

Figure S1. **Sequence alignment of MINT orthologs.** Figure shows sequence alignment for orthologous MINT proteins corresponding to the region that is necessary for interacting with CSL. Numbering corresponds to the *M. musculus* (Mm) ortholog used in this study. Absolutely conserved residues between all orthologs are colored blue. The blue and magenta bars beneath the sequence correspond to construct (2776-2833) used in this study and the region identified by Oswald et al. (2002) to be necessary for interacting with CSL, respectively.

Fig. S1

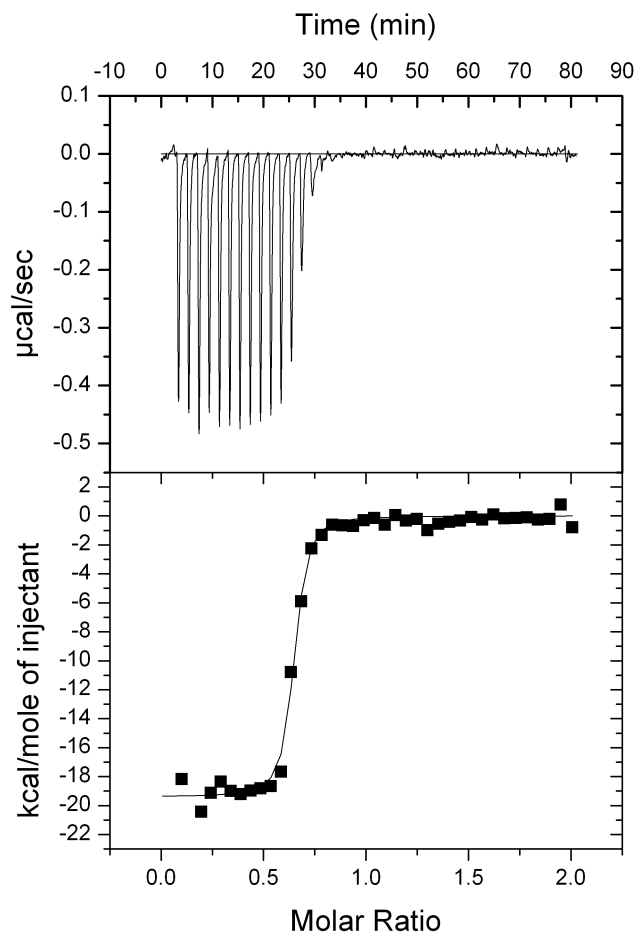
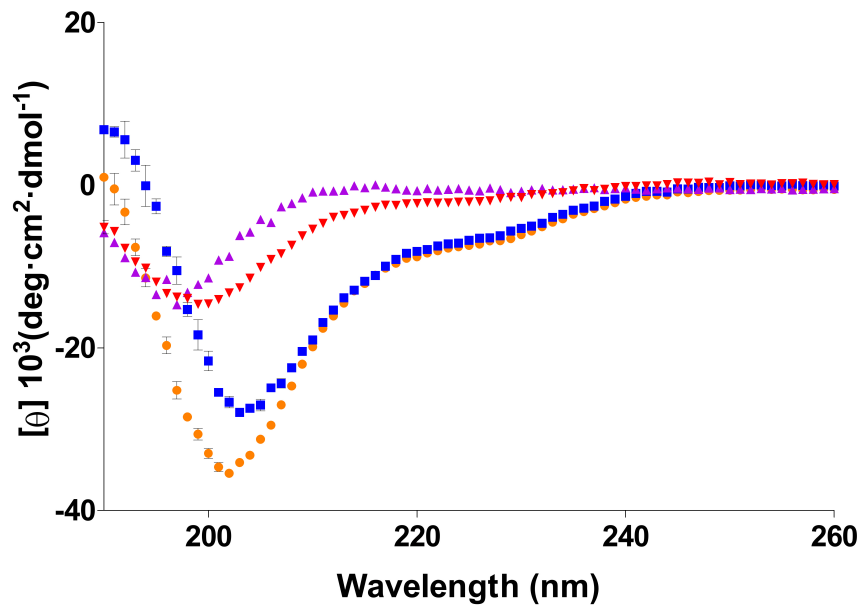


Figure S2. **CSL-MINT control ITC binding experiment.** Figure shows representative thermogram (raw heat signal and nonlinear least squares fit to the integrated data) of the complex formed by CSL and MINT (2776-2833), with CSL in the syringe and MINT in the cell.

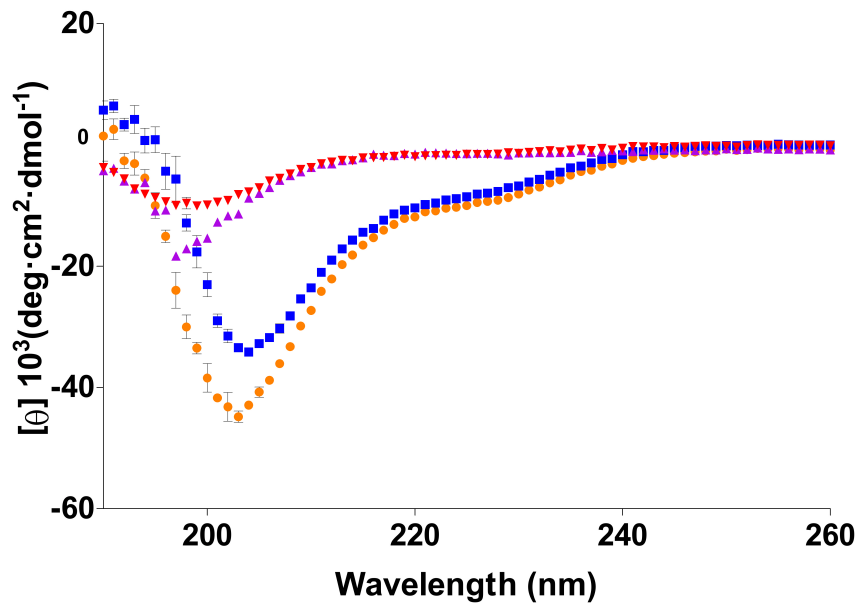
Fig. S2

Mint 2776-2833



- SMT3-MINT:2776-2833 (65uM)
- SMT3 (61uM)
- 2776-2833 Peptide (85uM)
- SMT3Mint - SMT3

Mint 2776-2820



- SMT3-MINT:2776-2820 (95uM)
- SMT3 (94uM)
- 2776-2820 Peptide (100uM)
- SMT3MINT - SMT3

Figure S3. **Comparison of CD for MINT peptides and corresponding SMT3-MINT fusion proteins.** Experiments were performed as described in the Experimental Procedures. CD data are shown for MINT constructs (2776-2833), top, and (2776-2820), bottom. Construct concentrations for CD analysis are denoted. MINT and SMT3-MINT fusion proteins were analyzed in a buffer containing 50mM NaPi pH 6.5 and 150mM NaF. [SMT3MINT - SMT3] represent the calculated spectra from subtracting the collect SMT3 spectra from the corresponding SMT3-MINT fusion protein spectra.

Fig. S3

	MINT	K (M ⁻¹)	Kd (μM)	ΔG (kcal/mol)	ΔH (kcal/mol)	TΔS (kcal/mol)
CSL	2752 - 2833	1.87E+08 ± 1.01E+07	0.005 ± 0.00028	-11.3 ± 0.032	-14.8 ± 0.992	-3.52 ± 1.007
	smt 2776 - 2833	1.21E+08 ± 2.00E+06	0.008 ± 0.0013	-11.0 ± 0.010	-18.0 ± 0.626	-7.0 ± 0.626
	2776 - 2833	9.39E+07 ± 1.19E+07	0.011 ± 0.0014	-10.9 ± 0.078	-14.6 ± 0.154	-3.7 ± 0.164
	smt 2776 - 2820	3.77E+08 ± 1.09E+08	0.003 ± 0.0007	-11.7 ± 0.165	-19.3 ± 0.545	-7.6 ± 0.698
	2776 - 2820	5.80E+07 ± 1.17E+07	0.018 ± 0.0038	-10.6 ± 0.124	-10.0 ± 1.241	0.6 ± 1.280
	smt 2801 - 2833	5.49E+05 ± 7.53E+04	1.845 ± 0.2698	-7.8 ± 0.084	-7.4 ± 1.209	0.4 ± 1.169
	2801 - 2833	1.13E+05 ± 1.41E+03	8.850 ± 0.1107	-6.9 ± 0.007	-11.3 ± 0.120	-4.4 ± 0.148
	smt 2776 - 2800	2.45E+05 ± 1.87E+04	4.104 ± 0.3294	-7.3 ± 0.047	-4.9 ± 0.607	2.4 ± 0.591
	smt 2776 - 2812	1.39E+08 ± 4.92E+07	0.008 ± 0.0023	-11.1 ± 0.196	-14.0 ± 1.051	-2.9 ± 1.246
	smt 2791 - 2812	9.43E+04 ± 1.28E+04	10.746 ± 1.5570	-6.8 ± 0.084	-10.6 ± 1.260	-3.8 ± 1.346
	smt 2791 - 2820	8.21E+04 ± 1.83E+04	12.654 ± 3.1515	-6.7 ± 0.141	-12.8 ± 1.948	-6.1 ± 2.075
	smt 2801 - 2820	1.71E+05 ± 7.35E+04	6.504 ± 2.3590	-7.1 ± 0.240	-19.0 ± 2.170	-11.9 ± 2.232
BTD	2776 - 2833	2.46E+04 ± 3.02E+03	41.044 ± 4.8050	-6.0 ± 0.071	-14.9 ± 3.573	-8.9 ± 3.529
	2801 - 2833	9.11E+04 ± 3.16E+04	11.804 ± 3.5800	-6.7 ± 0.196	-8.2 ± 1.606	-1.4 ± 1.797
	smt 2776 - 2812	NBD	NBD	NBD	NBD	NBD
	smt 2791 - 2812	NBD	NBD	NBD	NBD	NBD
	smt 2791 - 2820 **	5.25E+04 ± 3.05E+04	23.338 ± 11.4040	-6.2 ± 0.445	-12.3 ± 4.685	-6.1 ± 4.629
	smt 2801 - 2820	7.35E+04 ± 2.38E+04	14.458 ± 3.9470	-6.6 ± 0.180	-7.6 ± 1.450	-1.0 ± 1.612
	smt 2776 - 2800	NBD	NBD	NBD	NBD	NBD
CTD	2801 - 2833	NBD	NBD	NBD	NBD	NBD
	2776 - 2833	1.68E+04 ± 2.21E+03	60.330 ± 7.8390	-5.8 ± 0.078	-7.7 ± 1.864	-2.0 ± 1.946
	smt 2776 - 2800	8.82E+03 ± 2.50E+03	120.942 ± 40.3150	-5.4 ± 0.186	-12.7 ± 3.187	-7.4 ± 3.368
BTD-CTD	2776 - 2833	1.04E+06 ± 1.18E+05	0.969 ± 0.1130	-8.2 ± 0.069	-14.2 ± 1.635	-6.0 ± 1.672

Supplemental Table I.

All experiments were performed at 25°C, except for the BTD/SMT(2791-2820) complex, which was performed at 15°C (**). Values are the mean of at least three independent experiments and errors represent the standard deviations of multiple experiments. NBD = no binding detected.