Supporting information

Inhibition of light chain 6aJL2-R24G amyloid fiber formation associated with AL amyloidosis.

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Figure S1.

Native gel (9 % acrilamide) electrophoresis reveals that 6aJL2-R24G is mainly monomeric in solution with a small fraction forming probably dimers. The addition of EGCG does not change equilibrium. Line 1: 6aJL2-R24G; line 2: 6aJL2-R24G + EGCG 1:1 incubated 2 hrs at 4 °C; line 3: 6aJL2-R24G + EGCG 1:1 incubated 4 hrs at 4 °C ; line 5: 6aJL2-R24G + EGCG 1:1 incubated 6 hrs at 4 °C; line 5: reference proteins: Carbonic anhydrase 29 kDa, Ovalbumin 43 kDa and Conalbumin 75 kDa.
Figure S2.

Variation of the intensity correlation function with time for (A) 6aJL2-R24G and (B) 6aJL2-R24G + EGCG. Translational diffusion coefficients were obtained through measurement of the decay rates of scattered light and the auto-correlation curves. The addition of EGCG does not change the calculated diffusion coefficient (black), however after 5 hrs of the inhibition (red) the presence of soluble aggregates were detected.
Figure S3.

(A) Sequence alignment of germ line λ VI and III proteins (From top to bottom: 6a, 3h, 3r, 219, 3m, 3p, and 3l). The alignment was generated with CLUSTALW2. Red lettering indicates invariant residues, while blue boxes indicate residues implicated in EGCG binding by NMR and docking. Secondary structure elements observed in the NMR structure are shown. (B) Conservation alignments for AL patients from germ line VI and III. The size of the letter indicates the conservation percentage, with blue color indicates residues implicated in the EGCG binding.
**Figure S4.**

Isothermal titration calorimetry of 6aJL2 with EGCG at (A) 25 °C and (B) 37 °C. Heat exchanged from each injection of EGCG into a solution containing 6aJL2 are shown. Each experiment consisted of 1 µl injections, with an injection spacing of 180 s, the exothermic heat pulse detected after each injection was integrated (except for the first injection). The corresponding thermogram was fit to a one site-binding model (Origin 7.0).

**Table 1**

<table>
<thead>
<tr>
<th></th>
<th>n</th>
<th>Ka (M⁻¹)</th>
<th>ΔH (kcal/mol)</th>
<th>ΔG (kcal/mol)</th>
</tr>
</thead>
<tbody>
<tr>
<td>6JL2-R24G 25 °C</td>
<td>0.96 ± 0.07</td>
<td>1.3 x 10⁴ ± 2.8 x 10³</td>
<td>-1.02 ± 0.11</td>
<td>-5.63</td>
</tr>
<tr>
<td>6JL2-R24G 37 °C</td>
<td>0.86 ± 0.06</td>
<td>2.1 x 10⁴ ± 1.4 x 10³</td>
<td>-1.27 ± 0.13</td>
<td>-6.14</td>
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<tr>
<td>6JL2 25 °C</td>
<td>0.76 ± 0.02</td>
<td>3.8 x 10⁴ ± 5.2 x 10³</td>
<td>-0.53 ± 0.02</td>
<td>-6.25</td>
</tr>
<tr>
<td>6JL2 37 °C</td>
<td>0.73 ± 0.04</td>
<td>1.6 x 10⁴ ± 2.6 x 10³</td>
<td>-0.96 ± 0.07</td>
<td>-5.99</td>
</tr>
</tbody>
</table>
Figure S5.
Thermal (A) and chaotropic (B) unfolding of 6aJL2-R24G protein in the absence (black) and presence of 1 equivalent of EGCG (red). Thermal unfolding was induced by increasing the temperature from 25 to 60 °C at a rate of 1 °C min$^{-1}$ while chemical unfolding was induced by increasing urea concentrations from 0 to 6 M after incubation for 5 minutes at 25 °C. Both thermal and urea unfolding curves were fit to a single monophasic transition.