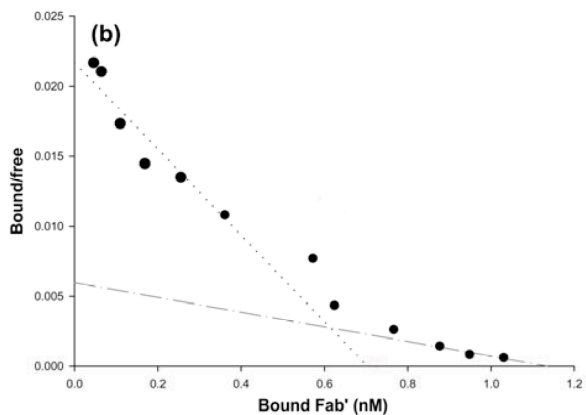
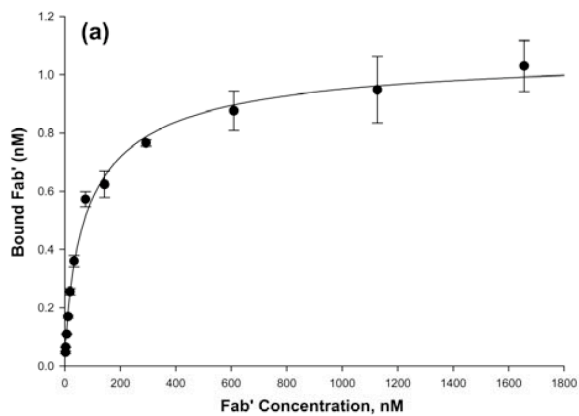


Synthesis and evaluation of multivalent branched HPMA copolymer-Fab' conjugates targeted to the B-cell antigen CD20

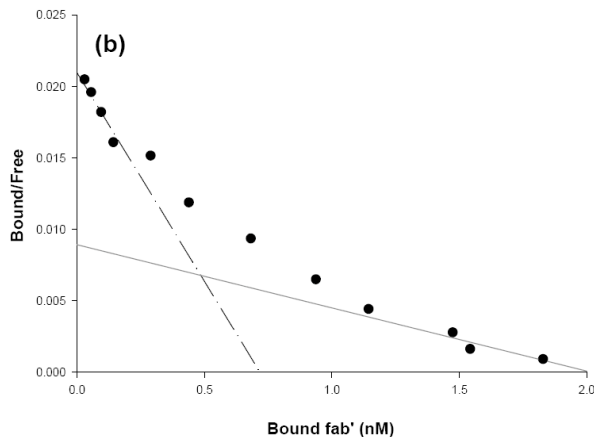
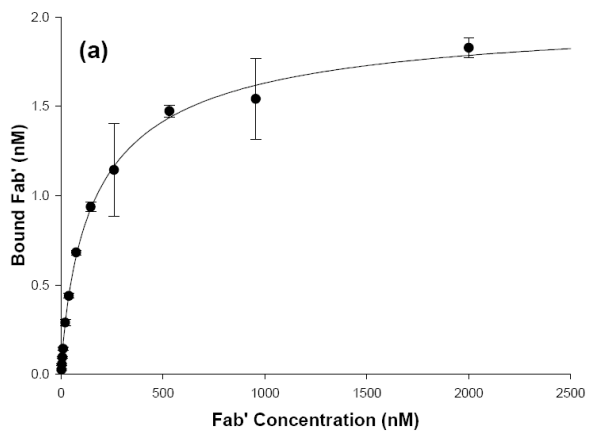
R. Johnson, P. Kopečková, and J. Kopeček

Supporting Information

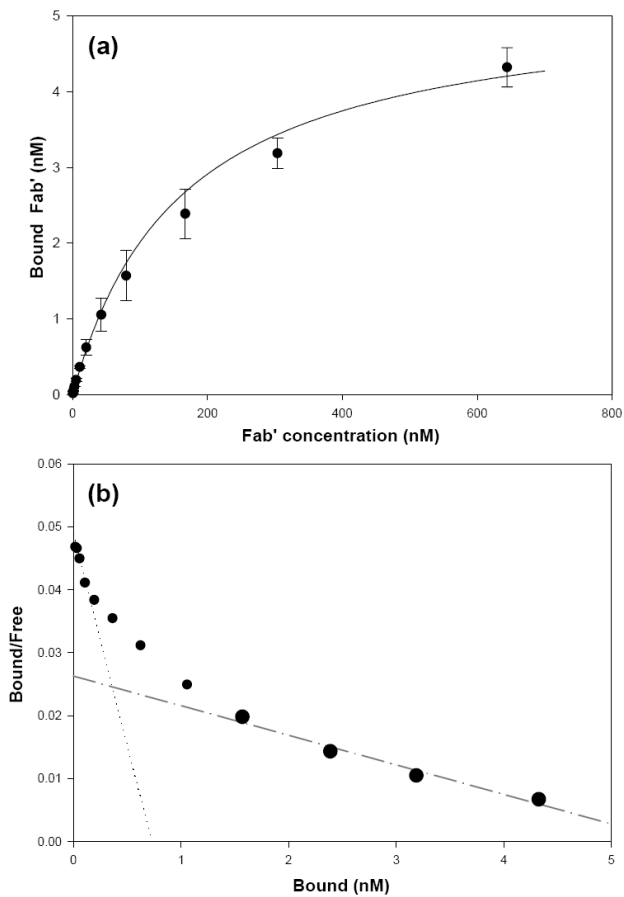
Binding analysis of each multivalent conjugate was performed as described in the Experimental Procedures section. Briefly, Raji cells grown in RPMI medium containing 10% fetal bovine serum (FBS) were washed twice with Hank's balanced salt solution (HBSS). The cells were adjusted to 4×10^6 cells/ml and split into two volumes. To one of the volumes of Raji cells, unlabeled anti-CD20 IgG was added to a final concentration of 500 nM to block CD20 for a negative control. Serial dilutions of ^{125}I -labeled anti-CD20 IgG, Fab', and multivalent Fab' conjugates were made from 2000 nM to 1 nM of Fab' fragment concentration. Millipore 96-well filter plates, coated with a 1% solution of nonfat dry milk in distilled water and incubated at 4 °C overnight, were washed with HBSS. For each of the serial dilutions, 25 μL of negative control cells were added to a single well, and 25 μL of unblocked cells were added to 3 different wells; then 25 μL of the respective dilutions were added to each well. The filter-well plates were incubated for 90 min at 120 rpm on a shaker at 25 °C. Following incubation, the Raji cells were washed twice with 200 μL of cold HBSS with 10% FBS, and then collected on filters. The filters were allowed to air-dry, removed from the plate and counted. Negative control wells were used to correct for non-specific binding. Isotherms were evaluated with the Sips equation using SigmaPlot software (Systat Software, San Jose, CA).



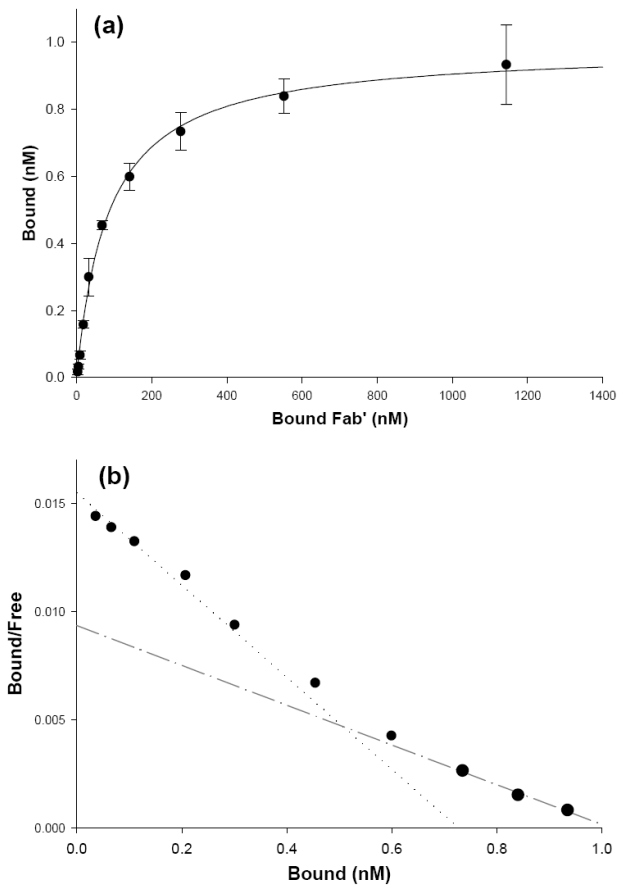
Supporting Information Figure 1. Binding analysis of conjugate *P-3Fab1.5*. (a) The isotherm for conjugate *P-3Fab1.5* was fitted with the Sips equation using the least squares method. (b) Scatchard plot of the binding data.



Supporting Information Figure 2. Binding analysis of conjugate *P-3Fab2.9*. (a) The isotherm for conjugate *P-3Fab2.9* was fitted with the Sips equation using the least squares method. (b) Scatchard plot of the binding data.



Supporting Information Figure 3. Binding analysis of conjugate *P-3Fab8.9*. (a) The isotherm for conjugate *P-3Fab2.9* was fitted with the Sips equation using the least squares method. (b) Scatchard plot of the binding data.



Supporting Information Figure 4. Binding analysis of conjugate *P-7Fab1.4*. (a) The isotherm for conjugate *P-3Fab2.9* was fitted with the Sips equation using the least squares method. (b) Scatchard plot of the binding data.