

2 Complex evolutionary footprints revealed in an analysis of reused protein segments of diverse lengths.

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There is a common belief in molecular biology, which states that domains are the basic units that define protein sequence evolution (although we note that the definition of domains is not universal). In this paper, the authors question this belief through a set of statistical analyses of the repeated use of 'short' fragments (at least 35 residues long) among a large collection of protein chains. They have shown that the repeated use of such fragments does not map with domain boundaries. They derive from these data a recursive model for protein evolution that goes beyond the concept of domains. This model is expected to prove useful for protein sequence design.

Disclosures

None declared

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Abstract:

ABSTRACT

Proteins share similar segments with one another. Such "reused parts"-which have been successfully incorporated into other proteins-are likely to offer an evolutionary advantage over de novo evolved segments, as most of the latter will not even have the capacity to fold. To systematically explore the evolutionary traces of segment "reuse" across proteins, we developed an automated methodology that identifies reused segments from protein alignments. We search for "themes"-segments of at least 35 residues of similar sequence and structure-reused within representative sets of 15,016 domains [Evolutionary Classification of Protein Domains (ECOD) database] or 20,398 chains [Protein Data Bank (PDB)]. We observe that theme reuse is highly prevalent and that reuse is more extensive when the length threshold for identifying a theme is lower. Structural domains, the best characterized form of reuse in proteins, are just one of many complex and intertwined evolutionary traces. Others include long themes shared among a few proteins, which encompass and overlap with shorter themes that recur in numerous proteins. The observed complexity is consistent with evolution by duplication and divergence, and some of the themes might include descendants of ancestral segments. The observed recursive footprints, where the same amino acid can simultaneously participate in several intertwined themes, could be a useful concept for protein design. Data are available at <http://trachel-srv.cs.haifa.ac.il/rachel/ppi/themes/>.

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