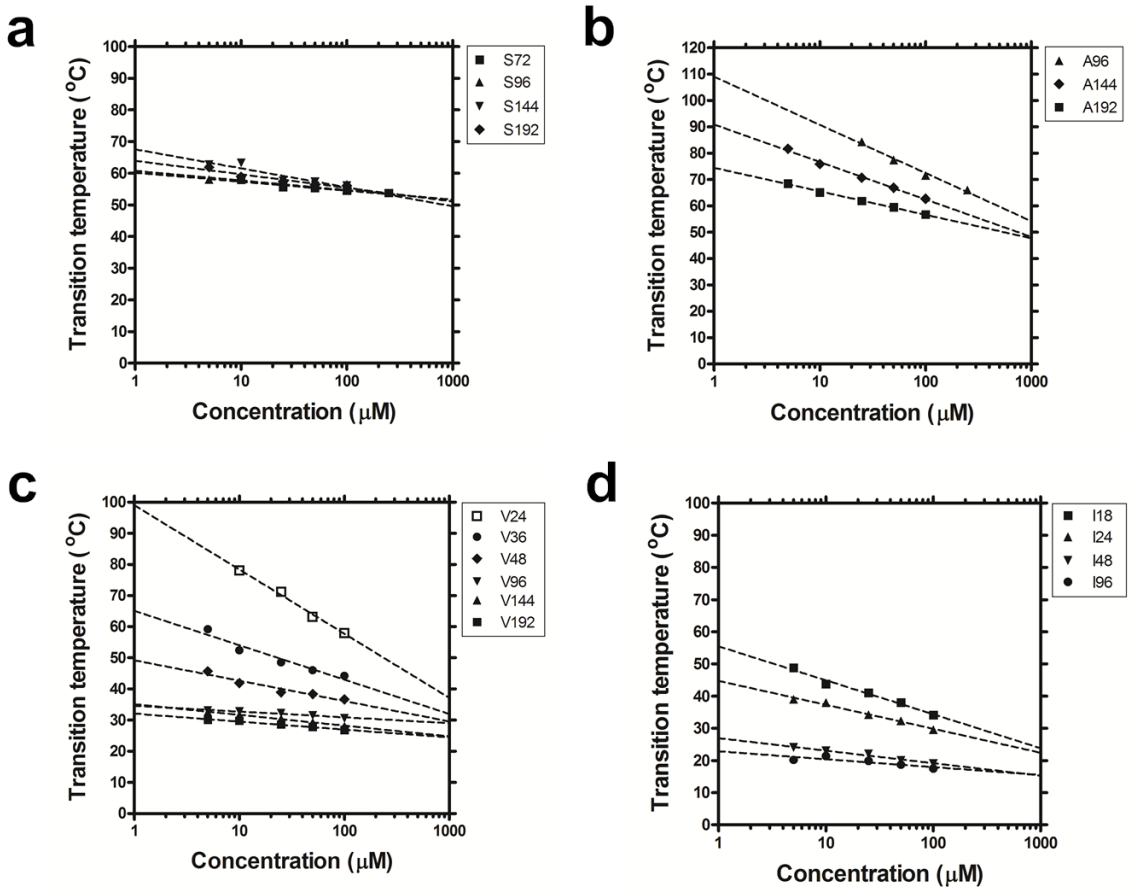
Supplementary data

Supplementary Table s1. Library of ELP genes expressed and characterized for phase behavior of monoblocks

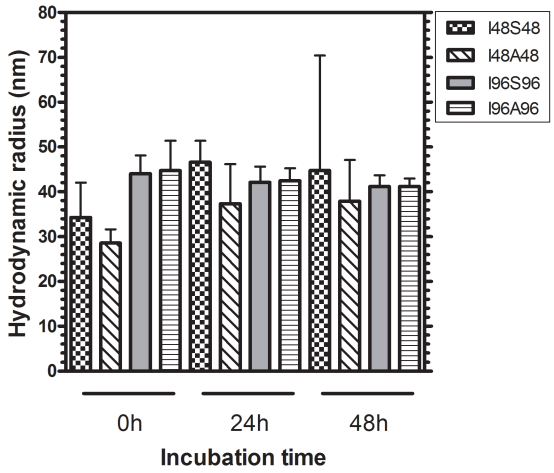
Nomenclature	*Nucleotide sequence of open reading frame	**Encoded amino acid sequence	ELP MW (Da)
S72	atg gg(t gtt ccg ggc tct ggt gta cca ggt agc ggt gta ccg ggt tct ggc gta cct ggc tcc ggt gtc ccg ggt tcc ggt gtt ccg ggt tct gg)$_{12}$ t tac tga	G(VPGSG)$_{72}$Y	28,853
S96	atg gg(t gtt ccg ggc tct ggt gta cca ggt agc ggt gta ccg ggt tct ggc gta cct ggc tcc ggt gtc ccg ggt tcc ggt gtt ccg ggt tct gg)$_{16}$ t tac tga	G(VPGSG)$_{96}$Y	38,392
S144	atg gg(t gtt ccg ggc tct ggt gta cca ggt agc ggt gta ccg ggt tct ggc gta cct ggc tcc ggt gtc ccg ggt tcc ggt gtt ccg ggt tct gg)$_{24}$ t tac tga	G(VPGSG)$_{144}$Y	57,468
S192	atg gg(t gtt ccg ggc tct ggt gta cca ggt agc ggt gta ccg ggt tct ggc gta cct ggc tcc ggt gtc ccg ggt tcc ggt gtt ccg ggt tct gg)$_{32}$ t tac tga	G(VPGSG)$_{192}$Y	76,545
A96	atg gg(t gtt ccg ggc gct ggt gta cca ggt gca ggt gta ccg ggt gcc ggc gta cct ggc gca ggt gtc ccg ggt gcc ggt gtt ccg ggt gct gg)$_{16}$t tac tga	G(VPGAG)$_{96}$Y	36,987
A144	atg gg(t gtt ccg ggc gct ggt gta cca ggt gca ggt gta ccg ggt gcc ggc gta cct ggc gca ggt gtc ccg ggt gcc ggt gtt ccg ggt gct gg)$_{24}$t tac tga	G(VPGAG)$_{144}$Y	55,296
A192	atg gg(t gtt ccg ggc gct ggt gta cca ggt gca ggt gta ccg ggt gcc ggc gta cct ggc gca ggt gtc ccg ggt gcc ggt gtt ccg ggt gct gg)$_{32}$t tac tga	G(VPGAG)$_{192}$Y	73,605
V24	atg gg(t gtt ccg ggc gtg ggt gta cca ggt gtc ggt gta ccg ggt gtc ggc gta cct ggc gtc ggt gtc ccg ggt gtt ggt gtt ccg ggt gta gg)$_{4}$t tac tga	G(VPGVG)$_{24}$Y	10,197
V36	atg gg(t gtt ccg ggc gtg ggt gta cca ggt gtc ggt gta ccg ggt gtc ggc gta cct ggc gtc ggt gtc ccg ggt gtt ggt gtt ccg ggt gta gg)$_{6}$t tac tga	G(VPGVG)$_{36}$Y	24,939
V48	atg gg(t gtt ccg ggc gtg ggt gta cca ggt gtc ggt gta ccg ggt gtc ggc gta cct ggc gtc ggt gtc ccg ggt gtt ggt gtt ccg ggt gta gg)$_{8}$t tac tga	G(VPGVG)$_{48}$Y	20,025
V96	atg gg(t gtt ccg ggc gtg ggt gta cca ggt gtc ggt gta ccg ggt gtc ggc gta cct ggc gtc ggt gtc ccg ggt gtt ggt gtt ccg ggt gta gg)$_{16}$t tac tga	G(VPGVG)$_{96}$Y	39,680
V144	atg gg(t gtt ccg ggc gtg ggt gta cca ggt gtc ggt gta ccg ggt gtc ggc gta cct ggc gtc ggt gtc ccg ggt gtt ggt gtt ccg ggt gta gg)$_{24}$t tac tga	G(VPGVG)$_{144}$Y	59,336
V192	atg gg(t gtt ccg ggc gtg ggt gta cca ggt gtc ggt gta ccg ggt gtc ggc gta cct ggc gtc ggt gtc ccg ggt gtt ggt gtt ccg ggt gta gg)$_{32}$t tac tga	G(VPGVG)$_{192}$Y	78,991
I18	atg gg(t gtt cct ggt atc ggt gtt ccg ggc atc ggt gta cct ggc att ggt gtc cca ggt att ggc gtt cca ggt atc ggc gta cca ggt att gg)$_{3}$t tac tga	G(VPGIG)$_{18}$Y	7,861
I24	atg gg(t gtt cct ggt atc ggt gtt ccg ggc atc ggt gta cct ggc att ggt gtc cca ggt att ggc gtt cca ggt atc ggc gta cca ggt att gg)$_{4}$t tac tga	G(VPGIG)$_{24}$Y	10,403
I48	atg gg(t gtt cct ggt atc ggt gtt ccg ggc atc ggt gta cct ggc att ggt gtc cca ggt att ggc gtt cca ggt atc ggc gta cca ggt att gg)$_{8}$t tac tga	G(VPGIG)$_{48}$Y	20,557
I96	atg gg(t gtt cct ggt atc ggt gtt ccg ggc atc ggt gta cct ggc att ggt gtc cca ggt att ggc gtt cca ggt atc ggc gta cca ggt att gg)$_{16}$t tac tga	G(VPGIG)$_{96}$Y	40,896

*Gene sequence confirmed by N and C terminal DNA sequencing and diagnostic restriction digestions. Parentheses indicate location of restriction cut sites (BserI, AcuI) used for recursive directional ligation. A BserI recognition site was located to the 5' direction of the start codon (atg). An AcuI recognition site was located to the 3' direction of the stop codon (tga).

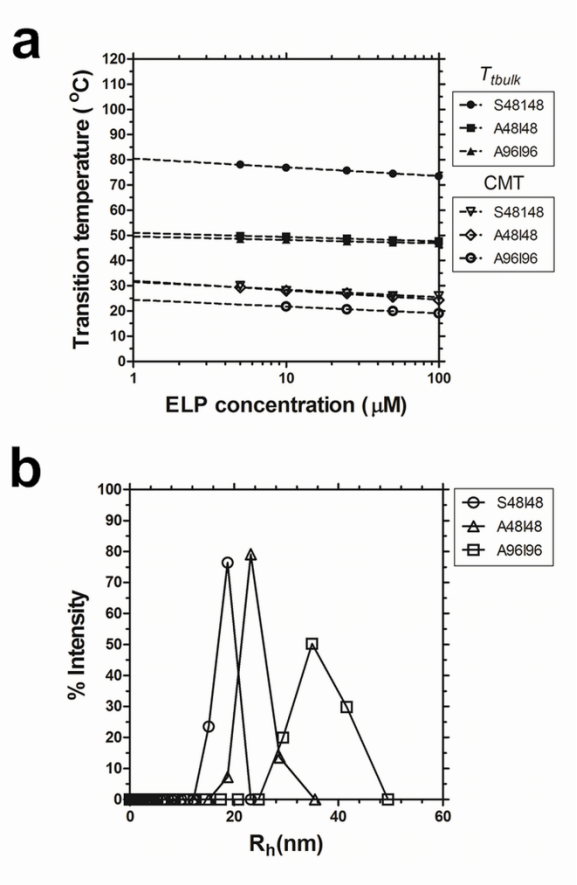
**Translation of open reading frame excluding start and stop codons. A carboxy terminal tyrosine was incorporated for $A_{280\ nm}$ quantification of ELP concentration (molar extinction coefficient 1,285 M^{-1} cm^{-1})



Supplementary Figure s1. Transition temperature for monoblock ELPs depends on molecular weight and hydrophobicity. ELP phase diagrams were characterized using optical density (350 nm) in phosphate buffered saline as a function of concentration, for which a best-fit line is indicated. **a**) Hydrophilic ELPs with Xaa=Ser and l = 72 to 192. **b**) Hydrophilic ELPs with Xaa=Ala and l = 96 to 192. **c**) Hydrophobic ELPs with Xaa=Val and l = 24 to 192. **d**) Hydrophobic ELPs with Xaa=Ile and l = 18 to 96. The complete library of genes encoding these ELPs can found in supplementary table s1.



Supplementary Figure s2. To determine the stability of the block copolymers over a period of time each of the samples were incubated either at room temperature (25^{o}C) or 37^{o}C for 24h and 48h. To ensure that the polypeptides are not subjected to premature proteolysis/degradation by residual bacterial enzymes, the samples were first filtered through a 0.2μM syringe filter. The filtered samples were then boiled for 5min and the antibiotics penicillin/streptomycin added.



Supplementary Figure s3. ELP assembly behavior and particle radius are independent of diblock orientation. ELP block copolymers were characterized for assembly using optical density and DLS in phosphate buffered saline. **a**) Concentration-temperature phase diagrams for ELP diblock copolymers S48I48, A48I48, A96I96. The reversal of orientation from hydrophobic-hydrophilic did not appear to influence the CMT or $T_{t,bulk}$. **b**) The distribution of hydrodynamic radii (37 °C) observed for S48I48, A48I48, and A96I96 roughly matches the particle radii observed for the equivalent block copolymers with the hydrophobic block at the amino terminus (Fig. 3).