seems contrary to the long-held hypothesis that an amino acid codes for a single unique 3-D structure.[60] Amyloid plaques or protein aggregations in the brain are also associated with Alzheimer's disease and Parkinson's disease, conditions not considered prion-based but also dependent on aberrant protein folding.[61] The primary structure does not absolutely determine the tertiary folding structure. It is now widely believed that gene expression alone largely, but not exclusively, controls the protein's 3-D properties.

III. Structurally similar, sequence dissimilar proteins

With the discovery of increasingly more protein structures, it has further become evident that many proteins that possess similar structures share only a very small number of identical residues in structurally associated positions.[62] Various structurally similar protein pairs have only a minimal amount of sequence identity. This suggests that many sequence positions do not play a significant role in structure determination, and folding determinants are restricted to a limited number of sequence residues.[63] Structurally similar proteins do therefore not necessarily reflect sequence-similar proteins.[64] Some proteins bearing diverse sequences with essentially no sequence homology, do fold into the same structure. With the protein's effect depending on the structure, large numbers of different proteins are able to perform the same functions.[65]

IV. Posttranslational modifications (PTM)

An important component of protein regulation and function is the modification of protein structures, which occur either co- or posttranslationally. Translation refers to

60 Tatzelt, Jorg/Winklhofer, Konstanze F., Folding and Misfolding of the Prion Protein in the Secretory Pathway, 11 Amyloid 2004, 162, 166.

61 Tatzelt, Jorg/Winklhofer, Konstanze F., Folding and Misfolding of the Prion Protein in the Secretory Pathway, 11 Amyloid 2004, 162, 162.

62 Jaenichen, Hans-Rainer/Mcdonell, Leslie A./Haley, James F., Jr., From Clones to Claims, Cologne, Berlin, Bonn, Munich 2002, 167; molecular biologists thus attempted to identify the common hidden information within these sequences that directs them to assume similar folds.

63 Kleist, Peter, Biomarker und Surrogat-Endpunkte: Garanten für eine schnellere Zulassung von neuen Arzneimitteln?, 83 Schweizerische Ärztezeitung 2022, 2347, 2350.

64 Wachenfeld, Joachim, The Patenting of Protein Structures, http://www.vossiusandpartner.com/eng/publication/mip-yearbook.html 2002.

65 Structural protein families are also called 'protein superfamilies'; see: Hultquist, Steven J./Robert Harrison, and Yongzhi Yang, Patenting Bioinformatic Inventions: Emerging Trends in the United States, 20 Nature Biotechnology 2002, 743; 771. A list of protein superfamilies with structure-based-sequence-alignment is available at: http://www-cryst.bioc.cam.ac.uk/~campass/superfamily.html, last checked on May 06, 2005.