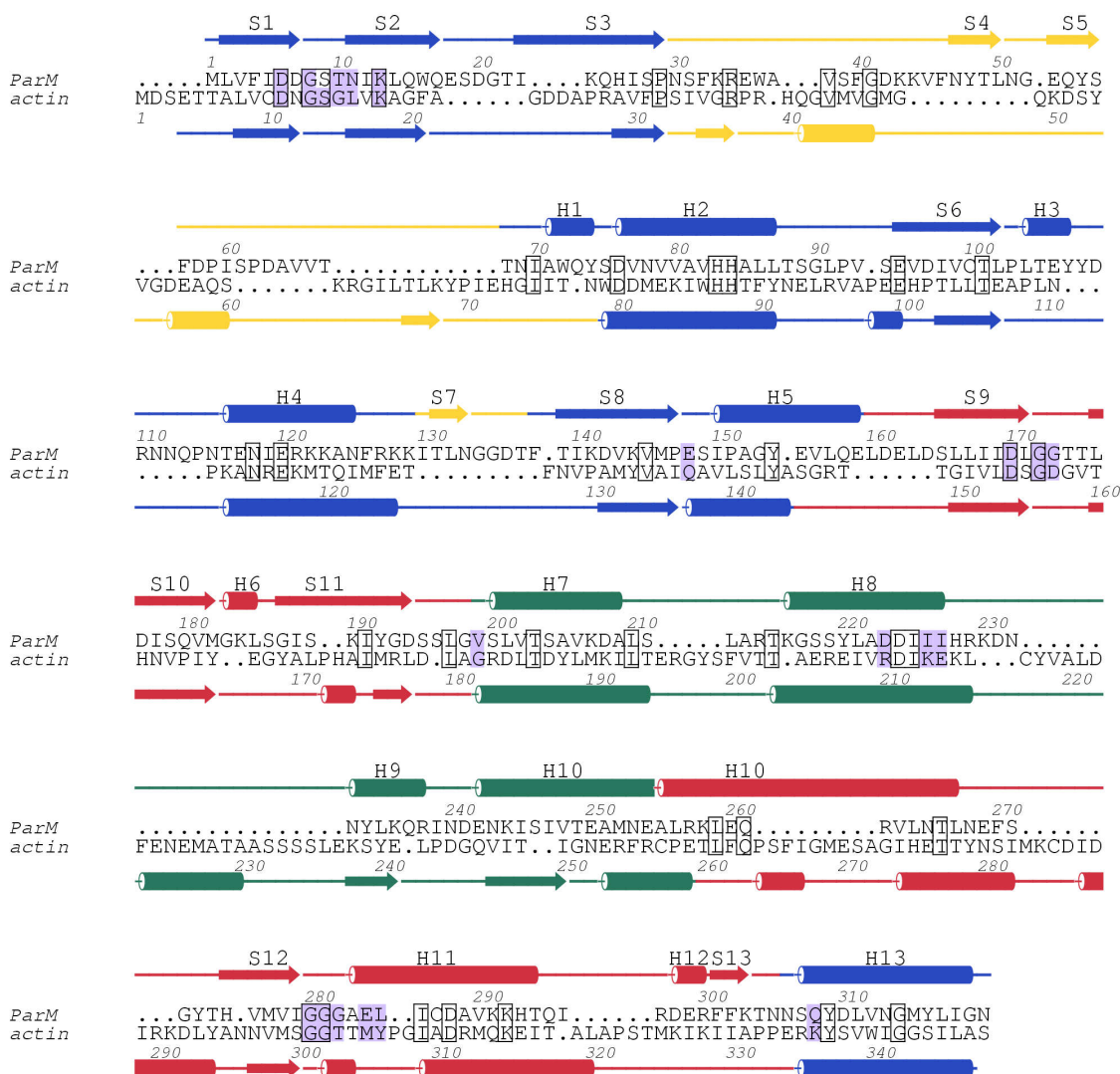




Structure-based sequence alignment between ParM and actin.

The alignment was made based on the three-dimensional comparison between ParM and ADP-bound actin (PDB entry 1J6Z; using the DALI-web server (Holmes et al., 1990)). Boundaries of the secondary structure elements were defined using the program DSSP (Kabsch and Sander, 1983). The colors of the secondary structure elements correspond to those of the subdomains shown in Figure 3. Active site residues are shaded purple. Conserved residues are blocked. The figure was prepared with the program ALSCRIPT (Barton, 1993).

References:

- Barton, G.J. (1993) ALSCRIPT: a tool to format multiple sequence alignments. *Protein Engineering*, **6**, 37-40.
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