

# Supplementary Data

**Table S1. Probability Estimates of Representative Mutations in Antibody DH270.6**

Mutation <sup>†</sup>	Number of Simulated Sequences Used in Mutation Probability Estimate					
	n=10,000		n=100,000		n=1,000,000	
	Mean Probability <sup>^</sup>	95% CI <sup>^</sup>	Mean Probability <sup>^</sup>	95% CI <sup>^</sup>	Mean Probability <sup>^</sup>	95% CI <sup>^</sup>
<b>N54Q</b>	0.0034	0.0030-0.0037	0.0032	0.0031-0.0033	0.0032	0.0031-0.0032
<b>K23A</b>	0.0059	0.0053-0.0064	0.0058	0.0056-0.0059	0.0059	0.0058-0.0059
<b>G57R</b>	0.0126	0.0123-0.0129	0.0127	0.0125-0.0128	0.0125	0.0124-0.0125
<b>R98T</b>	0.0190	0.0180-0.0199	0.0188	0.0186-0.0189	0.0187	0.0186-0.0188
<b>V11M</b>	0.0588	0.0576-0.0599	0.0593	0.0588-0.0598	0.0595	0.0593-0.0596
<b>A24P</b>	0.0810	0.0797-0.0824	0.0807	0.0802-0.0812	0.0808	0.0807-0.0809
<b>G31D</b>	0.1307	0.1286-0.1327	0.1322	0.1315-0.1328	0.1326	0.1325-0.1327
<b>R85S</b>	0.1223	0.1203-0.1244	0.1213	0.1208-0.1218	0.1215	0.1213-0.1217

<sup>†</sup> Representative set of DH270.6 mutations chosen over a range of probabilities varying from very low probability to very high probability.

<sup>^</sup> Means of probability and 95% confidence intervals were computed from n=10 independent ARMADiLLO runs with the DH270.6 antibody as the input sequence and using the specified number of simulated sequences (10,000, 100,000, or 1,000,000).