**SUPPLEMENTARY DATA**

The amino acid sequence including information about disulphide bridges and glycosylation site are as follows.

**Heavy chain**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QVTLKESGPT | LVKPTQTLTL | TCSFSGFSLS | TSGMGIGWIR | QPPGKALEWL | **50** |
| AHIWWDDDKR | YNPALKSRLT | ISKDTSKNQV | VLTMTNMDPV | DTATYYCARH | **100** |
| YGYDPYYAMD | YWGQGTLVTV | SSASTKGPSV | FPLAPCSRST | SESTAALGCL | **150** |
| VKDYFPEPVT | VSWNSGALTS | GVHTFPAVLQ | SSGLYSLSSV | VTVPSSSLGT | **200** |
| KTYTCNVDHK | PSNTKVDKRV | ESKYGPPCPP | CPAPEFEGGP | SVFLFPPKPK | **250** |
| DTLMISRTPE | VTCVVVDVSQ | EDPEVQFNWY | VDGVEVHNAK | TKPREEQFNS | **300** |
| TYRVVSVLTV | LHQDWLNGKE | YKCKVSNKGL | PSSIEKTISK | AKGQPREPQV | **350** |
| YTLPPSQEEM | TKNQVSLTCL | VKGFYPSDIA | VEWESNGQPE | NNYKTTPPVL | **400** |
| DSDGSFFLYS | RLTVDKSRWQ | EGNVFSCSVM | HEALHNHYTQ | KSLSLSLGK | **449** |

**Light chain**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| EIVLTQSPGT | LSLSPGERAT | LSCTASSSVS | SSYLHWYQQK | PGKAPKLLIY | **50** |
| RTSNLASGVP | SRFSGSGSGT | DYTLTISSLQ | PEDFATYYCH | QYHRSPPTFG | **100** |
| QGTKLEIKRT | VAAPSVFIFP | PSDEQLKSGT | ASVVCLLNNF | YPREAKVQWK | **150** |
| VDNALQSGNS | QESVTEQDSK | DSTYSLSSTL | TLSKADYEKH | KVYACEVTHQ | **200** |
| GLSSPVTKSF | NRGEC |  |  |  | **215** |

**Confirmed disulphide bridge locations**

The expected disulphide bridge pattern for an IgG4 molecule has been confirmed, and no signals consistent with scrambled disulphide bridges were observed on the heavy chain or light chain. No signals consistent with reduced cysteine were observed in the light chain. Minor signals consistent with reduced cysteine were observed in the heavy chain constant region among cysteine residues participating in intrachain disulphide bridging. The disulphide bridges are at

Intra-H 22-97 149-205 263-323 369-427

Intra-L 23-89 135-195

Inter H-L 136-215

Inter H-H 228-228 231-231