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(71) **Applicant** *(for all designated States except US)*: **CAMBRIDGE ENTERPRISE LIMITED** [GB/GB]; The Old Schools, Trinity Lane, Cambridge, Cambridgeshire CB2 1TN (GB).

(72) **Inventors; and**

(75) **Inventors/Applicants** *(for US only)*: **DOBSON, Christopher** [GB/GB]; Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge, Cambridgeshire CB2 1EW (GB). **PECHMANN, Sebastian** [DE/GB]; Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge, Cambridgeshire CB2 1EW (GB). **TARTAGLIA, Gian Gaetano** [IT/GB]; Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge, Cambridgeshire CB2 1EW (GB). **VENDRUSCOLO, Michele** [IT/GB]; Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge, Cambridgeshire CB2 1EW (GB).

(74) **Agent**: **MARKS & CLERK LLP**; 62-68 Hills Road, Cambridge, Cambridgeshire CB2 1LA (GB).

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(54) **Title**: PROTEIN AGGREGATION PREDICTION SYSTEMS

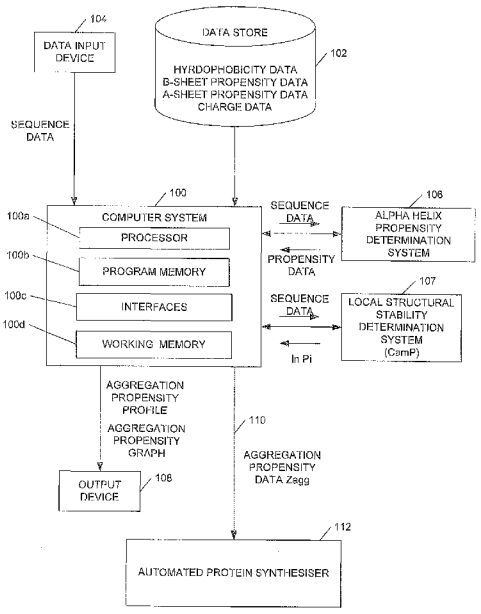


Figure 1a

(57) **Abstract**: This invention relates to methods for identifying aggregation-prone regions in structured (folded) proteins and to related methods for determining the aggregation propensity of a protein, to computer program code and equipment for implementing the methods, and to related methods of identifying new drugs and drug targets as well as protein toxicities. A method of identifying one or more regions in the amino acid sequence of a protein which, in the folded protein, are predicted to promote aggregation, the method comprising: determining, for amino acid positions (*i*) along said sequence, a local propensity for aggregation (A) at a said amino acid position, said local propensity for aggregation being determined by a combination of a hydrophobicity value, an α-helix propensity value, a β-sheet propensity value, a charge value and a pattern value for said amino acid position; determining local structural stability values for said amino acid positions, a said local structural stability value comprising a measure of local structural stability at a said amino position; and combining said determined local propensities for aggregation at said amino acid positions and said local structural stability values at said amino acid positions to identify one or more regions in said amino acid sequence which, in said folded protein, are predicted to promote aggregation.

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