SUPPLEMENTARY INFORMATION

BIOPRODUCTION AND CHARACTERIZATION OF $(E50I60)_2$

Standard molecular biology techniques were used to construct the ELP gene and its sequence was verified by automated DNA sequencing. Polymer production was carried out using cellular systems for genetic-engineering protein biosynthesis in *Escherichia coli*. The $(E50I60)_2$ biopolymer was purified by three cycles of temperature-driven precipitation and the final bioproduction yield was around 520 mg/L of bacterial culture. A purified sample of the biopolymer was analyzed by polyacrylamide gel electrophoresis in the presence of sodium dodecyl sulfate with copper staining, which indicated a polypeptide purity of 95% (Fig. S1).

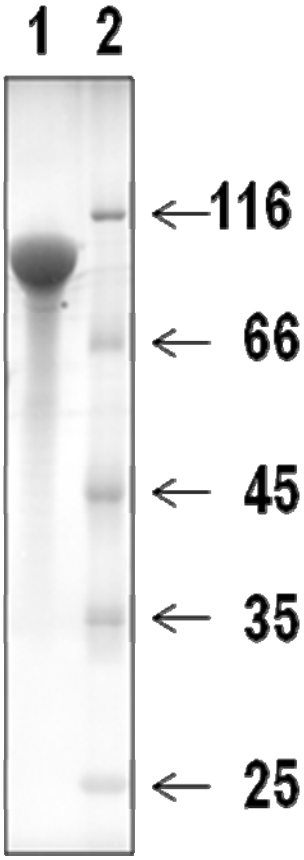

Fig. S1. Analysis of $(E50I60)_2$ biopolymer purity by SDS-PAGE after staining with copper chloride. Lane 1: 20 μg of the purified biopolymer. Lane 2: protein markers. The numbers on the right indicate the corresponding apparent molecular weight values of the standards (in kDa).

High-mass MALDI TOF MS analyses were performed using a Reflex IV MALDI TOF mass spectrometer (Bruker, Bremen, Germany) equipped with CovalX's HM2 high-mass detector system and focusing on different mass ranges from 0 to 1500 kDa. An external calibration with clusters of Insulin, BSA and IgG was applied to calibrate the instrument. Three spots were analyzed for the sample (300 laser shots per spot). The MS data were analyzed using the Complex Tracker analysis software.

The main protein detected in the three different spots for the $(E50I60)_2$ biopolymer corresponds to a protein with a molecular weight of 92,892±19 Da. The predicted molecular weight for this polymer is 93,176 Da. This is a variation of 0.3%, which is perfectly reasonable for this technique (Fig. S2).

The following results were obtained for the three spots:

$(E50I60)_2$	Concentration	Observed Molecular Weight (Da)
Spot 1	1 mg/ml	92,897
Spot 2	1 mg/ml	92,871
Spot 3	1 mg/ml	92,908

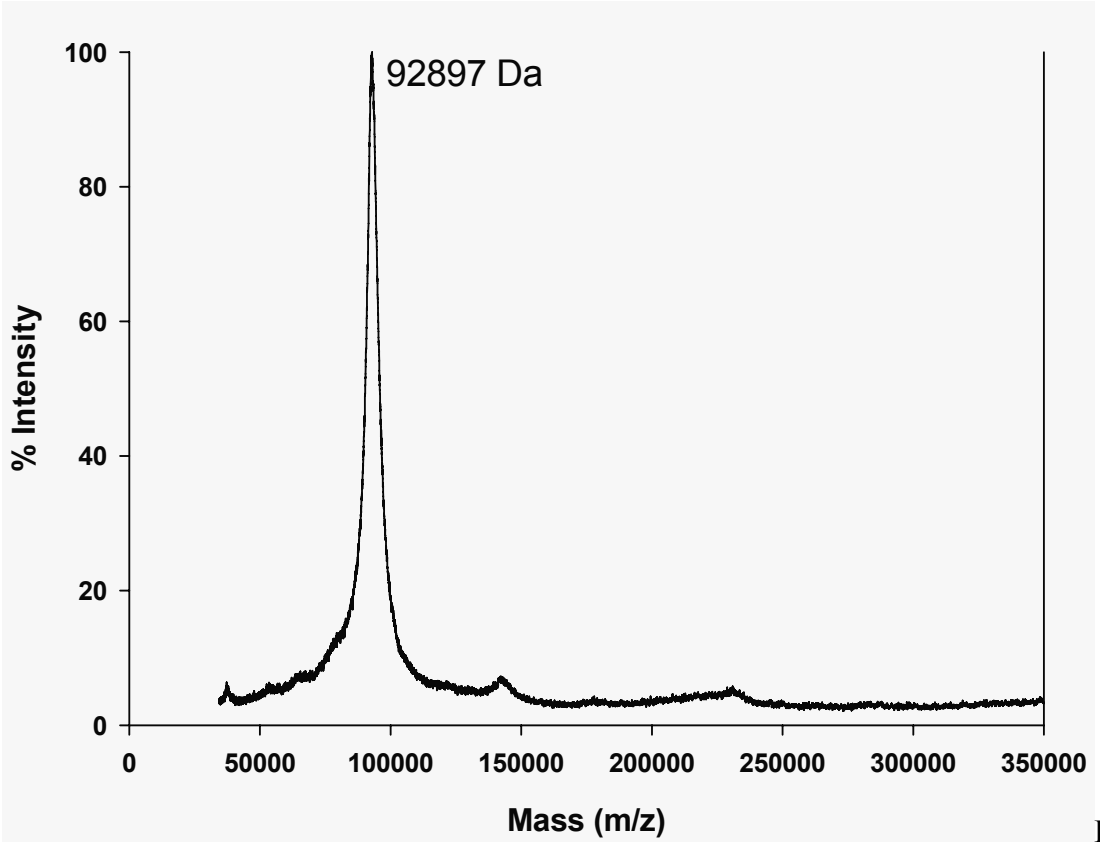

Fig. S2. MALDI-TOF spectra of one of the spots analyzed for the $(E50I60)_2$ biopolymer.

The polymer's amino acid composition was determined by the AccQ-Tag Waters method. The derivatized amino acids were analyzed by high performance liquid chromatography (HPLC) with UV detection, using a WATERS600 HPLC gradient system with a WATERS2487 detector. Quantification of the most represented amino acids was performed using the 1/10 dissolution.

The results of the amino acid composition analysis match the predicted amino acid composition very well taking into account the endogenous error inherent to this technique and the peculiar composition of this sample (Fig. S3).

	Predicted	Experimental
Asp	**0**	**0.47**
Ser	**1**	**1.09**
Glu	**21**	**22.01**
Gly	**440**	**432.83**
Thr	**0**	**0.22**
Ala	**0**	**0.37**
Pro	**221**	**224.02**
Tyr	**0**	**0.22**
Val	**301**	**304.8**
Lys	**0**	**0.22**
Ile	**120**	**119.34**
Leu	**2**	**1.91**

Fig. S3. Predicted and measured amino acid compositions for the $(E50I60)_2$ biopolymer.

The reversible process undergone by $(E50I60)_2$ was monitored by DSC, which showed a transition temperature (T_t) of 8.11 °C on heating and 7.35 °C on cooling (Fig. S4). Experiments were performed with a Mettler Toledo 822e with a liquid-nitrogen cooler. The solution was prepared at 15.0 wt % in sodium phosphate buffer (PBS) solution. For analysis, 25 μL of the solution was placed in a standard 40 μL aluminum pan and sealed hermetically. The same volume of PBS was placed in the reference pan. The following thermal procedure was used for heating-cooling cycle measurements:

isotherm at –10 °C for 5 min, ramp 1.0 °C·min^{-1} from –10 to 20 °C, isotherm at 20 °C for 1 min, and ramp 1.0 °C·min^{-1} from 20 to –10 °C.

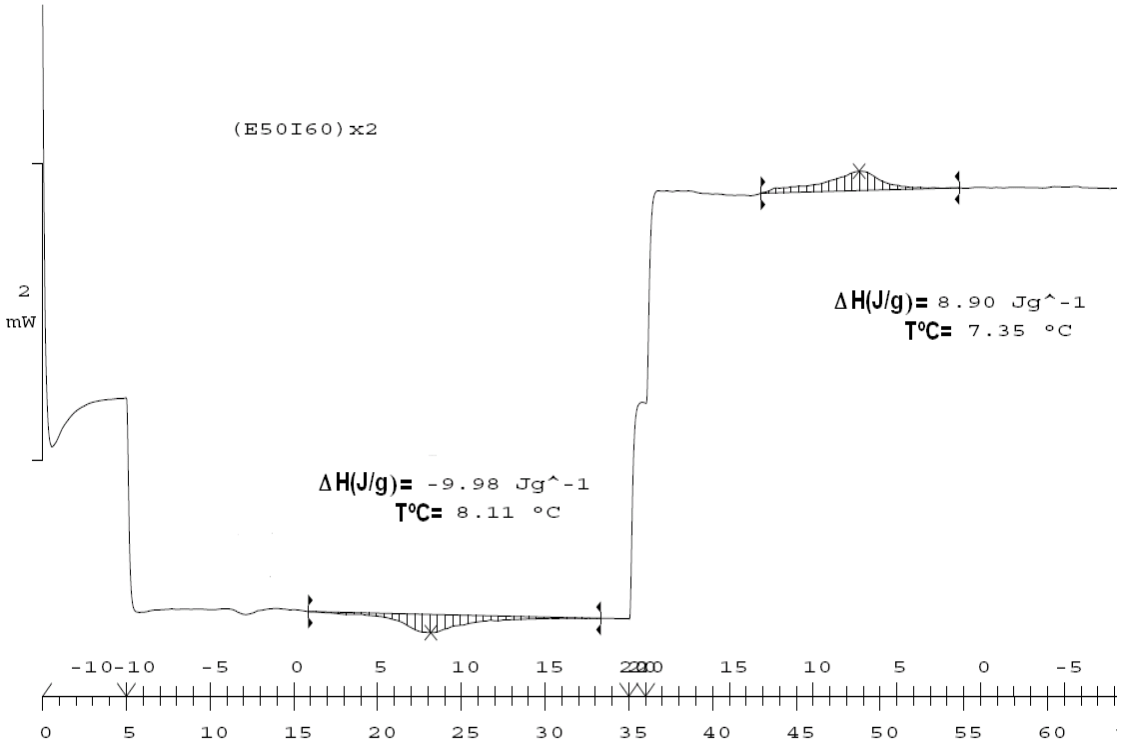

Fig. S4. DSC thermo grams for a heating–cooling cycle (1.0 °C·min^{-1}) for $(E50I60)_2$ at 15.0 wt % in sodium phosphate buffer (PBS) solution.