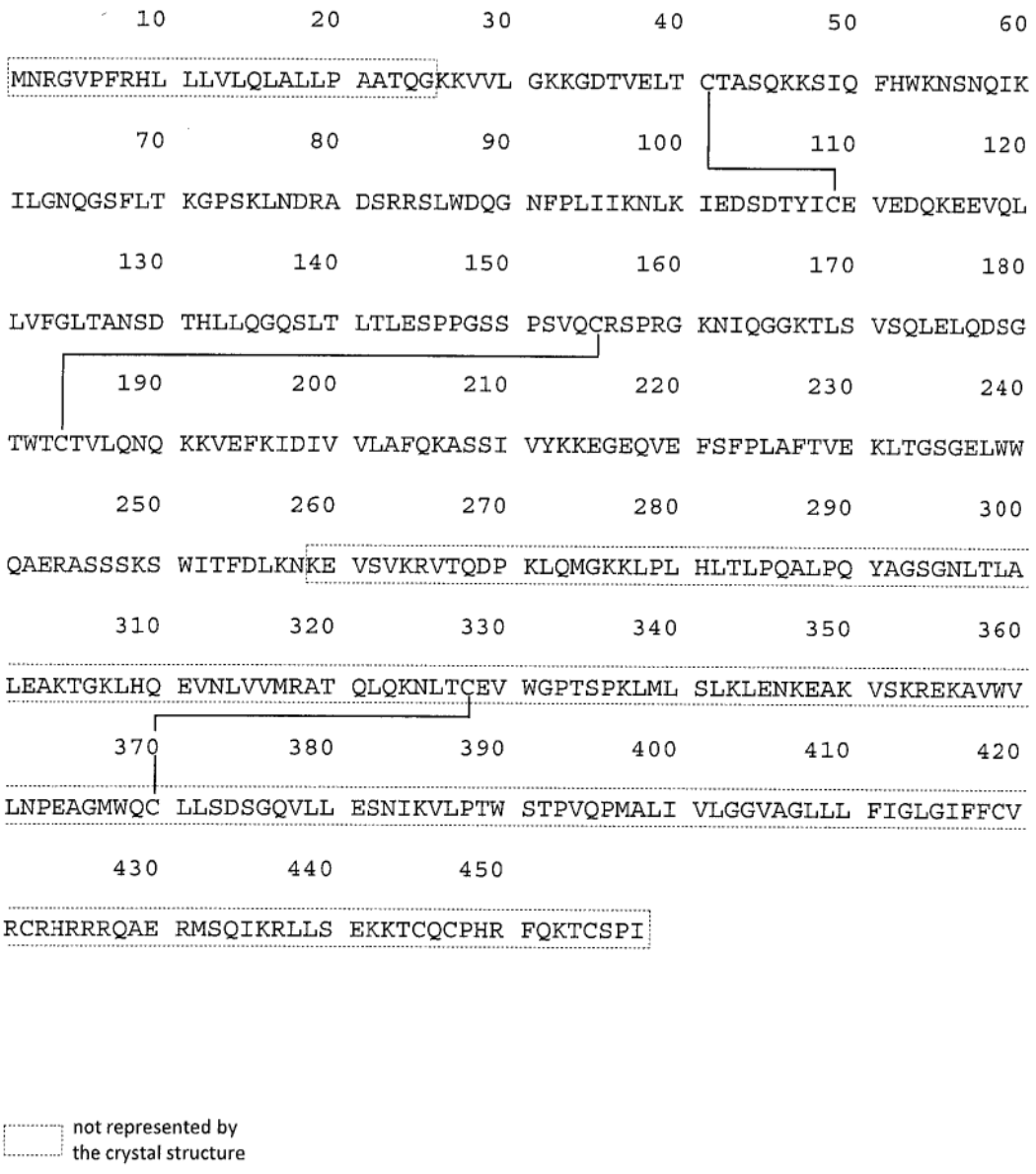

10 20 30 40 50 60
MNRGVPFRHL LLVLQLALLP AATQGKKVVL GKKGDTVELT CTASQKKSIQ FHWKNSNQIK
70 80 90 100 110 120
ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIIKNLK IEDSDTYICE VEDQKEEVQL
130 140 150 160 170 180
LVFGLTANSD THLLQGQSLT LTLESPPGSS PSVQCRSPRG KNIQGGKTLS VSQLELQDSG
190 200 210 220 230 240
TWTCTVLQNQ KKVEFKIDIV VLAFQKASSI VYKKEGEQVE FSFPLAFTVE KLTGSGELWW
250 260 270 280 290 300
QAERASSSKS WITFDLKNKE VSVKRVTQDP KLQMGKKLPL HLTLPQALPQ YAGSGNLTLA
310 320 330 340 350 360
LEAKTGKLHQ EVNLVVMRAT QLQKNLTCEV WGPTSPKLML SLKLENKEAK VSKREKAVWV
370 380 390 400 410 420
LNPEAGMWQC LLSDSGQVLL ESNIKVLPTW STPVQPMALI VLGGVAGLLL FIGLGIFFCV
430 440 450
RCRHRRRQAE RMSQIKRLLS EKKTCQCPHR FQKTCSPI
not represented by the crystal structure

Figure 1

A. Light chain.

```
         10          20          30          40          50          60
                                CDR1                               CDR2
DIVMTQSPDS LAVSLGERAT INCRASKSVS TSGYSYIYWY QQKPGQPPKL LIYLASILES

         70          80          90         100         110         120
                                          CDR3
GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQHSRELPW TFGQGTKVEI KRTVAAPSVF

        130         140         150         160         170         180

IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS

        190         200         210

STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC
```

Figure 2A

B. Heavy chain.

```
        10          20          30          40          50          60
EEQLVESGGG LVKPGGSLRL SCAASGFSFS DCRMYWLRQA PGKGLEWIGV ISVKSENYGA
                                CDR1                        CDR2

        70          80          90          100         110         120
CDR2                                                CDR3
NYAESVRGRF TISRDDSKNT VYLQMNSLKT EDTAVYYCSA SYYRYDVGAW FAYWGQGTLV

        130         140         150         160         170         180
TVSSASTKGP SVFPLAPSSK STSGGTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV

        190         200         210         220         230         240
LQSSGLYSLS SVVTVPSSSL GTQTYICNVN HKPSNTKVDK KVEPKSCDKT HTCPPCPAPE

        250         260         270         280         290         300
LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE

        310         320         330         340         350         360
EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP

        370         380         390         400         410         420
SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSKLTVD

        430         440         450
KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK
```

not represented by the crystal structure

Figure 2B

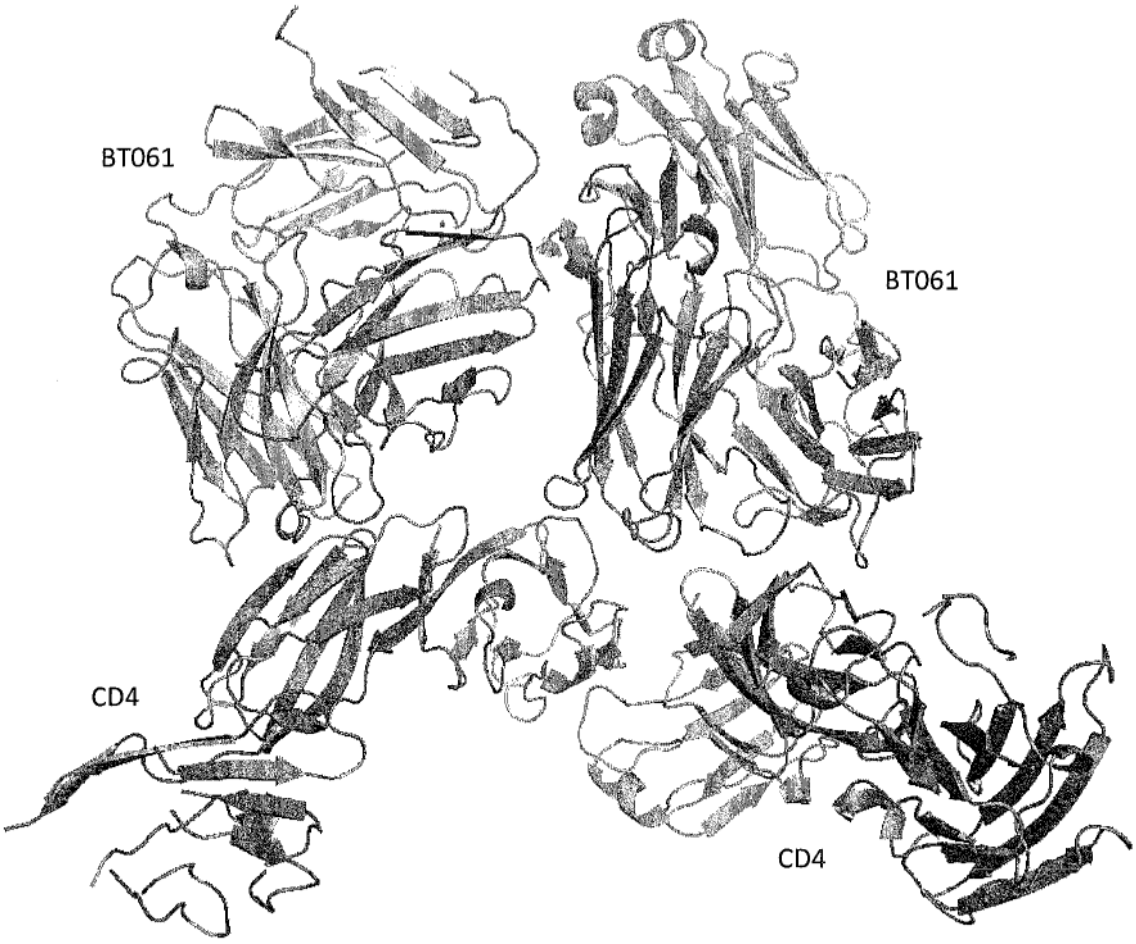


FIGURE 3

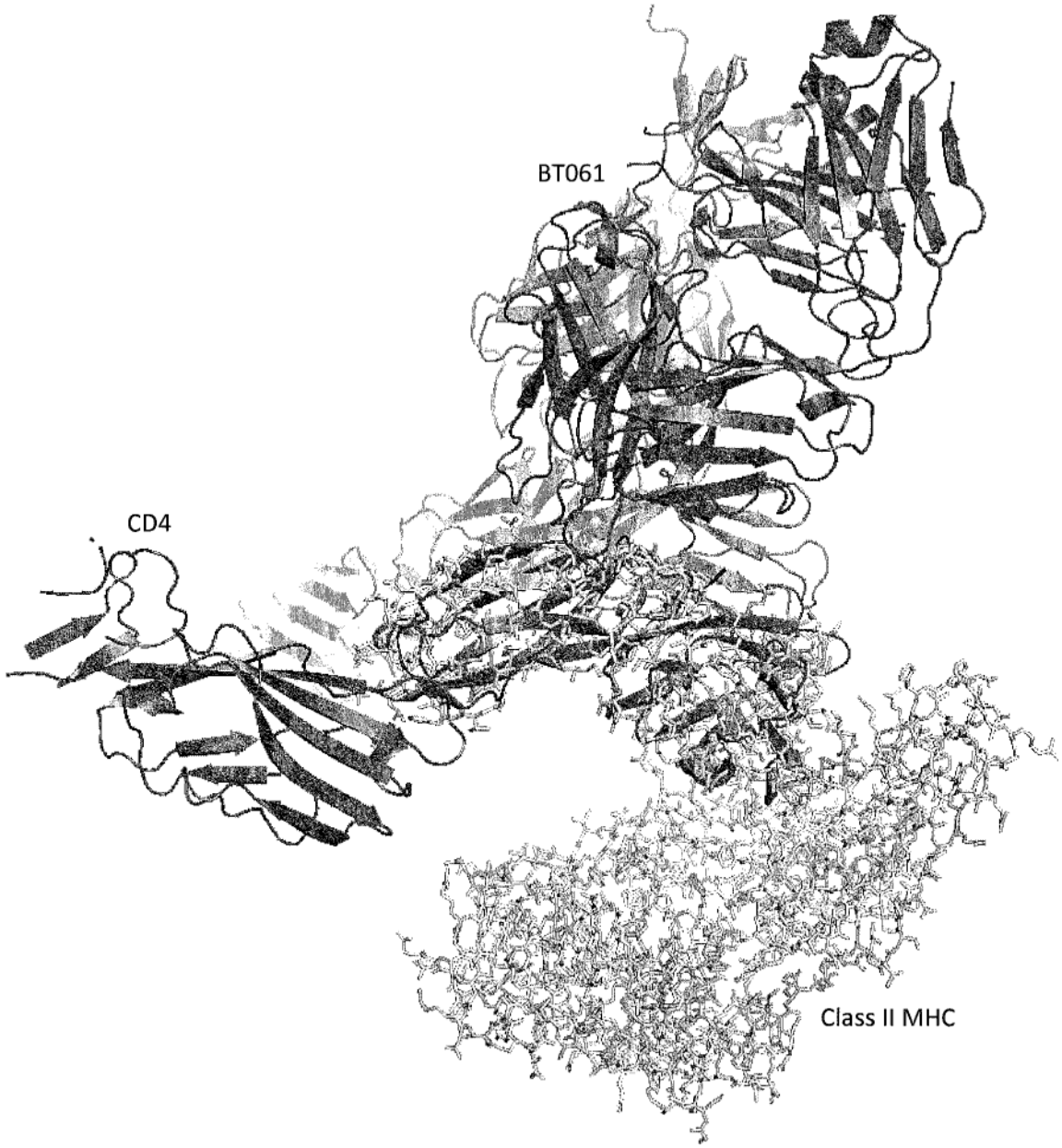


Figure 4

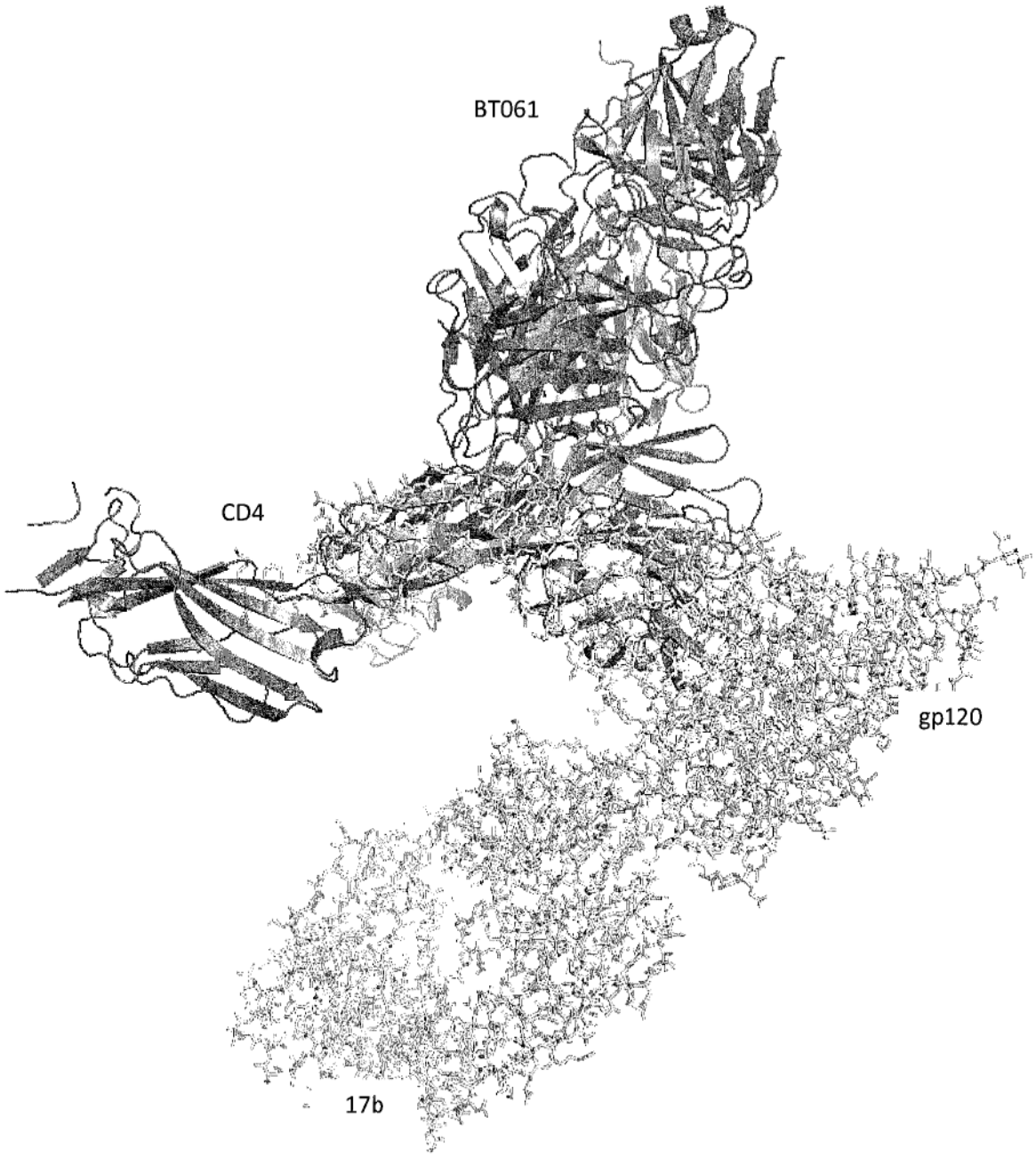


Figure 5

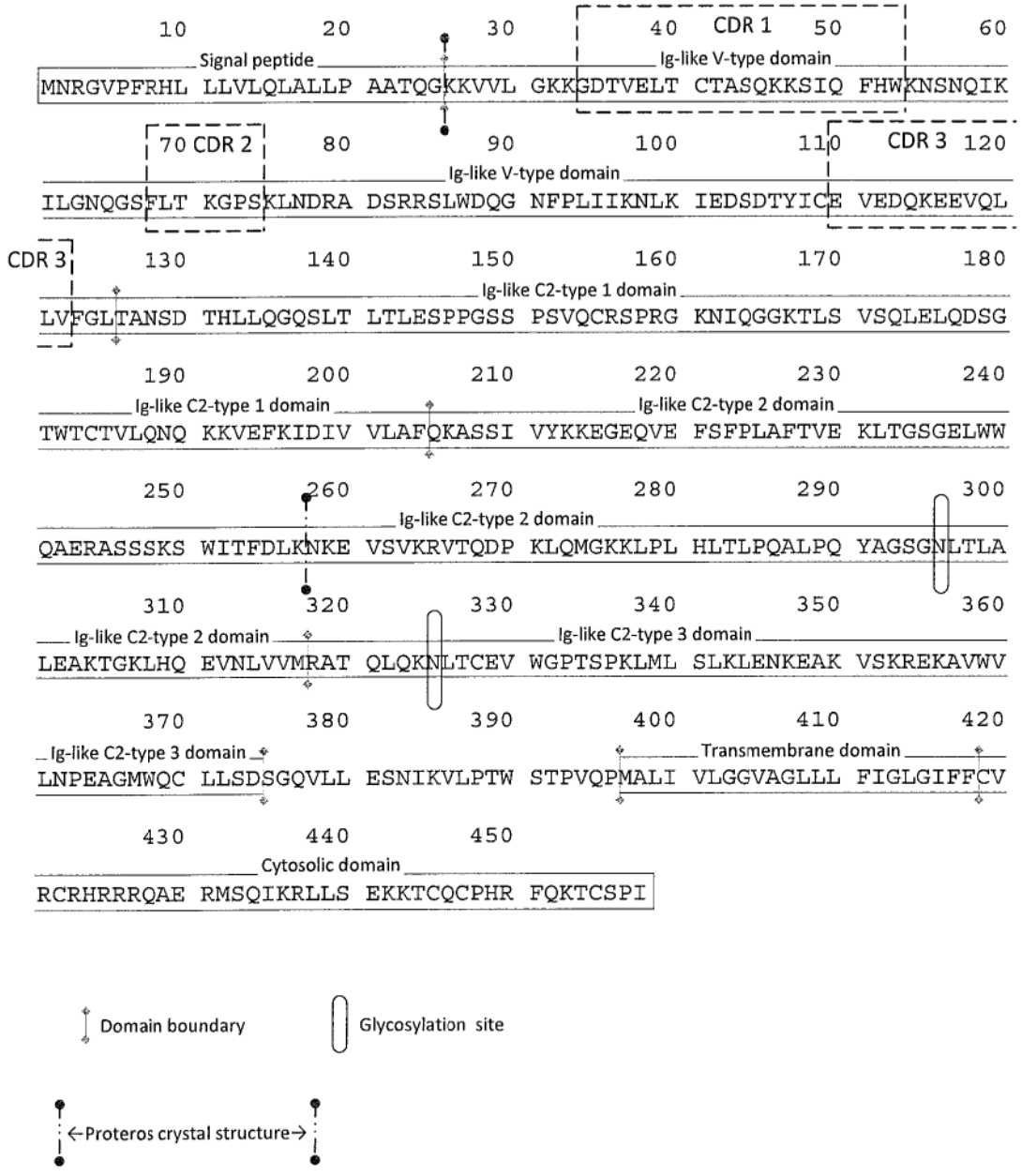

10 20 30 40 CDR 1 50 60
Signal peptide
Ig-like V-type domain
MNRGVPFRHL LLVLQLALLP AATQGKKVVL GKKGDTVELT CTASQKKSIQ FHWKNSNQIK
70 CDR 2 80 90 100 110 CDR 3 120
Ig-like V-type domain
ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIIKNLK IEDSDTYICE VEDQKEEVQL
CDR 3 130 140 150 160 170 180
Ig-like C2-type 1 domain
LVFGLTANSD THLLQGQSLT LTLESPPGSS PSVQCRSPRG KNIQGGKTLS VSQLELQDSG
190 200 210 220 230 240
Ig-like C2-type 1 domain
Ig-like C2-type 2 domain
TWTCTVLQNQ KKVEFKIDIV VLAFQKASSI VYKKEGEQVE FSFPLAFTVE KLTGSGELWW
250 260 270 280 290 300
Ig-like C2-type 2 domain
QAERASSSKS WITFDLKNKE VSVKRVTQDP KLQMGKKLPL HLTLPQALPQ YAGSGNLTLA
310 320 330 340 350 360
Ig-like C2-type 2 domain
Ig-like C2-type 3 domain
LEAKTGKLHQ EVNLVVMRAT QLQKNLTCEV WGPTSPKLML SLKLENKEAK VSKREKAVWV
370 380 390 400 410 420
Ig-like C2-type 3 domain
Transmembrane domain
LNPEAGMWQC LLSDSGQVLL ESNIKVLPTW STPVQPMALI VLGGVAGLLL FIGLGIFFCV
430 440 450
Cytosolic domain
RCRHRRRQAE RMSQIKRLLS EKKTCQCPHR FQKTCSPI
Domain boundary
Glycosylation site
←Proteros crystal structure→

Figure 6

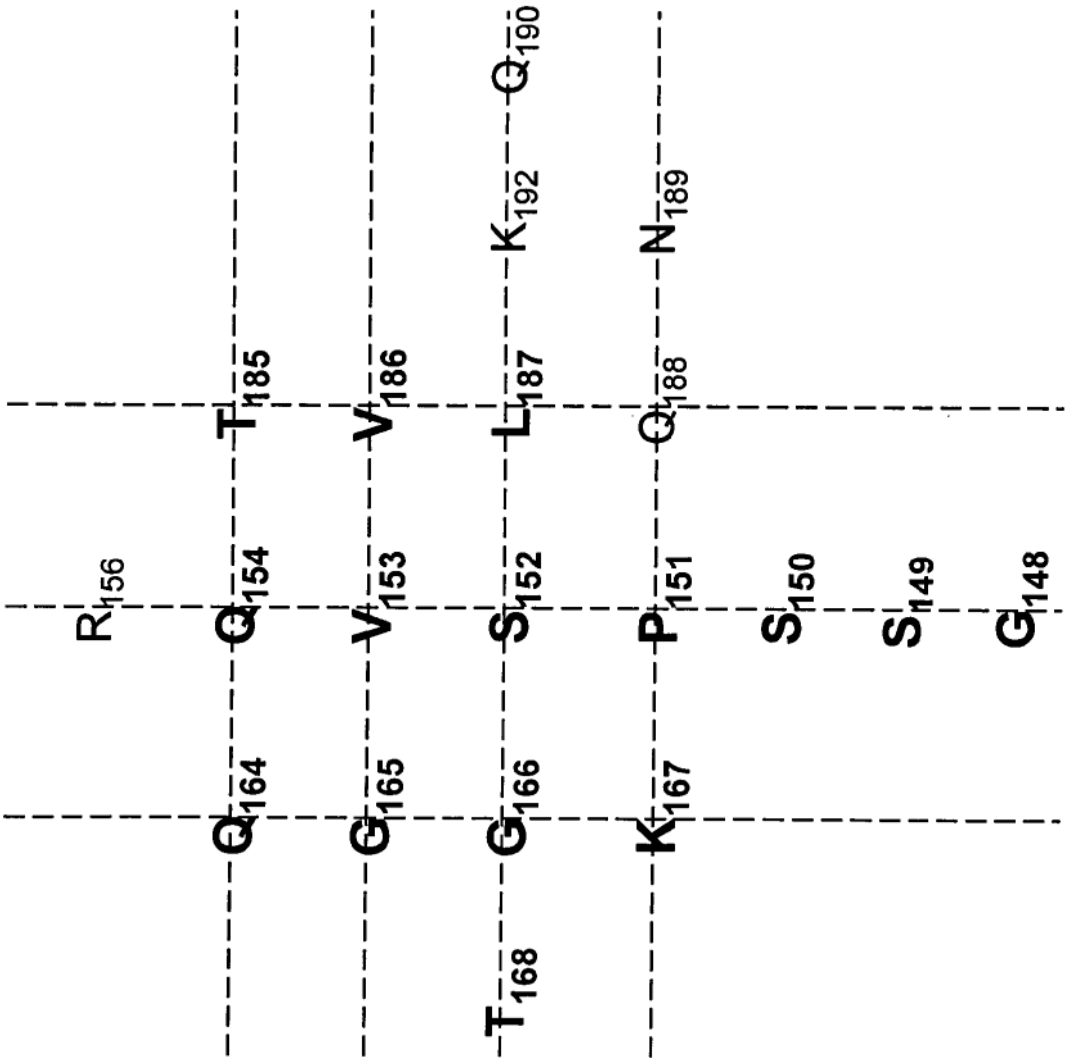

R156
Q154
V153
S152
P151
S150
S149
G148
T185
V186
L187
Q188
N189
K192
Q190
Q164
G165
G166
K167
T168

Figure 7

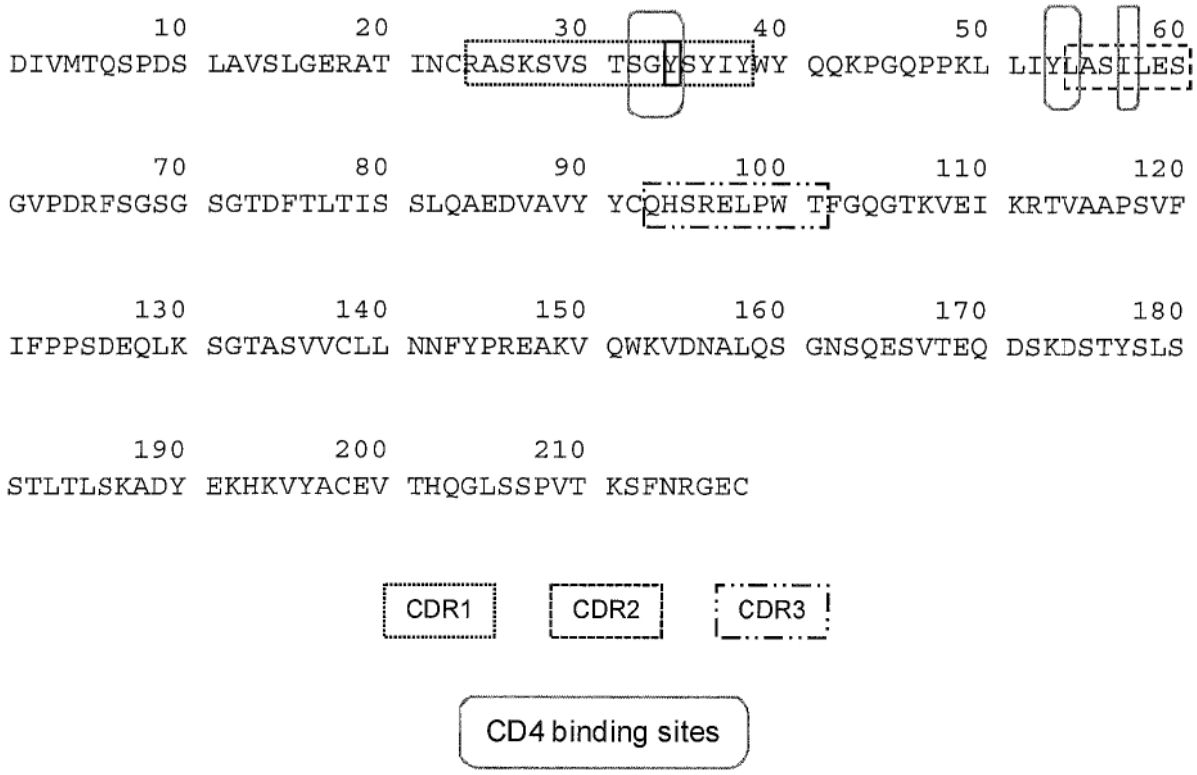

10 20 30 40 50 60
DIVMTQSPDS LAVSLGERAT INCRASKSVS TSGYSYIYWY QQKPGQPPKL LIYLASILES
70 80 90 100 110 120
GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQHSRELPW TFGQGTKVEI KRTVAAPSVF
130 140 150 160 170 180
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
190 200 210
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC
CDR1
CDR2
CDR3
CD4 binding sites

Figure 8

```
        10          20          30          40          50          60
EEQLVESGGG LVKPGGSLRL SCAASGFSFS DCRMYWLRQA PGKGLEWIGV ISVKSENYGA

        70          80          90         100         110         120
NYAESVRGRF TISRDDSKNT VYLQMNSLKT EDTAVYYCSA SYYRYDVGAW FAYWGQGTLV

       130         140         150         160         170         180
TVSSASTKGP SVFPLAPSSK STSGGTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV

       190         200         210         220         230         240
LQSSGLYSLS SVVTVPSSSL GTQTYICNVN HKPSNTKVDK KVEPKSCDKT HTCPPCPAPE

       250         260         270         280         290         300
LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE

       310         320         330         340         350         360
EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP

       370         380         390         400         410         420
SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSKLTVD

       430         440         450
KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK
```

CDR1 CDR2 CDR3

CD4 binding sites

Figure 9

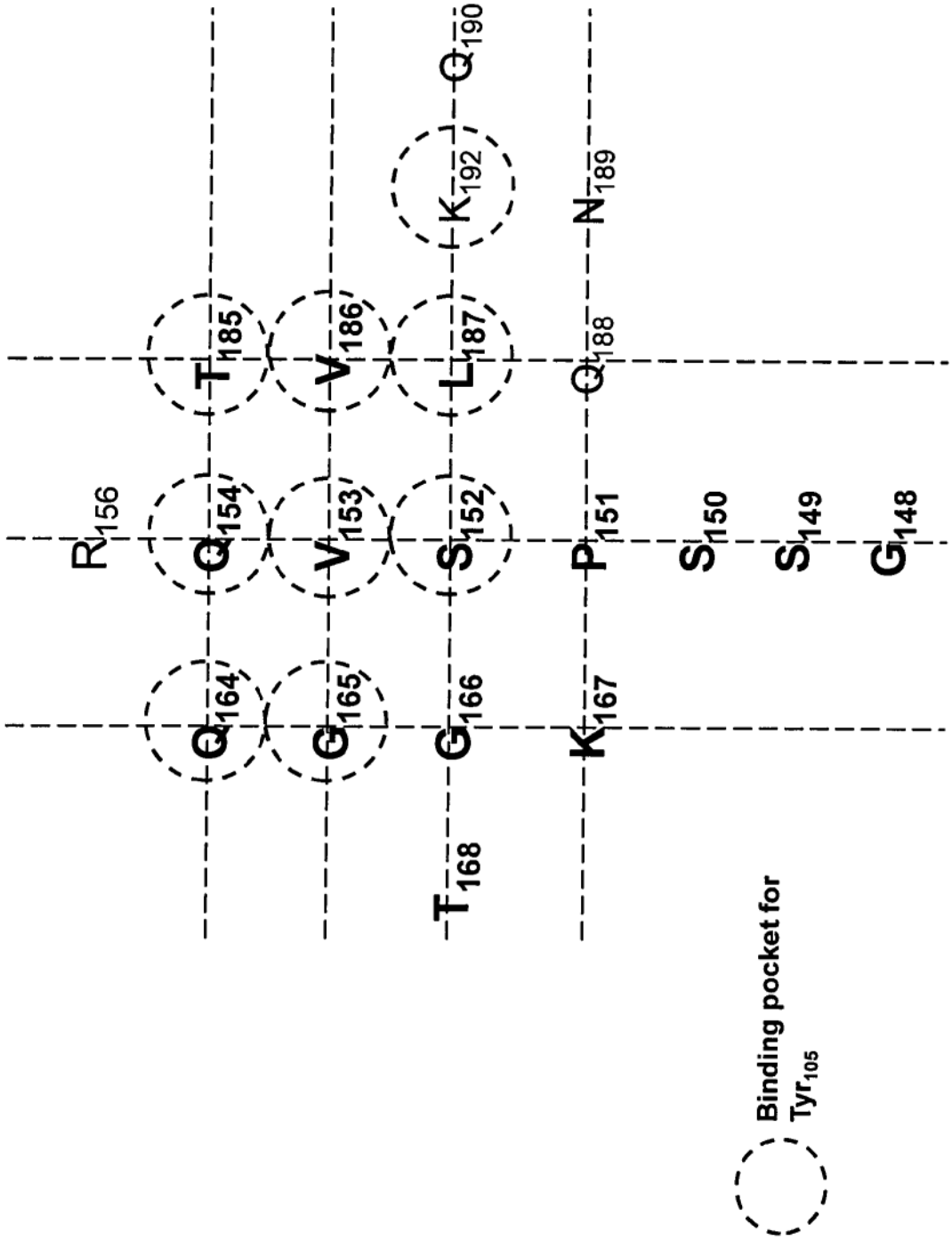

R156
Q154
T185
V186
L187
Q188
P151
S150
S149
G148
V153
S152
Q164
Q165
G166
K167
T168
K192
Q190
N189
Binding pocket for Tyr105

Figure 10

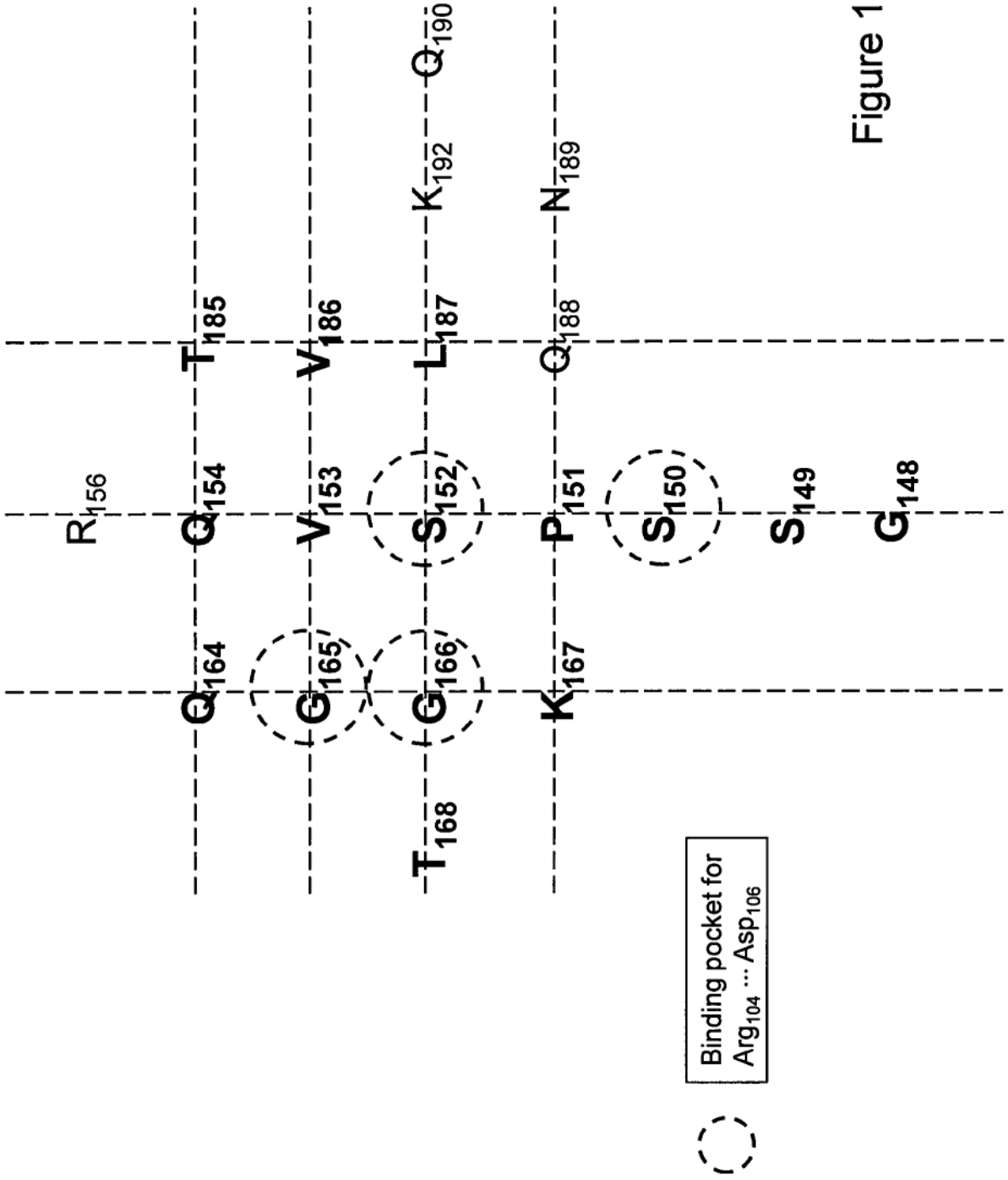

R156
Q154
Q164
G165
T185
V186
V153
G166
T168
L187
S152
K192
Q190
Q188
P151
K167
N189
S150
S149
G148
Binding pocket for Arg104 ··· Asp106

Figure 11

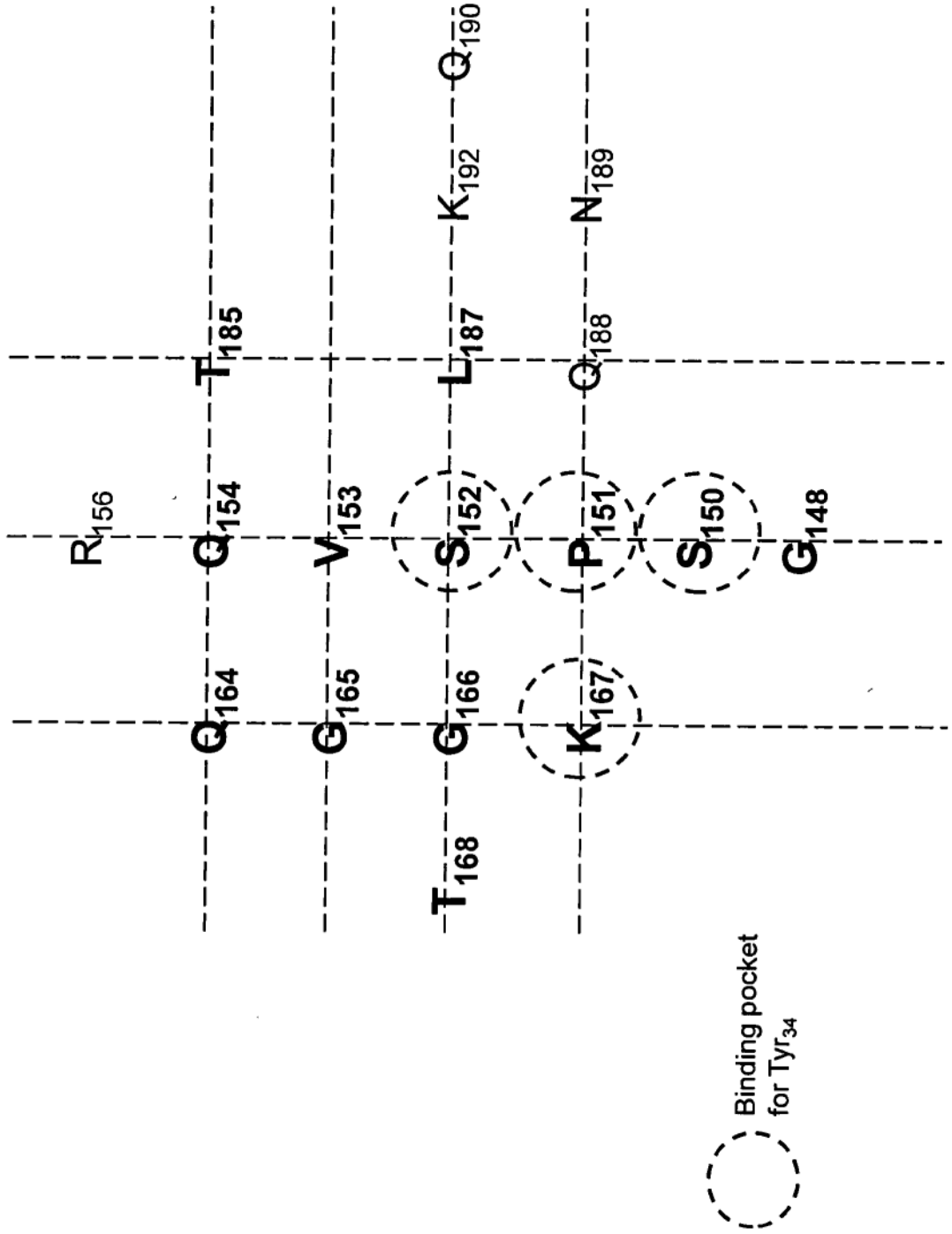

Q190
K192
N189
T185
L187
Q188
R156
Q154
V153
S152
P151
S150
G148
Q164
G165
G166
K167
T168
Binding pocket for Tyr34

Figure 12