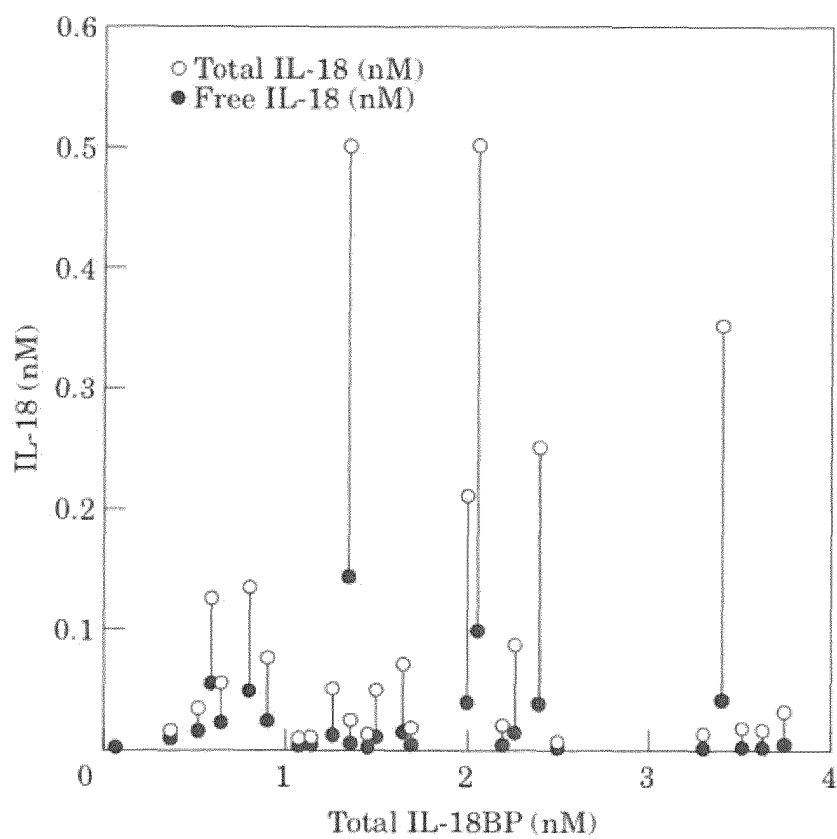


**Figure 1**

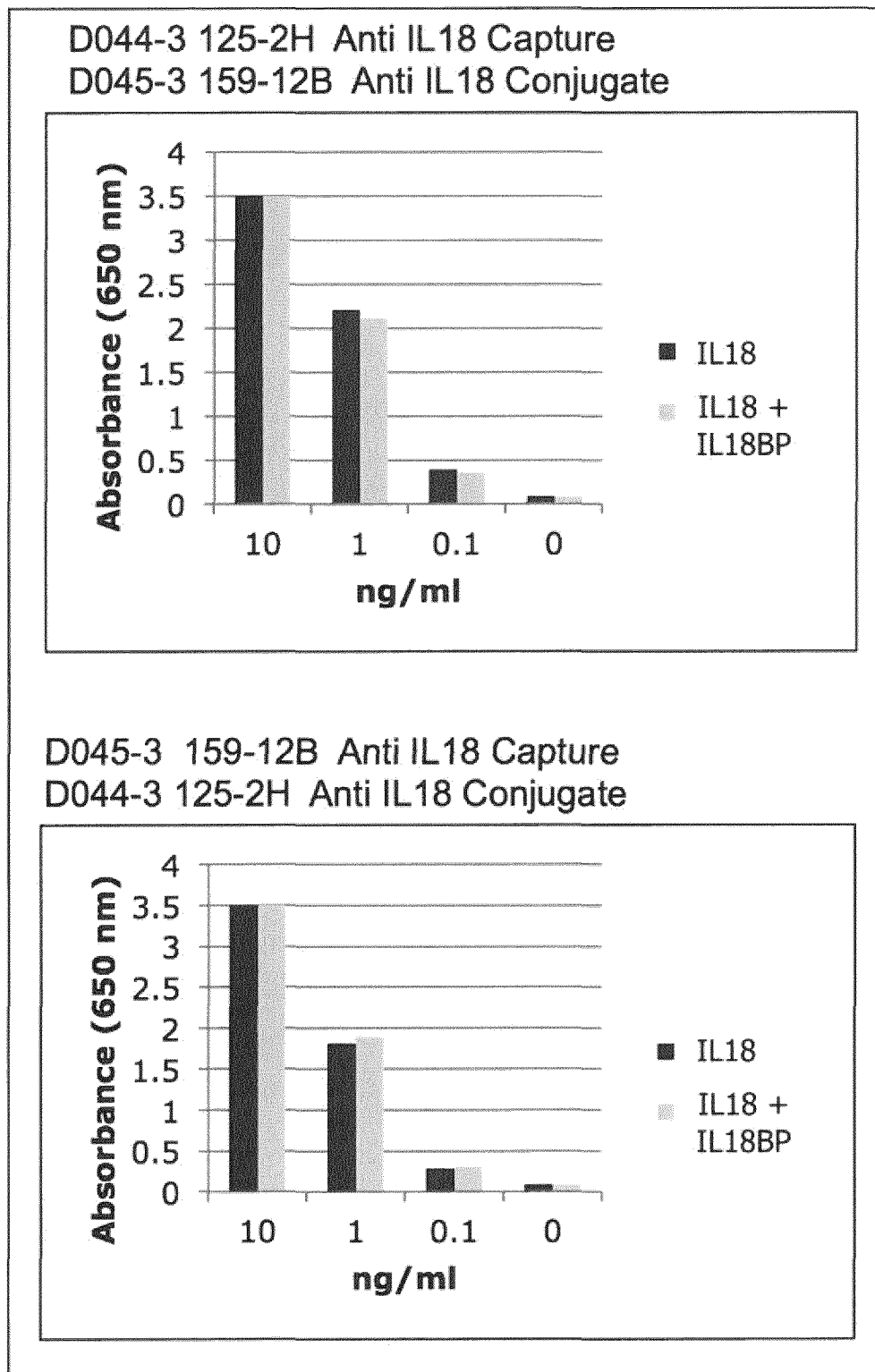


Figure 2

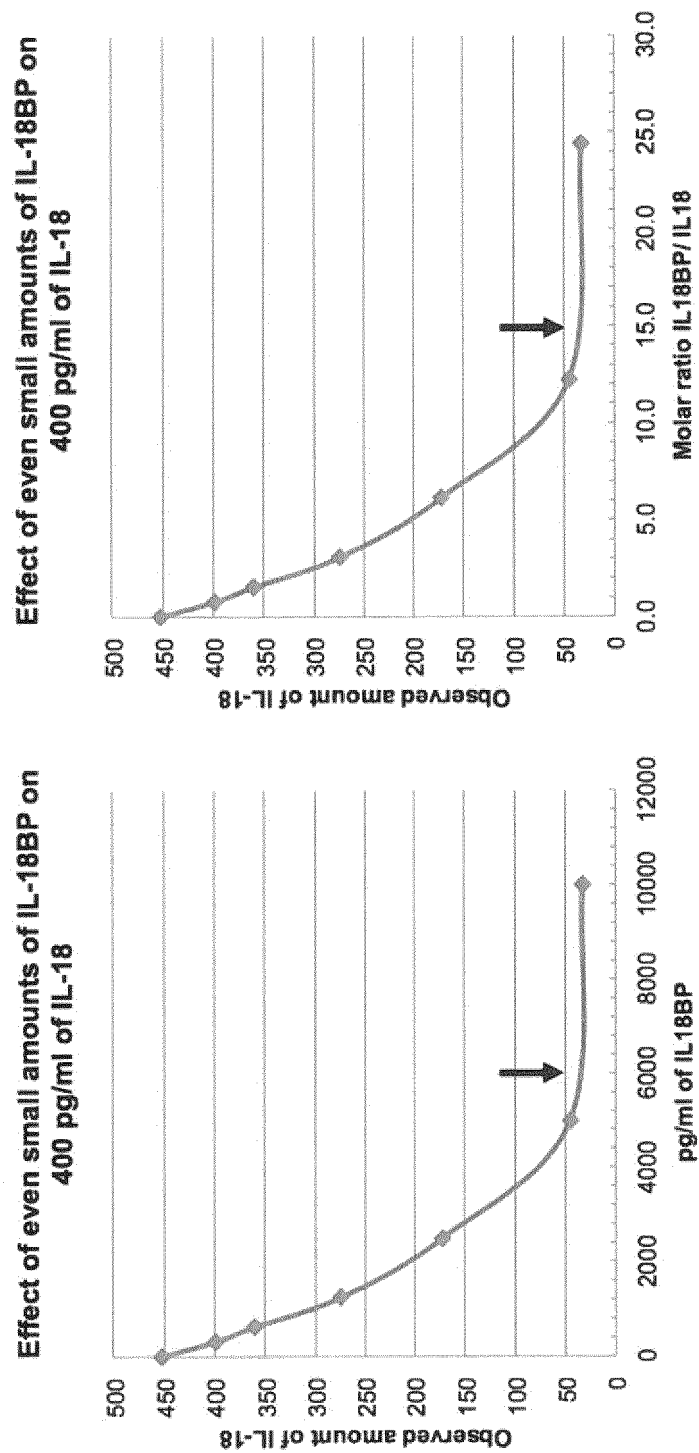


Figure 3

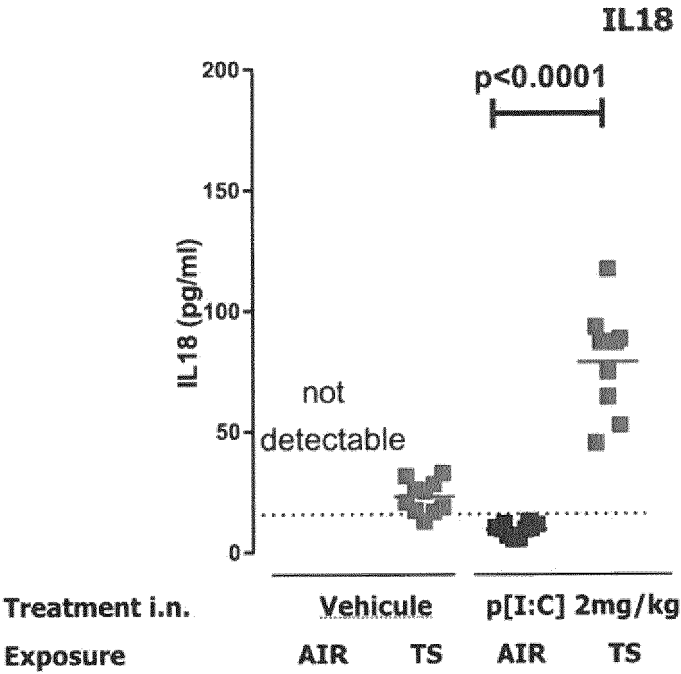


Figure 4

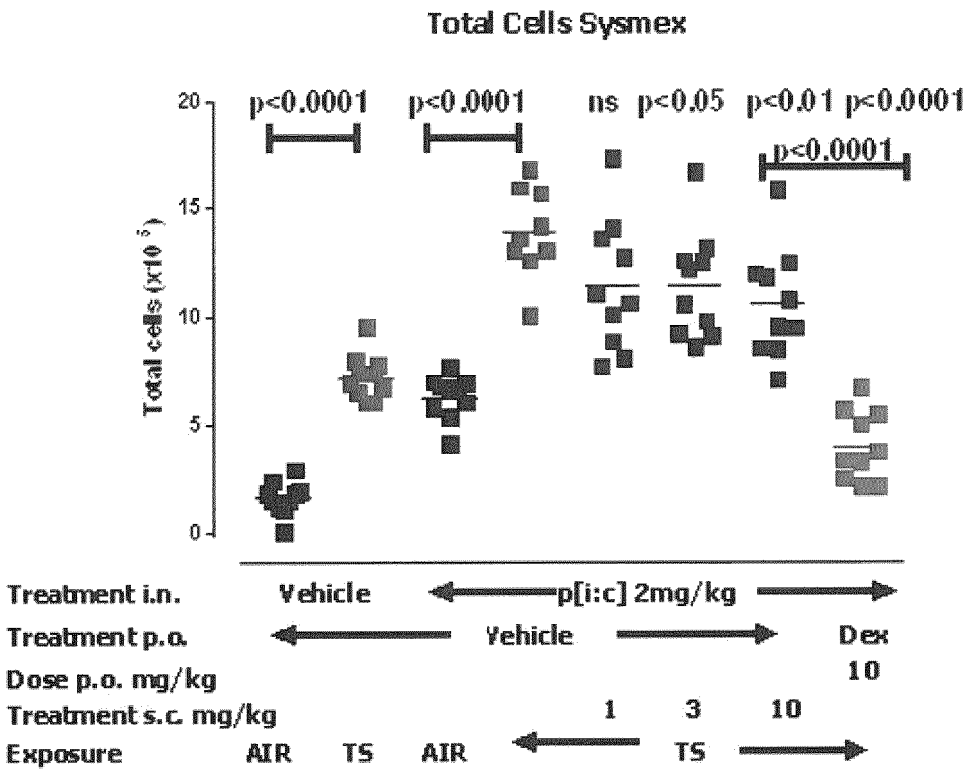


Figure 5

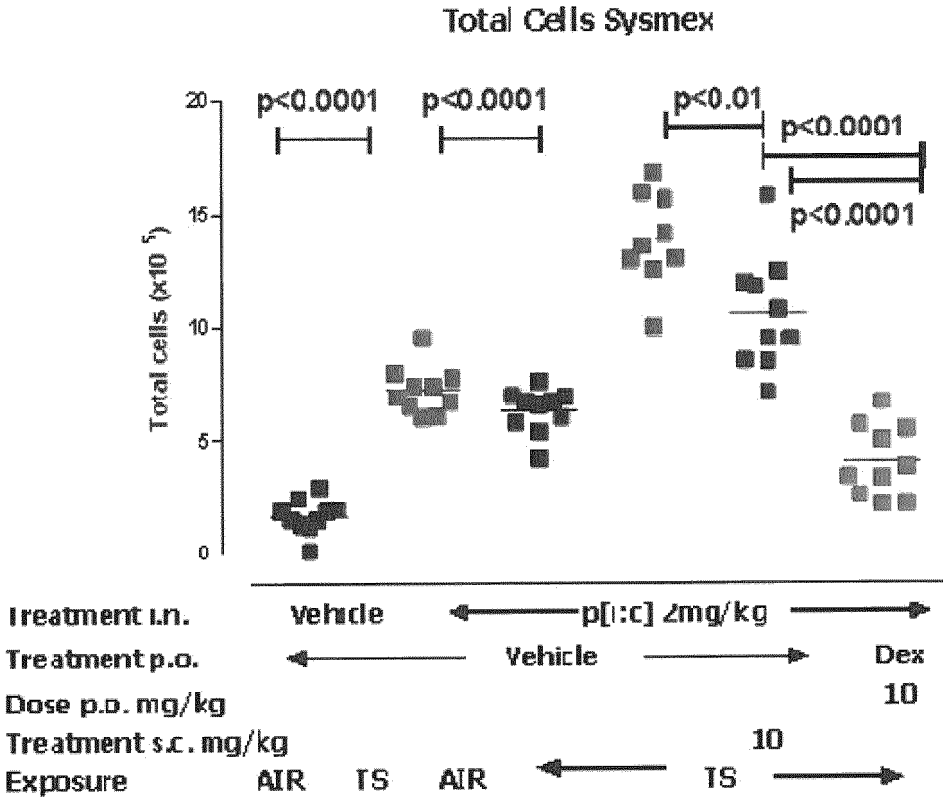


Figure 6

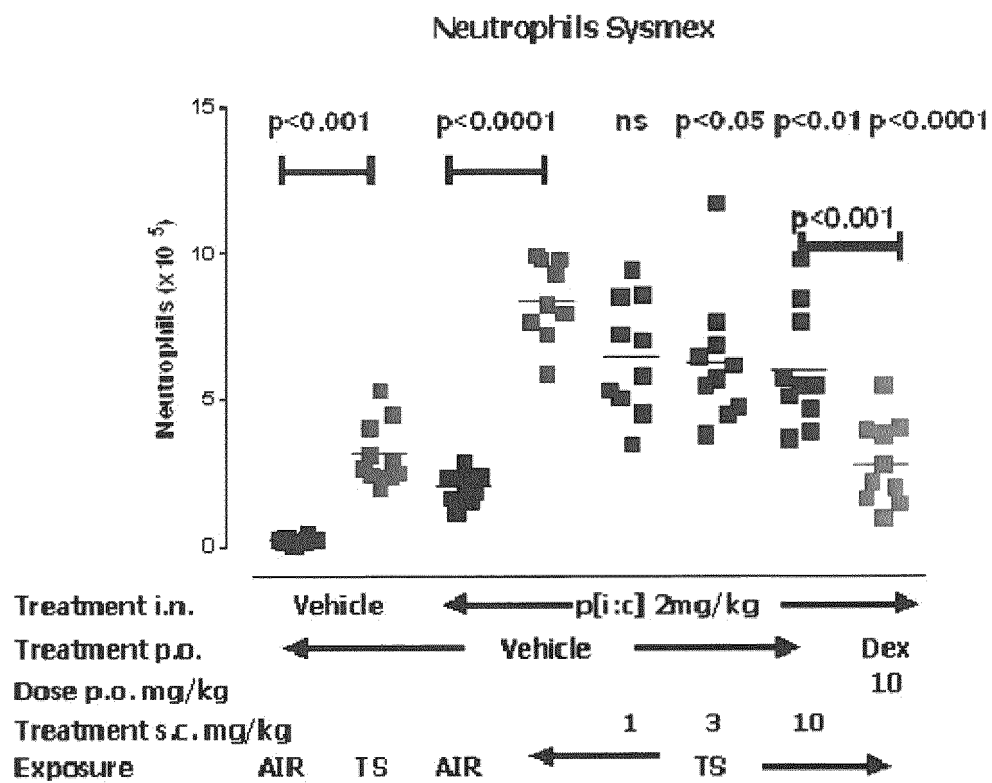
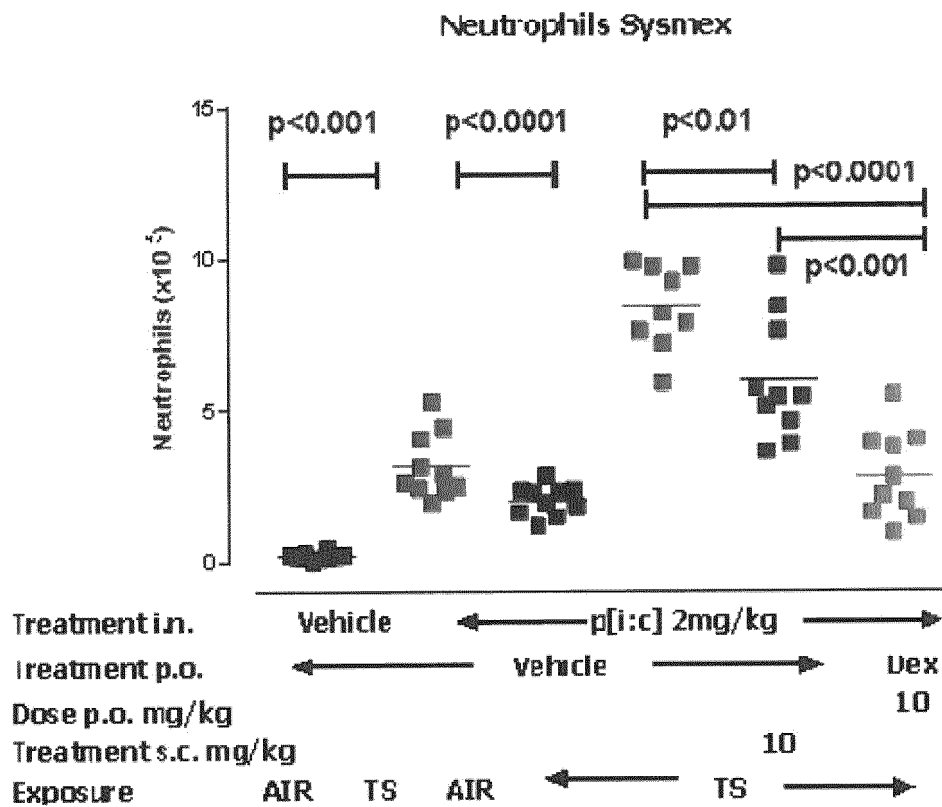


Figure 7

**Figure 8**

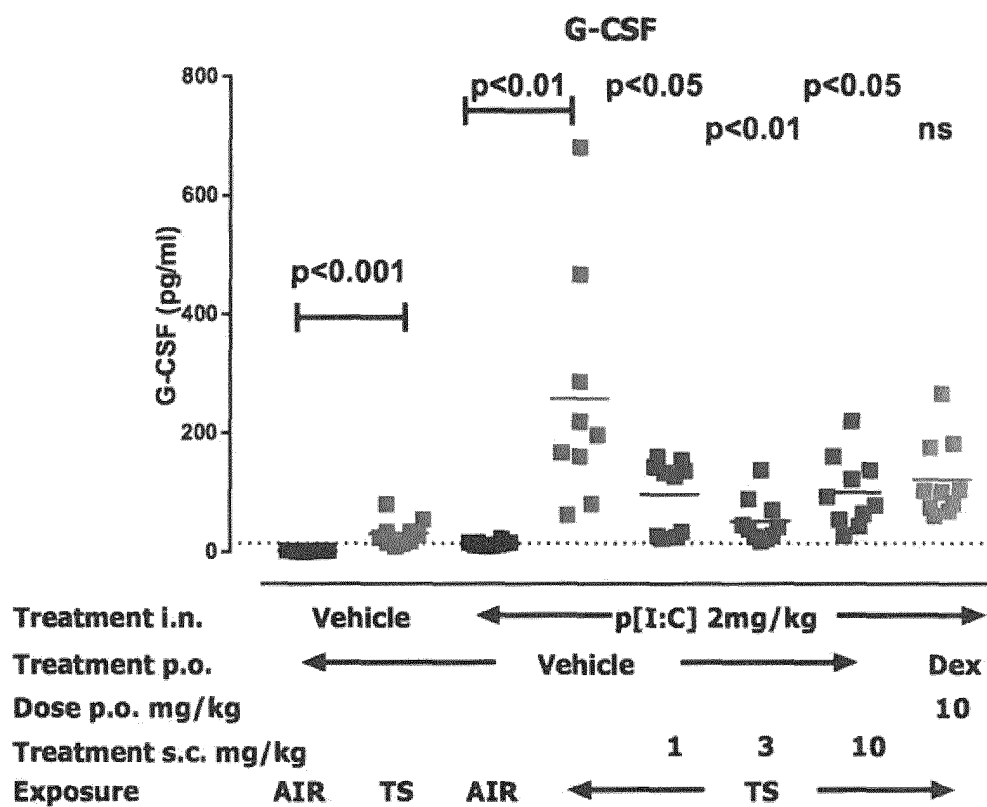


Figure 9

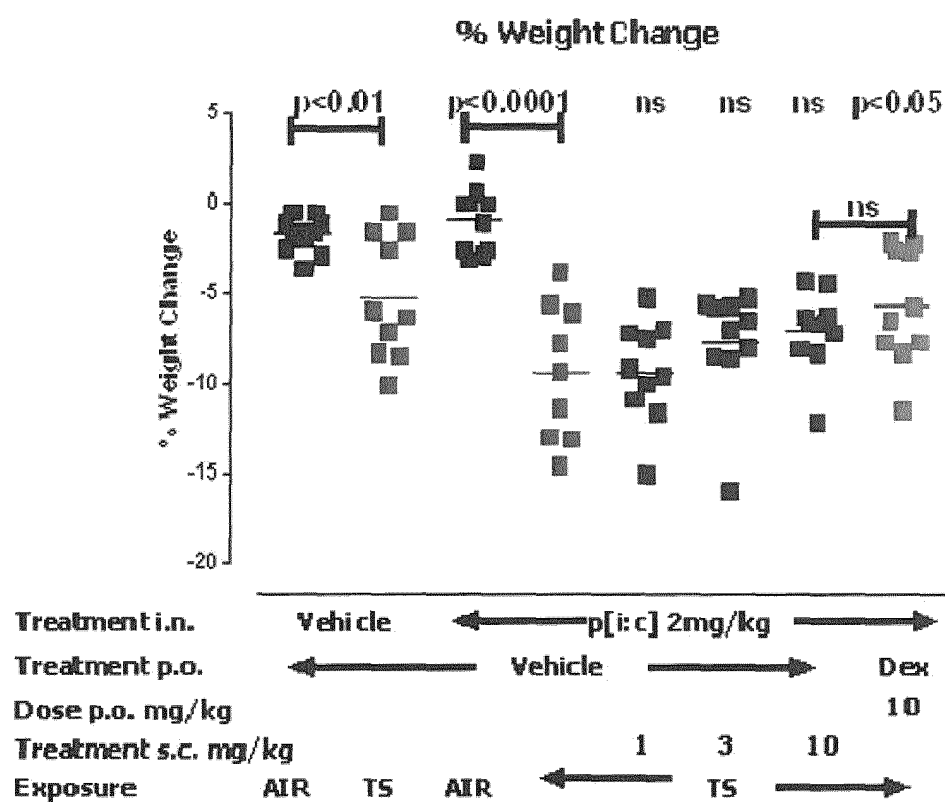


Figure 10

131B4-2

VH Amino Acid Sequence: (SEQ ID NO: 387)

EVQLQQSGAELVKPGASVKLSCTASGFKIK**DTYI**HWLKQRPEQGLEWIG**RIDPANG**
NTIYGSKFQGKATITADTSSNTAYIQLSSLTSGDTAVYFCAG**YVWFAY**WGQGTLVTV
SA

VK Amino Acid Sequence: (SEQ ID NO: 19)

DAVLTQTPLSLPVSLGDQASISCT**TSSQSLVHSNGNTYL**HWYLQKPGQSPKLLIY**KVS**
DRFSGVPDRFSGSGSGTDFTLMITRVEAEDLGVI**FC****SQSSLVPWT**FGGGTKLEVK

Figure 11

Human interleukin-18 binding protein isoforms (Kim SH et al 2000)***Isoform a***

TPVSQTTTAA TASVRSTKDP CPSQPPVFPA AKQCPALEVT WPEVEVPLNG
TSLSLSCVACS RFPNFSILYW LGNGSFIEHL PGRLWEGSTS RERGSTGTQL
CKALVLEQLT PALHSTNFSC VLVDPEQVVQ RHVVLAQLWA GLRATLPPTQ
EALPSSHSSP QQQG (SEQ ID NO 7)

MW = 17630

pI = 6.37

Isoform b

TPVSQTTTAA TASVRSTKDP CPSQPPVFPA AKQCPALEVT WPEVEVPL
SWAEGNLAPH PRSPALQPQQ STAAGLRLST GPAAAQP (SEQ ID NO 388)

MW = 8751

pI = 6.44

Isoform c

TPVSQTTTAA TASVRSTKDP CPSQPPVFPA AKQCPALEVT WPEVEVPLNG
TSLSLSCVACS RFPNFSILYW LGNGSFIEHL PGRLWEGSTS RERGSTGTQL
CKALVLEQLT PALHSTNFSC VLVDPEQVVQ RHVVLAQLWV RSPRRGLQEQ
EELCFHMGWK GGLCQSSL (SEQ ID NO 389)

MW: 18404

pI: 6.82

Isoform d

TPVSQTTTAA TASVRSTKDP CPSQPPVFPA AKQCPALEVT WPEVEVPLNG
TSLSLSCVACS RFPNFSILYW LGNGSFIEHL PGRLWEGSTS RERGSTGWAE
GNLAPHPRSP ALQPQQSTAA GRLSTGPAAA QP (SEQ ID NO 390)

MW: 13896

pI: 7.64

Figure 12