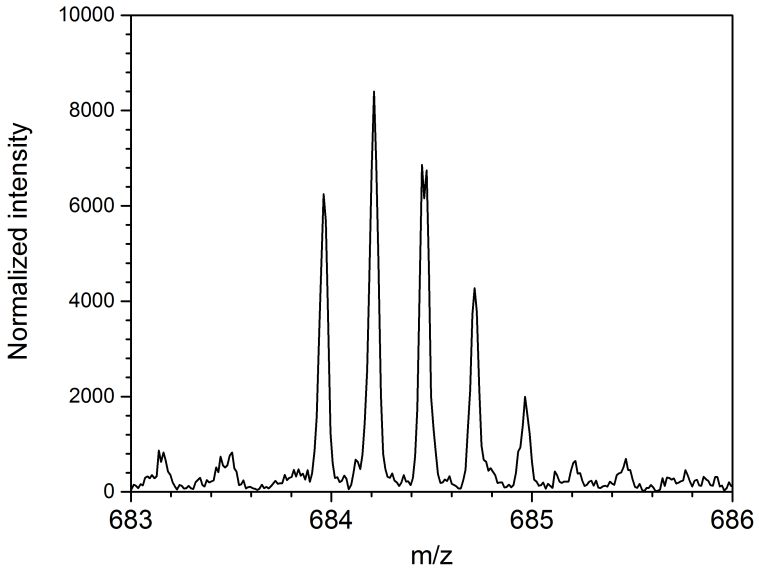
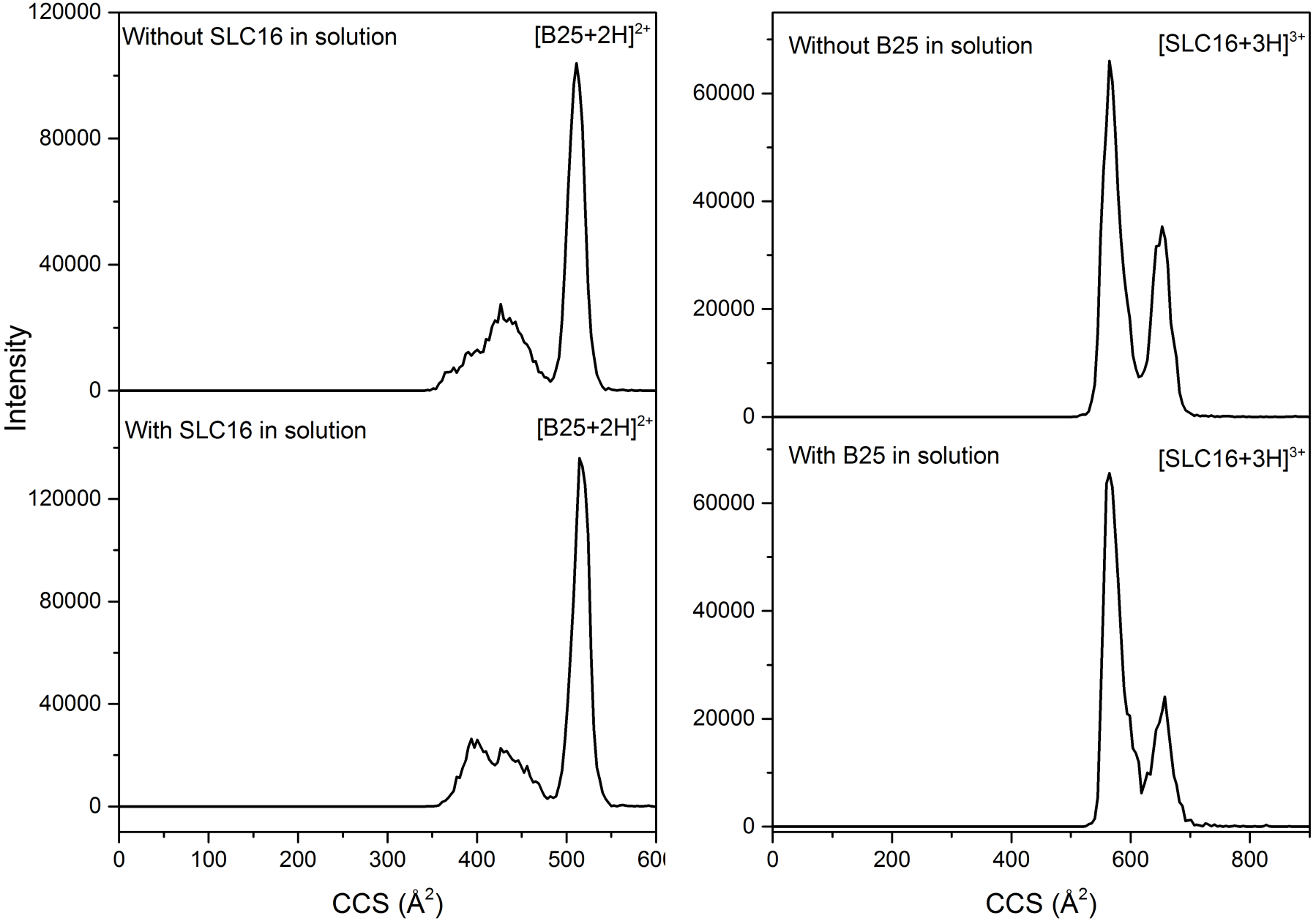
	Elution Volume (mL)	Elution Time (min)	Peak Area (mL*mAU)	RNA amount (nano moles)
SLC16 only	14.01	56.04	275.15	7.00
mSLC16 only	14.04	56.16	267.95	7.00
U16 only	13.7	54.8	176	7.00
B26 only (Major)	14.02	56.08	6.5	5.95
B26 only (Minor)	12.7	50.8	1.15	1.05
Bound SLC16 in a mixture of SLC16-B26	12.7	50.8	90.86	2.31
Unbound SLC16 in a mixture of SLC16-B26	14.04	56.16	184.29	4.69
Bound mSLC16 in a mixture of mSLC16-B26	13.07	52.28	51.53	1.35
Unbound mSLC16 in a mixture of mSLC16-B26	14.01	56.04	216.42	5.65
Bound U16 in a mixture of U16-B26	12.7	50.8	17.8	~0
Unbound U16 in a mixture of U16-B26	13.7	54.8	193.8	7.71

Supplementary Table 1. Detailed data for each of the peaks for B26 peptide, SLC16, mSLC16, U16 RNAs and their peptide-RNA mixtures from size exclusion column chromatography.

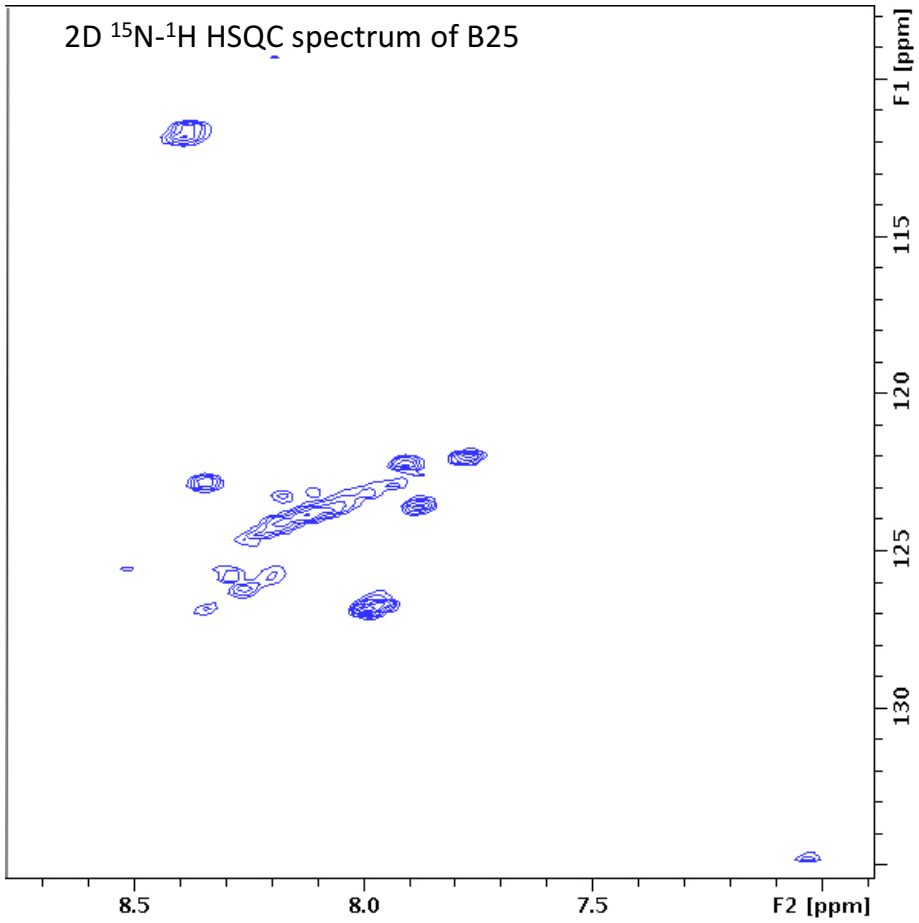


Ace-STSGTGKMTRAQRRAAARRNRWTAR $[M+4H]^{4+}$

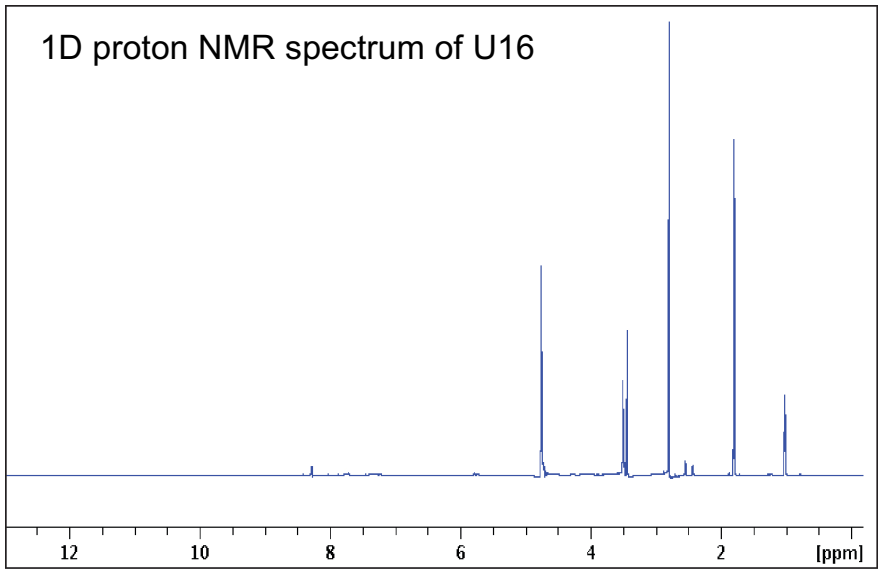
Supplementary Figure 1. Mass spectrum of the proteolyzed BMV CP treated with trypsin. The truncations occur in the N-terminal arm after residue 26.



Supplementary Figure 2. Collision cross section distributions of B25 (left) and SLC16 (right), without (top) and with (bottom) the respective binding partners. Cross section distributions shift when the binding partner is present, suggesting the loss of conformation when the two species bind.



Supplementary Figure. 3. 2D ^{15}N-^{1}H HSQC shows only a few broad crosspeaks, indicating that the N-H bonds of the peptide backbone of B25 is flexible and consistent with B26 existing in a disordered state.

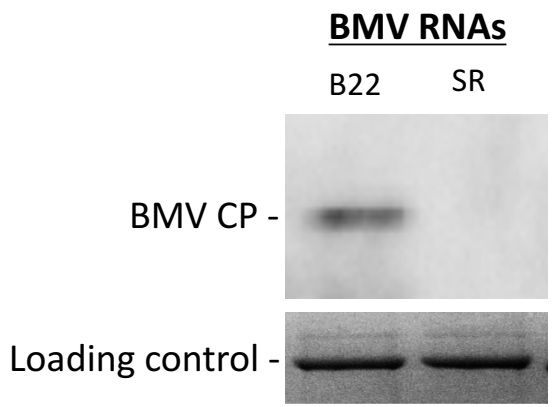


Supplementary Figure 4. A lack of well-defined conformations of U16 RNA and B26 peptide as examined by 1D proton NMR spectrum of U16. Lack of imino proton peaks that should be present at 11-13 ppm, indicates lack of base-paired stem region in this RNA.

A

```
B22   STSGTGKMTRAQRRAAARRNR
SR    TSAQSSSAAASSNS
```

B



Supplemental Figure 5. The N-terminal Arm of the BMV CP can stimulate BMV CP accumulation in the barley protoplasts. **A.** Sequences of the peptides used. **B.** Western blot detecting the BMV CP. Transcripts of the BMV genomic RNAs were transfected into barley protoplasts with a ca. 100-fold molar excess of the peptides. The BMV CP was detected by Western blotting of lysates from protoplasts lysed 7 h after transfection. The loading control is the small subunit of the Rubisco protein that was obtained from the blot membrane after staining with Coomassie brilliant blue.