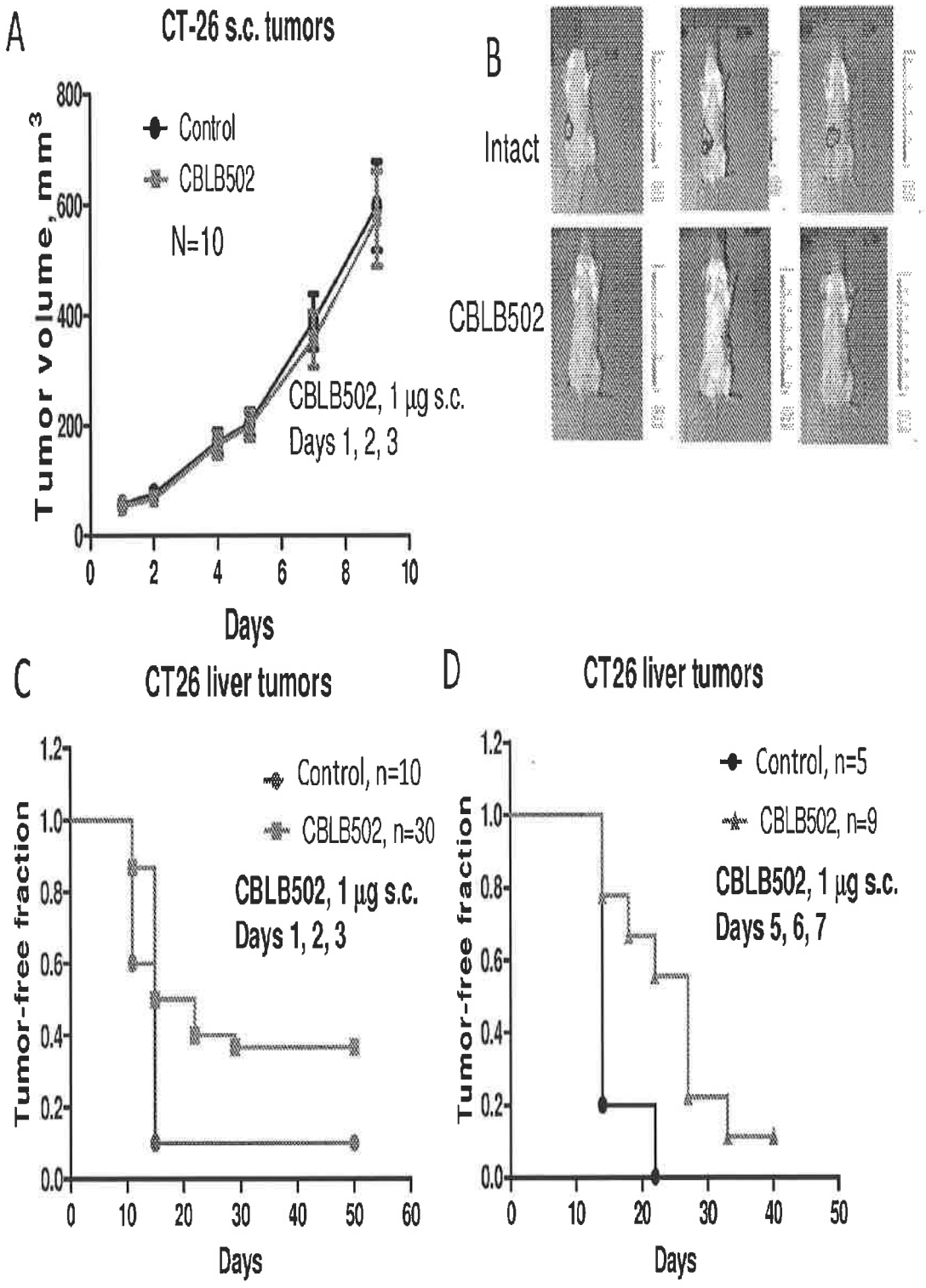

A
CT-26 s.c. tumors
Tumor volume, mm3
800
600
400
200
0
Control
CBLB502
N=10
CBLB502, 1 µg s.c.
Days 1, 2, 3
0 2 4 6 8 10
Days
B
Intact
CBLB502
C
CT26 liver tumors
Tumor-free fraction
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Control, n=10
CBLB502, n=30
CBLB502, 1 µg s.c.
Days 1, 2, 3
0 10 20 30 40 50 60
Days
D
CT26 liver tumors
Tumor-free fraction
Control, n=5
CBLB502, n=9
CBLB502, 1 µg s.c.
Days 5, 6, 7
0 10 20 30 40 50
Days

FIGURE 23 CONTINUED

E

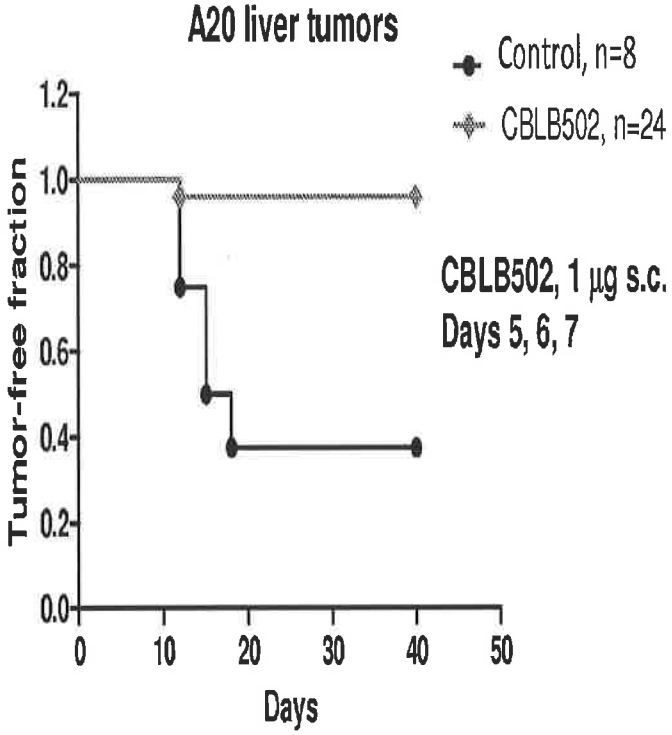


FIGURE 24

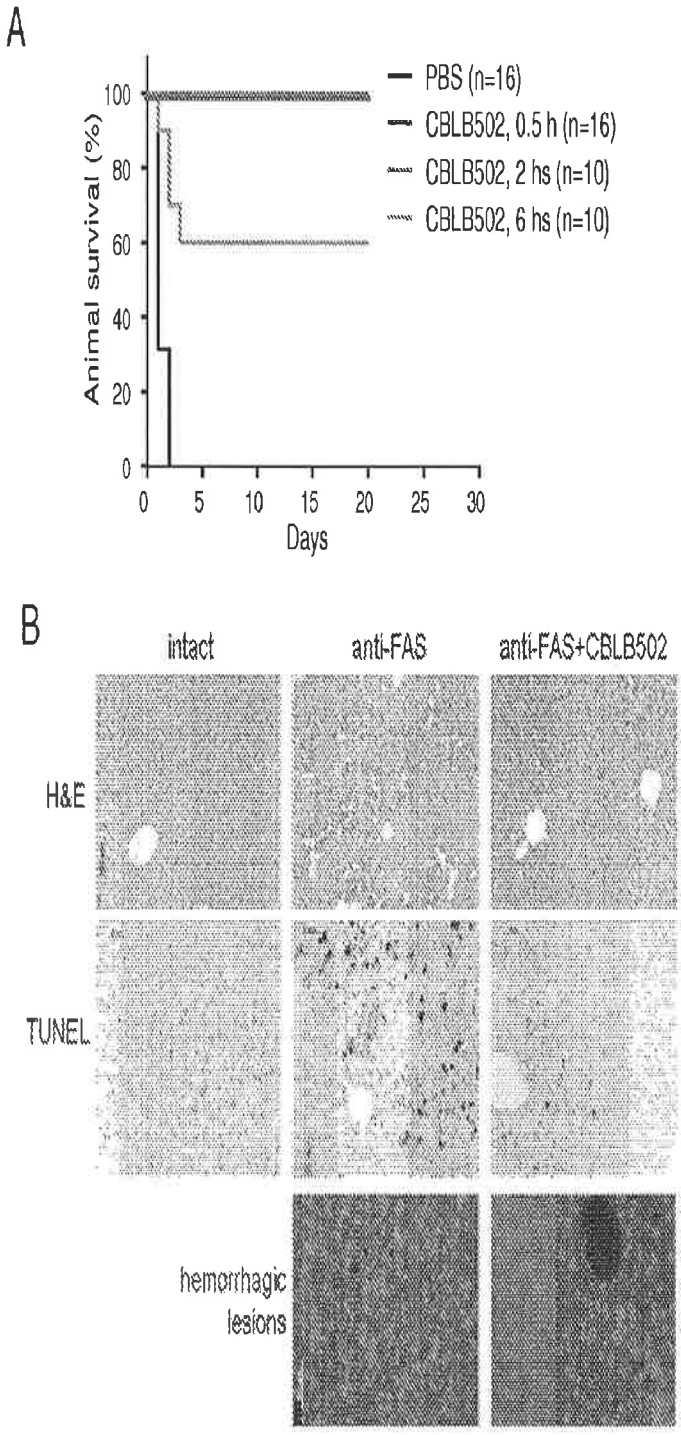

A
Animal survival (%)
100
80
60
40
20
0
0
5
10
15
20
25
30
Days
PBS (n=16)
CBLB502, 0.5 h (n=16)
CBLB502, 2 hs (n=10)
CBLB502, 6 hs (n=10)
B
intact
anti-FAS
anti-FAS+CBLB502
H&E
TUNEL
hemorrhagic
lesions

FIGURE 25

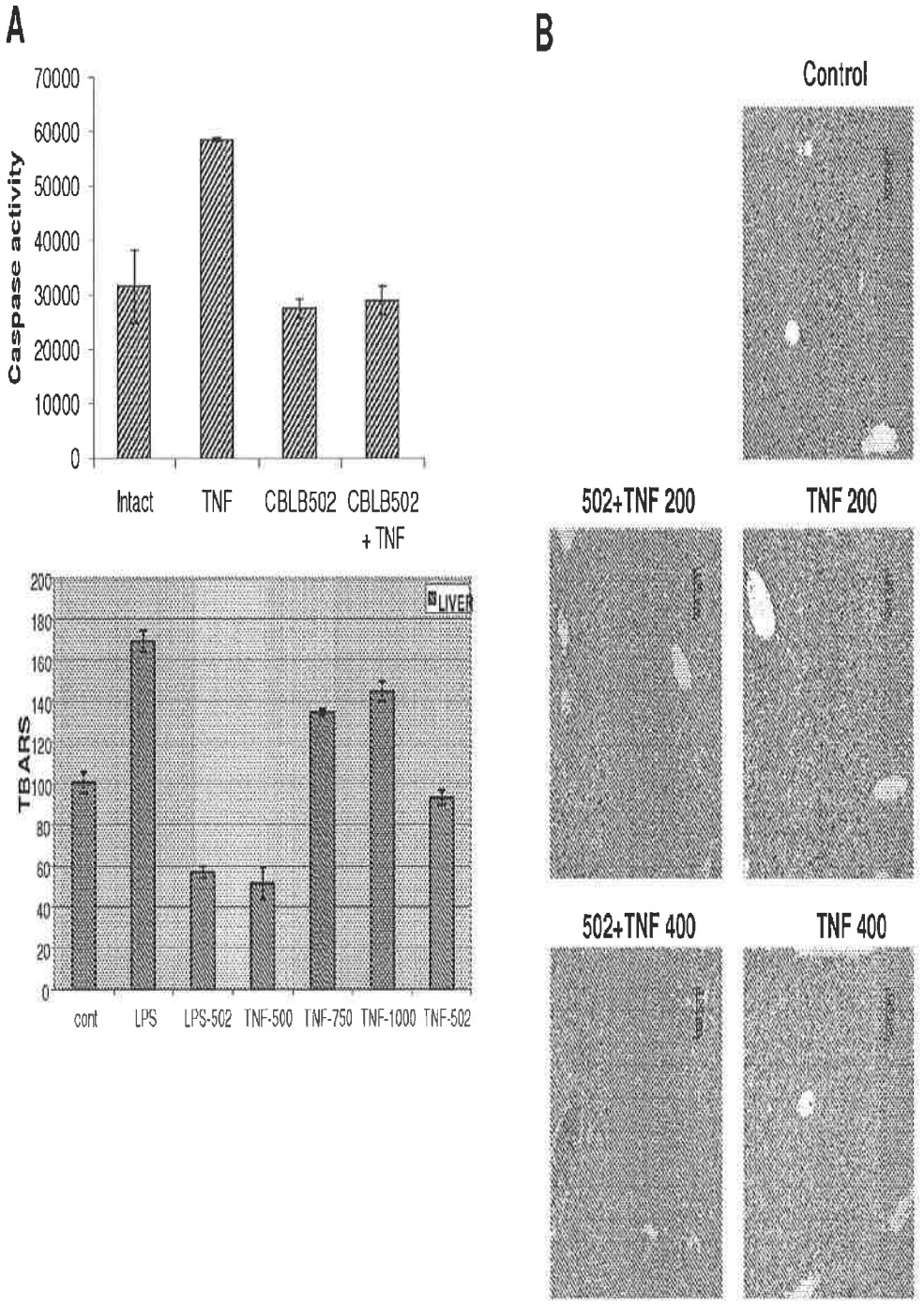

A
Caspase activity
70000
60000
50000
40000
30000
20000
10000
0
Intact
TNF
CBLB502
CBLB502 + TNF
TBARS
LIVER
200
180
160
140
120
100
80
60
40
20
0
cont
LPS
LPS-502
TNF-500
TNF-750
TNF-1000
TNF-502
B
Control
502+TNF 200
TNF 200
502+TNF 400
TNF 400

FIGURE 26

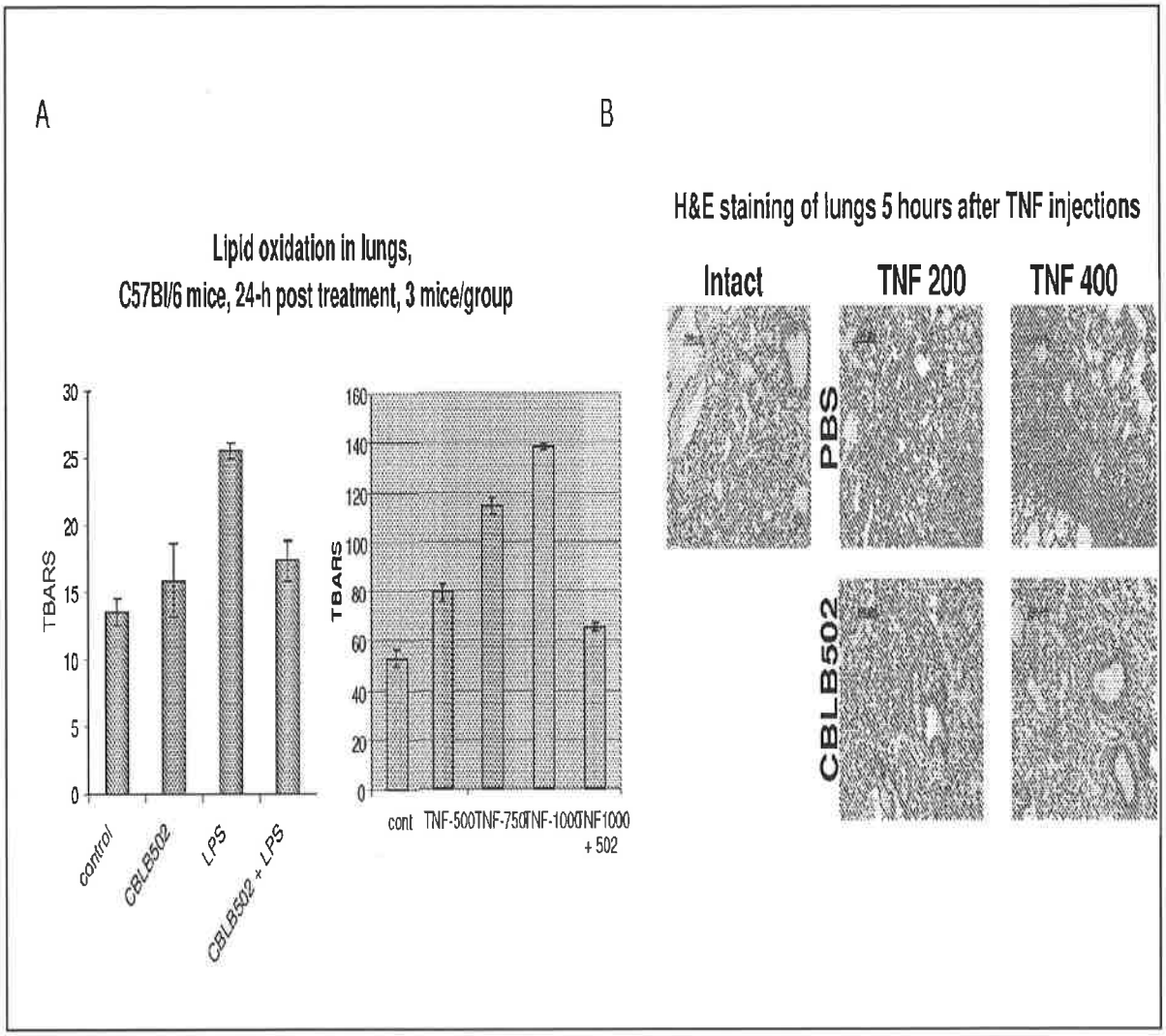

A
Lipid oxidation in lungs,
C57Bl/6 mice, 24-h post treatment, 3 mice/group
TBARS
30
25
20
15
10
5
0
control
CBLB502
LPS
CBLB502 + LPS
TBARS
160
140
120
100
80
60
40
20
0
cont
TNF-500
TNF-750
TNF-1000
TNF1000 + 502
B
H&E staining of lungs 5 hours after TNF injections
Intact
TNF 200
TNF 400
PBS
CBLB502

FIGURE 27

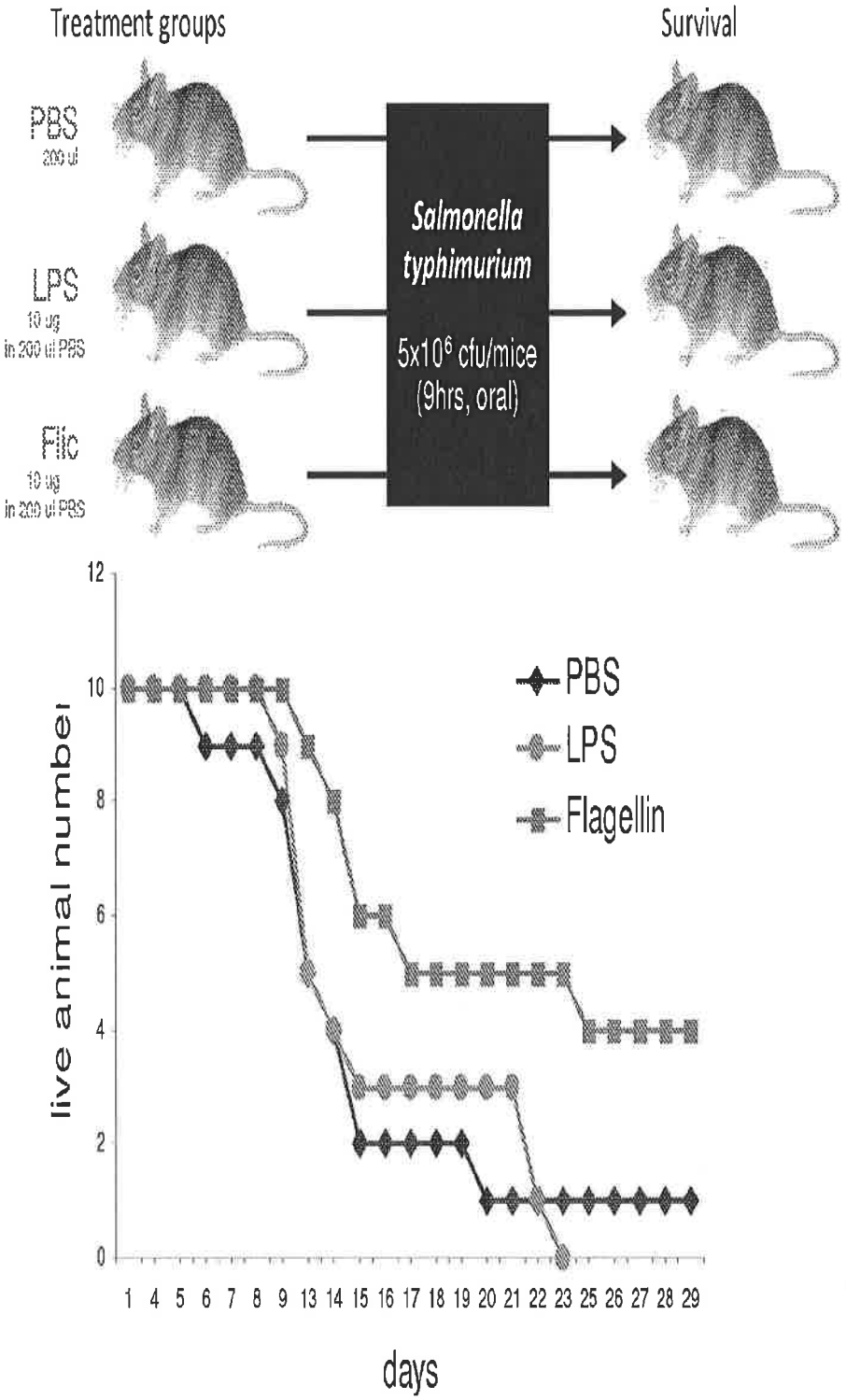
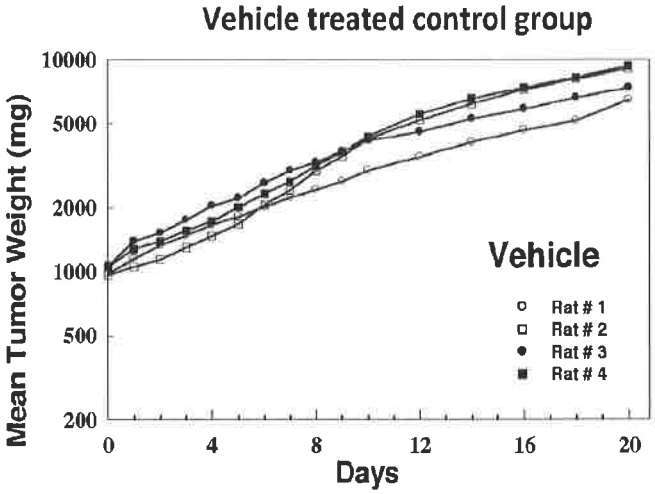
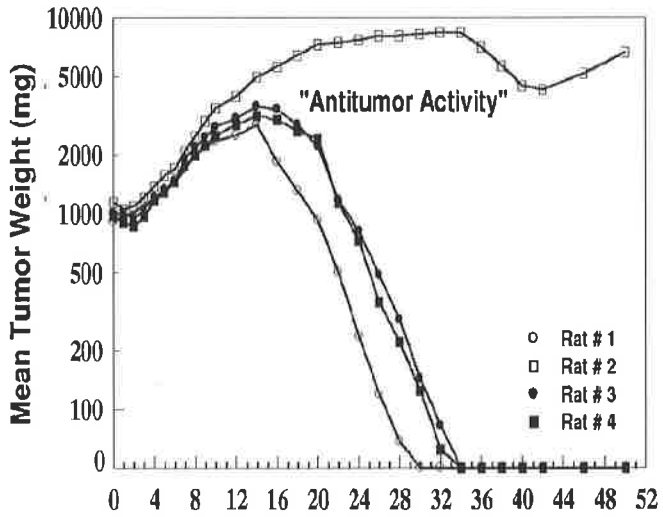

Treatment groups
Survival
PBS
200 ul
LPS
10 ug
in 200 ul PBS
Flic
10 ug
in 200 ul PBS
Salmonella typhimurium
5x10^6 cfu/mice
(9hrs, oral)
live animal number
0
2
4
6
8
10
12
1 4 5 6 7 8 9 13 14 15 16 17 18 19 20 21 22 23 25 26 27 28 29
days
PBS
LPS
Flagellin

FIGURE 28

A



B



C

