



**Supplementary Figure 1** Conserved residues in E3-19K proteins across Ad species. (a) Amino acid sequence alignment of different serotypes of E3-19K proteins of species B, C, D, and E. Strictly (blue) and highly (cyan) conserved residues are indicated. Secondary structural elements of the Ad2 E3-19K structure are shown above the sequences;  $\beta$  strands are represented by letter-coded arrows as in Figure 1(b) and the  $\alpha$ -helix is indicated by a coil. The strictly and highly conserved residues in Ad2 E3-19K at interaction sites 1, 2, 3, and 4 are indicated by red numbers, and core-forming residues (>90% buried) are indicated by a \* (see legend of Figure 2). GenBank accession numbers are as follows: Ad2, AP\_000184; Ad1, AP\_000521; Ad5, AP\_000220; Ad6, ACN88120; Ad3, ABB17785; Ad7, AAB28959; Ad11a, ACV41300; Ad16, BAB70718; Ad35, AP\_000594; Ad4, AAT97507; Ad8, BAH18792; Ad9, CAI05977; Ad17, ADY18438; Ad19, AFA46737; Ad37, BAH19152; Ad56, ADM66125; Ad60a, AEM45926