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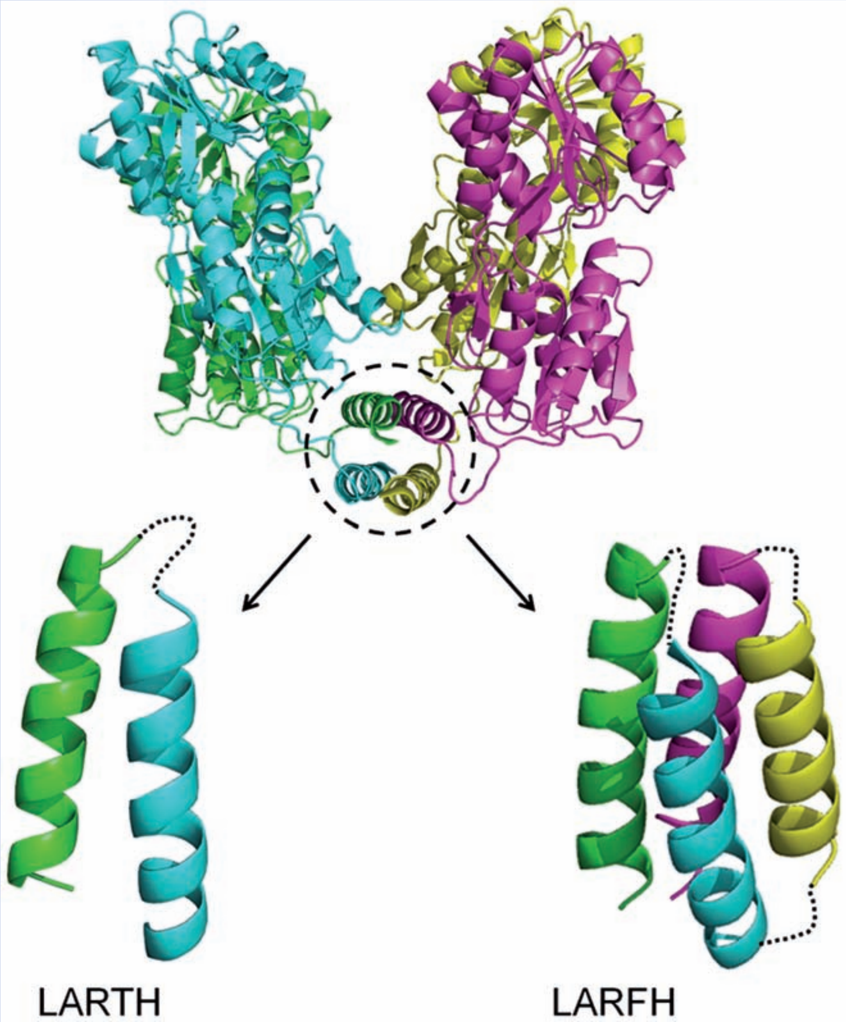

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	Extracellular Matrices and Cell Adhesion Molecules
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Author Index

COVER: The tertiary and quaternary structures of an *Escherichia coli* Lac repressor missing its N-terminal DNA binding domains (top); and models for a helix-loop-helix protein, LARTH, and its duplicated version, LARFH (bottom). LARTH and LARFH were engineered by connecting two and four copies of the C-terminal α-helix of the Lac repressor, respectively. LARTH exists predominantly as a homodimer that likely maintains a four-helix bundle motif. Thermal stability of LARTH is considerably higher than that of the tetrameric four-helix bundle formed by a peptide having a similar sequence to that of the C-terminal helix of the Lac repressor. Moreover, monomeric LARFH is significantly more thermally stable than is dimeric LARTH. Thus, evolution of homo-oligomeric protein into the monomer with internal symmetry results in a more robust protein. In addition, the thermally stable monomeric four-helix bundle may provide a robust scaffold for future development of new biomaterials. [See Akanuma *et al.*; p. 371].