

80/02

Poster 20

The Solution Structure of the Multifunctional Repeated Motif-1 in Human Bifunctional tRNA Synthetase: Structural Basis of Protein-protein, Protein-nucleic Acid Interactions

Eui-Jun Jeong^{1,2}, Geum-Sook Hwang^{1,3}, Minjung Kim³, Sunghoon Kim³ and Key-Sun Kim¹

¹Structural Biology Center, KIST,

²The Graduate School of Biotechnology, Korea University, and ³Dept. of Biol. Sci., Natl. Res. Center for ARS Network, Sung Kyun Kwan University

A multi-tRNA synthetase complex consists of nine synthetases and 3 auxiliary proteins. Among the synthetases, glutamyl-prolyl-tRNA synthetase (EPRS) is known to have a repeated motif that is involved in protein-protein, and protein-nucleic acid interactions. The repeated motif is 208 amino acids long and contains three repeated motifs of 57 amino acids. A repeated motif is known to interact with both tRNA synthetase and tRNA. The solution structure of motif-1 solved by NMR spectroscopy shows that it consists of two helices linked by a tight turn. The overall fold is similar to RNA binding domain of ROP and ribosomal binding protein S15. The surface potential generated by a program GRASP indicates that motif-1 is two-faced, one face is positively charged and the other is hydrophobic. The tRNA binding site mapped by chemical shift perturbation resides in the hydrophobic side of protein. And the tRNA binding site appears to be overlapped with the binding site of isoleucyl-tRNA synthetase motif.