Membrane protein integration, folding and assembly processes \textit{in vivo} depend on complex targeting, translocation, chaperoning, and sorting machineries that somehow read the "molecular code" built into the nascent polypeptide, ultimately producing a properly folded protein integrated into the correct target membrane. Although the main molecular constituents and the basic mechanistic principles of many of these machines are known in outline, the codes remain poorly defined and there is essentially no quantitative information on how protein sequence affects the final structure of membrane proteins. By carefully designing model protein constructs, we have derived the first true "biological" hydrophobicity scale and have been able to get a first idea of how the position of a given kind of residue within a transmembrane segment affects its ability to promote membrane insertion.


**Insertion of proteins into the ER membrane**

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