OPEN ACCESS Freely available online

Enzyme Engineering

ISSN: 2329-6674

Perspective

Protein Complexes: A Biological Tool for Cellular Biosynthesis

Aryal Franco*

Department of Comparative Pathobiology, Purdue University, West Lafayette, IN, 47907, USA

DESCRIPTION

A group of two or more associated polypeptide chains is referred to as a protein complex or multiprotein complex. Protein complexes differ from multienzyme complexes, which have multiple catalytic domains in a single polypeptide chain. Non-covalent protein-protein interactions link the proteins together in a protein complex. These complexes are the basis of the majority, if not all, biological processes. It is believed that the cell is made up of modular supramolecular complexes, each of which carries out a distinct, independent biological activity. These complexes are the basis of the majority biological processes. The cell is seen to be made up of modular supramolecular complexes, each of which performs out an independent, unique biological function.

Higher cellular efficiency can result from proximity, which greatly increases the speed and selectivity of binding interactions between enzyme complexes and substrates. The process of identifying a complex's constituent parts is made more difficult by the fact that many of the methods used to penetrate cells and isolate proteins are inherently disruptive to such massive complexes. The proteasome, which breaks down molecules, and the majority of RNA polymerases are two examples of protein complexes. The proteasome, which breaks down molecules, and the majority of RNA polymerases are two examples of protein complexes.

Functions

Protein complex formation can resemble phosphorylation in that, it has the ability to activate or inhibit one or more of the complex components. Several protein complexes can contain a same protein. The functions that distinct complexes perform vary, and the same complex can perform out many functions depending on a variety of conditions. Factors include:

- Cell compartment location
- Cell cycle stage
- Cell nutritional status

It is generally known that several protein complexes exist, especially in the model organism Saccharomyces cerevisiae (yeast). The elucidation of the majority of the protein complexes in this relatively simple organism is still ongoing, and protein complexes are currently being studied across the entire genome. RoseTTAFold and AlphaFold, two deep learning programmes, were utilised to identify the structures of 712 eukaryotic complexes. They compared 6000 yeast proteins with 2026 different fungi and 4325 different eukaryotes.

Types of protein complexes

Obligate *vs.* non-obligate protein complex: A protein complex is referred to as a "non-obligate protein complex" if it can produce a stable, well-folded structure *in vivo* without the involvement of any other proteins. Yet, some proteins can be found as a part of a protein complex that stabilises the constituent proteins rather than being able to form a stable, well-folded structure on their own. Obligate protein complexes are these types of protein complexes.

Transient *vs.* permanent/stable protein complex: Transient protein complexes develop and degrade quickly, whereas permanent complexes have a relatively long half-life. While non-obligatory interactions have been found to be either permanent or transient, obligate interactions—protein-protein interactions in an obligate complex—typically last forever. It should be noted that there is no obvious separation between obligate and non-obligate interaction; instead, there is a continuum between them that depends on a variety of factors, such as pH, protein concentration, etc. Transient interactions are much less conserved than stable interactions, and transient interactions are much less co-localized than stable interactions. Additionally, interacting proteins on opposite sides of a stable interaction have a higher tendency to be co-expressed than those of a transient interaction (in fact, the co-expression probability between two transiently interacting proteins is not higher than two random proteins). Although transient by nature, transient interactions are crucial for cell biology because they are the dominant players in gene regulation and signal transduction, are enriched in the human interactome, and are found to be present in proteins with intrinsically disordered regions (IDRs, which are regions of

Correspondence to: Dr. Aryal Franco, Department of Comparative Pathobiology, Purdue University, West Lafayette, IN, 47907, USA, E-mail: aryal@franco.edu

Received: 28-Feb-2023, Manuscript No. EEG-23-22329; **Editor assigned:** 02-Mar-2023, Pre QC No. EEG-23-22329 (PQ); **Reviewed:** 16-Mar-2023, QC No. EEG-23-22329; **Revised:** 23-Mar-2023, Manuscript No. EEG-23-22329 (R); **Published:** 30-Mar-2023, DOI: 10.35248/2329-6674.23.12.206

Citation: Franco A (2023) Protein Complexes: A Biological Tool for Cellular Biosynthesis. Enz Eng. 12:206

the protein that exhibit dynamic inter-converting structures in their native state).

Fuzzy complex: In the bound state, fuzzy protein complexes exhibit several structural forms or dynamic structural disorder. This means that in both temporary and long-term complexes, proteins might not fold entirely. As a result, certain complexes may have unclear interactions that change based on environmental signals. Hence, various structural ensembles produce various (even completely opposite) biological activities. The conformational ensembles of fuzzy complexes are modified by post-translational alterations, protein interactions, or alternative splicing to fine-tune the affinity or specificity of contacts. Within the eukaryotic transcription apparatus, several methods are frequently employed for regulation.

CONCLUSION

Two or more connected polypeptide chains form a protein complex. Each modular supramolecular structure in them performs a unique, autonomous biological function. The capacity of protein complexes to activate or inhibit one or more of the complex's components can make them mimic phosphorylation. Transient interactions are substantially less co-localized than stable interactions and less preserved than stable interactions. Fuzzy complexes have several structural configurations or dynamic structural disorder, and to fine-tune the affinity or selectivity of connections, post-translational modifications, protein interactions, or alternative splicing alter their conformational ensembles.