-continued

```
                405                 410                 415

Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys
            420                 425                 430

Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys
        435                 440                 445

Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe
    450                 455                 460

Ser Arg Thr Pro Gly Arg Lys Arg Arg Ala Pro Val Lys Gln Thr Leu
465                 470                 475                 480

Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
                485                 490                 495

Pro Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val
            500                 505                 510

Pro Gly Ser Thr Gly Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu
        515                 520                 525

Ala Val Ser Val Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln
    530                 535                 540

Ser Leu Leu Asn Ser Arg Asn Gln Lys Asn His Leu Ala Trp Tyr Gln
545                 550                 555                 560

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
                565                 570                 575

Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Asp Gly Ser Gly Thr
            580                 585                 590

Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val
        595                 600                 605

Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Arg Thr Phe Gly Gly Gly Thr
    610                 615                 620

Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe
625                 630                 635                 640

Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
                645                 650                 655

Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
            660                 665                 670

Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln
        675                 680                 685

Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
    690                 695                 700

Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
705                 710                 715                 720

Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
                725                 730                 735
```

1. An isolated or purified antibody or fragment thereof, comprising:

a) a light chain comprising a complementarity determining region (CDR) L1 sequence of $QSLLNSX_1X_2QKNX_3$ (SEQ ID NO:1) where X_1=R or D, X_2=N or T, X_3=H or F; a CDR L2 sequence of X_1AS (SEQ ID NO:35) where X_1=W or F; and a CDR L3 sequence of $QQYYX_1X_2X_3X_4T$ (SEQ ID NO:2) where X_1=T or S, $X_{2=}$Y or I, X_3=P or no amino acid, $X_{4=}$R or L;

and

b) a heavy chain comprising a complementarity determining region (CDR) H1 sequence of $GYX_1X_2TX_3DYY$ (SEQ ID NO:3) where X_1=S or T, X_2=I or F, X_3=S or no amino acid;

a CDR H2 sequence selected from the group consisting of $IGYDGX_1K$ (SEQ ID NO:4) where X_1=S or T, and IYPGNGHT (SEQ ID NO:5); and

a CDR H3 sequence selected from the group consisting of TRDRANWDDYFDY (SEQ ID NO:6) and AYDLFNY (SEQ ID NO:7).