Table Table S1. Radius of gyration and cis-trans isomerization.

	$R_g(\mathrm{Q}_n)$		$R_g(\mathrm{Q}_n\mathrm{P}_6)$		trans content							all-trans
n	mean	st.dev.	mean	st.dev.	P^1	P^2	P^3	P^4	P^5	P^6	**average**	population
40	14.06	1.80	14.45	2.41	85	88	98	92	93	96	**92**	60
30	12.96	1.71	-	-	-	-	-	-	-	-	-	-
18	8.20	0.96	8.01	0.95	68	67	69	80	87	91	**77**	23
12	5.83	0.65	5.81	0.67	69	68	68	78	87	94	**77**	22
9	4.69	0.57	4.47	0.53	71	64	63	82	89	93	**77**	18
6	3.62	0.57	3.73	0.67	73	73	52	64	84	91	**73**	12

The mean radius of gyration and its standard deviation (in $\mathring{A}$) for Q_n and $\mathrm{Q}_n\mathrm{P}_6$ peptides, along with the trans content (as a percentage) of all prolyl bonds of $\mathrm{Q}_n\mathrm{P}_6$ peptides along with their averages are given. The population of all-trans structures for each $\mathrm{Q}_n\mathrm{P}_6$ peptide is given as well.