Vivaldi: visualisation and validation of biomacromolecular NMR structures from the PDB (Supporting information)

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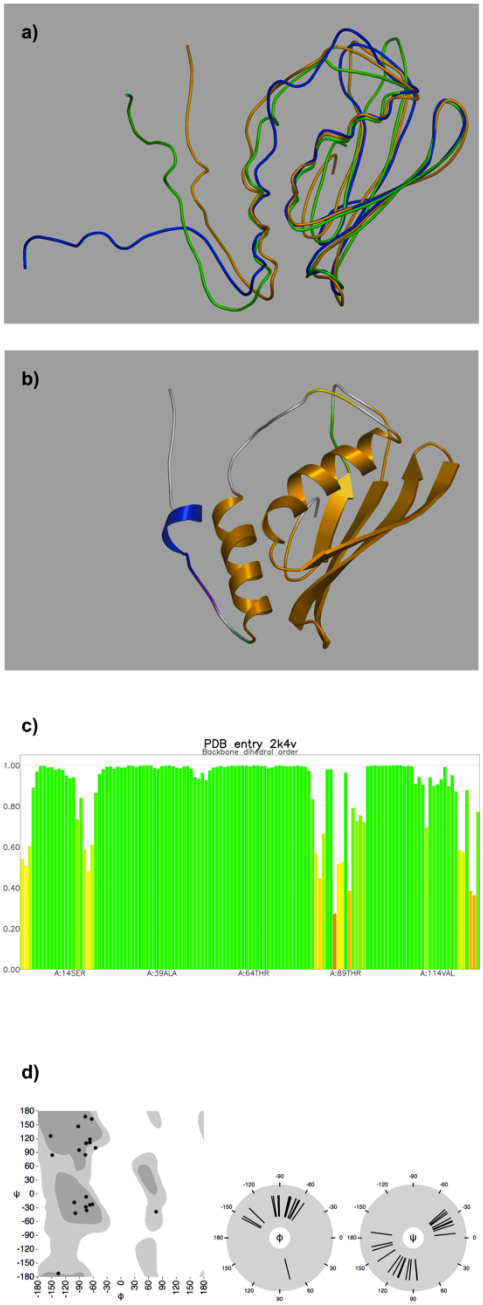

Figure S1. Various options available in Vivaldi to display conformational flexibility applied to protein PA1076 from *Pseudomonas aeruginosa* (2k4v)[15]. (a) Representative models from each cluster identified by OLDERADO[14]. (b) Ribbon view of the most representative model coloured by OLDERADO domains. (c) Dihedral order parameters per residue calculated by Vivaldi. (d) Ramachandran and pie-chart representation of backbone conformational flexibility in the deposited ensemble for residue Ile88, which is located in a poorly defined loop of the protein.