

Supplementary material

SAMPLEX: Automatic mapping of perturbed and unperturbed regions of proteins and complexes.

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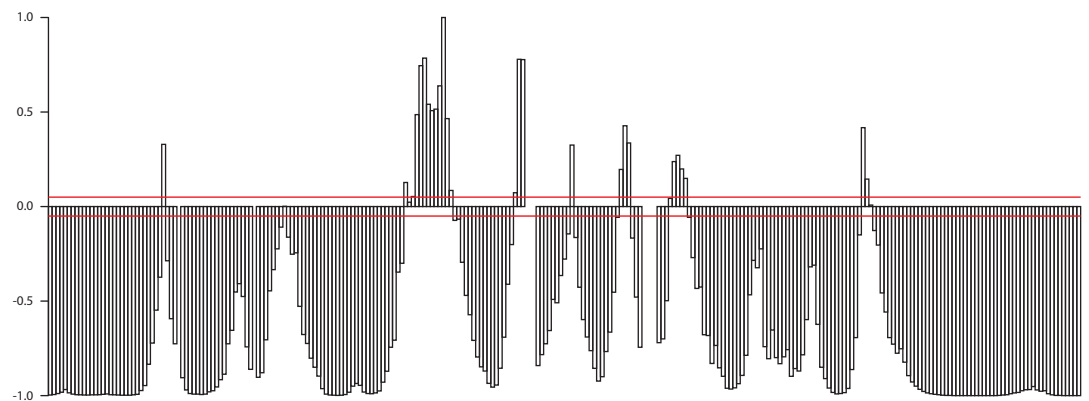
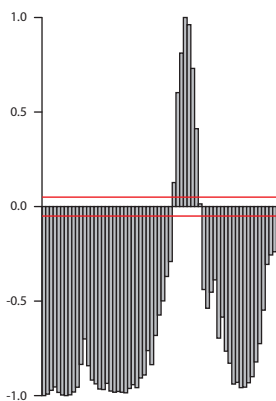
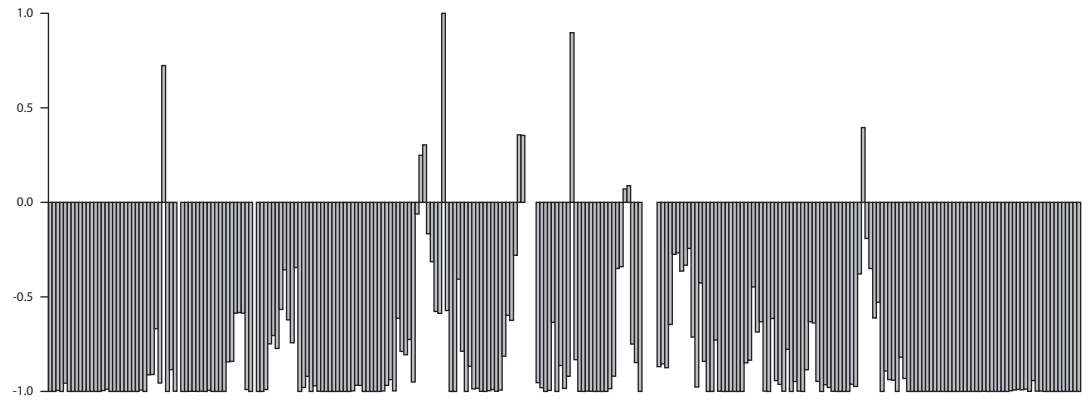
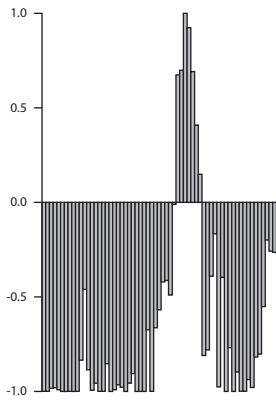
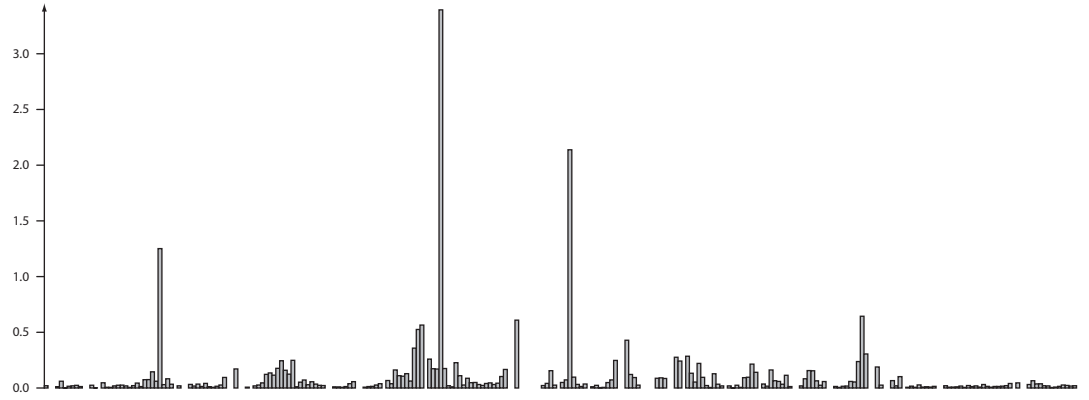
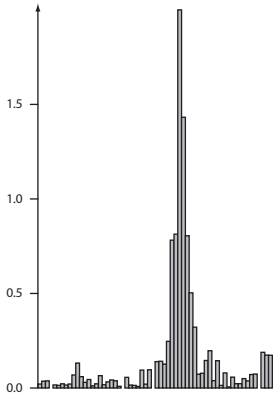
RB: r.boelens@uu.nl

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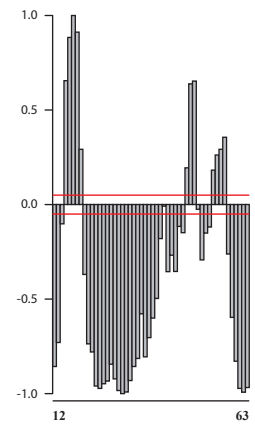
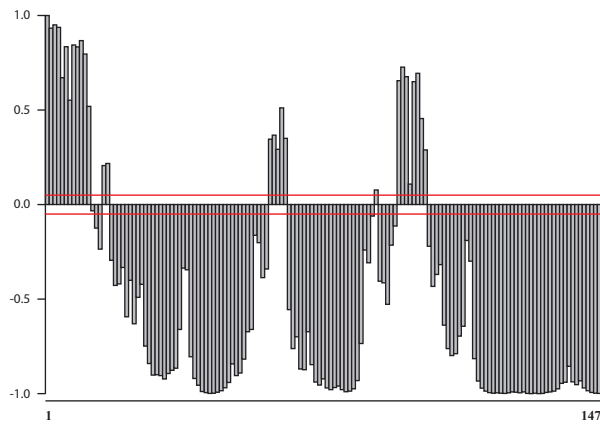
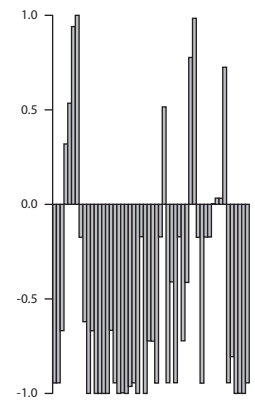
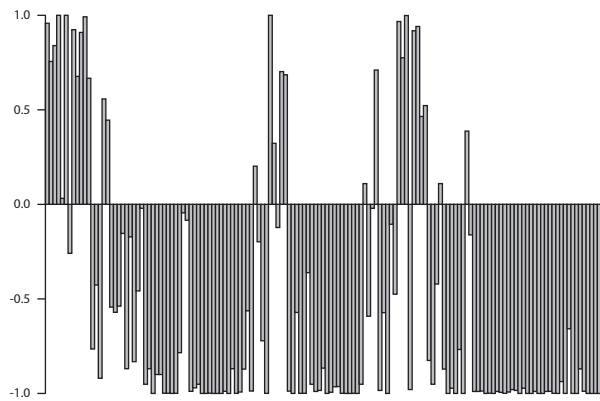
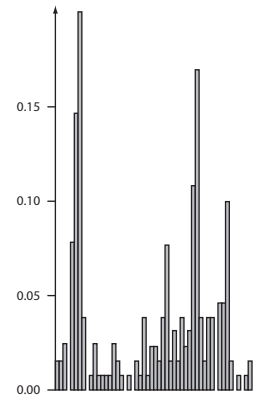
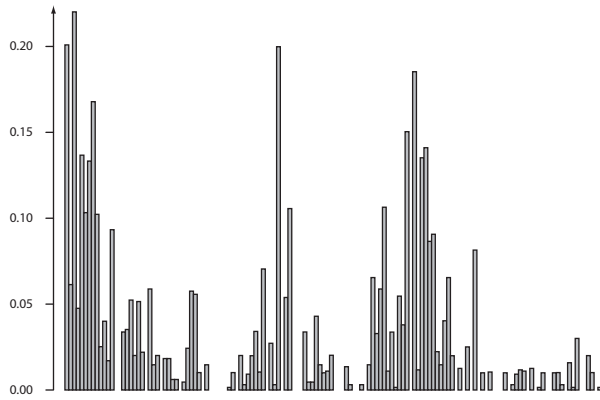
This document contains the chemical shift perturbations and derived confidences as function of the residue sequence for the diverse test cases described in the paper.

For each vertical panel, the top row displays raw CSP data, the middle row represents the starting and inferred confidences and the bottom row shows the confidences after homogenization, as well as the limits -0.05 and 0.05 (red bars) between which data are classified as ambiguous.

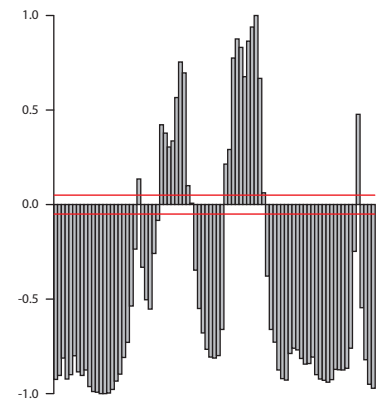
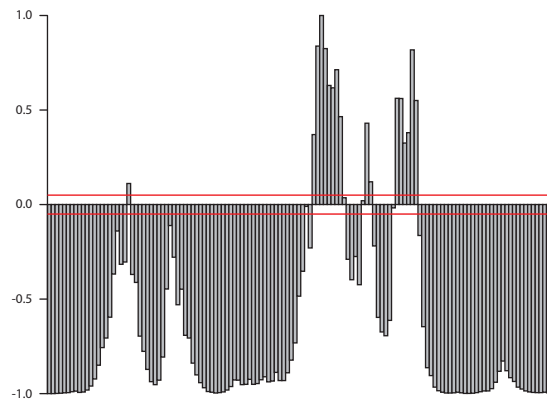
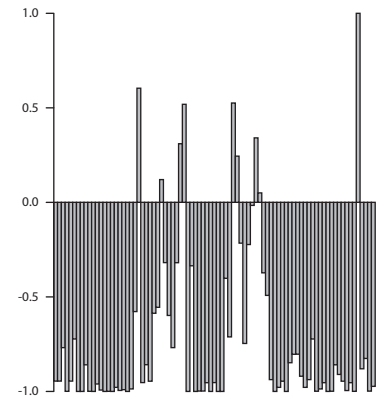
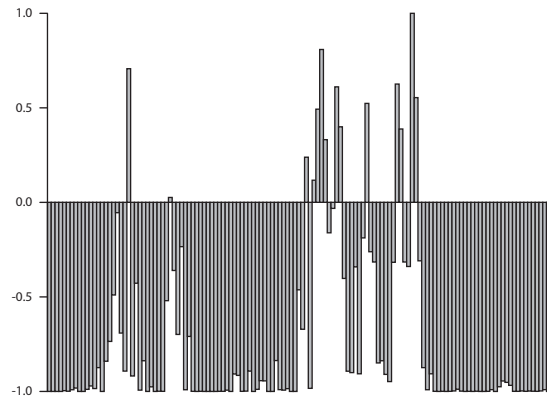
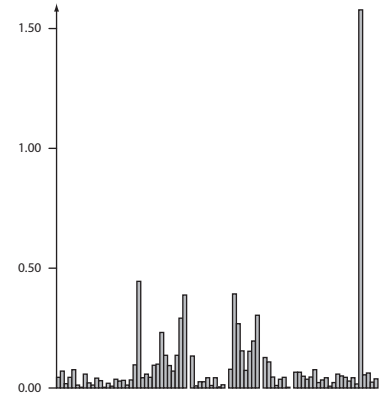
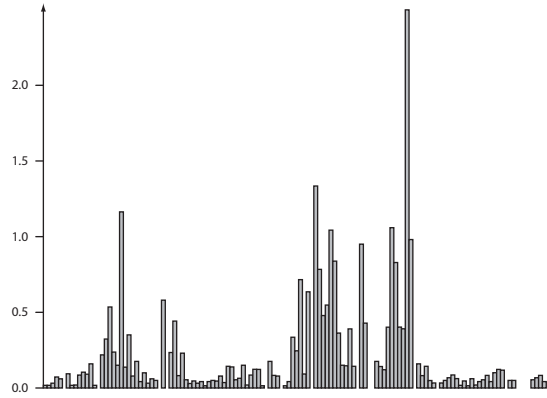
CI2 / Subtilisin



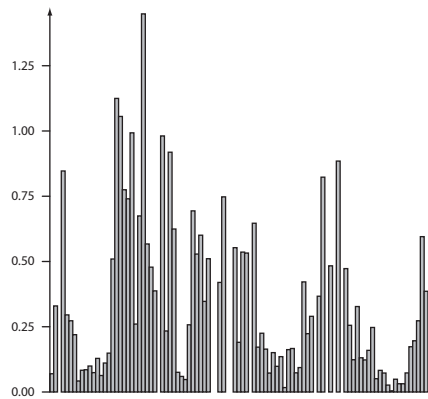
UBCH5 / CNOT4



CE9 / Im9



PYP



Lac repressor (IPTG)

