

SUPPORTING INFORMATION

STRUCTURAL BASIS FOR THE 14-3-3 PROTEIN-DEPENDENT INHIBITION OF G-PROTEIN SIGNALING 3 (RGS3) FUNCTION

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FIGURE LEGENDS

Fig. S1. Theoretical prediction of RGS3 (human isoform 1) disorder. The disorder was predicted using the web-based program GlobPlot (<http://globplot.embl.de/>). The black and the gray bars denote the N-terminal part (residues 255-383) and the C-terminal RGS domain (residues 384-513), respectively. The position of the phosphorylation site (S264) is labeled as (P).

Fig. S2. Peptide mapping of 14-3-3 ζ after the digestion on the pepsin column. The blue bars represent all identified peptides (sequence coverage 100%), red bars are peptides for which the H/D exchange kinetics was followed (sequence coverage 98%). The secondary structure elements (helices H1-H9) are shown above the sequence.

Fig. S3. Peptide mapping of RGS3 after digestion on the pepsin column. The blue bars represent all identified peptides (sequence coverage 100%), the red bars represent peptides for which the H/D exchange kinetics was followed (sequence coverage 99%). The secondary structure elements are shown above the sequence.

Fig. S4. Circular dichroism spectroscopy. (A) The comparison of the far-UV CD spectra of pRGS3 WT (red line) and AEDANS-labeled pRGS3(C456) (black line). (B) The comparison of the sum of the individual far-UV CD spectra of pRGS3 and 14-3-3 ζ (red line) with the far-UV CD spectrum of the 14-3-3 ζ :pRGS3 complex (black line). The mean residue ellipticity (MRE) is plotted as a function of the wavelength.

Figure S1

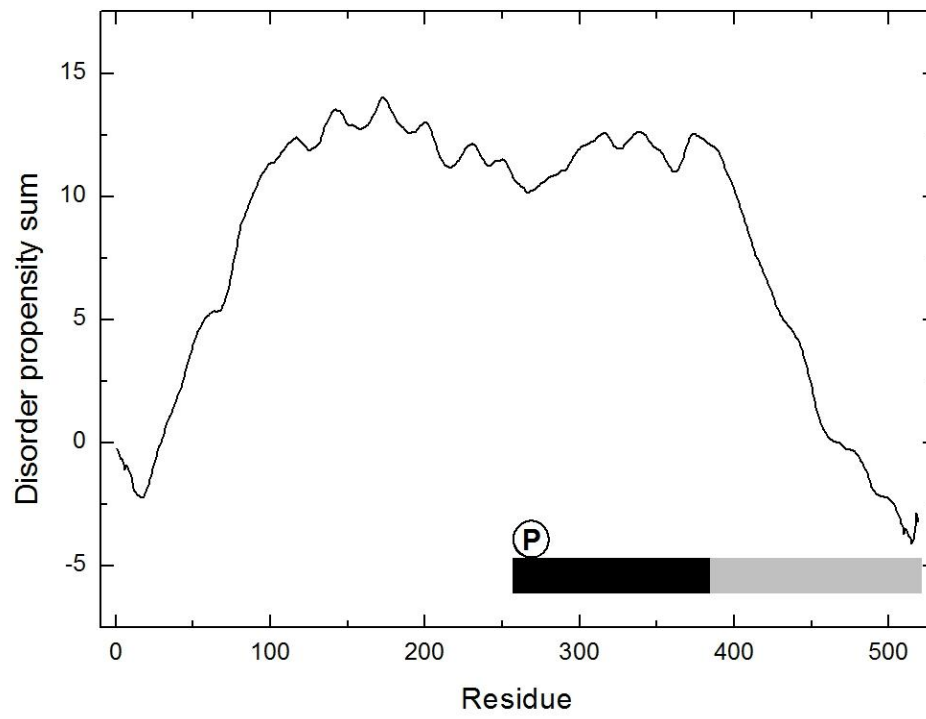


Figure S2

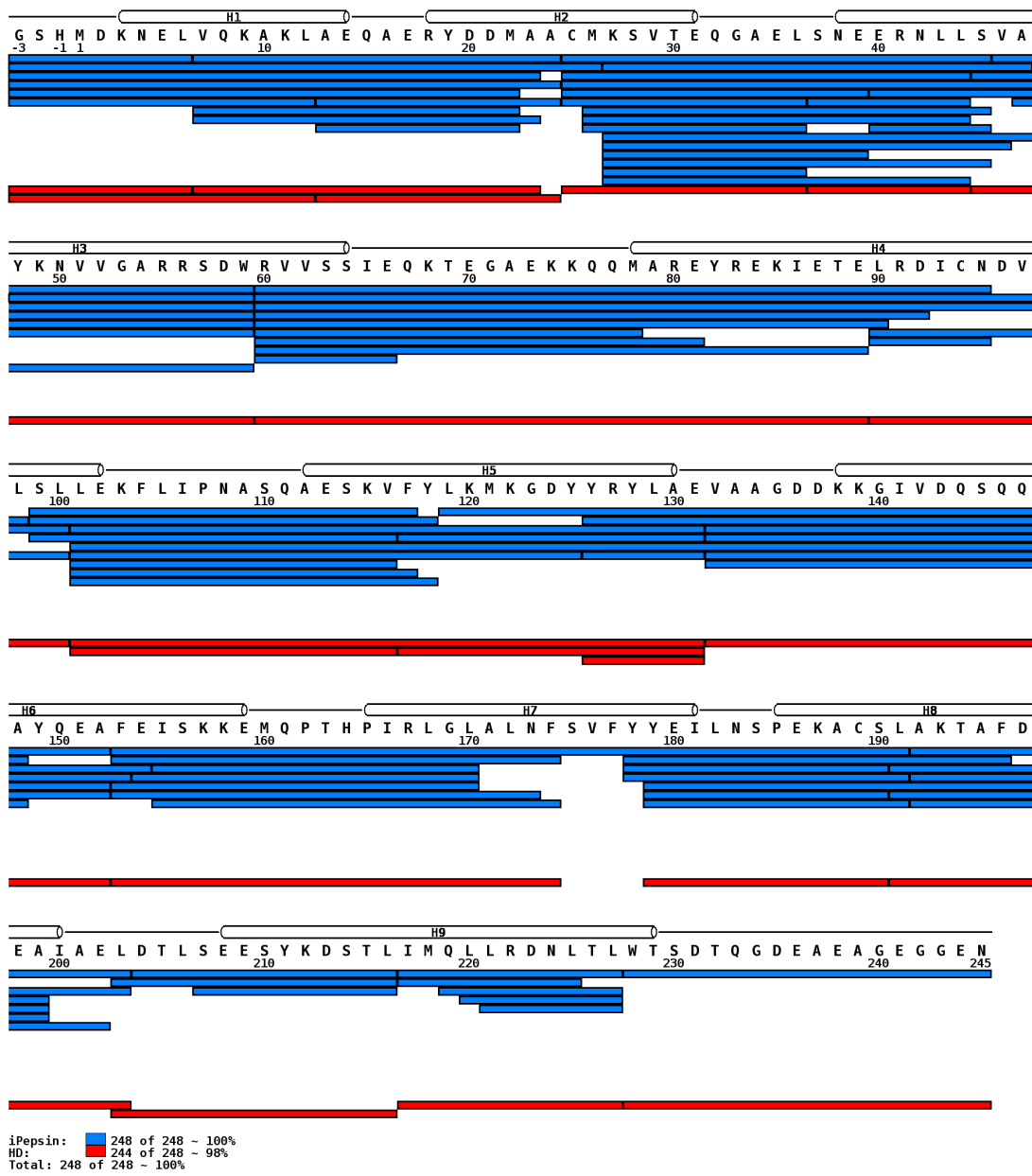


Figure S3

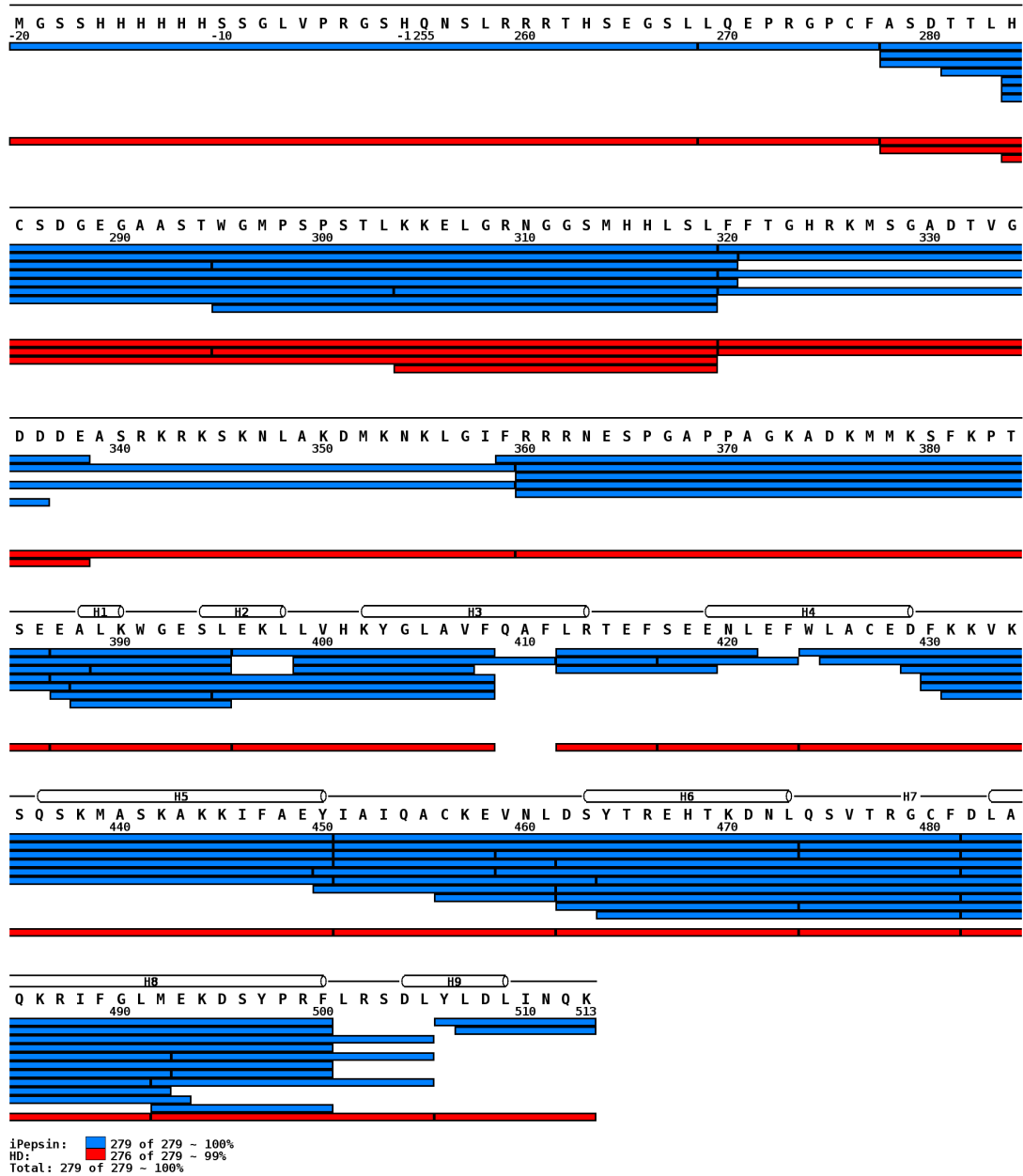


Figure S4

