

Error of Science? The Truth About Proteins and Antibodies

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It is a fact that to date no three-dimensional resolution and biochemical characterization of an isolated protein is possible, and thus its unequivocal existence as an independent molecule and effect is still pending. In current science, proteins are not defined as solid structures, but are constantly changing their three-dimensional shape. This continuous “wobbling” means that assumed proteins never remain stable long enough to serve as constant target structures for antibodies.

Even the smallest changes in the tissue environment can lead to completely different forms of an assumed protein. We are talking about intrinsic randomness here!

- So how can antibodies be specific when their target is constantly changing shape?
- How can the specificity of a protein be asserted if it can neither be isolated nor clearly characterized in three dimensions?
- How is it possible to distinguish a not clearly characterized and constantly changing protein from other proteins and assign it to a specific, never isolated virus?

Tests and diagnoses based on the assumption that antibodies can specifically recognize a constantly changing protein are

therefore scientifically untenable.

In a laboratory test tube, where environmental variables are meticulously controlled, specific reactions can be forced under certain circumstances – but the smallest deviations or disturbances in the conditions lead to different results! In a natural organism or in natural environments, these laboratory conditions are impossible simply because of the constant interaction and reciprocity with nature.

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