

Heavy chain

1 - SDVQLQESGP GLVKPSQSLS LTCTVT GYSI TSDYAWNWIR QFPGNKLEWM
51 - GYSISYSGSTN YKPSLKSRSV ITRDTSKNQF FLQLNSVTTE DTATYYC ARS
101 - GISYYPGTD WGQGTTLTVS SAKTTPPSVY PLAPGSAAQT NSMVTLGCLV
151 - KGYFPEPVTV TWNSGSLSSG VHTFPAVLQS DLYTLSSSVT VPSSTWPSET
201 - VTCNVAHPAS STKVDKIVP RDCGCKPCIC TVPEVSSVFI FPPKPKDVLV
251 - ITLTPKVTCV VVDISKDDPE VQFSWFVDDV EVHTAQTQPR EEQFNSTFRS
301 - VSELPIMHQD WLNKKEFKCR VNSAAFPAPI EKTISKTKGR PKAPQVYTIP
351 - PPKEQMAKDK VSLTCMITDF FPEDITVEWQ WNGQPAENYK NTQPIMDTDG
401 - SYFVYSKLVN QKSNWEAGNT FTCSVLHEGL HNHHTEKSL S HSPGK

Light chain

1 - SENVLTQSPA IMSASLGEKV TMSCRAS SSV NYMYWYQQKS DASPKLWIYY
51 - TSNLAPGVPT RFSGSGSGNS YSLTISSMEG EDAATYYC RS FTSSEPTFGG
101 - GTKLEIKADA APTVSIFFPS SEQLTSGGAS VVCFLNNFYP KDINVKWKID
151 - GSERQNGVLN SWTDQDSKDS TYSMSSTLTL TKDEYERHNS YTCEATHKTS
201 - TSPIVKSFNR NEC

Supplementary file 2: Figure S2. The predicted amino acid sequences of heavy and light chain of mAb6-9-1 based on mouse immunoglobulin gamma 1 chain AAB06744 (GenBank), kappa light chain BAB33402 (GenBank) and the sequence of cDNA encoding variable fragments of scFv 6-9-1. Peptides determined by mass spectrometry analysis of mAb6-9-1 are shown in red (75% and 72% of the heavy and light chains, respectively). Complementarity determining regions CDR1, CDR2 and CDR3 are underlined and highlighted in yellow, blue and green, respectively.