



CDR3

**Supplementary Fig. 1. MW1 sequence and comparison with other antibodies.** (a) The amino acid sequences of the MW1 V<sub>H</sub> and V<sub>L</sub> domains as derived from the nucleotide sequences of the genes. CDRs 1, 2, and 3 are highlighted in yellow. Peptides identified by mass spectroscopic sequencing of the MW1 Fab (see Supplementary Methods) are underlined. (b) Structure-based sequence alignment of the MW1 V<sub>L</sub> domain (a λ light chain) with the V<sub>L</sub> domain from a mouse cyclosporin A-binding antibody (a κ light chain) (PDB code 1ikf). The locations of the β-strands in the MW1 V<sub>L</sub> domain structure are shown above the sequence as arrows. Conserved residues are red and conservatively-substituted residues are green. (c) Sequence alignment of the MW1 V<sub>L</sub> domain with the sequences of mouse κ light chains of known crystal structures. Residues within CDR loops are highlighted in yellow and a deletion in the strand A to A' region is highlighted in red. The sequence of the V<sub>L</sub> domain that is used for structural comparisons (PDB-1ikf) is listed directly below the MW1 sequence. The other V<sub>L</sub> domain sequences are listed in