

<b>Construct</b>	<b>Chimera aa residue</b>	<b>Length of substituted AE2 TMD segment (aa)</b>	<b>% aa seq. identity with corresponding AE1 seq.</b>
3	AE2 <sub>(1-1119)</sub> /AE1 <sub>(812-929)</sub>	118	<b>62%</b>
4	AE2 <sub>(1-920)</sub> /AE1 <sub>(613-929)</sub>	317	67%
5	AE2 <sub>(1-920)</sub> /AE1 <sub>(613-811)</sub> /AE2 <sub>(1120-1237)</sub>	199	70%
6	AE2 <sub>(1-703)</sub> /AE1 <sub>(423-811)</sub> /AE2 <sub>(1120-1237)</sub>	416	67%
7	AE2 <sub>(1-703)</sub> /AE1 <sub>(423-612)</sub> /AE2 <sub>(921-1237)</sub>	218	<b>65%</b>
8	AE1 <sub>(1-612)</sub> /AE2 <sub>(921-1237)</sub>	317	67%
9	AE2 <sub>(1-703)</sub> /AE1 <sub>(423-929)</sub>	534	66%
10	AE2-AE1(EC3)	50	divergent
11	AE1-AE2(EC3)		divergent

**Supplemental Table 2. Comparing sequence identity of AE transmembrane segments**