

Uniquely Localized Intra-Molecular Amino Acid Concentrations at the Glycolytic Enzyme Catalytic/Active Centers of Archaea, Bacteria and Eukaryota are Associated with Their Proposed Temporal Appearances on Earth

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Abstract The distributions of amino acids at most-conserved sites nearest catalytic/active centers (C/AC) in 4,645 sequences of ten enzymes of the glycolytic Embden-Meyerhof-Parnas pathway in Archaea, Bacteria and Eukaryota are similar to the proposed temporal order of their appearance on Earth. Glycine, isoleucine, leucine, valine, glutamic acid and possibly lysine often described as prebiotic, i.e., existing or occurring before the emergence of life, were localized in positional and conservational defined aggregations in all enzymes of all Domains. The distributions of all 20 biologic amino acids in most-conserved sites nearest their C/ACs were quite different either from distributions in sites less-conserved and further from their C/ACs or from all amino acids regardless of their position or conservation. The major concentrations of glycine, e.g., perhaps the earliest prebiotic amino acid, occupies $\approx 16\%$ of all the most-conserved sites within a volume of $\approx 7\text{--}8\text{ \AA}$ radius from their C/ACs and decreases linearly towards the molecule's peripheries. Spatially localized major concentrations of isoleucine, leucine and valine are in the mid-conserved and mid-distant sites from their C/ACs in protein interiors. Lysine and glutamic acid comprise $\approx 25\text{--}30\%$ of all amino acids within an irregular volume bounded by $\approx 24\text{--}28\text{ \AA}$ radii from their C/ACs at the most-distant least-conserved sites. The unreported characteristics of these amino acids: their spatially and conservationally identified concentrations in Archaea, Bacteria and Eukaryota, suggest some common structural organization of glycolytic enzymes that may be relevant to their evolution and that of other proteins. We discuss our data in relation to enzyme evolution, their reported

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