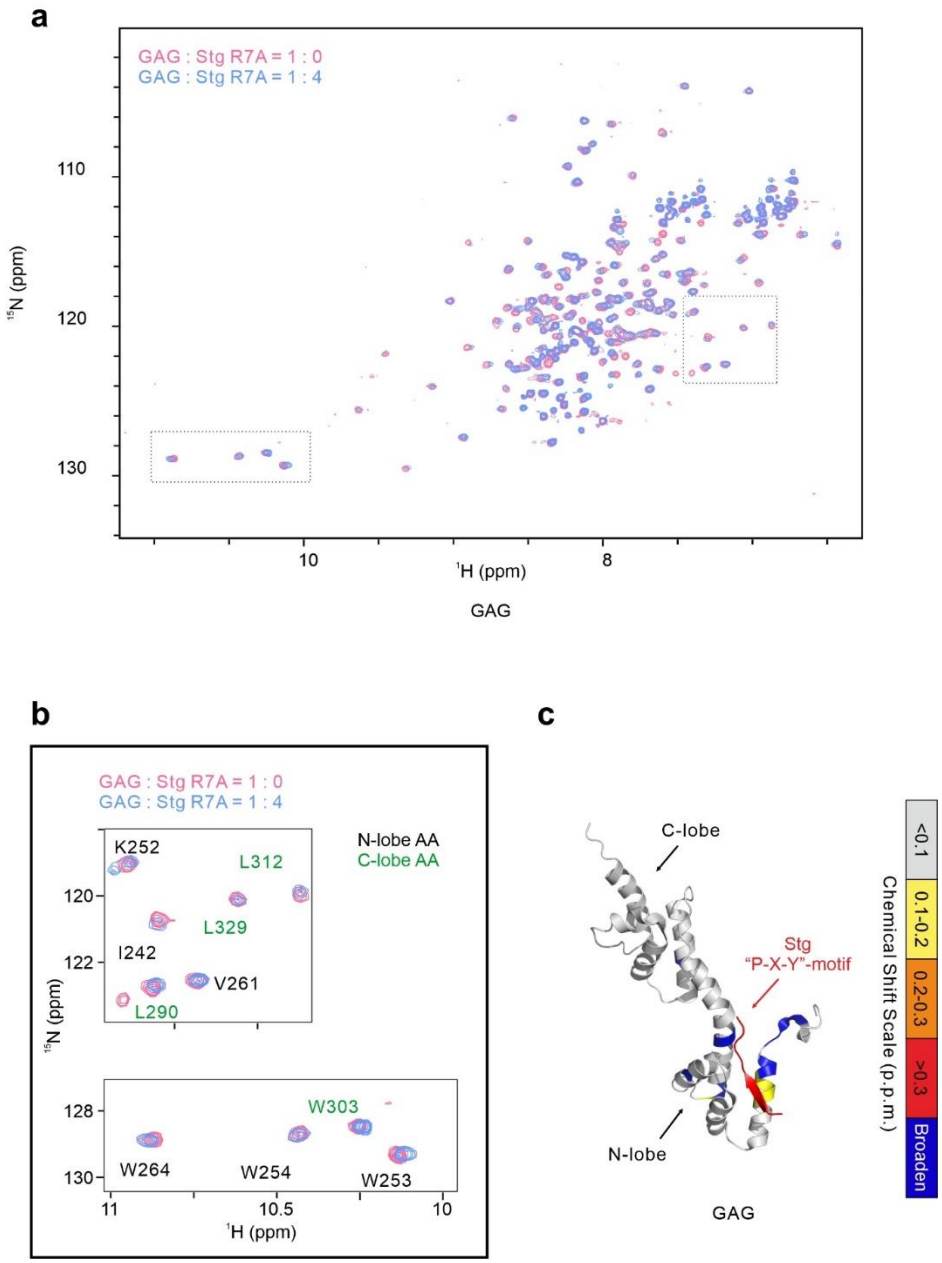

Supplementary information, Fig. S4: NMR-based study of the interaction between Stg R7A and the Arc GAG domain

- **a,** An overlay plot of ^{1}H, ^{15}N-HSQC spectra of Arc GAG along (0.1 mM) (pink) and the protein with the presence of 4 molar ratio amount of unlabeled Stg R7A (blue).
- **b,** Two selected regions of the overlayed ^{1}H, ^{15}N-HSQC spectra in panel A, with the residue assignment labeled. The chemical shift assignment of Arc GAG is adapted from an earlier study (Nielsen et al, 2019).
- **c,** Mapping of the backbone amide chemical shift changes of GAG induced by Stg R7A binding to the structure of the GAG domain. In this representation, the combined ^{1}H and ^{15}N chemical shift changes are defined as: $\Delta_{p.p.m} = [(\Delta\delta_{HN})^2 + (\Delta\delta_N \times \alpha_N)^2]^{1/2}$, where $\Delta\delta_{HN}$ and $\Delta\delta_N$ represent chemical shift differences of amide proton and nitrogen chemical shifts of each residue of the GAG domain with and without the presence of Stg R7A. The scaling factor (α_N) used to normalize the ^{1}H and ^{15}N chemical shifts is 0.17.