SUPPLEMENTAL MATERIAL

Fig. S1: *Purification of C-terminal mCRYCCtail and mBMAL1 fragments.* SDS-PAGE analysis of purified C-terminal mCRY- and mBMAL1 fragments concentrated to about 5 mg/ml. All 4 proteins display aberrant running behaviours on SDS gels, but their correct mass and identity has been confirmed by mass spectrometry (data not shown).

Fig. S2: *Analysis of mCRYCCtail- and mBMAL1 fragments by analytical ultracentrifugation sedimentation velocity experiments.* Representative figure showing sedimentation coefficient distributions c(s) obtained from the analysis of the sedimentation profiles of the monomeric mCRY1[471-606] (A) and mBMAL1[490-625] (B) proteins. Concentrations correspond to OD_{280} = 0.5 (0.96 mg/ml for mCRY1[471-606]; 0.84 mg/ml for mBMAL1[490-625]). The c(s) distributions were normalized to facilitate the comparison.

Fig. S3: *CD spectra of the mCRYCCtail- and mBMAL1 fragments (A) and the synthetic mCRY peptides P1 and P2 (B).* The mean molar ellipticity $[\Theta]_R$ per amino acid residue after buffer correction is plotted against the wavelength. The spectra suggest, that the mBMAL1 and mCRY proteins are partially disordered (Table 2). Peptide P1 has a high α-helical content, whereas peptide P2 is largely unstructured.

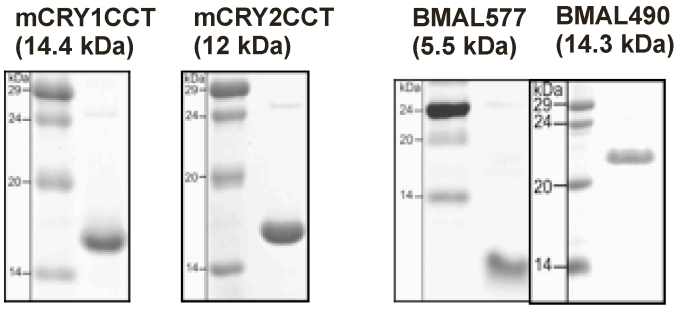
mCRY1CCT
(14.4 kDa)
mCRY2CCT
(12 kDa)
BMAL577
(5.5 kDa)
BMAL490
(14.3 kDa)
kDa
29
24
20
14

Fig. S1

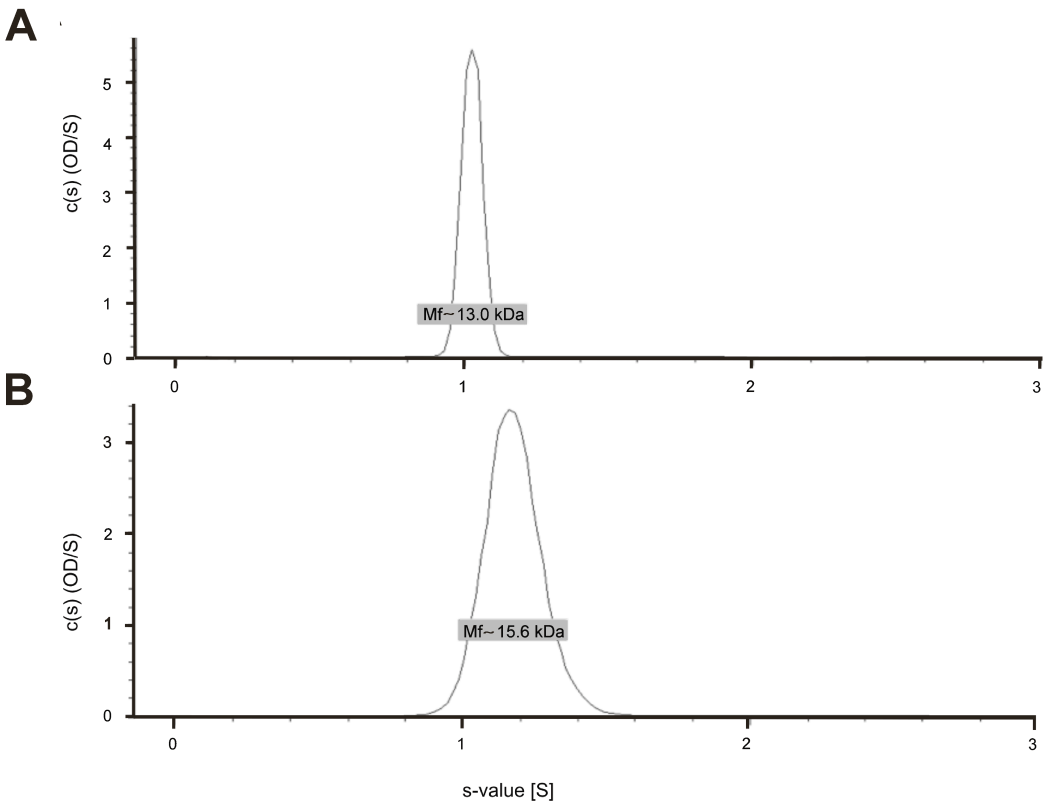

Fig. S2

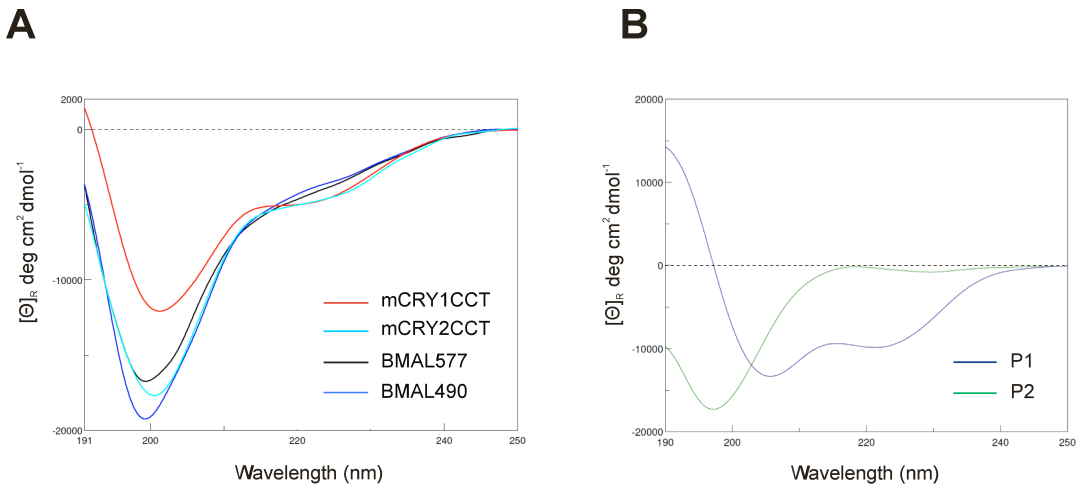
A
B
2000
0
-10000
-20000
191
200
220
240
250
[Θ]R deg cm2 dmol-1
Wavelength (nm)
mCRY1CCT
mCRY2CCT
BMAL577
BMAL490
20000
10000
0
-10000
-20000
190
200
220
240
250
[Θ]R deg cm2 dmol-1
Wavelength (nm)
P1
P2

Fig. S3