



Figure 4. Illustration and explanatory note taken from (Honegger and Pluckthun, 2001) **(a)** Representative structures of disparate Ig fold domains from V_{L1} (PDB entries 1MFA, 2FB4, and 8FAB pink), V_{L2} (PDB entries 1A2Y, 1F58, 1FLR, 1HIL, 25C8, and 2FBJ magenta), V_H (PDB entries 1A2Y, 1A6V, 1F58, 1FLR, 1MFA, 1MRC, and 2HMI cyan), T Cell Receptor Va (PDB entries 1A07, 1B88, 1BD2, 1KB5, 1NFD, and 1TCR orange), T Cell Receptor Vb (PDB entries 1A07, 1BD2, 1KB5, 1NFD, 1TCR green) and T Cell Receptor Vd (PDB entry 1TVD red) were aligned by a least-squares fit of the C^α atoms of residues 3-7, 20-24, 41-47, 51-57, 78-82, 89-93, 102-108 and 138-144 (indicated in white). **(b)** Structure and main-chain hydrogen bonding pattern of immunoglobulin variable domains. Arrows indicate hydrogen bonds that are present in the majority of the structures in all types of immunoglobulin variable domains. The loop and turn regions that accommodate gaps are indicated in yellow. Gray areas underlie the residues whose C^α positions were used for least-squares superposition of the structures.