

**Table 3. Impact of differences in cleavage rate constants between the minor and major subpopulations on the average cleavage rate constant**

<b>Variant</b>	<b><math>\rho</math></b>	<b><math>k_{\text{cleav,I}}</math></b>	<b><math>k_{\text{cleav,II-IV}}</math></b>	<b>Res. sq.</b>	<b><math>f_1</math></b>	<b><math>k_{\text{cleav}}</math></b>
	10	0.02	0.19	0.0030	0.62	0.09
	6	<i>0.03</i>	<i>0.17</i>	<i>0.0026</i>	<i>0.62</i>	<i>0.08</i>
WT	3	0.05	0.16	0.0028	0.62	0.09
	1	0.15	0.15	0.0035	0.62	0.15
	0.33	0.45	0.15	0.0039	0.62	0.33
	15	0.05	0.76	0.0033	0.62	0.32
	<i>10</i>	<i>0.07</i>	<i>0.67</i>	<i>0.0025</i>	<i>0.62</i>	<i>0.30</i>
dC12	3	0.19	0.57	0.0065	0.62	0.34
	1	0.56	0.56	0.0102	0.62	0.56
	0.33	1.72	0.57	0.0186	0.62	1.28
	10	0.03	0.29	0.0150	0.64	0.12
	5	<i>0.04</i>	<i>0.19</i>	<i>0.0035</i>	<i>0.64</i>	<i>0.09</i>
dA38	3	0.05	0.14	0.0012	0.64	0.08
	1	0.08	0.08	0.0305	0.64	0.08
	0.33	0.13	0.04	0.1133	0.64	0.10
	10	0.01	0.12	0.0008	0.64	0.05
	8	<i>0.01</i>	<i>0.11</i>	<i>0.0003</i>	<i>0.64</i>	<i>0.05</i>
C39S3	3	0.02	0.06	0.0149	0.64	0.04
	1	0.04	0.04	0.0620	0.64	0.04
	0.33	0.14	0.05	0.1153	0.64	0.11
	10	0.002	0.019	0.0062	0.48	0.011
	4	<i>0.003</i>	<i>0.012</i>	<i>0.0029</i>	<i>0.48</i>	<i>0.007</i>
RzAS3	3	0.003	0.010	0.0031	0.48	0.007
	1	0.006	0.006	0.0103	0.48	0.006
	0.33	0.015	0.005	0.0248	0.48	0.010
	10	0.002	0.024	0.0056	0.53	0.012

<b>Variant</b>	<b><math>\rho</math></b>	<b><math>k_{\text{cleav,I}}</math></b>	<b><math>k_{\text{cleav,II-IV}}</math></b>	<b>Res. sq.</b>	<b><math>f_1</math></b>	<b><math>k_{\text{cleav}}</math></b>
	<i>6</i>	<i>0.003</i>	<i>0.017</i>	<i>0.0045</i>	<i>0.53</i>	<i>0.010</i>
RzAS3/C39S3	3	0.004	0.011	0.0083	0.53	0.007
	1	0.006	0.006	0.0338	0.53	0.006
	0.33	0.012	0.004	0.0964	0.53	0.008

The rate of cleavage ( $k_{\text{cleav}}$ ) was derived from an analytical fit to the experimental data as described above, while keeping the ratio  $\rho = k_{\text{cleav,II-IV}}/k_{\text{cleav,I}}$  of the cleavage rate constants of the minor ( $k_{\text{cleav,II-IV}}$ ) to that of the major sub-populations ( $k_{\text{cleav,I}}$ ) constant at the tabulated value. Res. sq. indicates the sum of the squared residuals between fit and data. The average rate of cleavage was calculated as  $k_{\text{cleav,ave}} = f_1 \times k_{\text{cleav,I}} + (1 [\text{minus}] f_1) \times k_{\text{cleav,II-IV}}$ . The values for the optimal  $\rho$  (resulting in the lowest Res. sq.) are in italics.