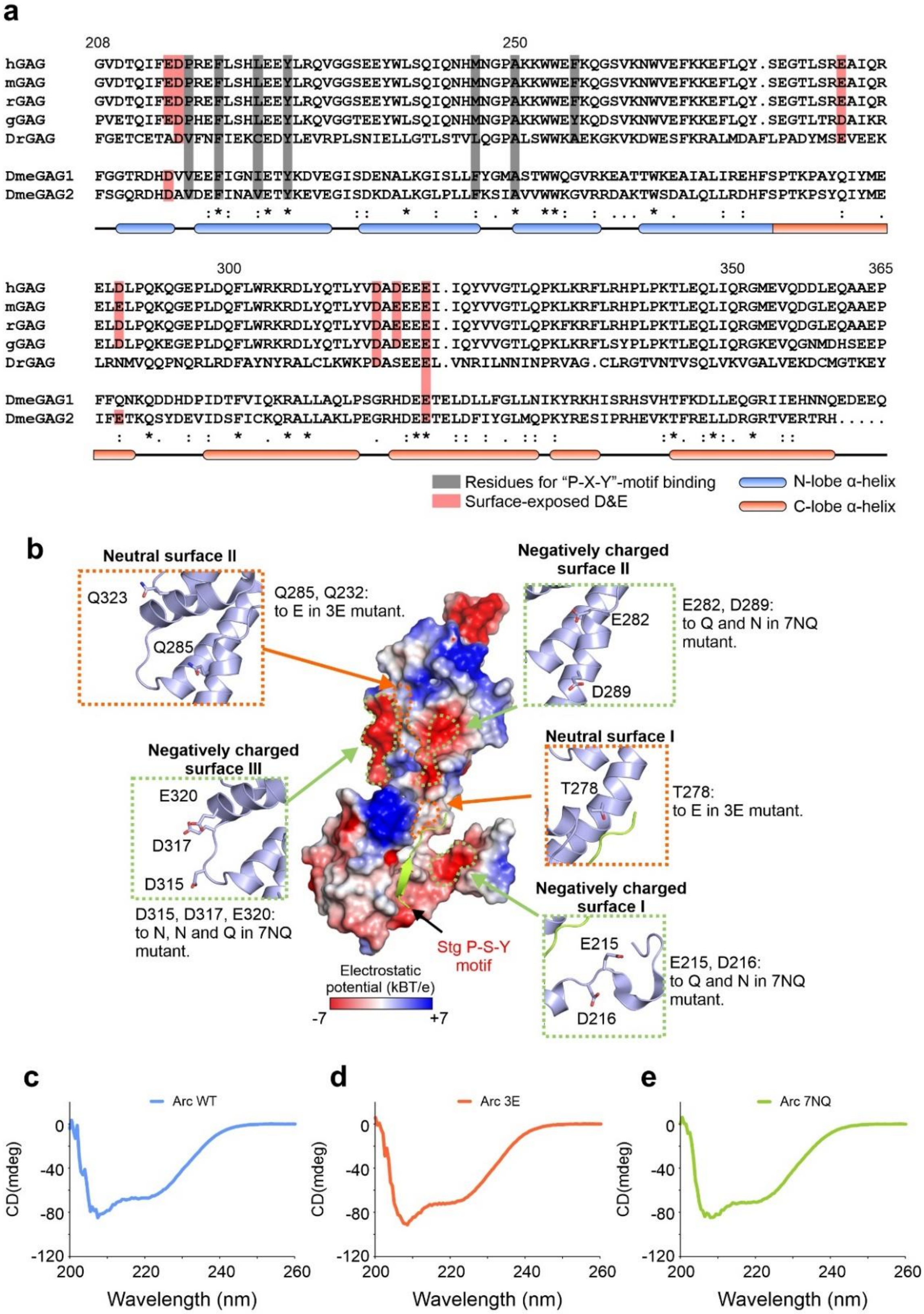

Supplementary information, Fig. S5: Conservation and surface charge property of the Arc GAG domain

- **a,** Structure-based sequence alignment of Arc GAG from different species. H, Homo sapiens; m, Mus musculus; r, Rattus norvegicus; g, Gallus gallus; Dr, Danio rerio; Dme, Drosophila melanogaster. Residues responsible for binding to “P-X-Y”-motif are highlighted in gray, and residues required for the Arg-motif binding are marked in orange.
- **b,** Detailed illustrations of the positions of amino acid residues selected for replacements in Arc 3E and Arc 7NQ mutants. The surface charge distributions are contoured as in Fig. 2f. The apo GAG structure was obtained from previous study (PDBID: 6GSE) [38]. The complex structure of GAG and Stg P-S-Y motif was generated by Auto-Dock.

- **c-e,** CD spectra of the full-length Arc WT (C), Arc 3E (D) and Arc 7NQ(E) showing that replacements of residues in the Arc 3E or Arc 7NQ mutants do not alter the overall folding of the protein.