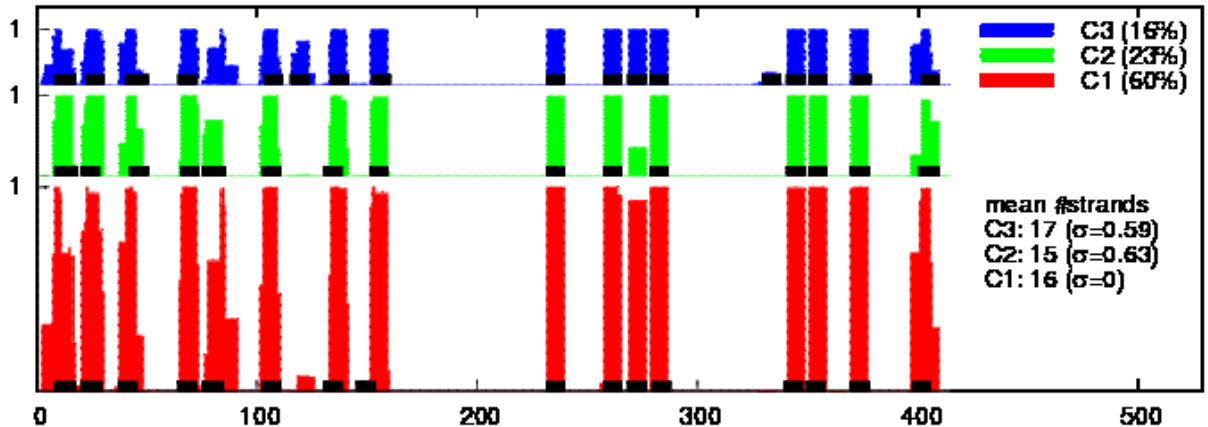
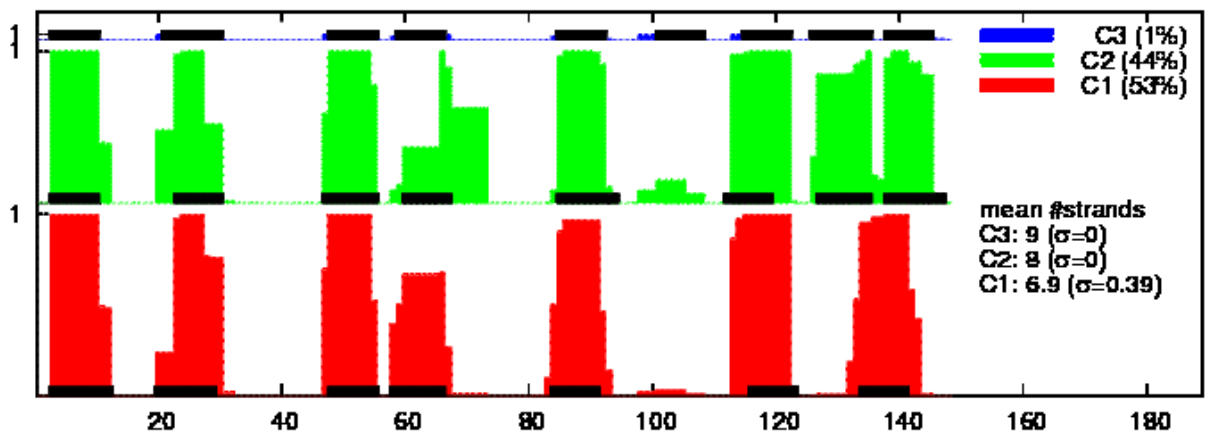


1 **S1 Data. Per-residue β -sheet propensity for the full-length Vicilin protein and its**
 2 **domains, Cupin-1.1 and Cupin-1.2.**



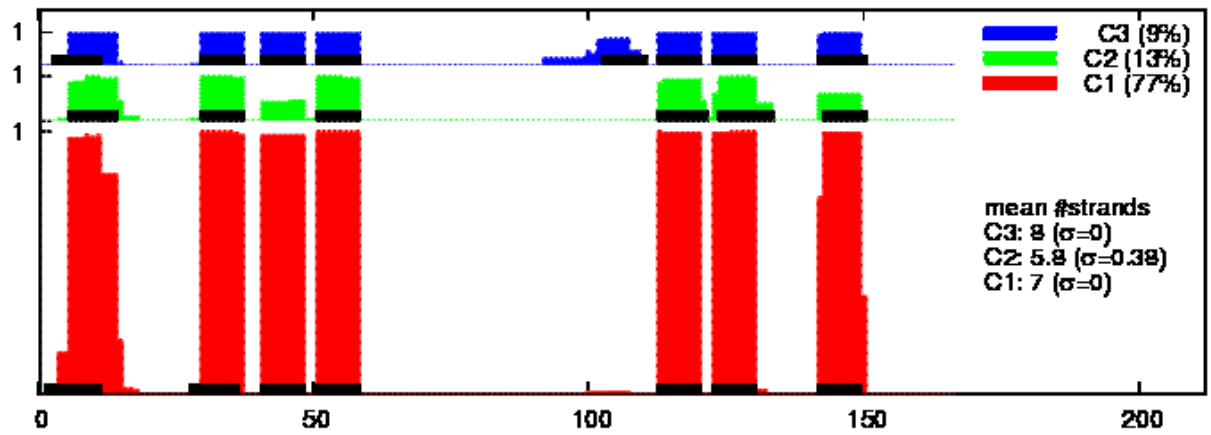
3 **Fig 1.** Per-residue β -sheet propensity for full-length Vicilin predicted by the AmyloidMutants¹
 4 program. The x-axis indicates residue position. Each cluster ("C1","C2",...) is given its own
 5 color, one on top of another, with the relative size of that cluster in the ensemble indicated by its
 6 vertical size and the percentage in the legend. The largest cluster is the most probable
 7 structure. The y-axis the β -sheet propensity of each residue position, for each cluster. Black
 8 lines indicate the β -sheet assignment of a single representative mediod structure that is at the
 9 center of each cluster.
 10

11



12 **Fig 2.** Per-residue β -sheet propensity for Cupin-1.1 predicted by the AmyloidMutants¹
 13 program. The x-axis indicates residue position. Each cluster ("C1","C2",...) is given its own
 14 color, one on top of another, with the relative size of that cluster in the ensemble indicated by
 15 its vertical size and the percentage in the legend. The largest cluster is the most probable
 16 structure. The y-axis the β -sheet propensity of each residue position, for each cluster. Black
 17 lines indicate the β -sheet assignment of a single representative mediod structure that is at the
 18 center of each cluster.
 19

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21 **Fig 3.** Per-residue β -sheet propensity for Cupin-1.2 predicted by the AmyloidMutants¹ program.
 22 The x-axis indicates residue position. Each cluster ("C1","C2",...) is given its own color, one on
 23 top of another, with the relative size of that cluster in the ensemble indicated by its vertical size
 24 and the percentage in the legend. The largest cluster is the most probable structure. The y-axis
 25 the β -sheet propensity of each residue position, for each cluster. Black lines indicate the β -sheet
 26 assignment of a single representative mediod structure that is at the center of each cluster.

27

28 **Reference:**

- 29 1. O'Donnell, C. W. *et al.* A method for probing the mutational landscape of amyloid
 30 structure. *Bioinformatics* (2011). doi:10.1093/bioinformatics/btr238

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